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(54) **GENETICALLY CONTROLLED NANOSCOPY CONTRAST-GENERATING UNITS, GENETICALLY CONTROLLED STRUCTURAL ELEMENTS, GENETICALLY CONTROLLED SCAFFOLDS, NANOBIOMATERIAL BASED THEREON, AND USE THEREOF IN NANOSOCOPY METHODS**

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(2) Date: **Aug. 19, 2024**

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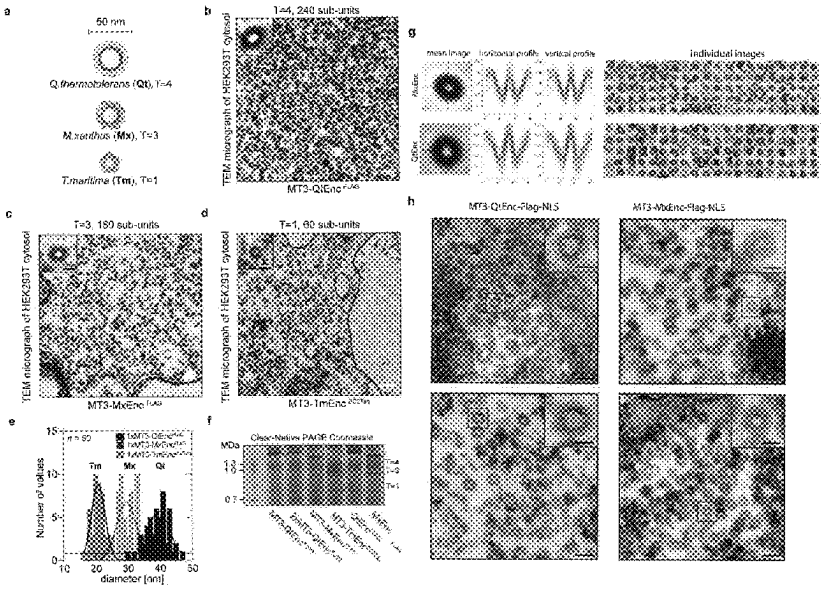
CPC ***G01N 33/5035*** (2013.01); ***C07K 14/415*** (2013.01); ***C07K 14/825*** (2013.01);
(Continued)

(57) **ABSTRACT**

The present invention relates to a genetically controlled nanoscopy contrast-generating unit comprising a metal interactor, wherein the metal interactor is compatible with nanoscopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols and wherein the metal interactor is a molecule to which metal ions can bind to or react with. The present invention also relates to a genetically controlled structural element, wherein said genetically controlled structural element organizes the genetically controlled nanoscopy contrast-generating unit. The genetically controlled structural element can be an encapsulin and the genetically controlled nanoscopy contrast-generating unit can be one or two murine metallothionein-3, or three chimeric metallothioneins. The present invention also relates to a genetically controlled scaffold, wherein said genetically controlled scaffold spatially organizes the genetically controlled structural elements. The present invention also relates to the use of such genetically controlled nanoscopy contrast-generating unit, such genetically controlled structural element, and/or such genetically controlled scaffold for nanoscopy detection methods. The present invention also relates to a nanobiomaterial consisting of the isolated genetically controlled structural elements, and/or genetically controlled scaffolds. The present invention also relates to vectors comprising a nucleic acid encoding a genetically controlled nanoscopy contrast-generating unit, a genetically controlled structural element, and/or a genetically controlled scaffold.

Specification includes a Sequence Listing.



Publication Classification

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C07K 14/415 (2006.01)
C07K 14/825 (2006.01)
G01N 33/58 (2006.01)

(52) **U.S. Cl.**
CPC ***G01N 33/582*** (2013.01); *B82Y 15/00* (2013.01); *C07K 2319/60* (2013.01)

Fig. 1

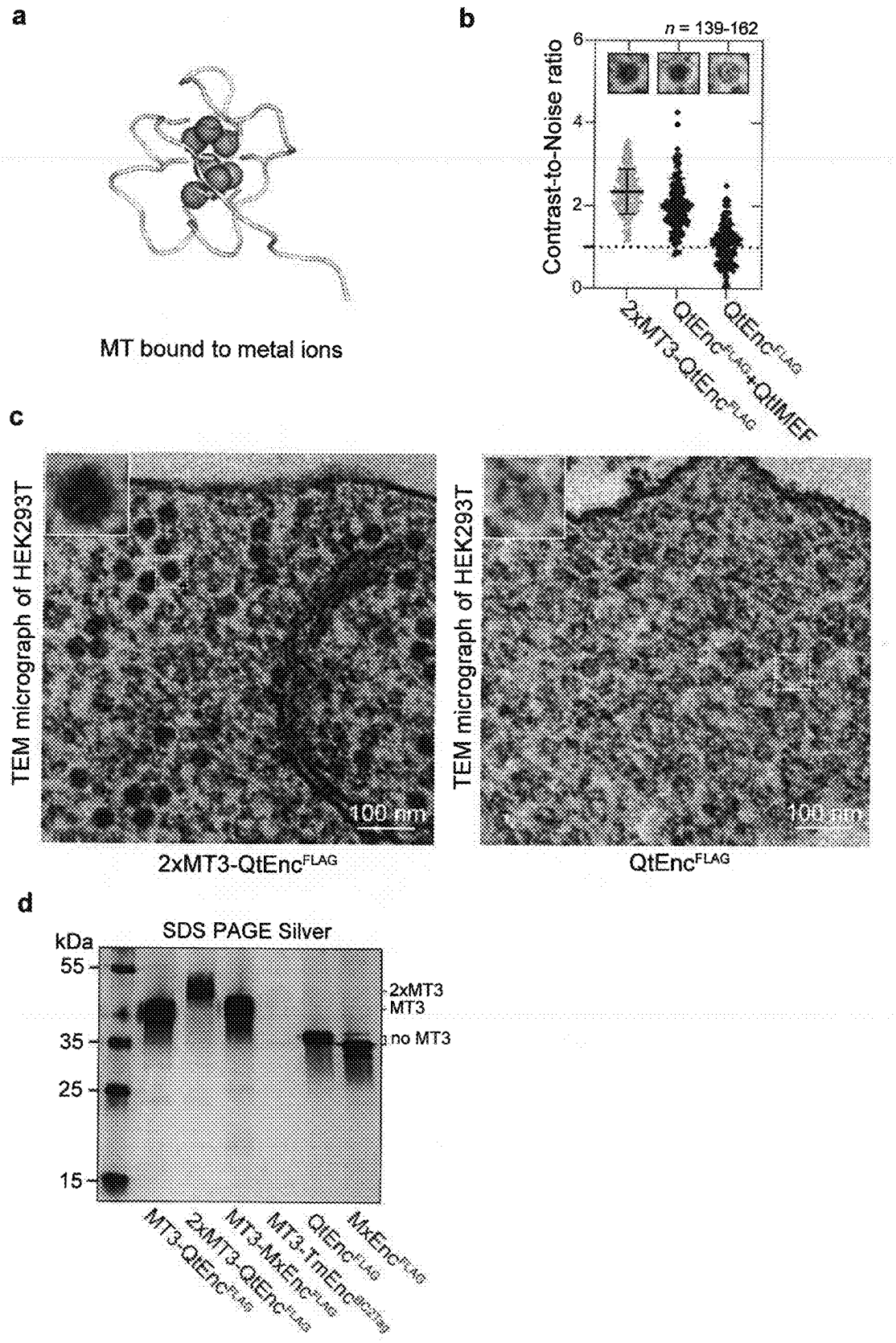

a
MT bound to metal ions
b
n = 139-162
Contrast-to-Noise ratio
6
4
2
0
2xMT3-QtEnc^FLAG
QtEnc^FLAG+QtIMEF
QtEnc^FLAG
c
TEM micrograph of HEK293T
100 nm
2xMT3-QtEnc^FLAG
TEM micrograph of HEK293T
100 nm
QtEnc^FLAG
d
SDS PAGE Silver
kDa
55
35
25
15
2xMT3
MT3
no MT3
MT3-QtEnc^FLAG
2xMT3-QtEnc^FLAG
MT3-MxEnc^FLAG
MT3-TmEnc^FLAG
QtEnc^FLAG
MxEnc^FLAG

Fig. 1 continued

e

f

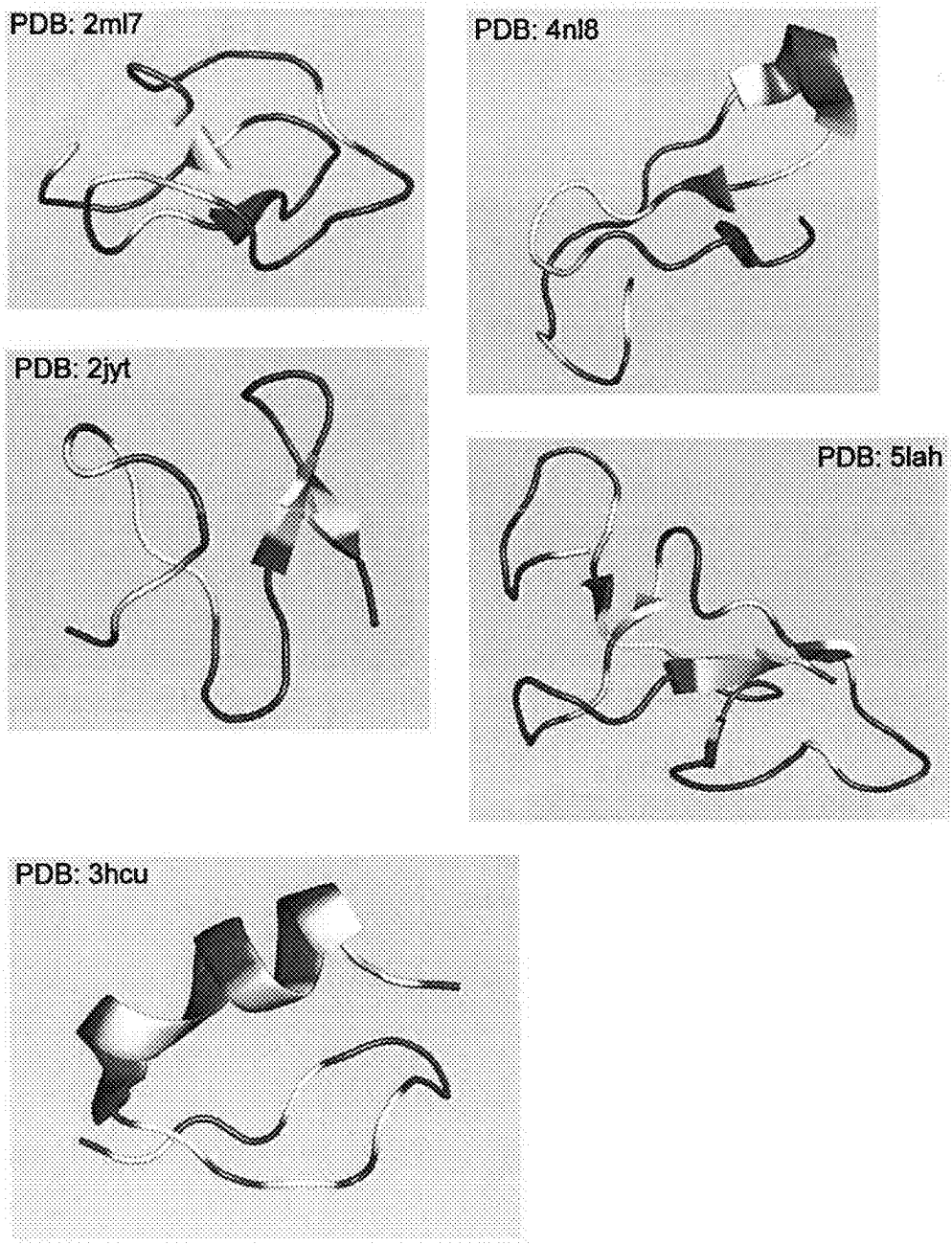


Fig. 2

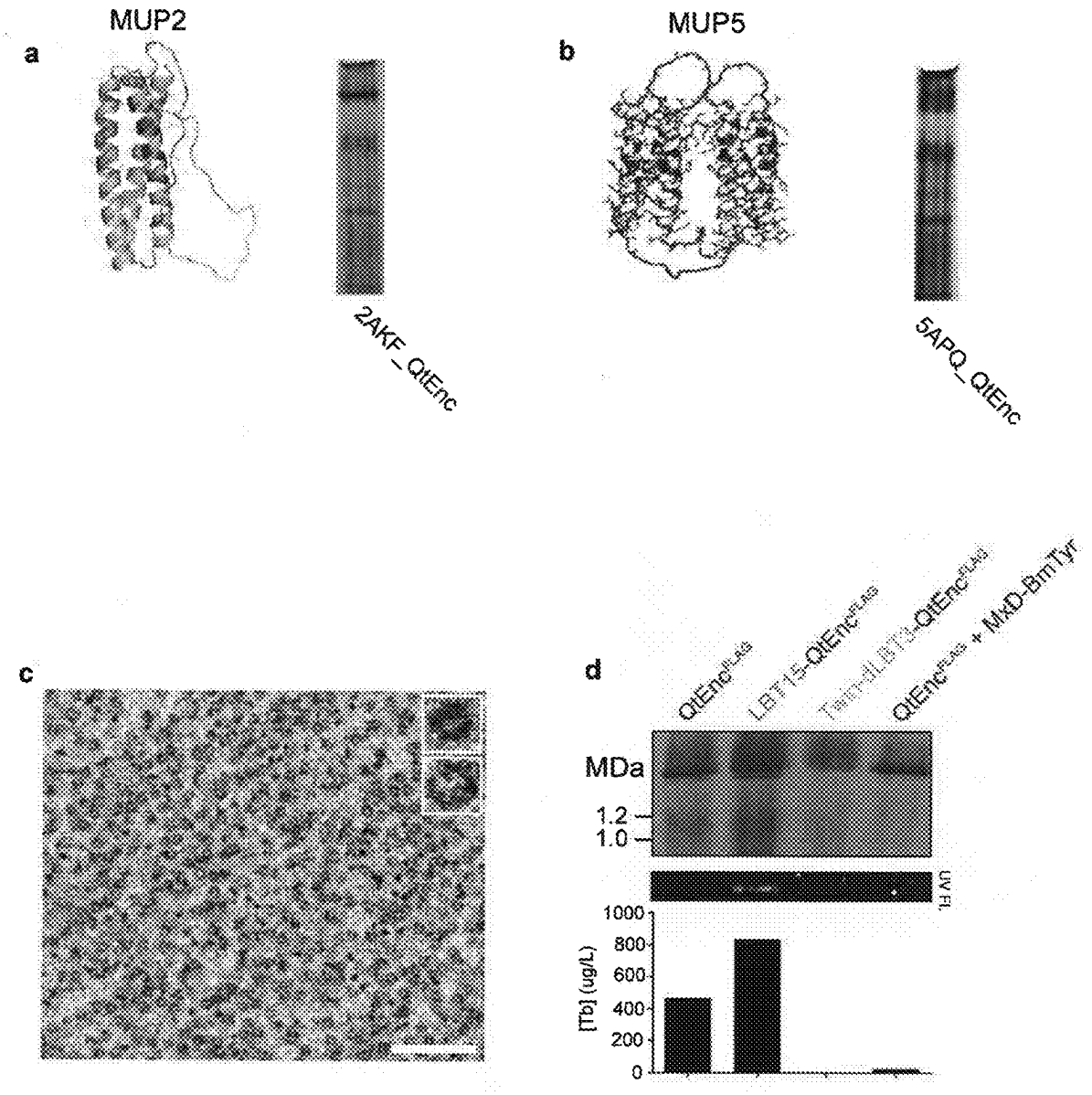
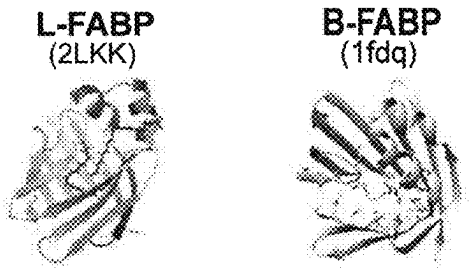
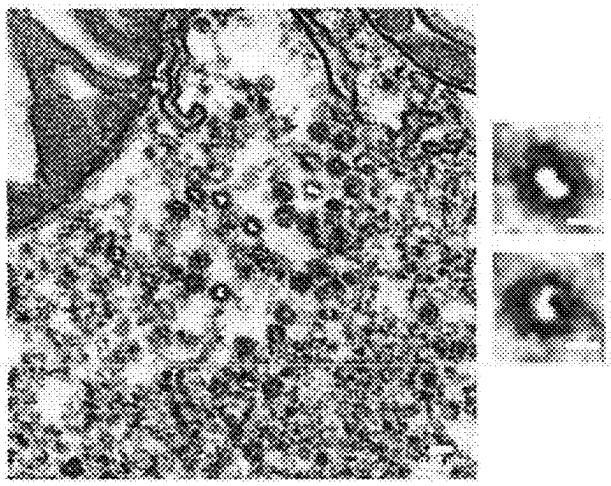

MUP2
a
2AKF_QtEnc
MUP5
b
5APQ_QtEnc
c
d
QtEnc
LBT15-QtEnc
Term-LBT3-QtEnc
QtEnc + MxD-BmTyr
MDa
1.2
1.0
UV FL
1000
800
600
400
200
0
[Tb] (ug/L)

Fig.3

a


L-FABP
(2LKK)
B-FABP
(1fdq)

b



c

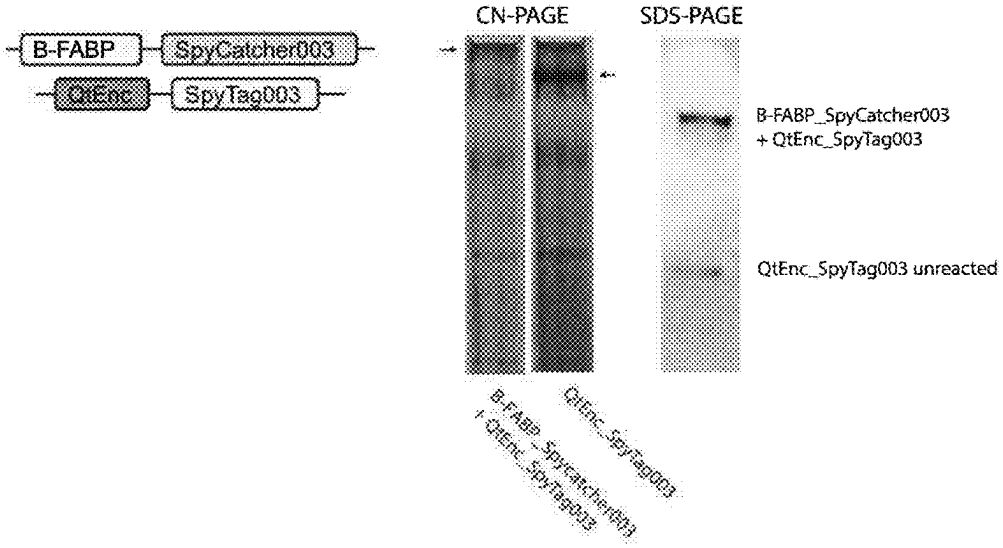
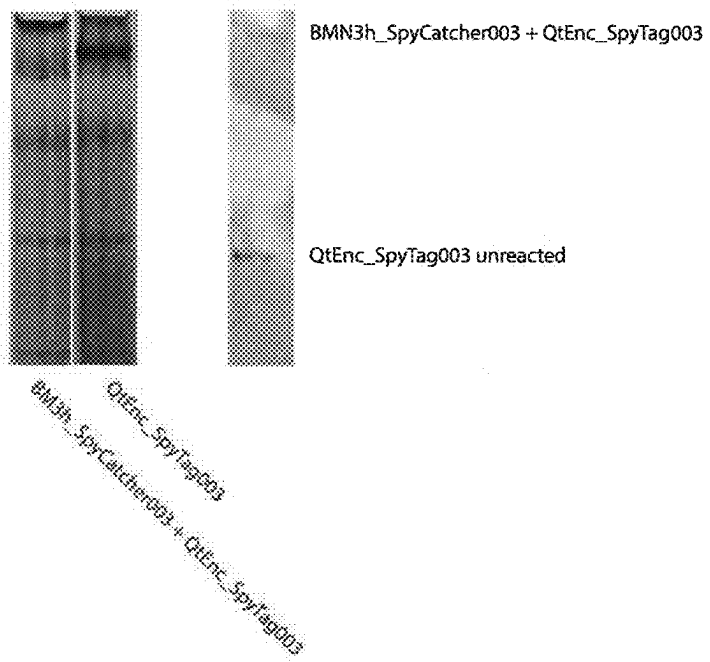

B-FABP
SpyCatcher003
QtEnc
SpyTag003
CN-PAGE
SDS-PAGE
B-FABP_SpyCatcher003
+ QtEnc_SpyTag003
QtEnc_SpyTag003 unreacted
B-FABP_SpyCatcher003
+ QtEnc_SpyTag003
QtEnc_SpyTag003

Fig. 3 continued

d

e



f

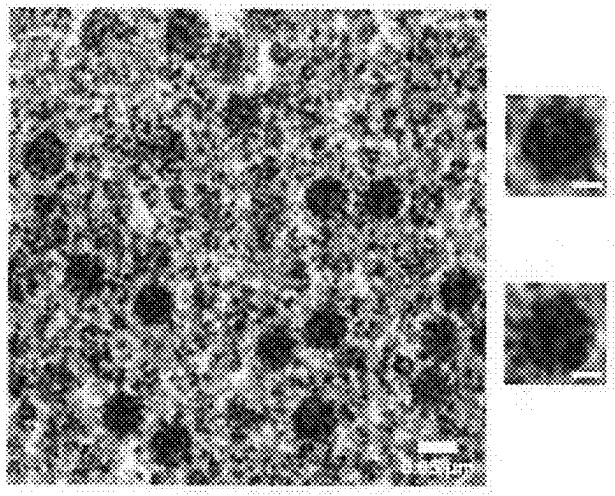


Fig. 4

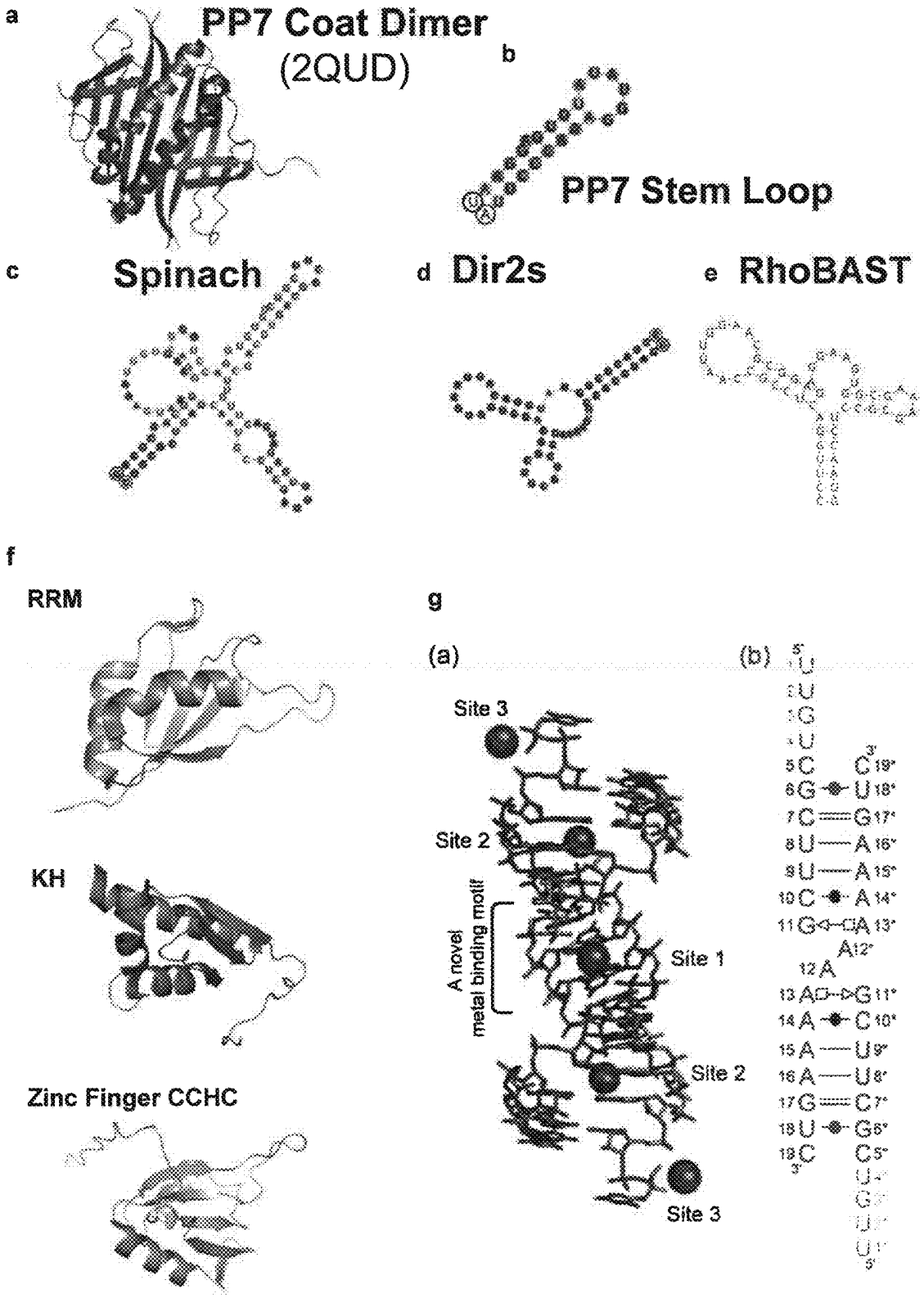
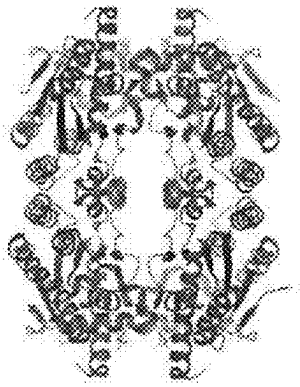

a
PP7 Coat Dimer
(2QUD)
b
PP7 Stem Loop
c
Spinach
d
Dir2s
e
RhoBAST
f
RRM
KH
Zinc Finger CCHC
g
(a)
Site 3
Site 2
A novel metal binding motif
Site 1
Site 2
Site 3
(b)

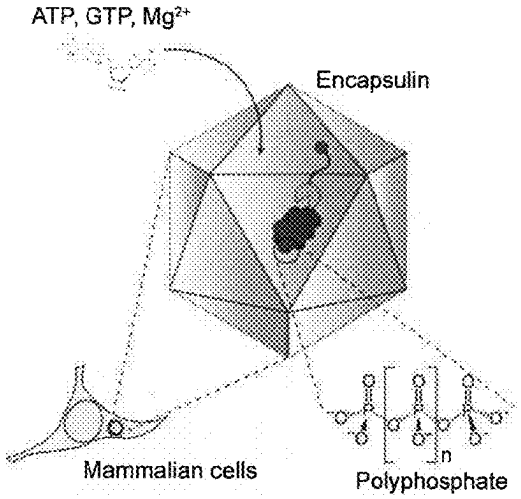
Fig. 5

a

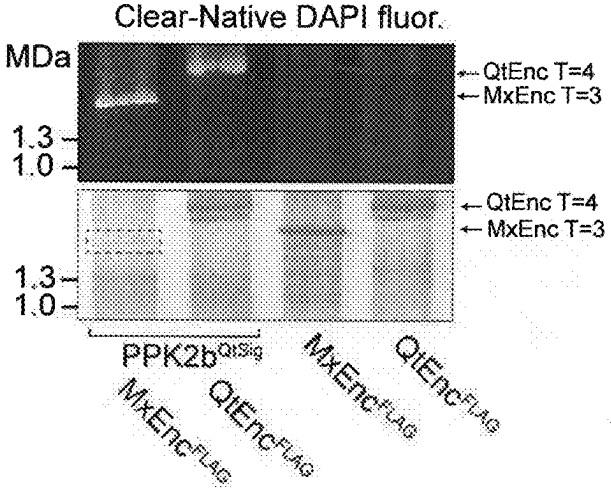


PPK2 tetramer

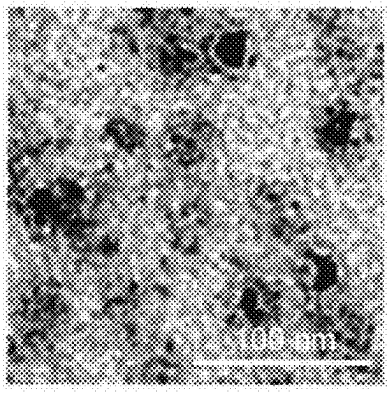
b



c



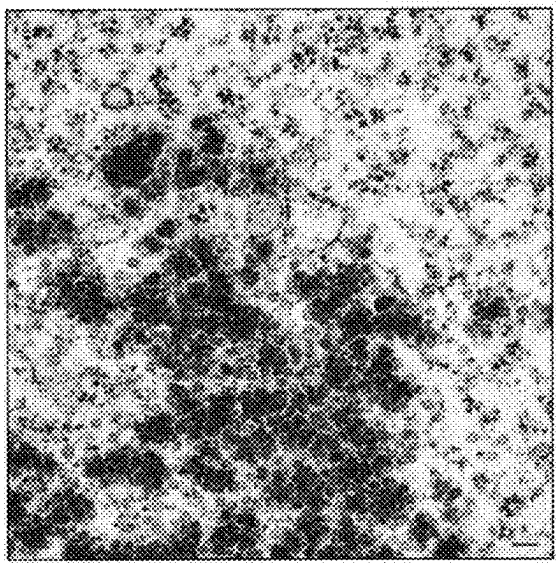
d



MxEnc FLAG + DD-CgPPK2b-QtSig

Fig. 5 continued

e



QtEnc^{FLAG} + AtPCS1-QtSig

f

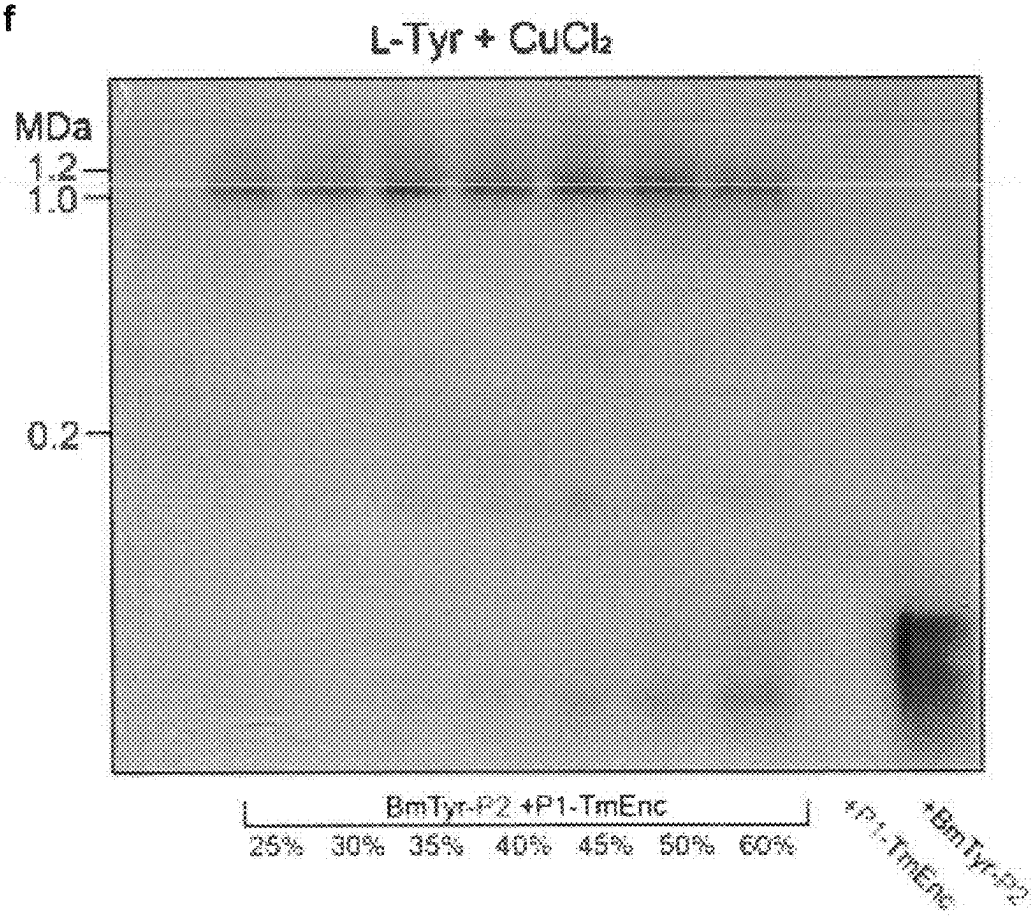


Fig. 6

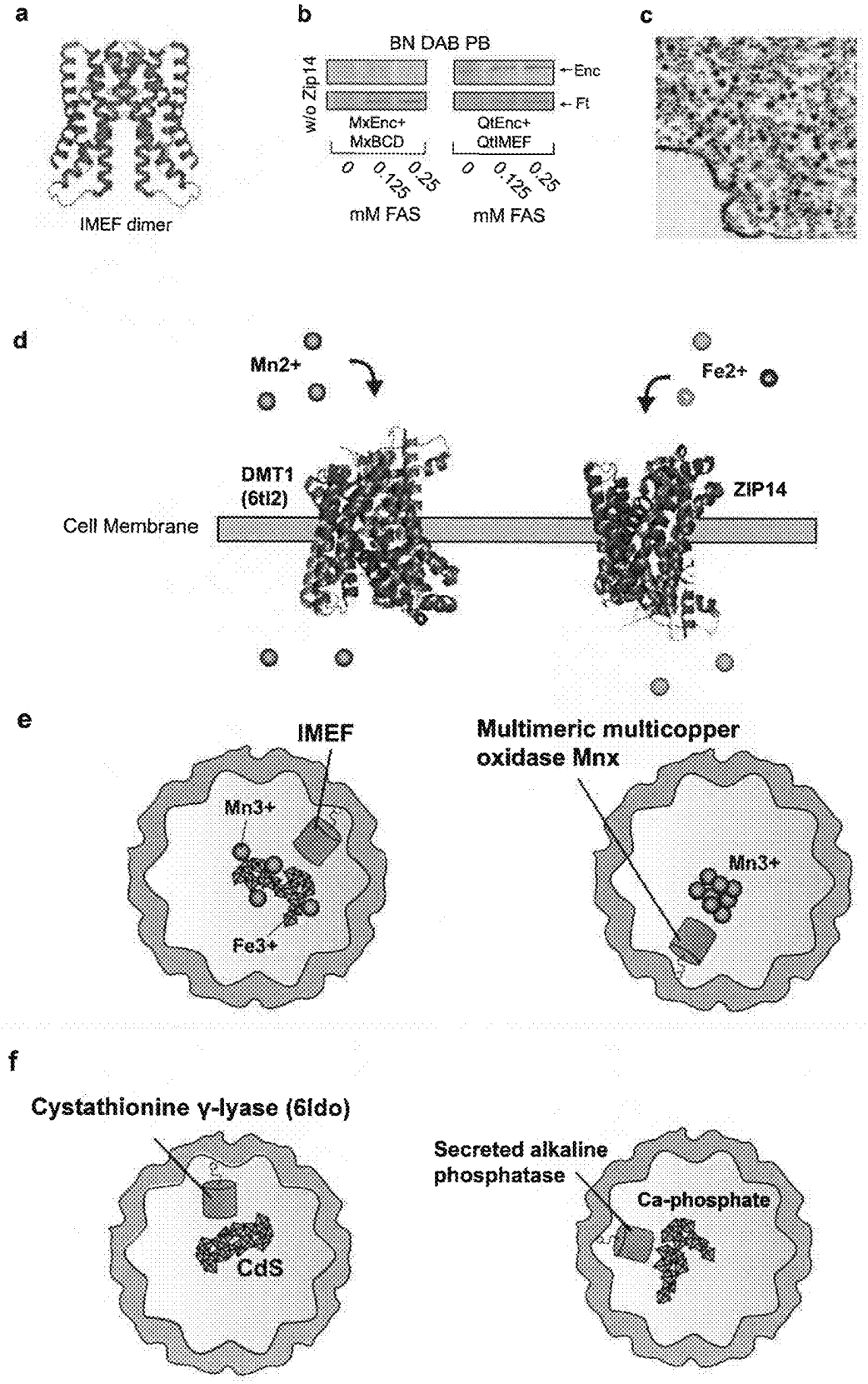

a
IMEF dimer
b
BN DAB PB
w/o Zip14
←Enc
←Ft
MxEnc+
MxBCD
QtEnc+
QtIMEF
0
0.125
0.25
mM FAS
c
d
Mn2+
Fe2+
DMT1
(6tl2)
ZIP14
Cell Membrane
e
IMEF
Mn3+
Fe3+
Multimeric multicopper
oxidase Mnx
Mn3+
f
Cystathionine γ-lyase (6ldo)
CdS
Secreted alkaline
phosphatase
Ca-phosphate

Fig. 7

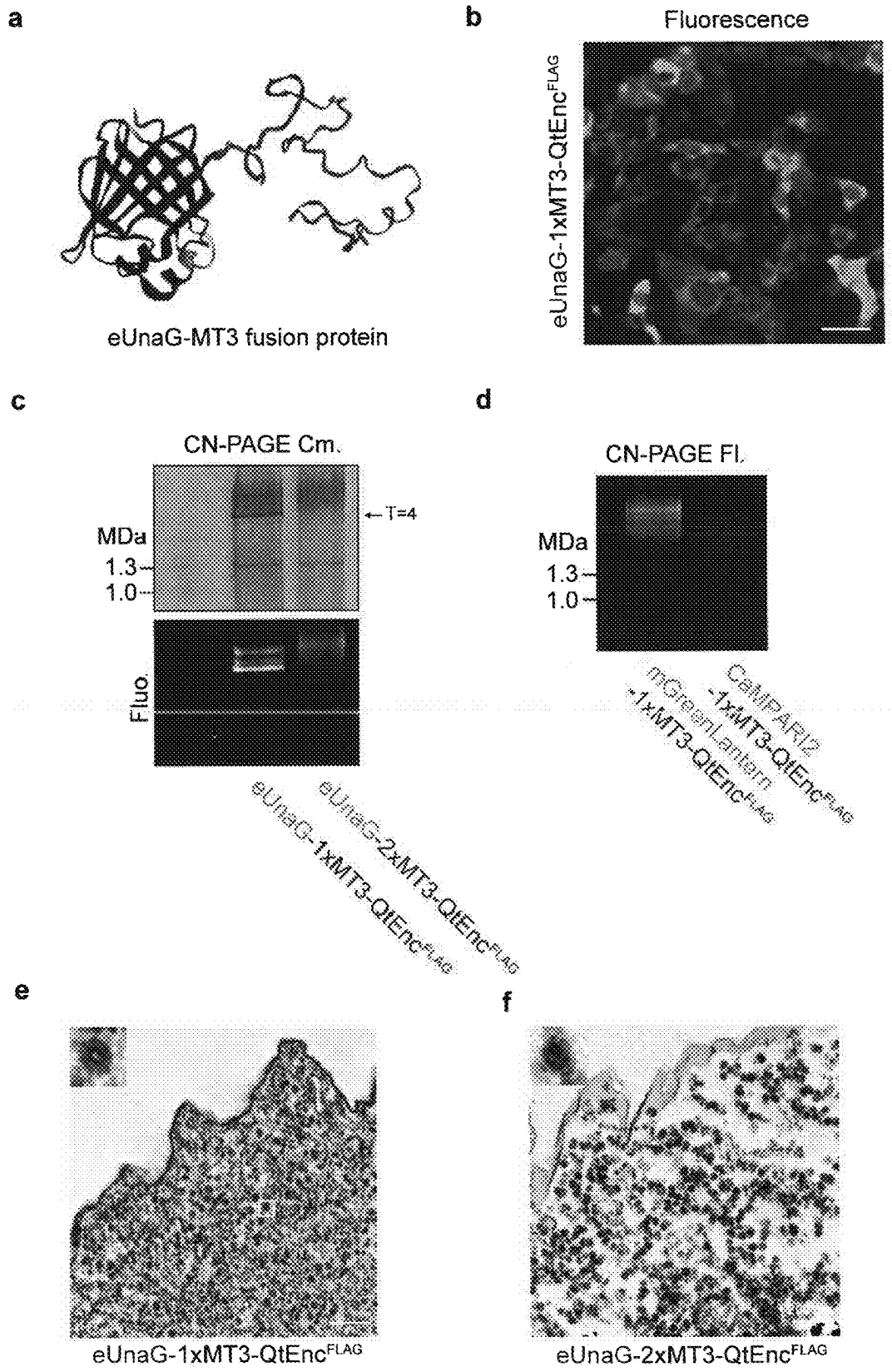

a
eUnaG-MT3 fusion protein
b
Fluorescence
eUnaG-1xMT3-QtEnc^FLAG
c
CN-PAGE Cm.
MDa
1.3
1.0
T=4
Fluo.
eUnaG-1xMT3-QtEnc^FLAG
eUnaG-2xMT3-QtEnc^FLAG
d
CN-PAGE Fl.
MDa
1.3
1.0
mGreenLantern -1xMT3-QtEnc^FLAG
CaMPARI2 -1xMT3-QtEnc^FLAG
e
eUnaG-1xMT3-QtEnc^FLAG
f
eUnaG-2xMT3-QtEnc^FLAG

Fig. 7

g

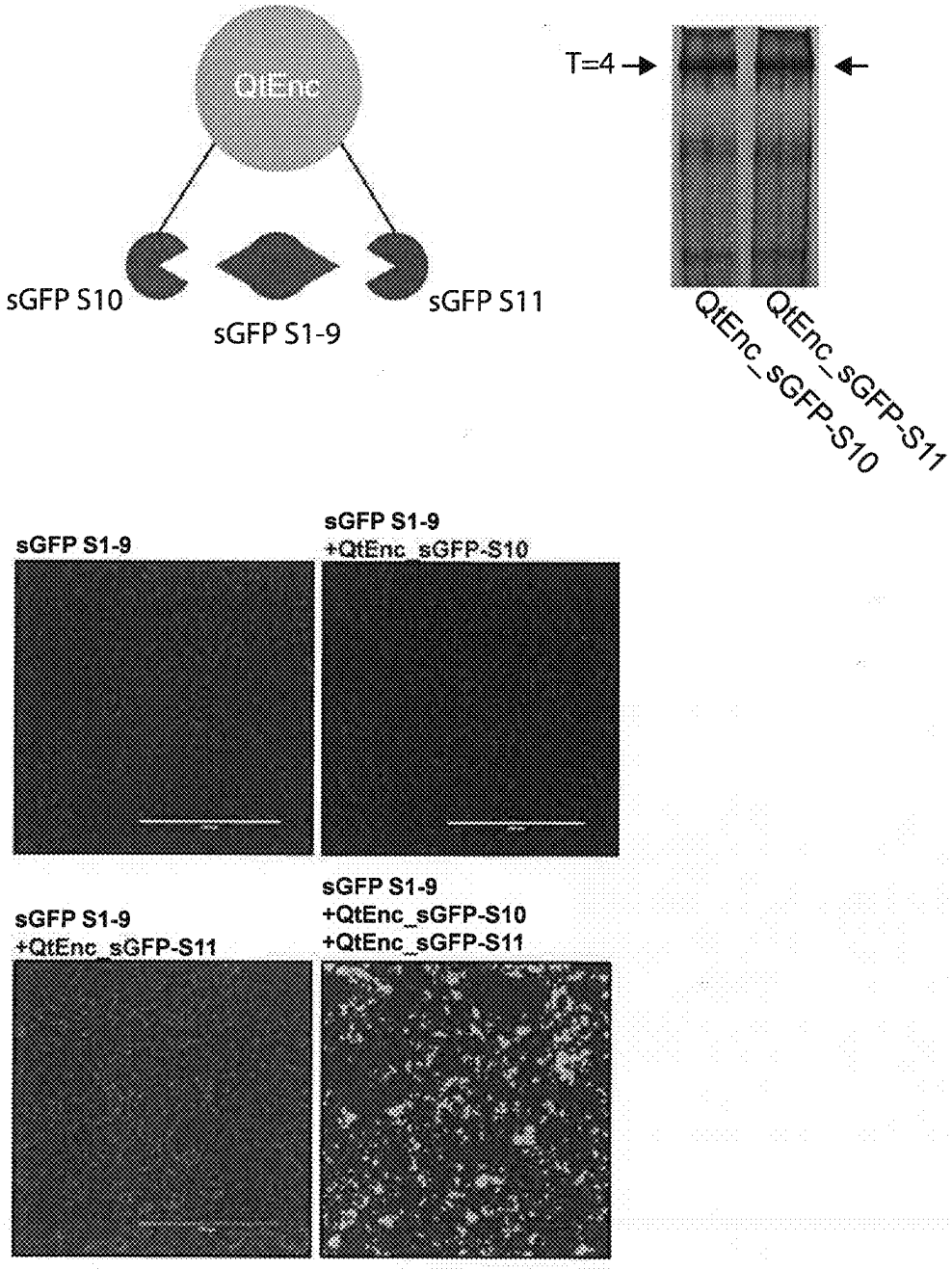
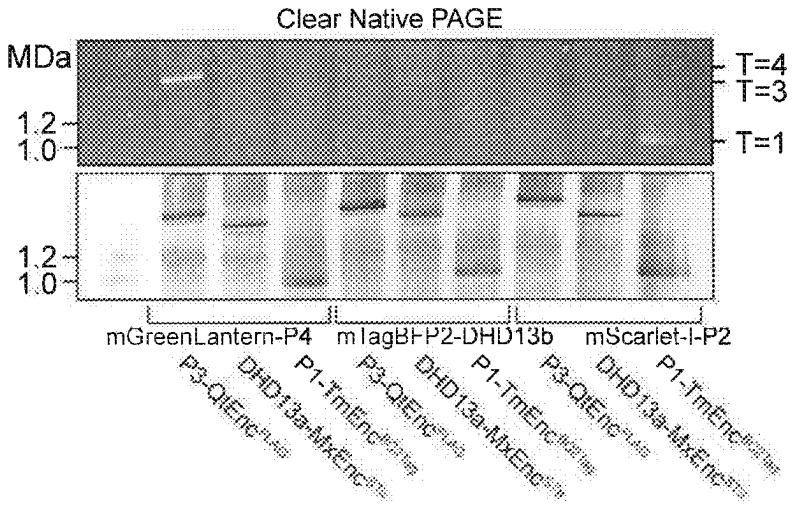

QtEnc
sGFP S10
sGFP S1-9
sGFP S11
T=4
QtEnc_sGFP-S10
QtEnc_sGFP-S11
sGFP S1-9
sGFP S1-9
+QtEnc_sGFP-S10
sGFP S1-9
+QtEnc_sGFP-S11
sGFP S1-9
+QtEnc_sGFP-S10
+QtEnc_sGFP-S11

Fig. 8

a


Clear Native PAGE
MDa
1.2
1.0
T=4
T=3
T=1
1.2
1.0
mGreenLantern-P4
mTagBFP2-DHD13b
mScarlet-I-P2
P3-QIEnc
DHD13a-MxEnc
P1-TmEnc
P3-QIEnc
DHD13a-MxEnc
P1-TmEnc
P3-QIEnc
DHD13a-MxEnc
P1-TmEnc

b

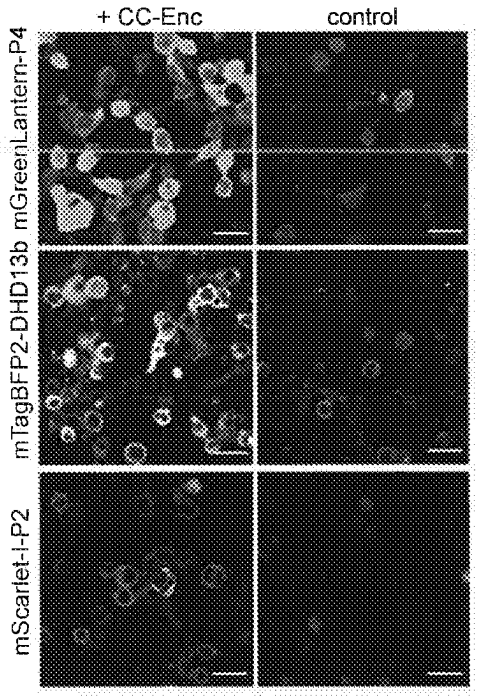

+ CC-Enc
control
mGreenLantern-P4
mTagBFP2-DHD13b
mScarlet-I-P2

Fig. 8 continued

c

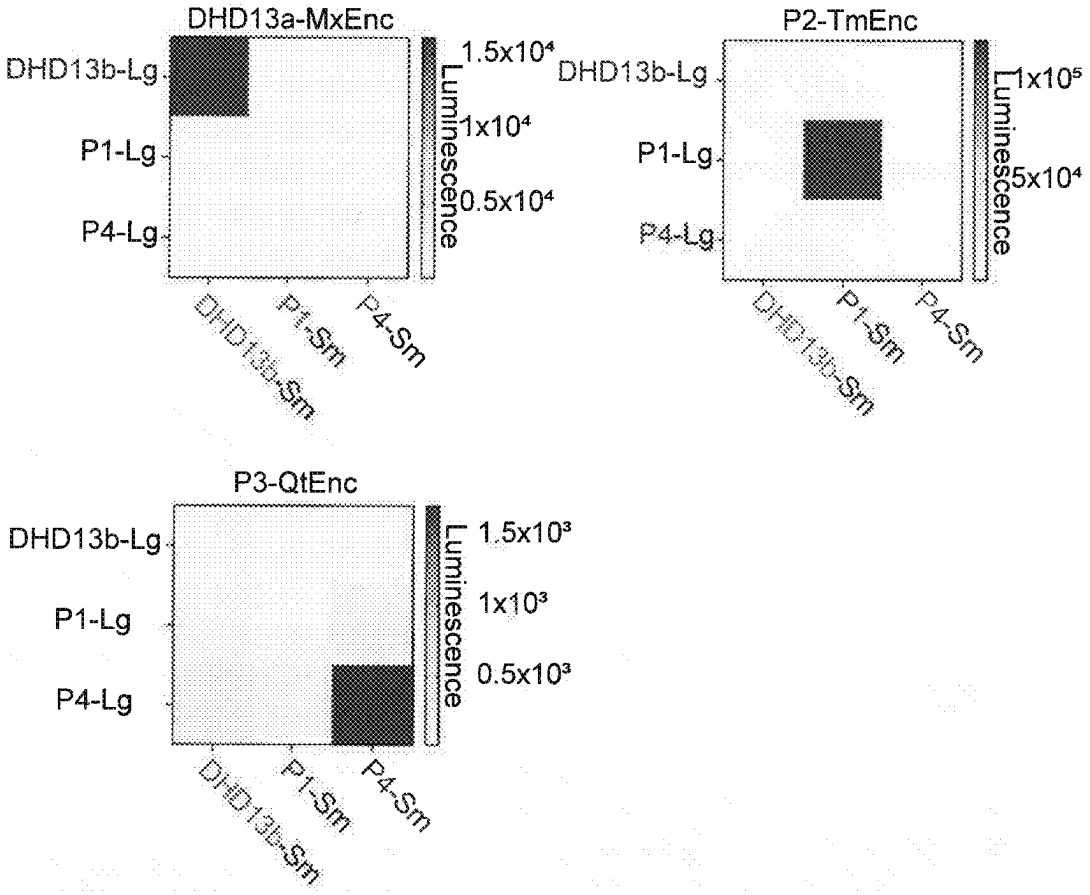


Fig. 9

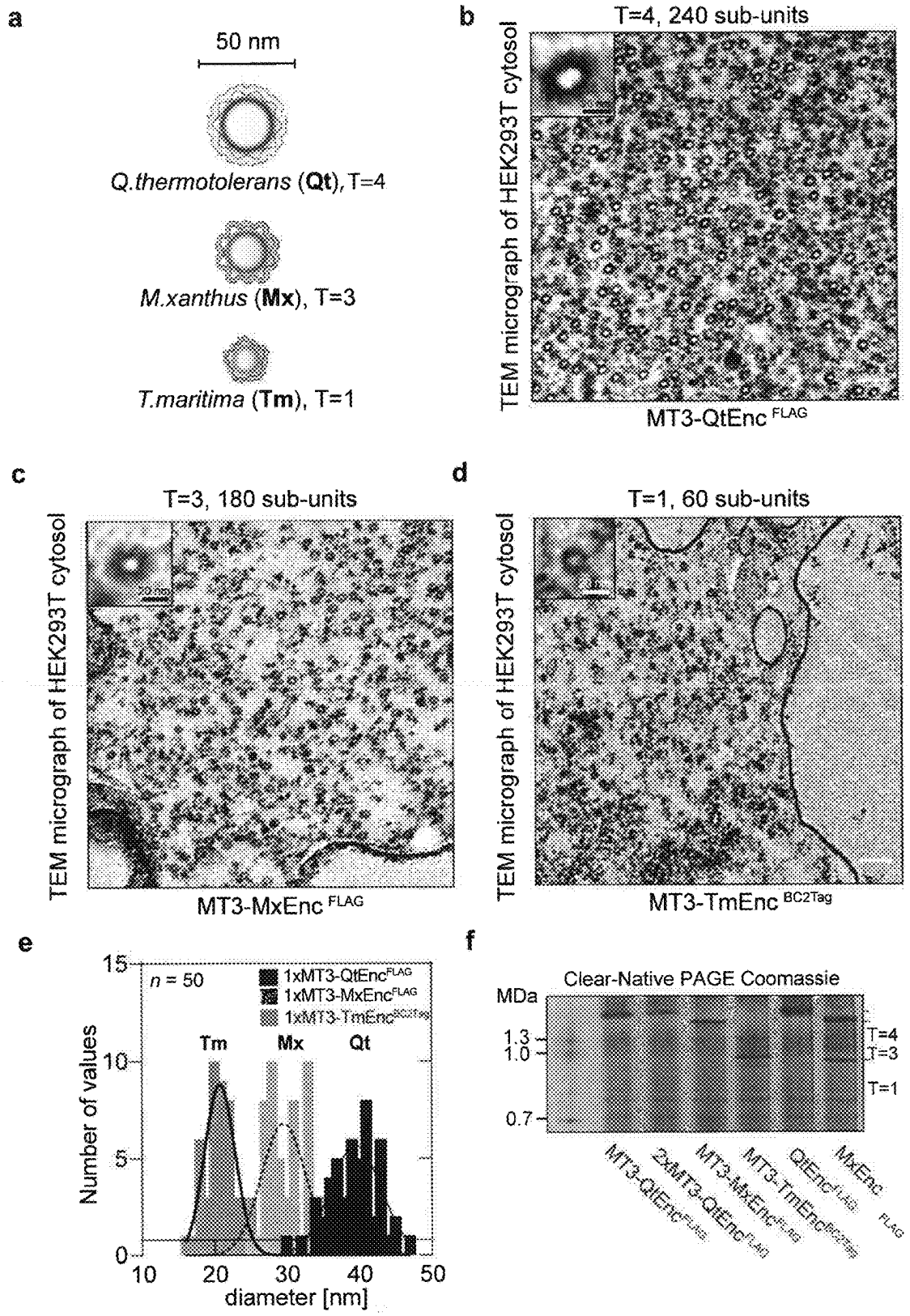
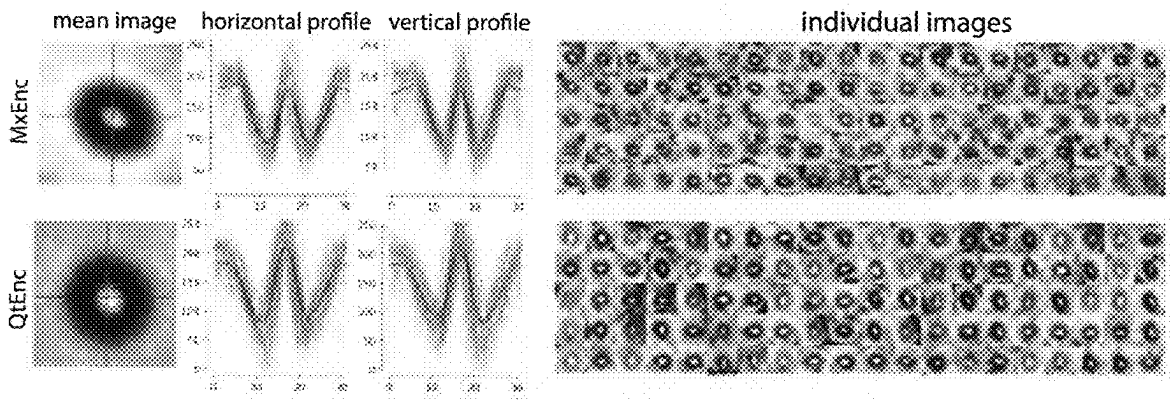

a
50 nm
Q.thermotolerans (Qt), T=4
M.xanthus (Mx), T=3
T.maritima (Tm), T=1
b
T=4, 240 sub-units
TEM micrograph of HEK293T cytosol
MT3-QtEnc FLAG
c
T=3, 180 sub-units
TEM micrograph of HEK293T cytosol
MT3-MxEnc FLAG
d
T=1, 60 sub-units
TEM micrograph of HEK293T cytosol
MT3-TmEnc BC2Tag
e
n = 50
1xMT3-QtEnc FLAG
1xMT3-MxEnc FLAG
1xMT3-TmEnc BC2Tag
Tm
Mx
Qt
Number of values
diameter [nm]
f
Clear-Native PAGE Coomassie
MDa
1.3
1.0
0.7
T=4
T=3
T=1
MT3-QtEnc FLAG
2xMT3-QtEnc FLAG
MT3-MxEnc FLAG
MT3-TmEnc BC2Tag
QtEnc FLAG
MxEnc FLAG

Fig. 9 continued

g



h

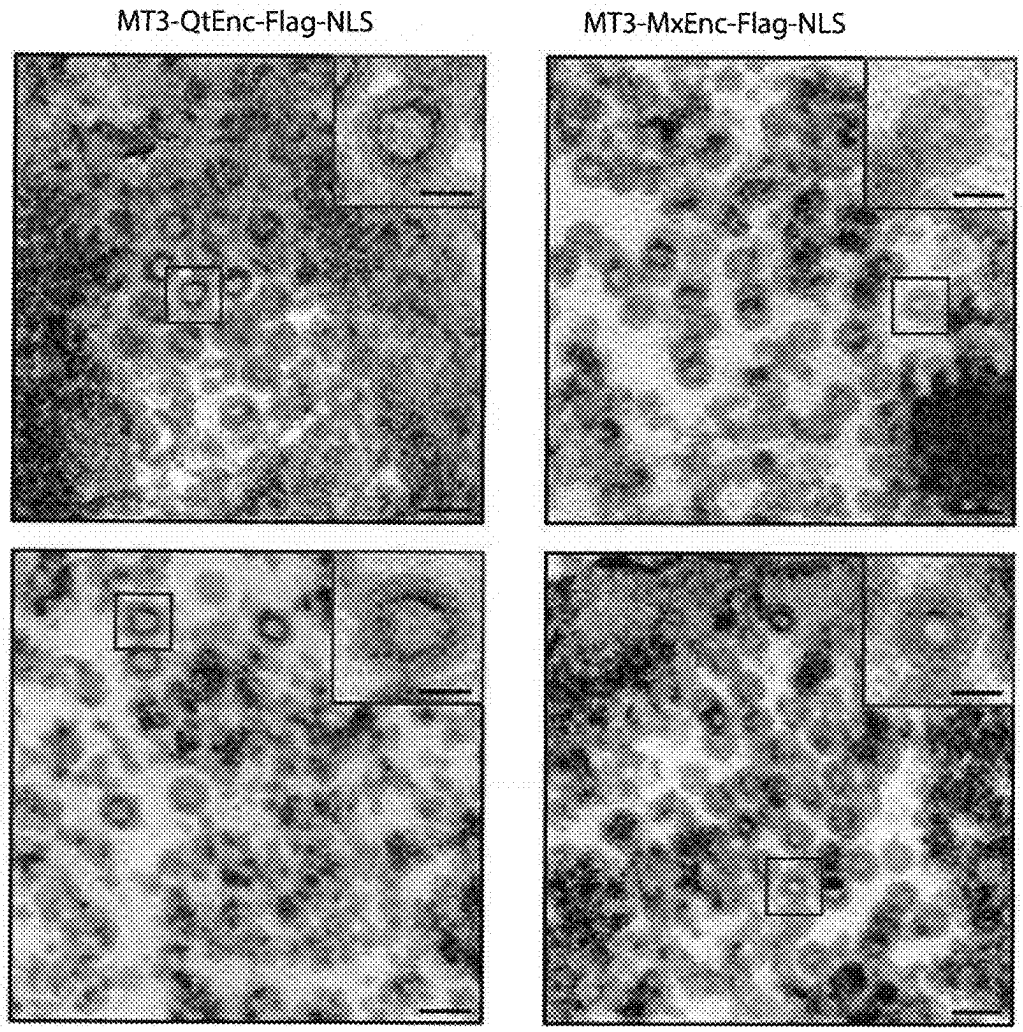


Fig. 9 continued

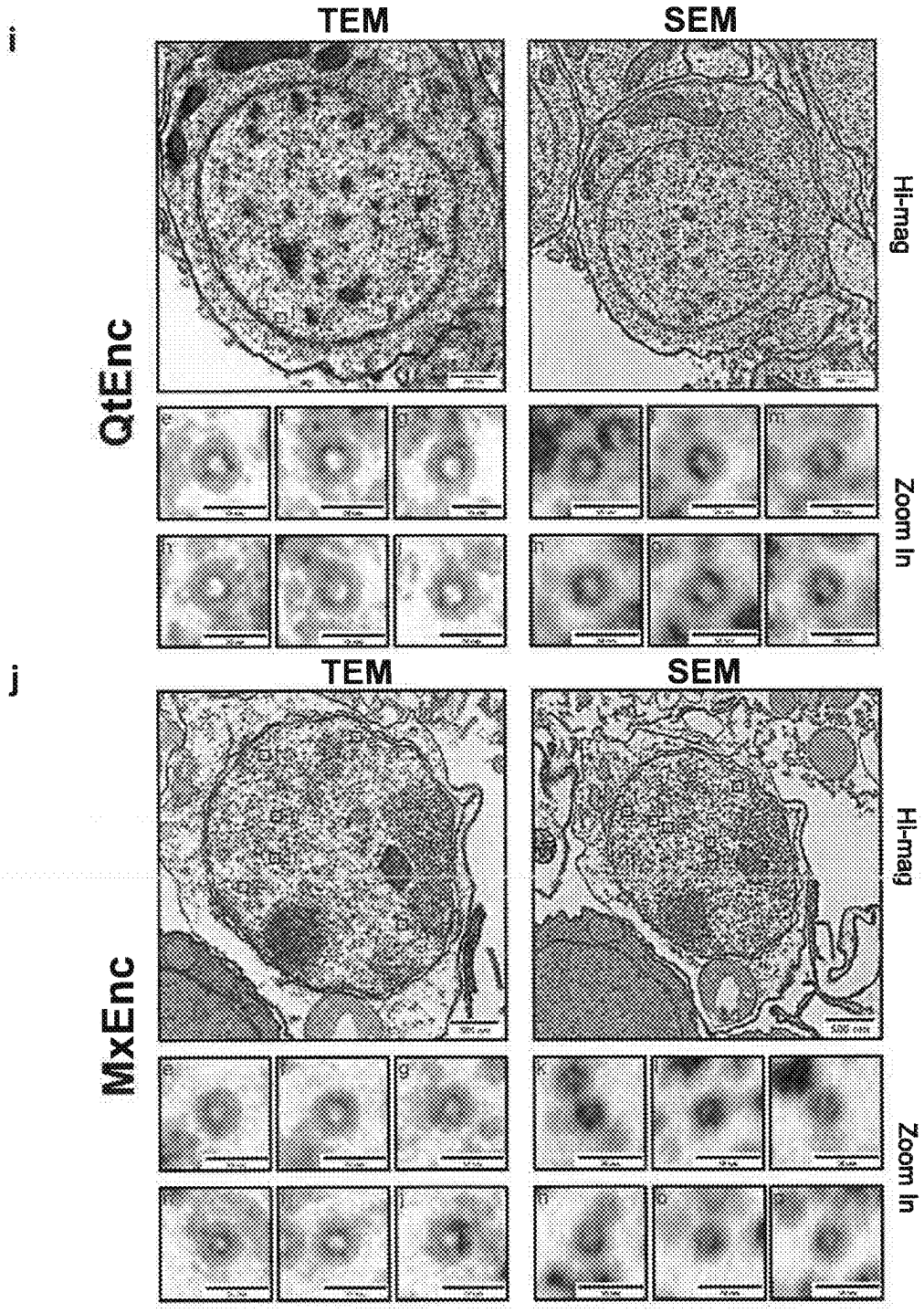


Fig. 9 continued

k

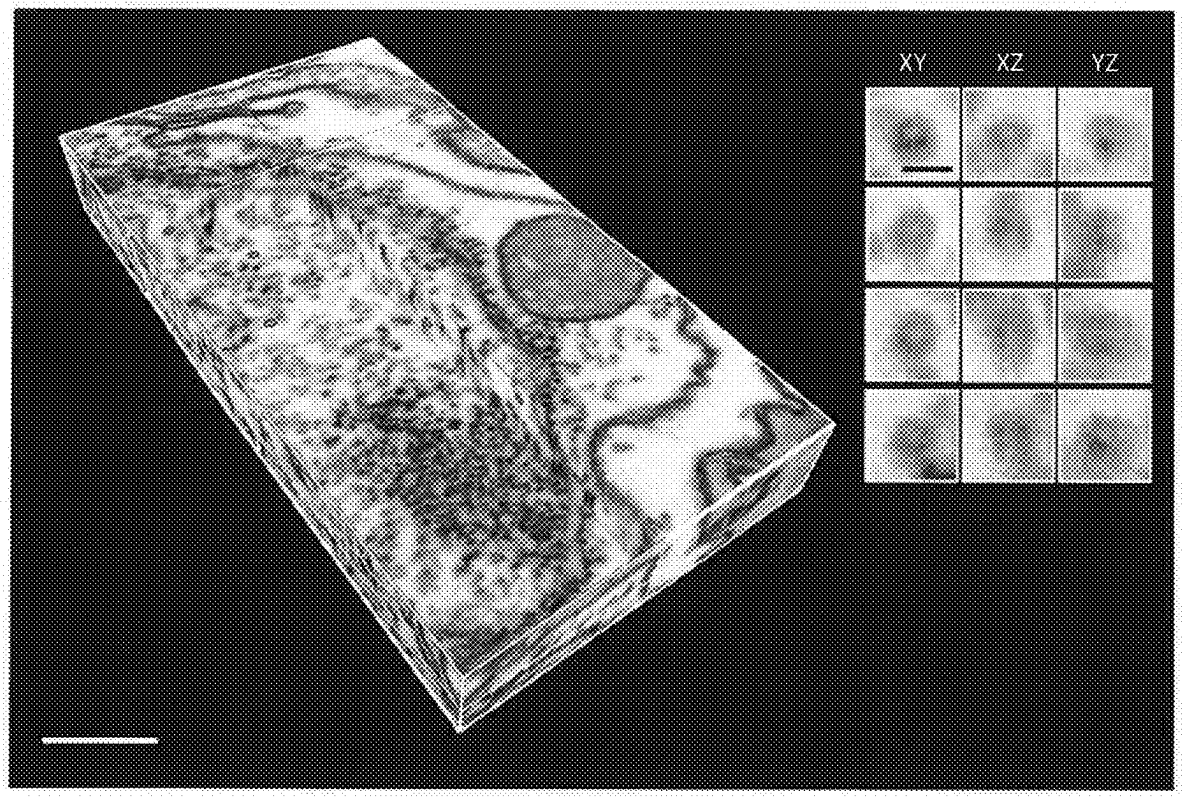


Fig. 10

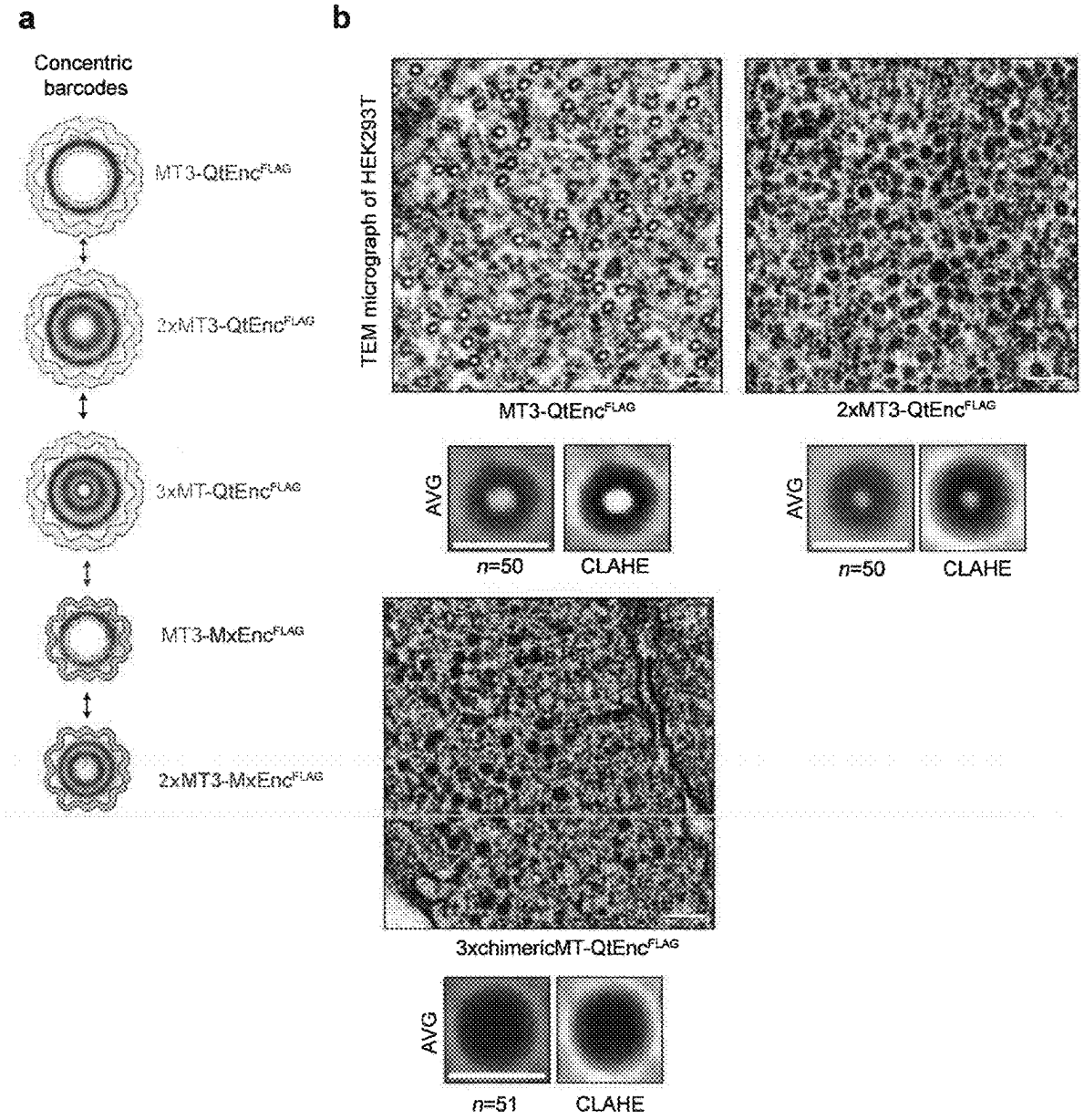
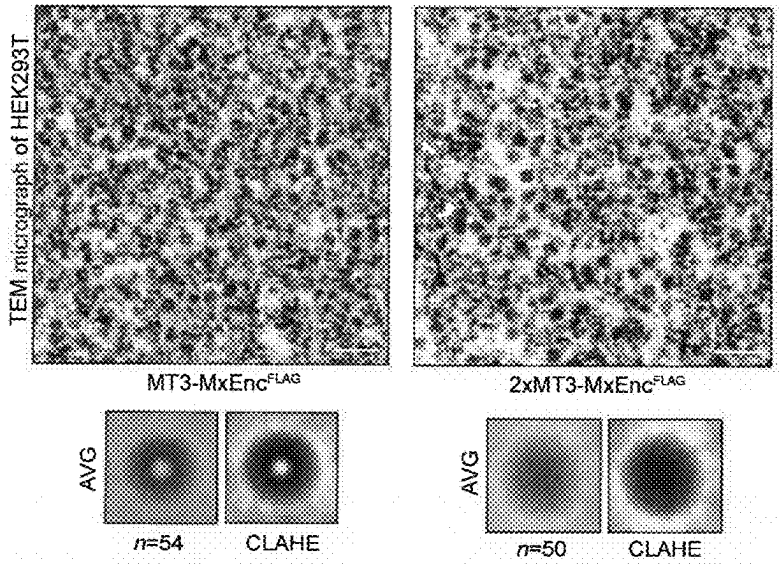
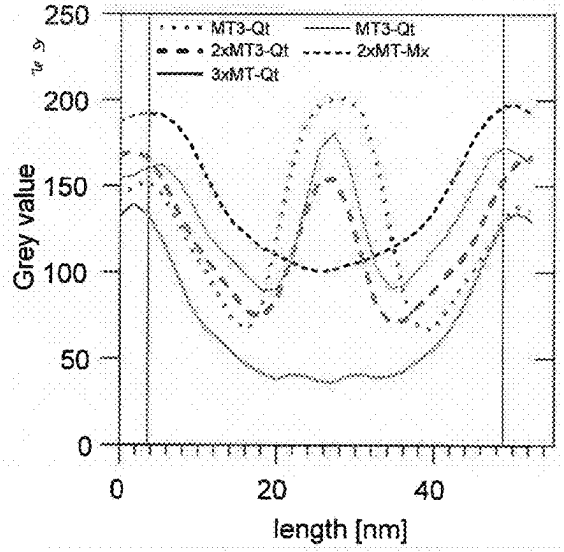

a
Concentric barcodes
MT3-QtEnc^{FLAG}
2xMT3-QtEnc^{FLAG}
3xMT-QtEnc^{FLAG}
MT3-MxEnc^{FLAG}
2xMT3-MxEnc^{FLAG}
b
TEM micrograph of HEK293T
MT3-QtEnc^{FLAG}
2xMT3-QtEnc^{FLAG}
AVG
n=50
CLAHE
AVG
n=50
CLAHE
3xchimericMT-QtEnc^{FLAG}
AVG
n=51
CLAHE

Fig. 10 continued

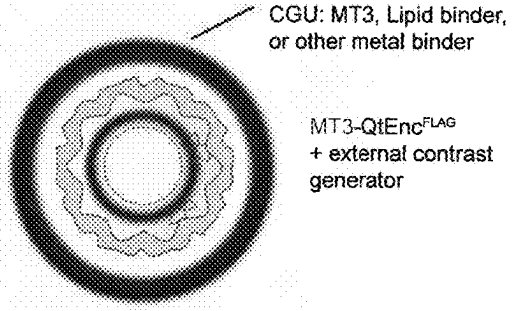
c



d



e



f

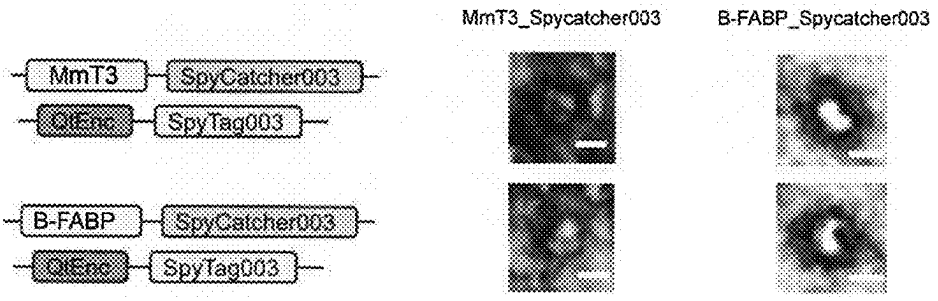
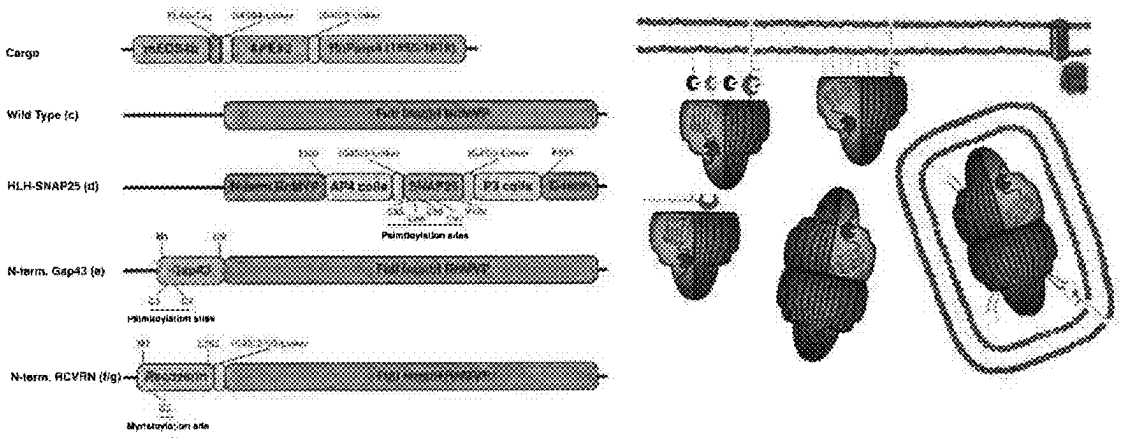
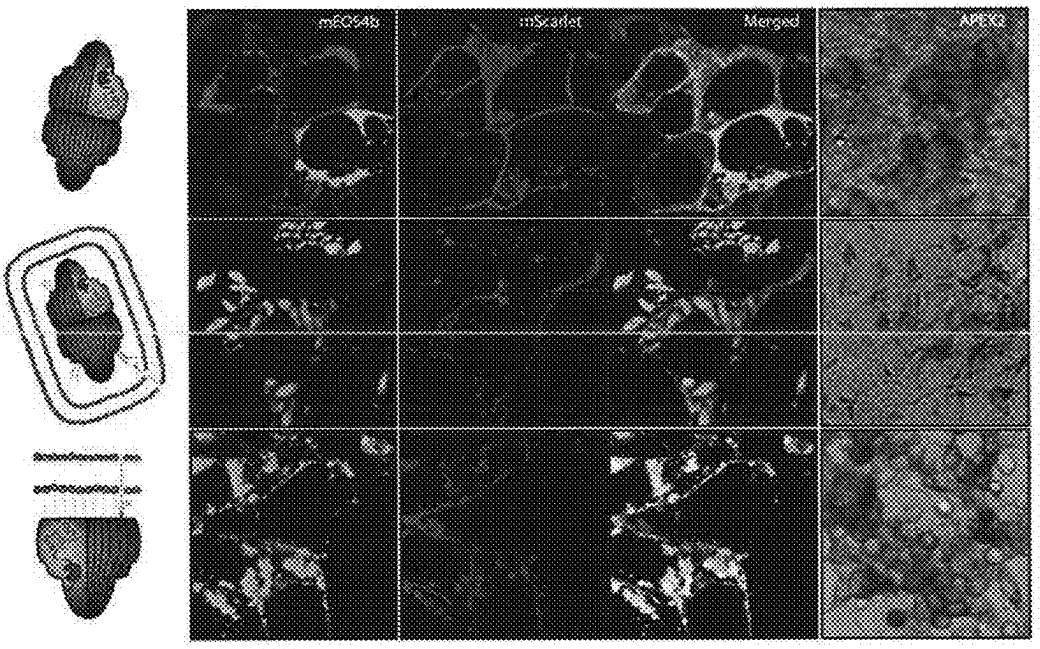


Fig. 11

a


Cargo
Wild Type (c)
HLH-SNAP25 (d)
N-term. Gap43 (e)
N-term. RCVRN (fig)

b


mEGFP
mScarlet
Merged
APH

c

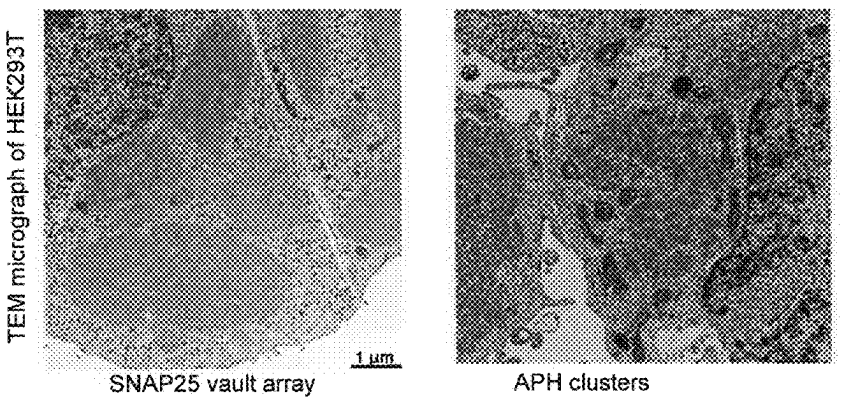
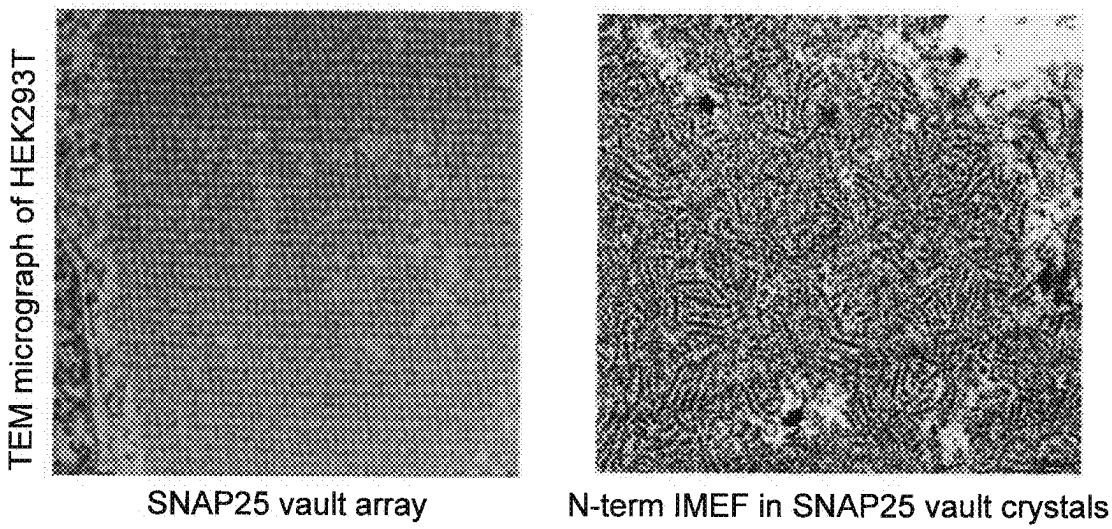

TEM micrograph of HEK293T
1 µm
SNAP25 vault array
APH clusters

Fig. 11 continued

d



e

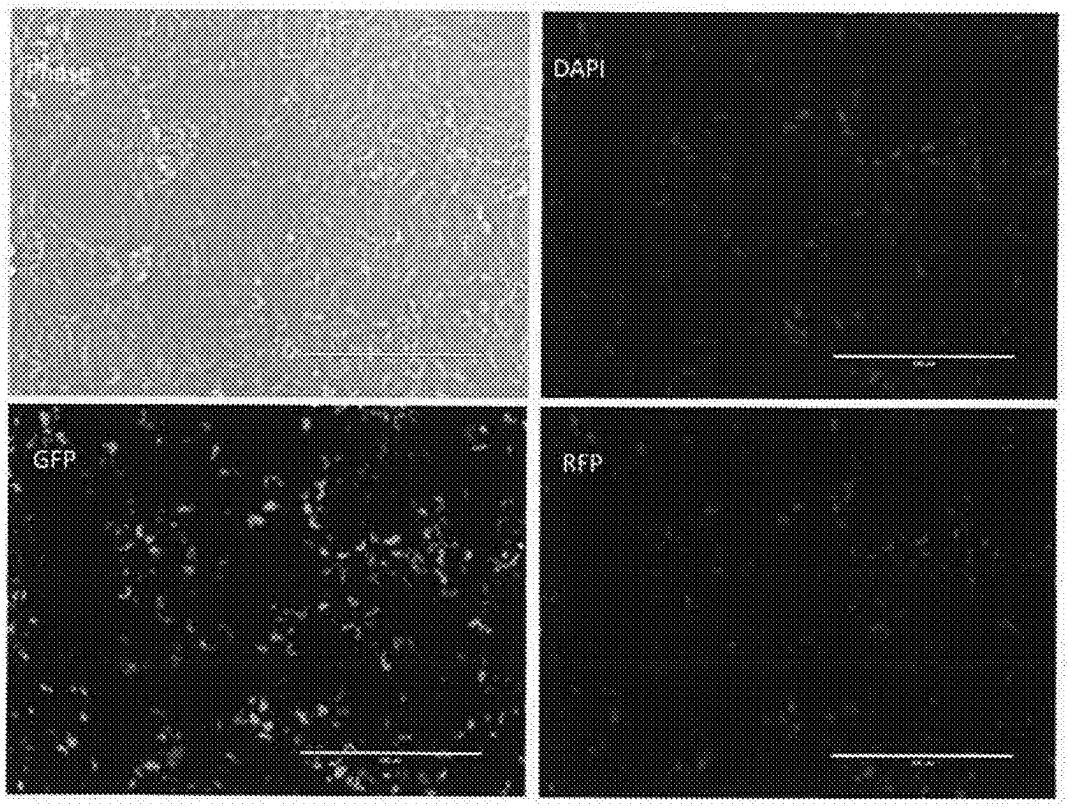


Fig. 12

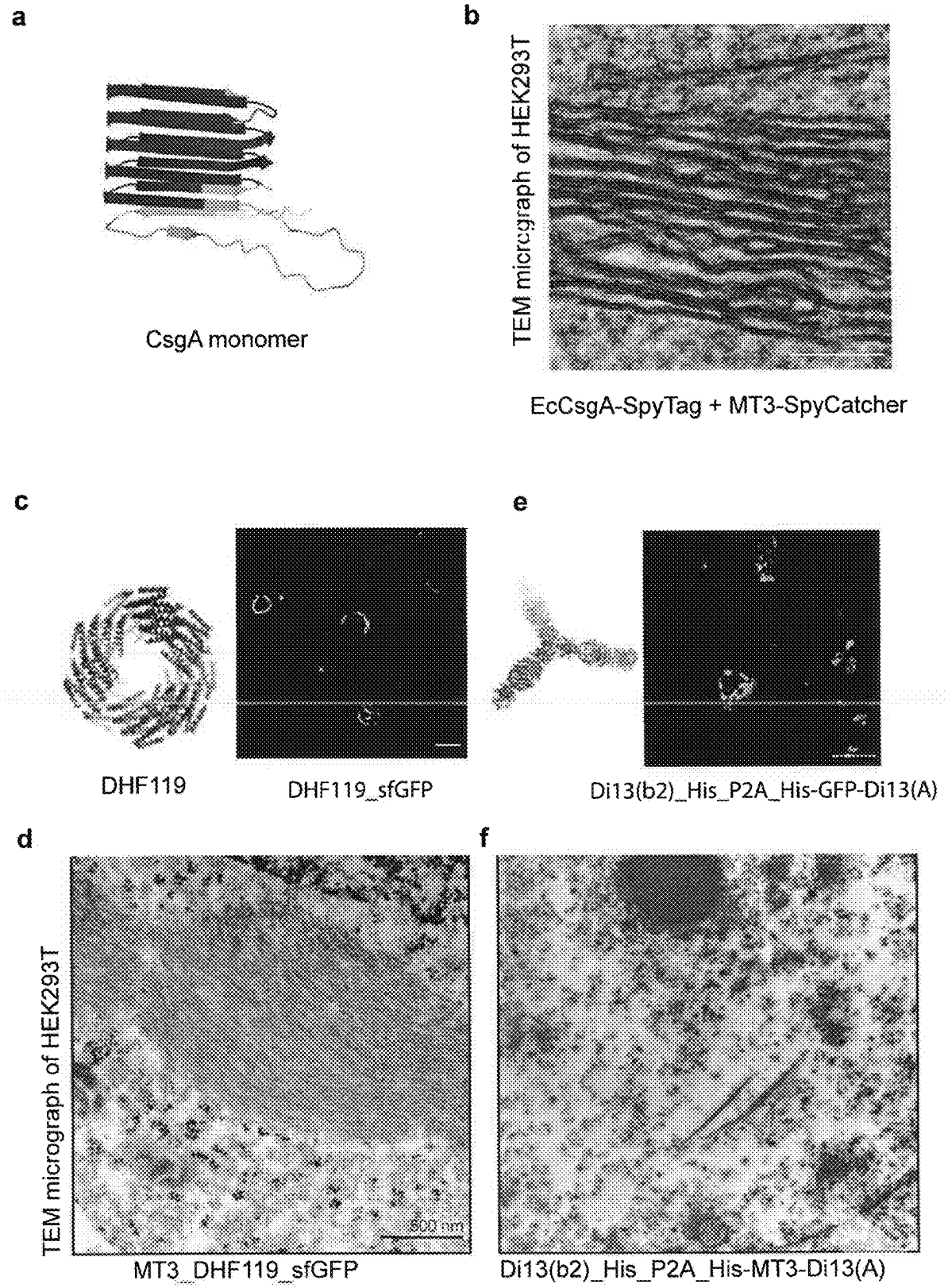
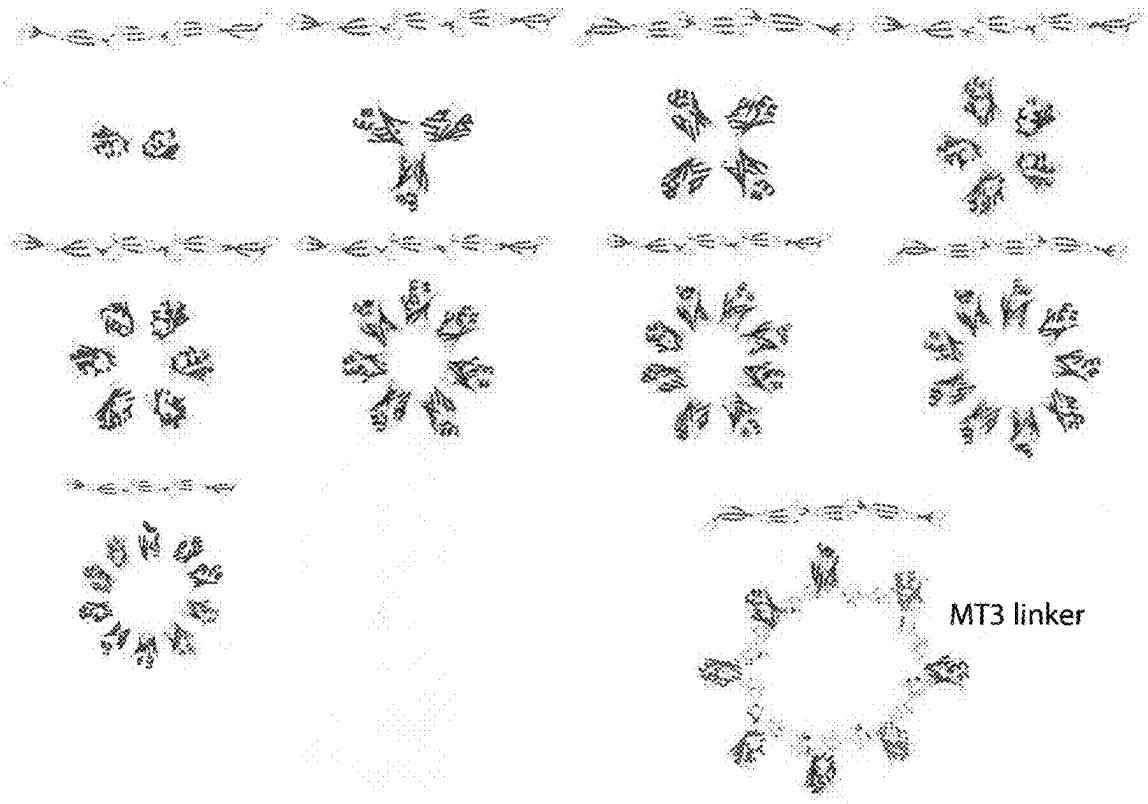
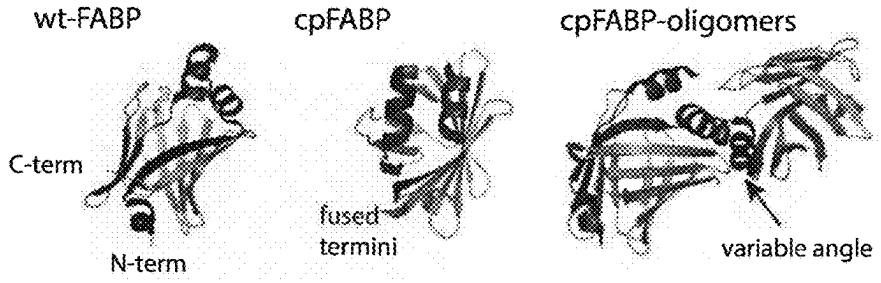

a
CsgA monomer
b
TEM micrograph of HEK293T
EcCsgA-SpyTag + MT3-SpyCatcher
c
DHF119
DHF119_sfGFP
e
Di13(b2)_His_P2A_His-GFP-Di13(A)
d
TEM micrograph of HEK293T
500 nm
MT3_DHF119_sfGFP
f
Di13(b2)_His_P2A_His-MT3-Di13(A)

Fig. 13

a


MT3 linker

b


wt-FABP
cpFABP
cpFABP-oligomers
C-term
N-term
fused
termini
variable angle

c

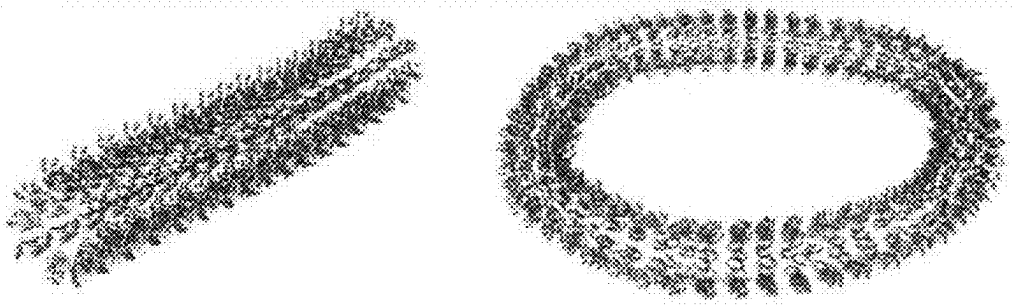


Fig. 14

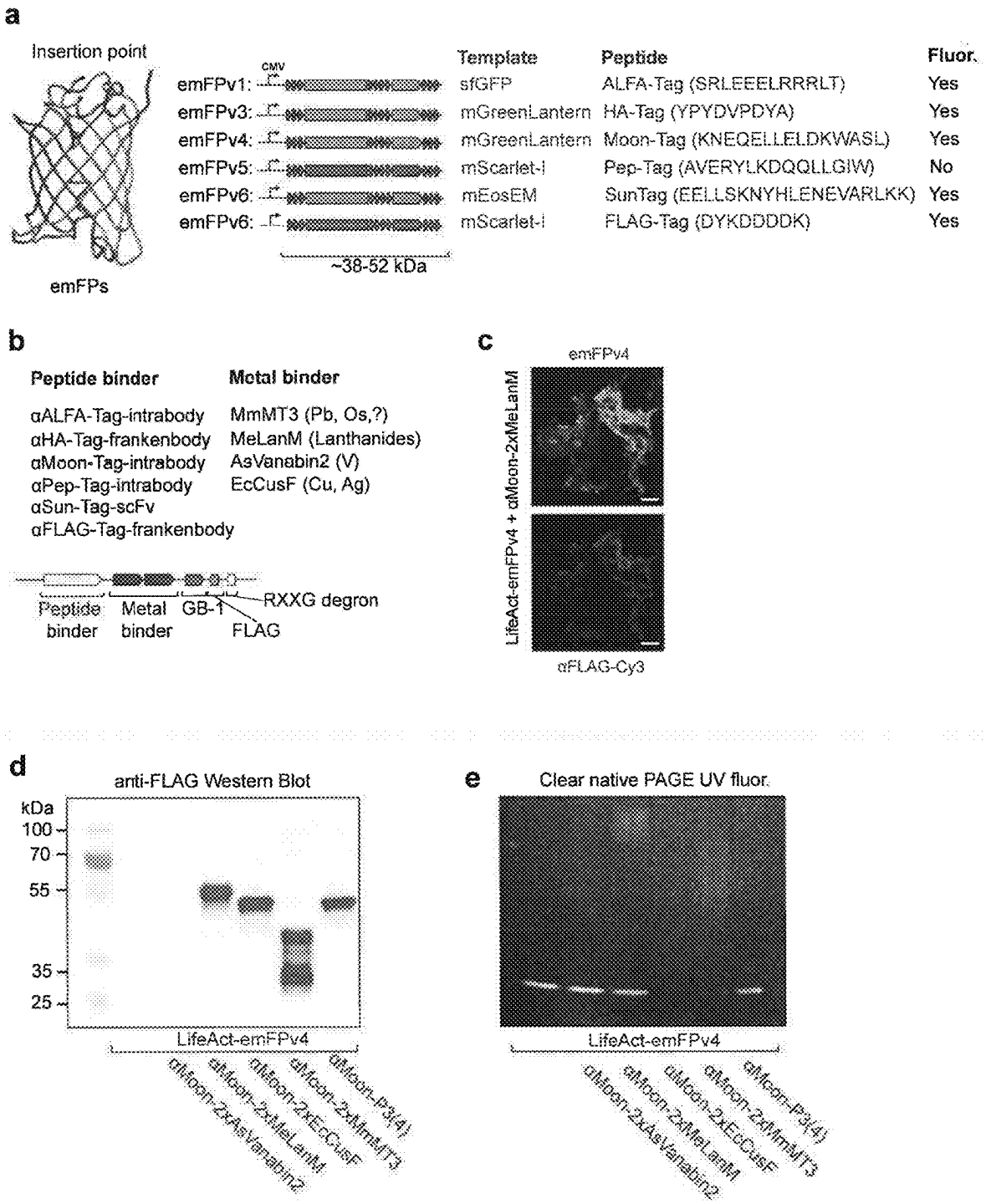
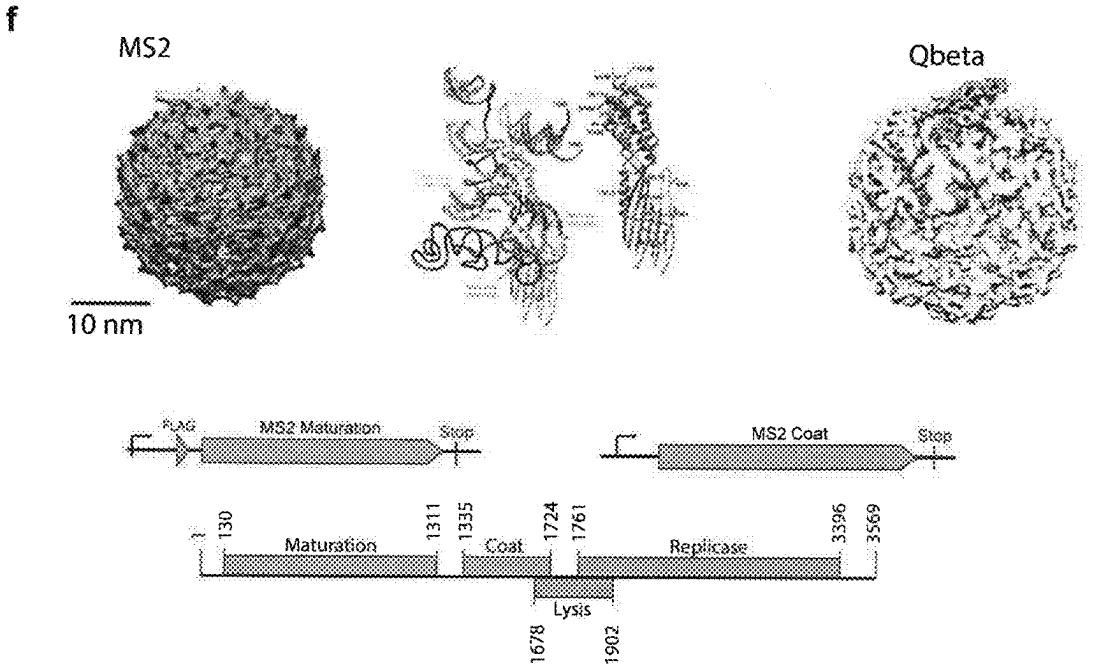
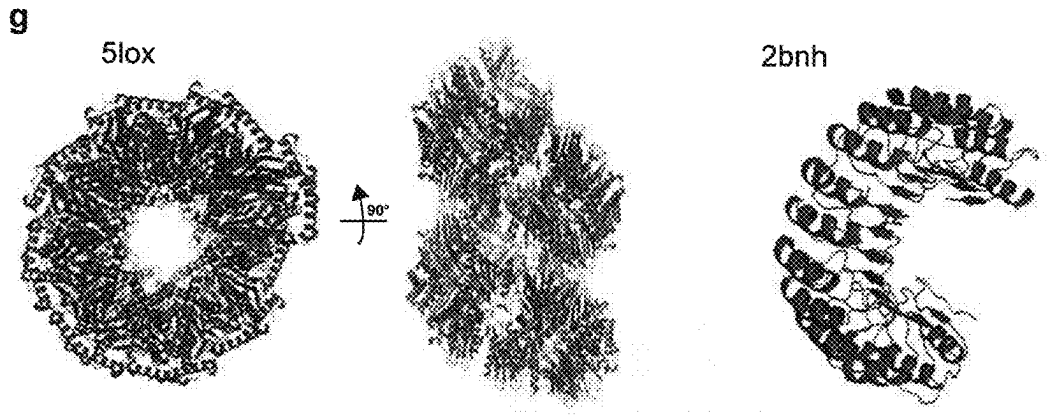

a
Insertion point
emFPs
CMV
emFPv1:
emFPv3:
emFPv4:
emFPv5:
emFPv6:
emFPv6:
~38-52 kDa
Template
Peptide
Fluor.
sfGFP
ALFA-Tag (SRLEEELRRRLT)
Yes
mGreenLantern
HA-Tag (YPYDVPDYA)
Yes
mGreenLantern
Moon-Tag (KNEQELLELDKWASL)
Yes
mScarlet-I
Pep-Tag (AVERYLKDQQLLGIW)
No
mEosEM
SunTag (EELLSKNYHLENEVARLKK)
Yes
mScarlet-I
FLAG-Tag (DYKDDDDK)
Yes
b
Peptide binder
Metal binder
αALFA-Tag-intrabody
αHA-Tag-frankenbody
αMoon-Tag-intrabody
αPep-Tag-intrabody
αSun-Tag-scFv
αFLAG-Tag-frankenbody
MmMT3 (Pb, Os,?)
MeLanM (Lanthanides)
AsVanabin2 (V)
EcCusF (Cu, Ag)
Peptide binder
Metal binder
GB-1
RXXG degron
FLAG
c
emFPv4
LifeAct-emFPv4 + αMoon-2xMeLanM
αFLAG-Cy3
d
anti-FLAG Western Blot
kDa
100
70
55
35
25
LifeAct-emFPv4
αMoon-2xAsVanabin2
αMoon-2xMeLanM
αMoon-2xEcCusF
αMoon-2xMmMT3
αMoon-P3(4)
e
Clear native PAGE UV fluor.
LifeAct-emFPv4
αMoon-2xAsVanabin2
αMoon-2xMeLanM
αMoon-2xEcCusF
αMoon-2xMmMT3
αMoon-P3(4)

Fig. 14 continued





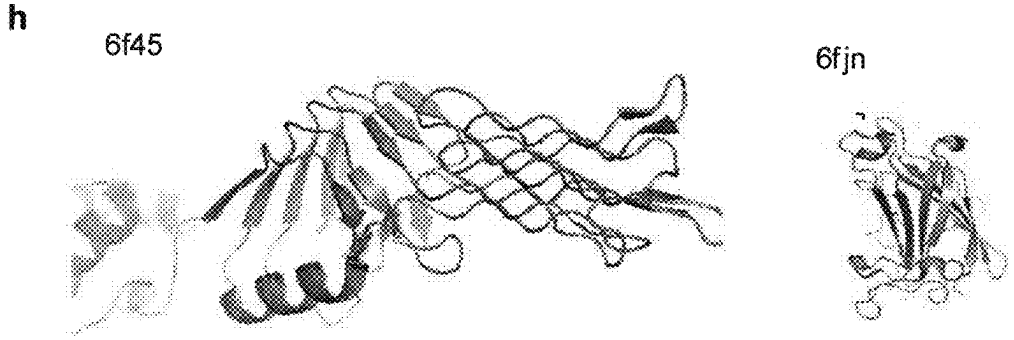
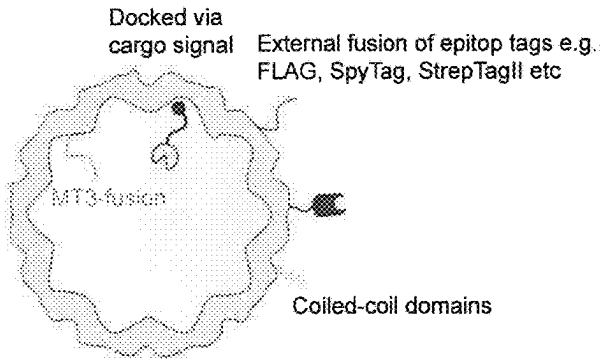
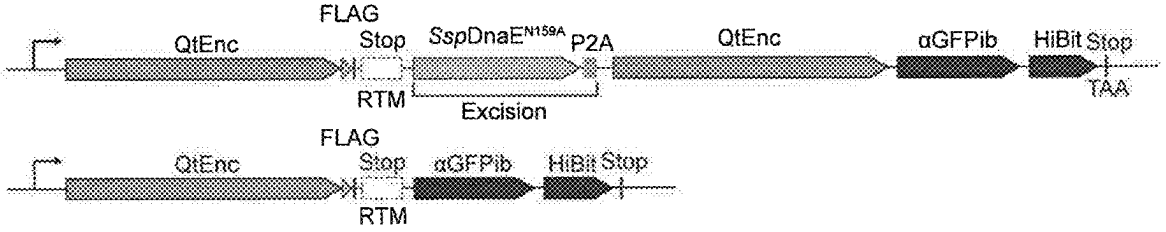


Fig. 15

a


Docked via
cargo signal
External fusion of epitop tags e.g.
FLAG, SpyTag, StrepTagII etc
MT3-fusion
Coiled-coil domains

b


FLAG
QtEnc
Stop
SspDnaE^{N159A}
P2A
QtEnc
αGFPib
HiBit
Stop
TAA
RTM
Excision
FLAG
QtEnc
Stop
αGFPib
HiBit
Stop
RTM

c

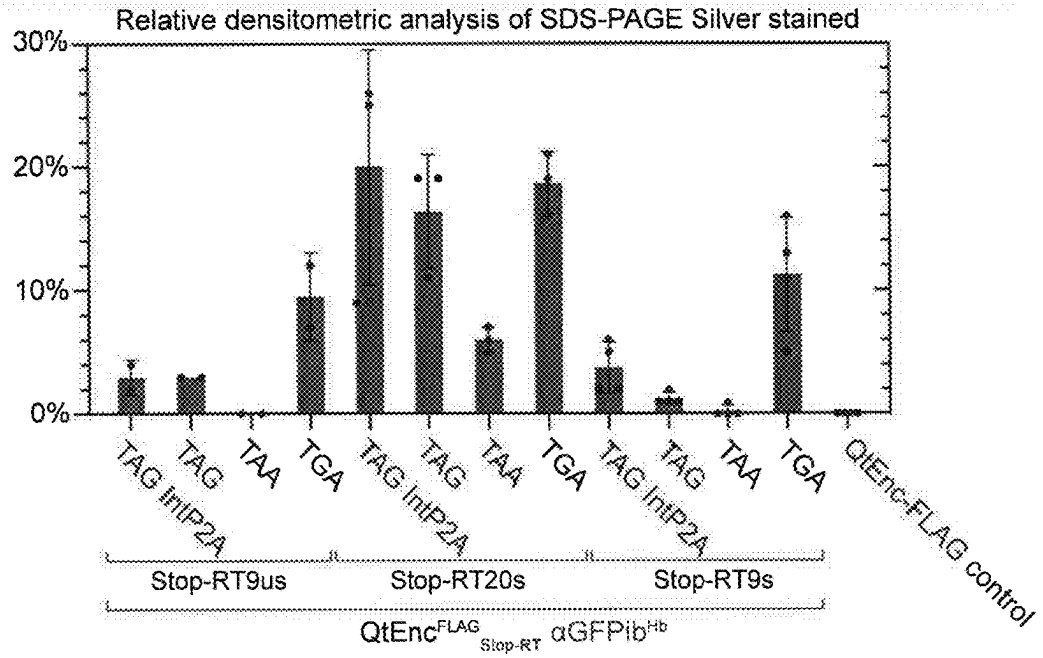
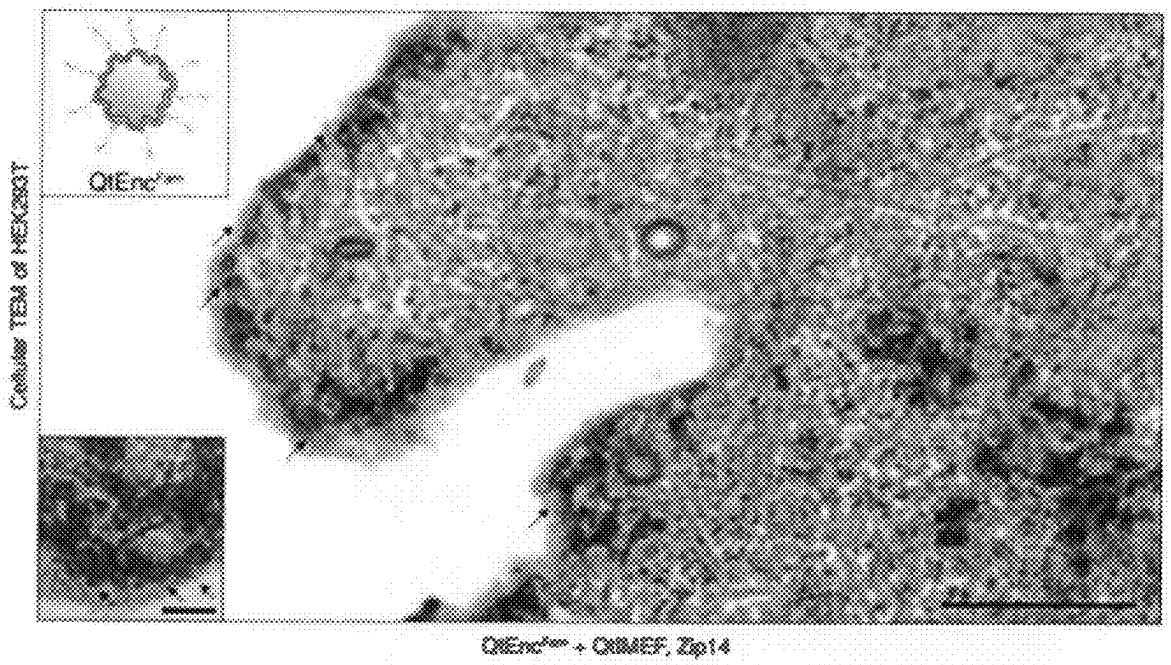
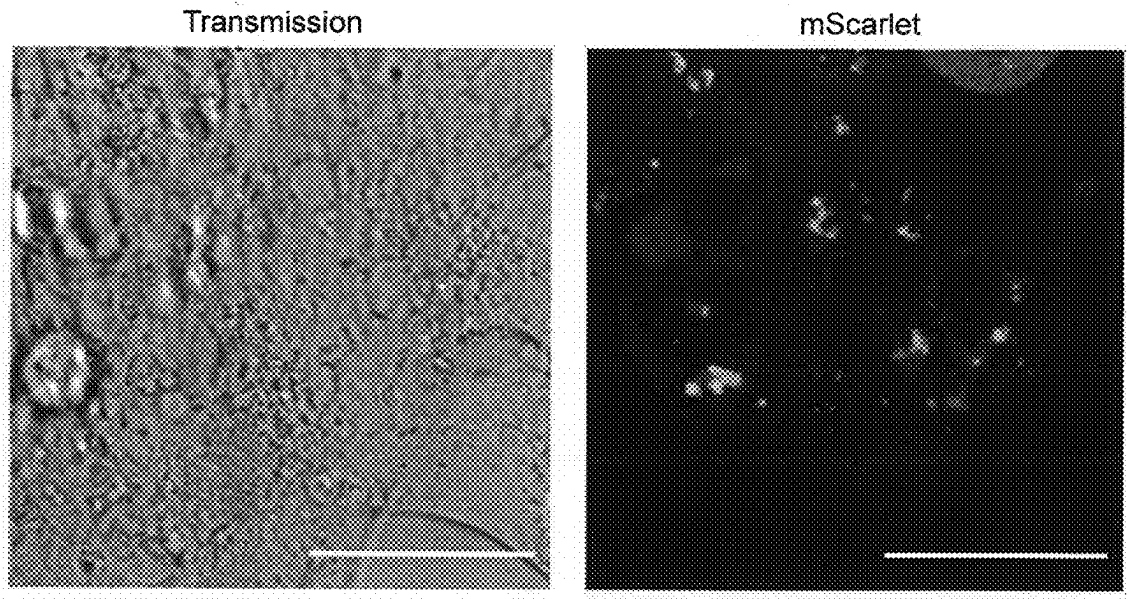

Relative densitometric analysis of SDS-PAGE Silver stained
30%
20%
10%
0%
TAG IntP2A
TAG
TAA
TGA
TAG IntP2A
TAG
TAA
TGA
TAG IntP2A
TAG
TAA
TGA
QtEnc-FLAG control
Stop-RT9us
Stop-RT20s
Stop-RT9s
QtEnc$^{FLAG}_{Stop\text{-}RT}$ αGFPib^{Hb}

Fig. 16

a



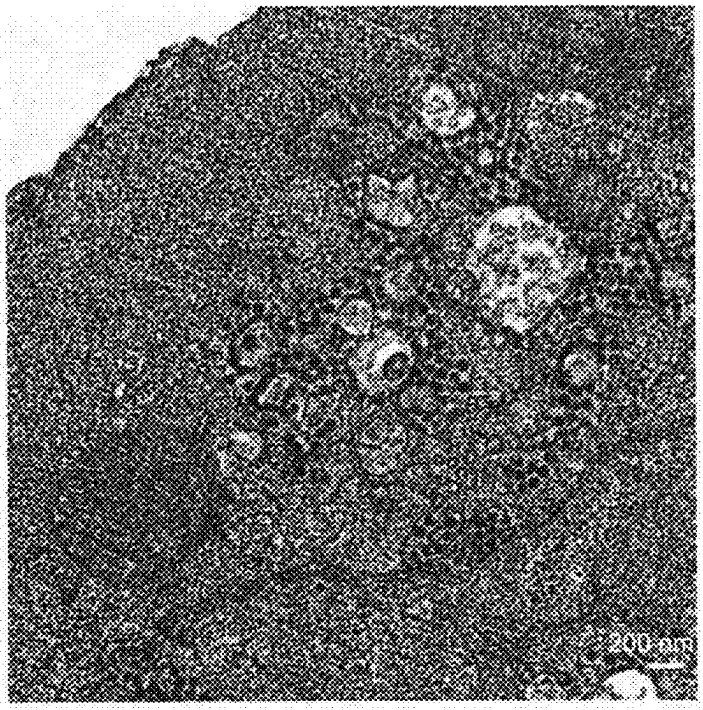
b



QtEnc^{KinTag} + DD-mScarlet-I-QtSig

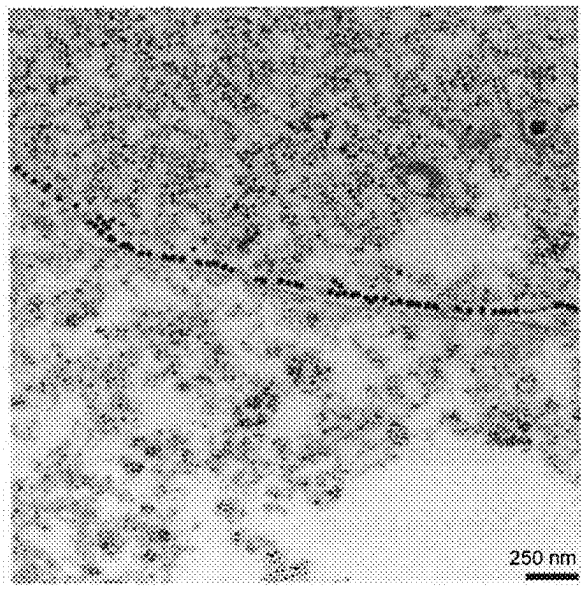
Fig. 16 continued

c

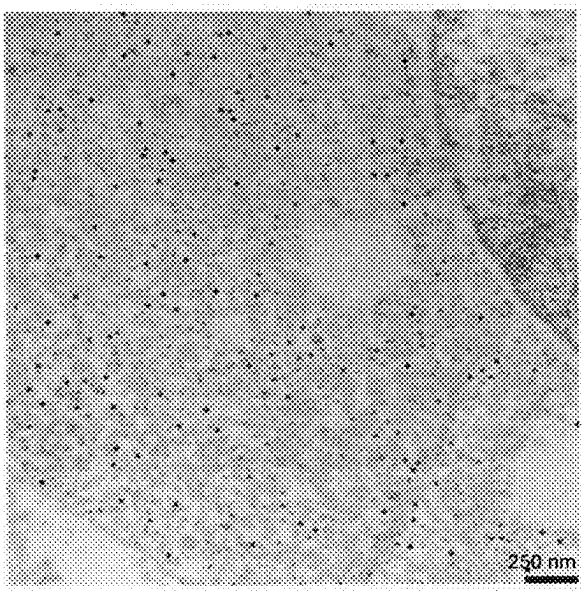


2xMT3-QtEnc^{antiGFPIB} + LAMP1-EGFP

d



eGFP-CAAX
+ QtEnc^{antiGFPIB} +IMEF
+ ZIP14



eGFP-CAAX
+ QtEnc^{FLAG}+IMEF
+Zip14

Fig. 17

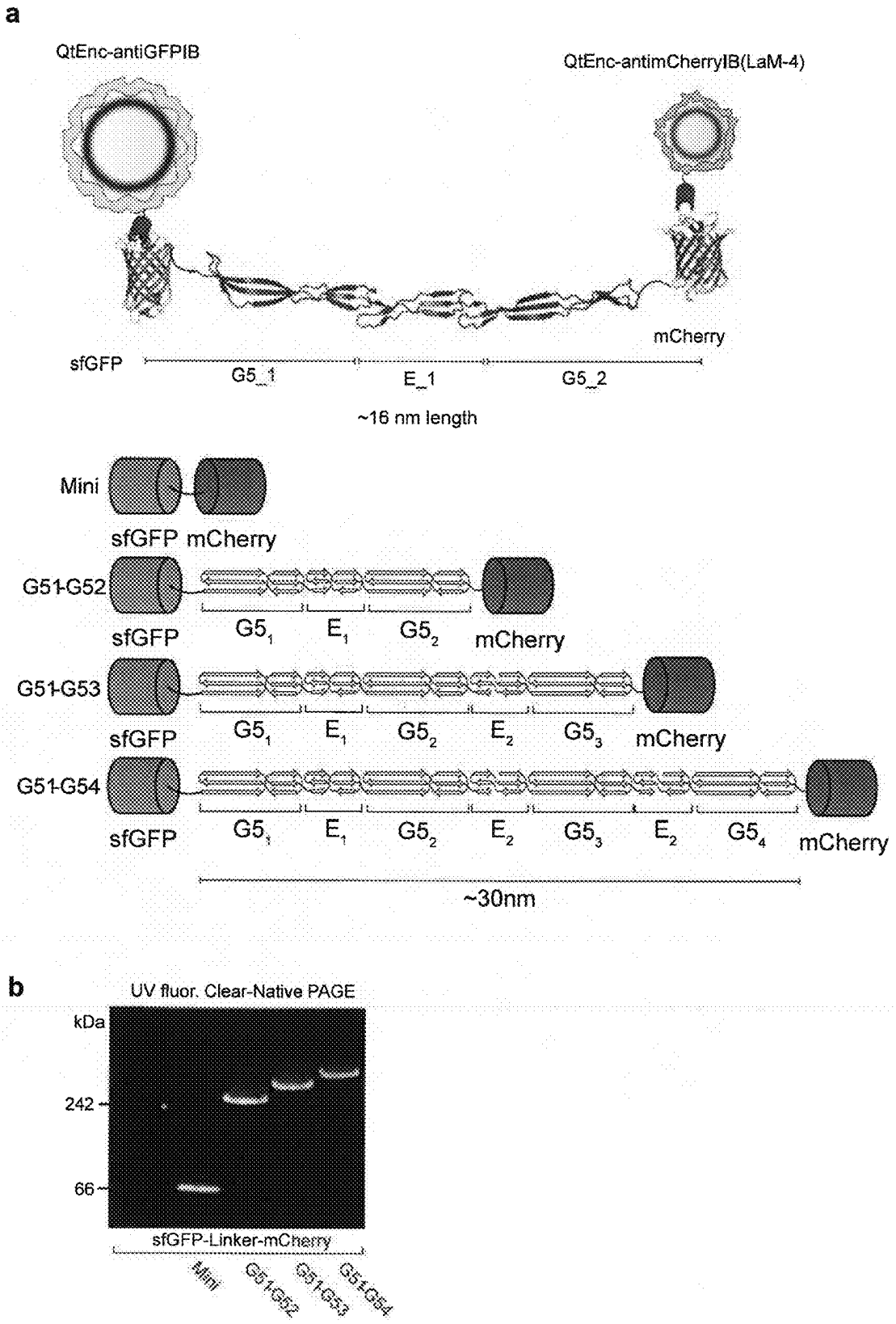
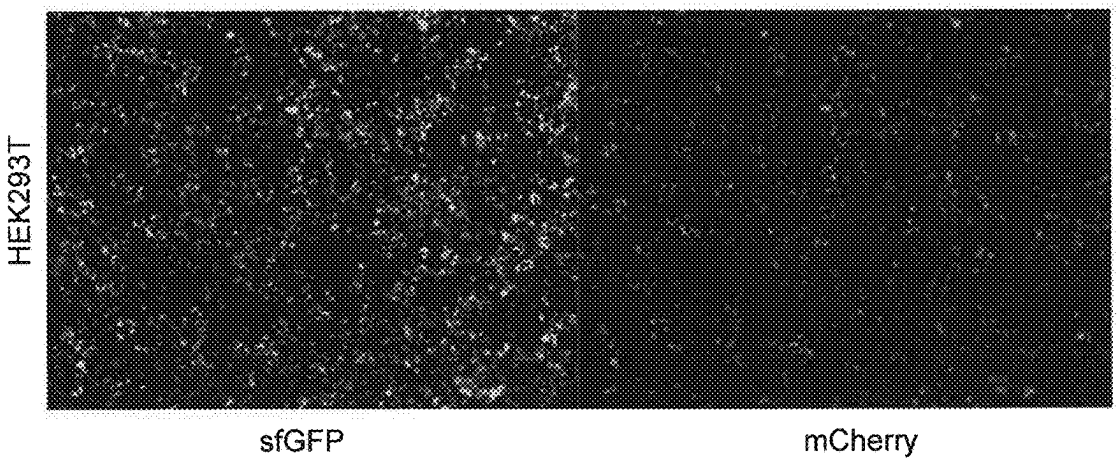
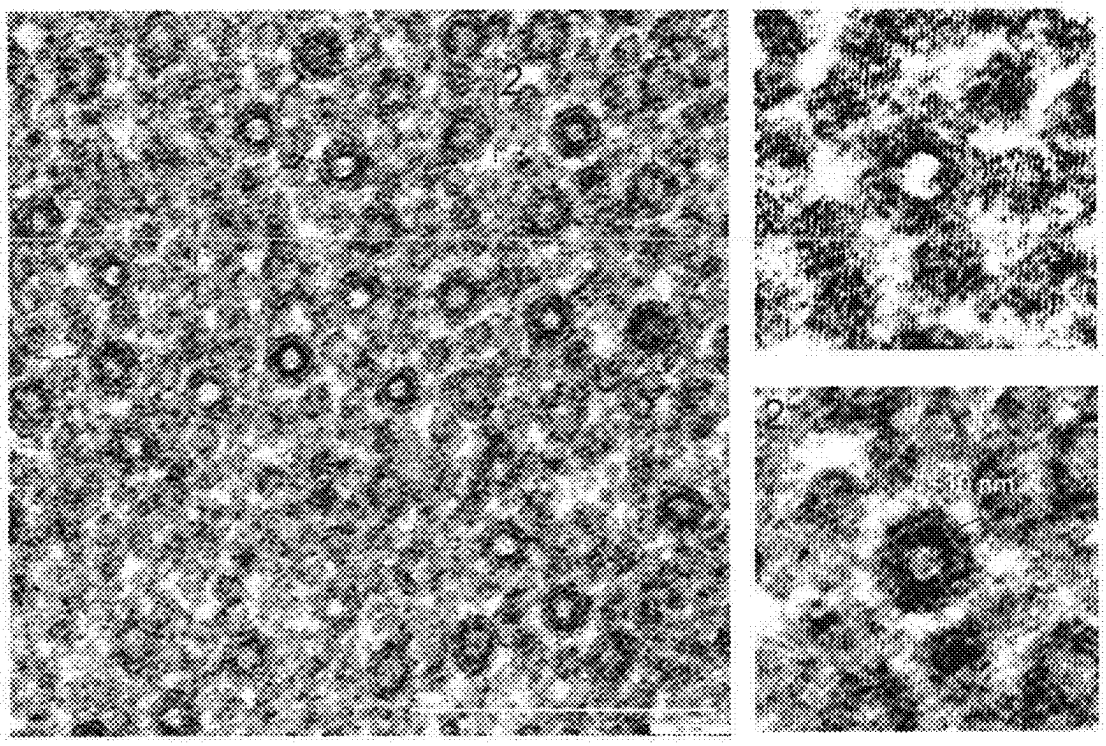

a
QtEnc-antiGFPIB
QtEnc-antimCherryIB(LaM-4)
mCherry
sfGFP
G5_1
E_1
G5_2
~16 nm length
Mini
sfGFP mCherry
G51-G52
sfGFP
G5₁ E₁ G5₂
mCherry
G51-G53
sfGFP
G5₁ E₁ G5₂ E₂ G5₃
mCherry
G51-G54
sfGFP
G5₁ E₁ G5₂ E₂ G5₃ E₂ G5₄
mCherry
~30nm
b
UV fluor. Clear-Native PAGE
kDa
242
66
sfGFP-Linker-mCherry
Mini
G51-G52
G51-G53
G51-G54

Fig. 17 continued

c sfGFP-SasGG5$_1$-G5$_2$-mCherry + MT3-QtEnc-antiGFPIB + P2-TmEnc-antimCherryIB (LaM-4)



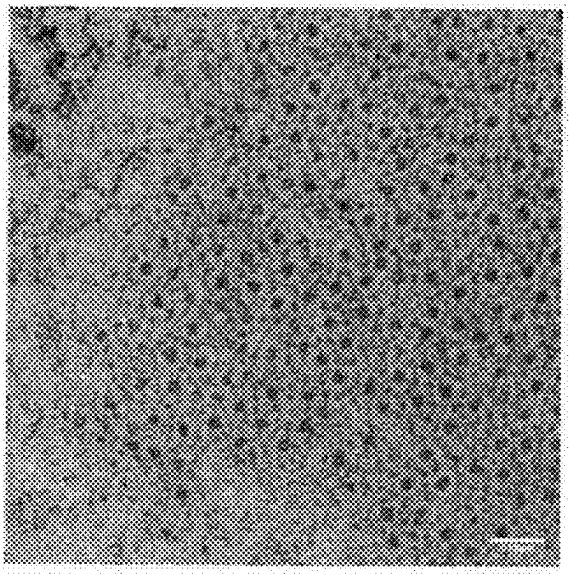
d



sfGFP-SasGG5$_1$-G5$_2$-mCherry + MT3-QtEnc-antiGFPIB + P2-TmEnc-antimCherryIB (LaM-4)

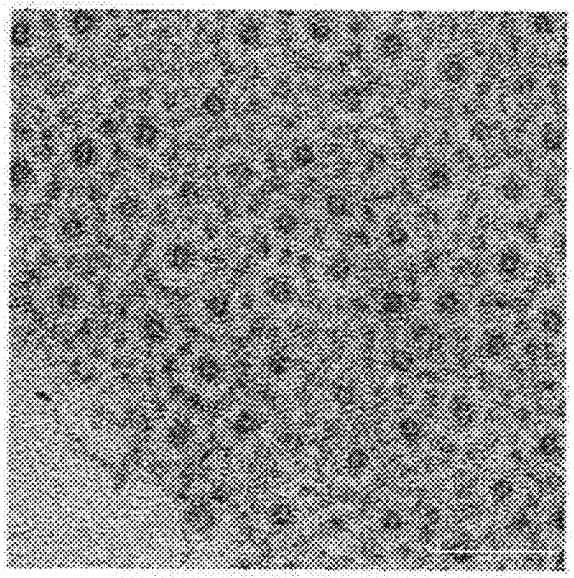
Fig. 17 continued

e

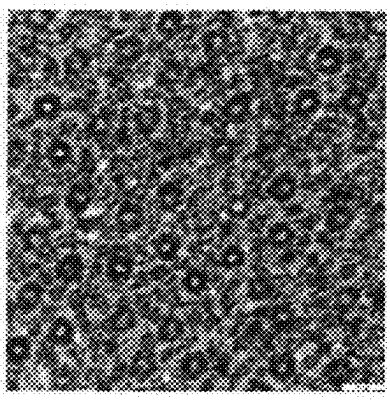


2xMT3-QtEnc^{antiGFPIgB} MT3-TmEnc$^{antimCherryIgB\ (LaM-4)}$
sfGFP-SasG-G5$_1$-G5$_4$-mCherry

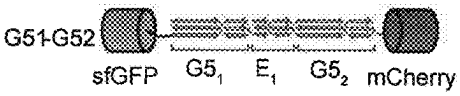
f



3x SasG Linker
„length fo vertices": ~100 nm



1x SasG Linker
„length of vertices": ~60 nm



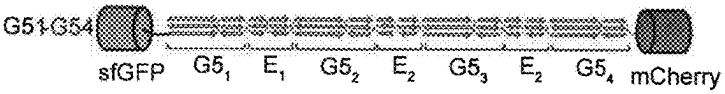
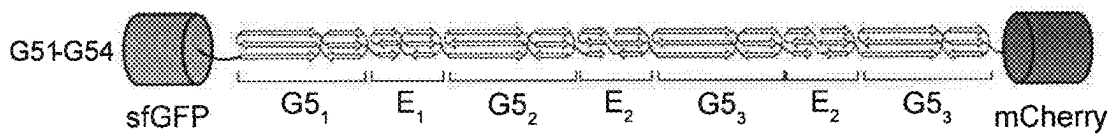


Fig. 17 continued

g



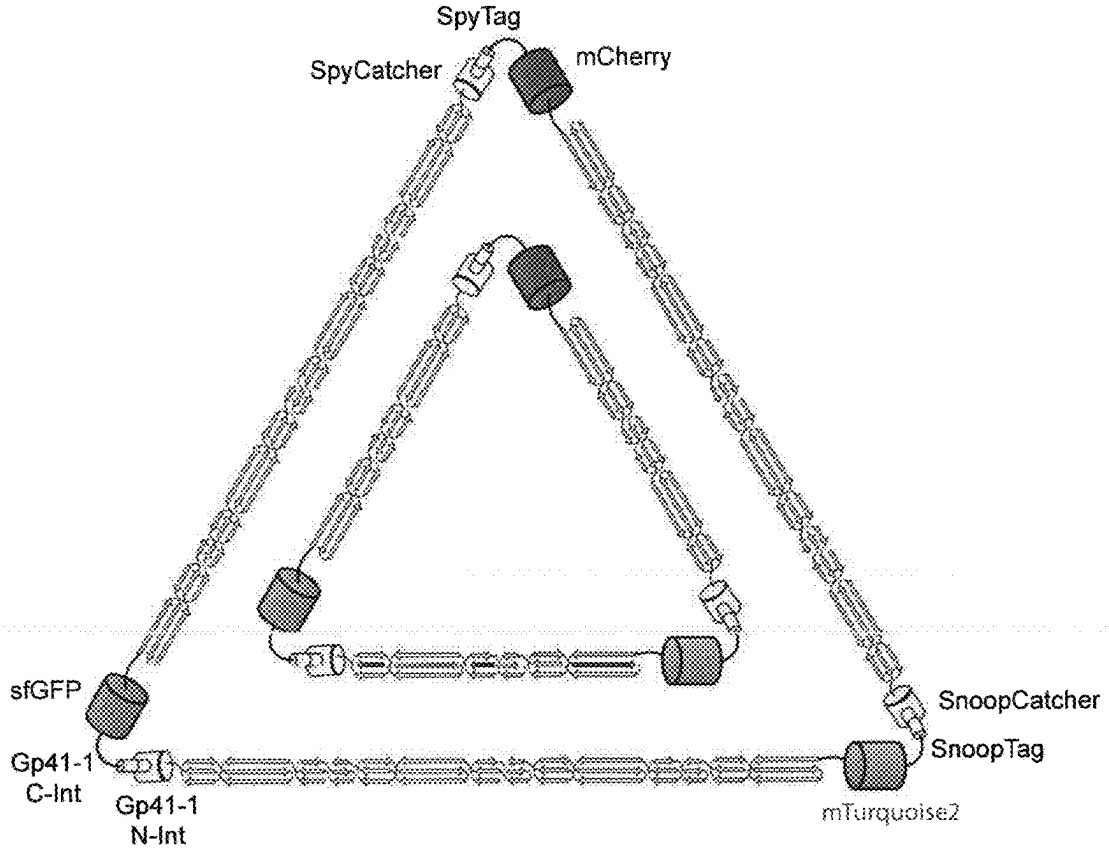


Fig. 17 continued

h

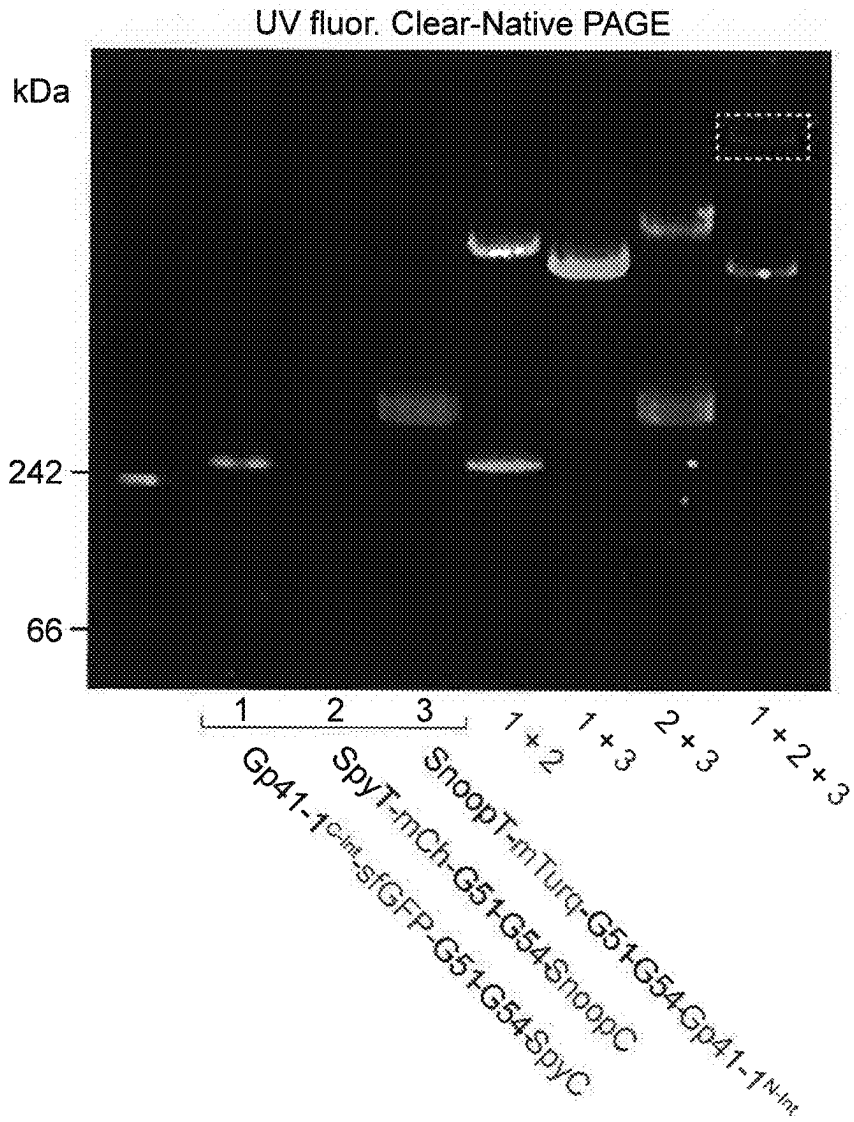
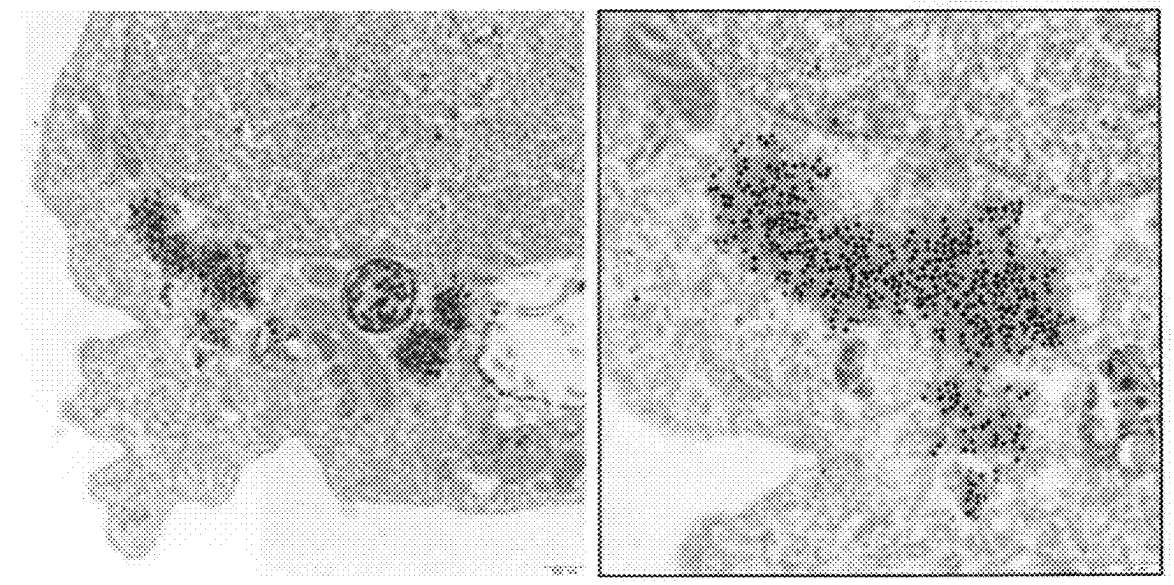


Fig. 17 continued



QtEnc-SpyTag + QtIMEF + I3-01-SpyCatcher

Fig. 17 continued

j

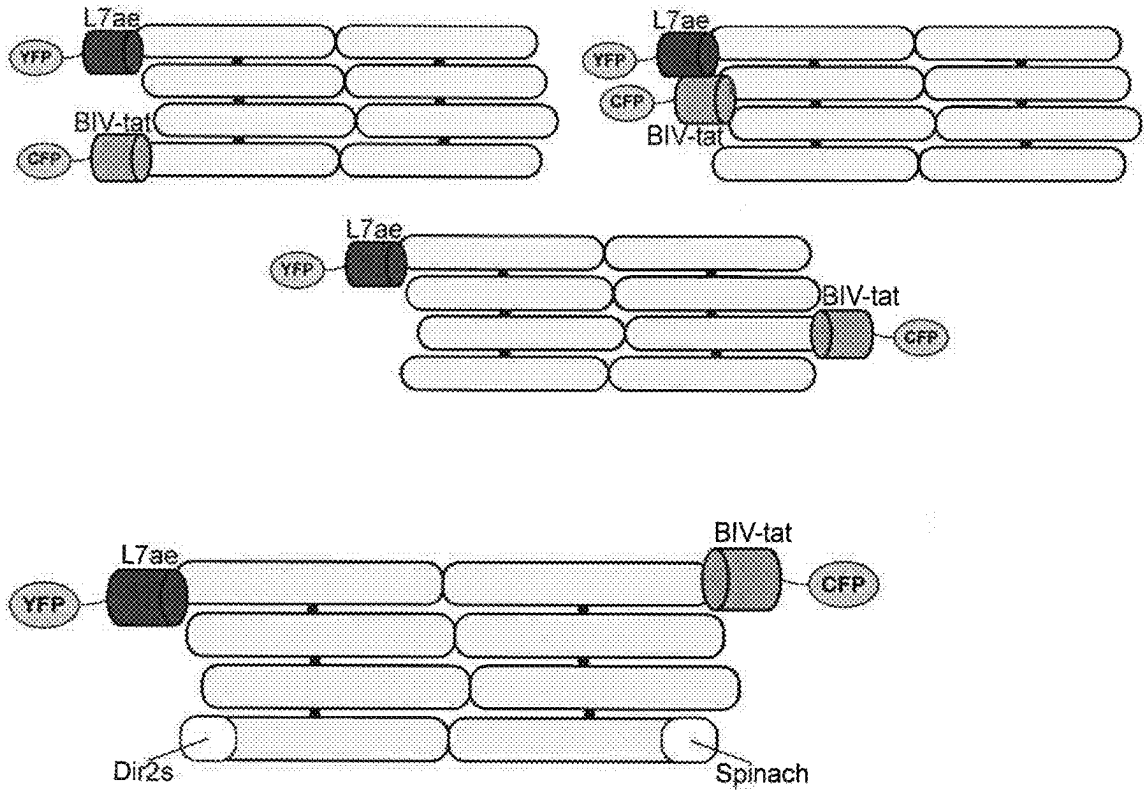
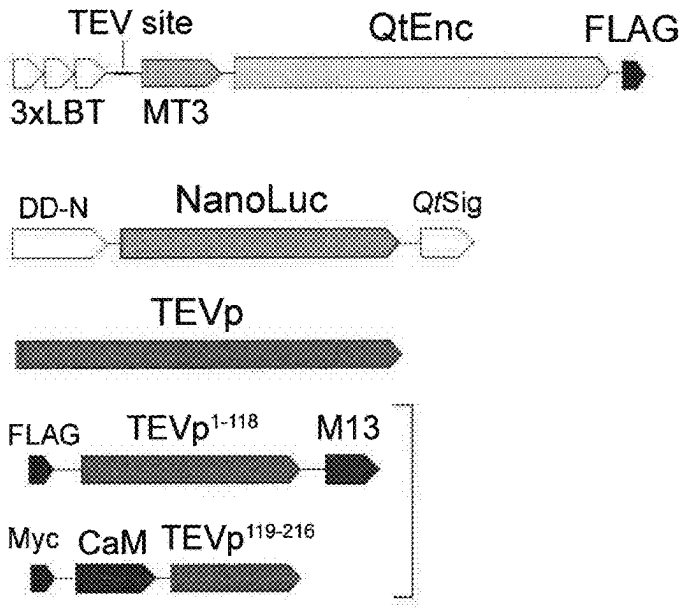


Fig. 18

a


TEV site
QtEnc
FLAG
3xLBT
MT3
DD-N
NanoLuc
QtSig
TEVp
FLAG
TEVp1-118
M13
Myc
CaM
TEVp119-216

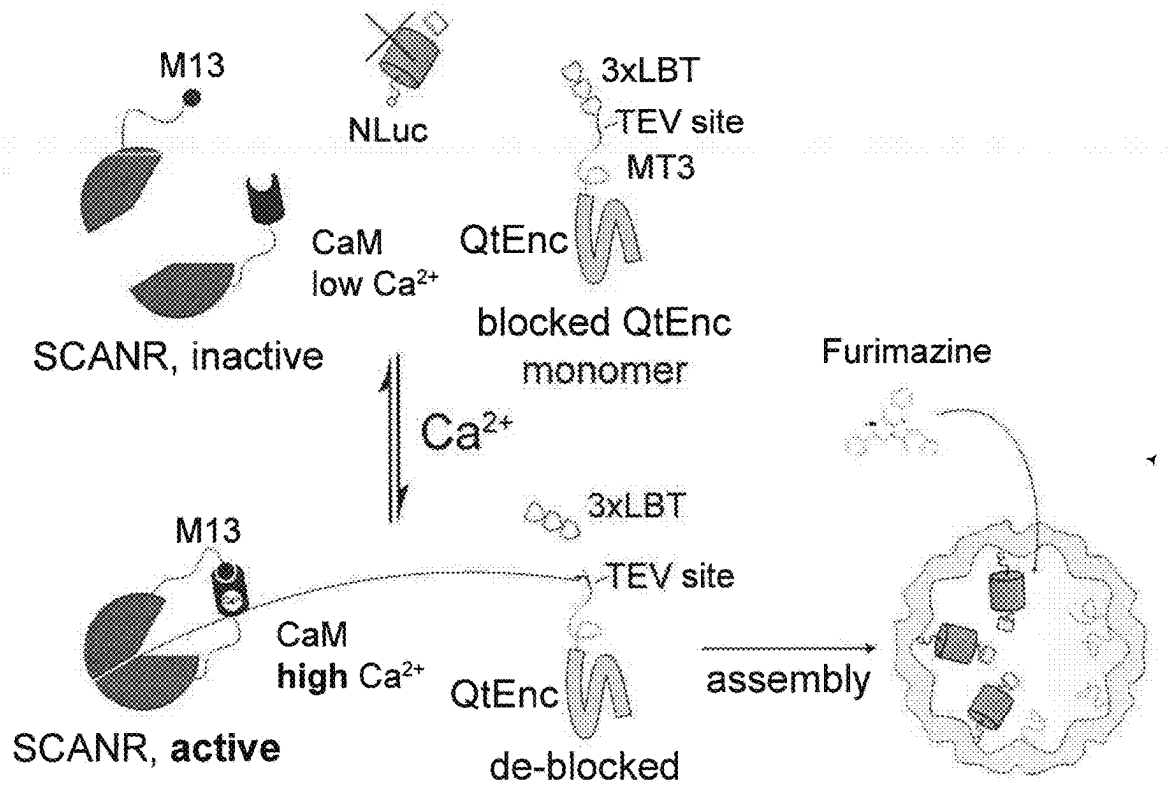
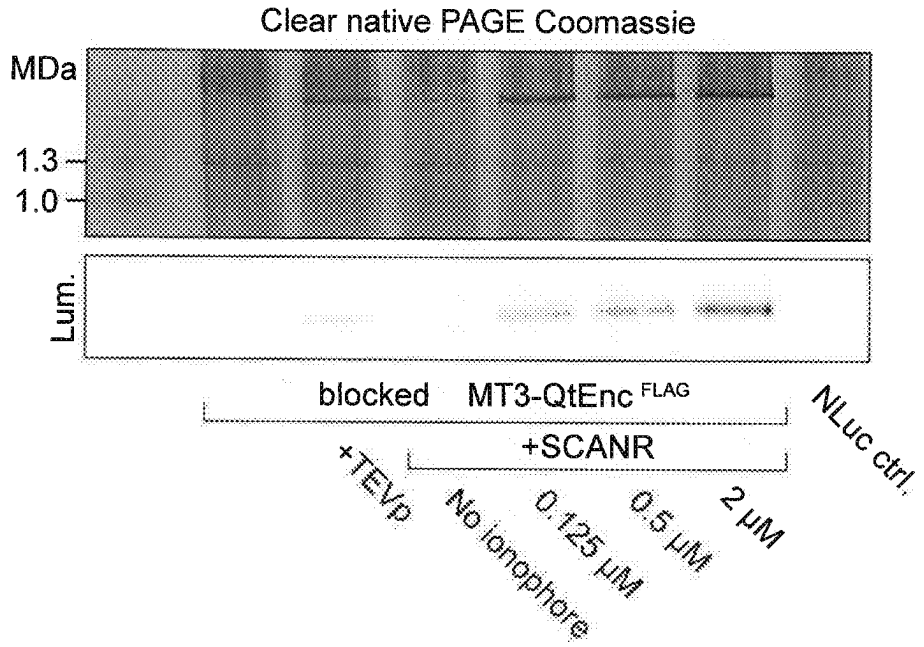

M13
NLuc
3xLBT
TEV site
MT3
CaM
low Ca2+
QtEnc
SCANR, inactive
blocked QtEnc
monomer
Furimazine
Ca2+
3xLBT
M13
TEV site
CaM
high Ca2+
QtEnc
assembly
SCANR, active
de-blocked

Fig. 18

b


Clear native PAGE Coomassie
MDa
1.3
1.0
Lum.
blocked MT3-QtEnc FLAG
NLuc ctrl.
+SCANR
+TEVp
No ionophore
0.125 μM
0.5 μM
2 μM

c

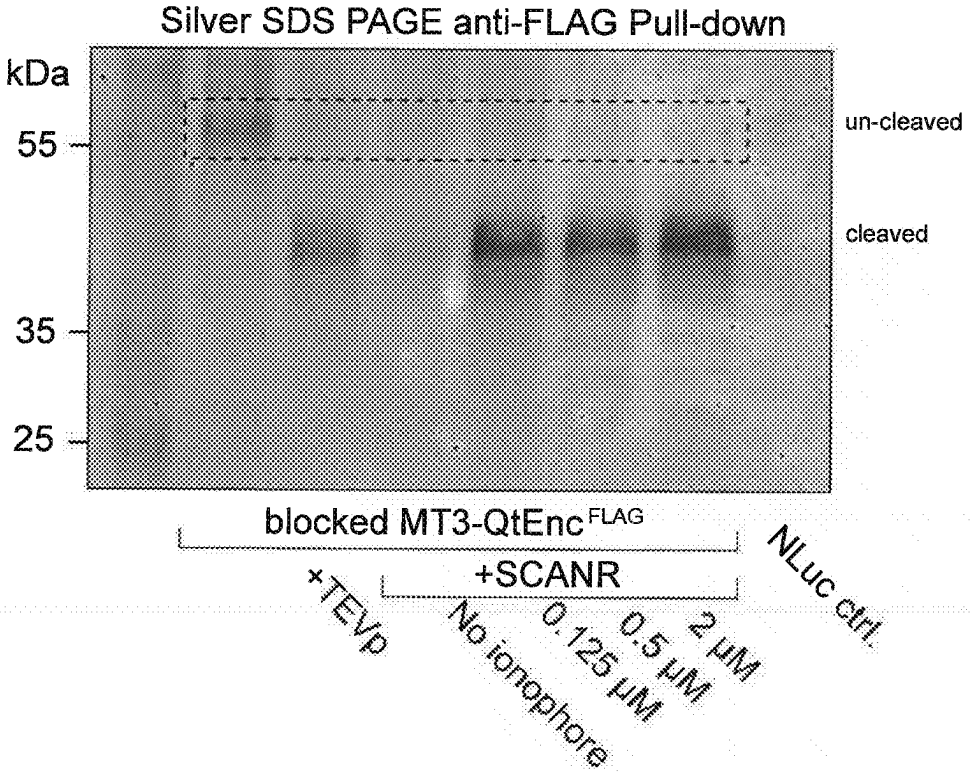
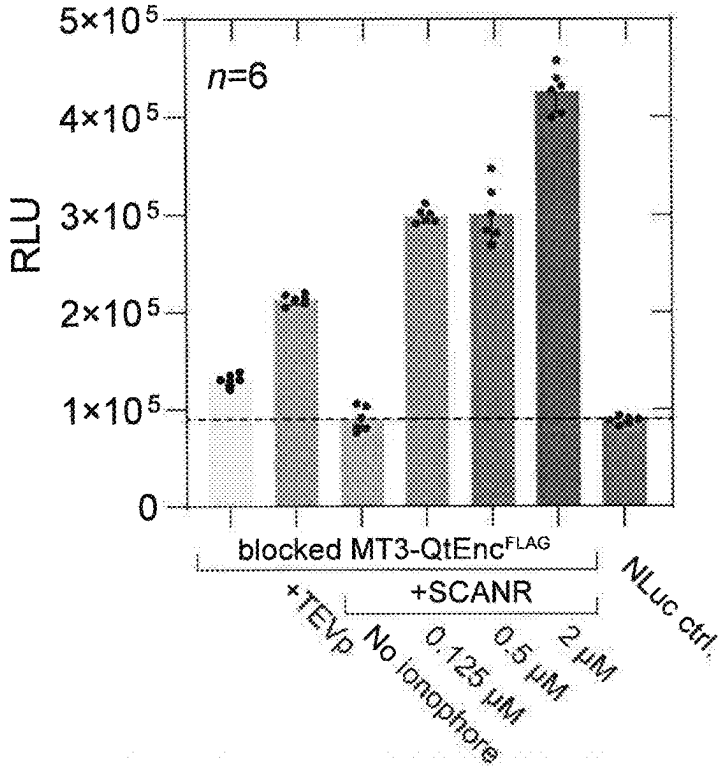

Silver SDS PAGE anti-FLAG Pull-down
kDa
55
35
25
un-cleaved
cleaved
blocked MT3-QtEnc FLAG
NLuc ctrl.
+SCANR
+TEVp
No ionophore
0.125 μM
0.5 μM
2 μM

Fig. 18 continued

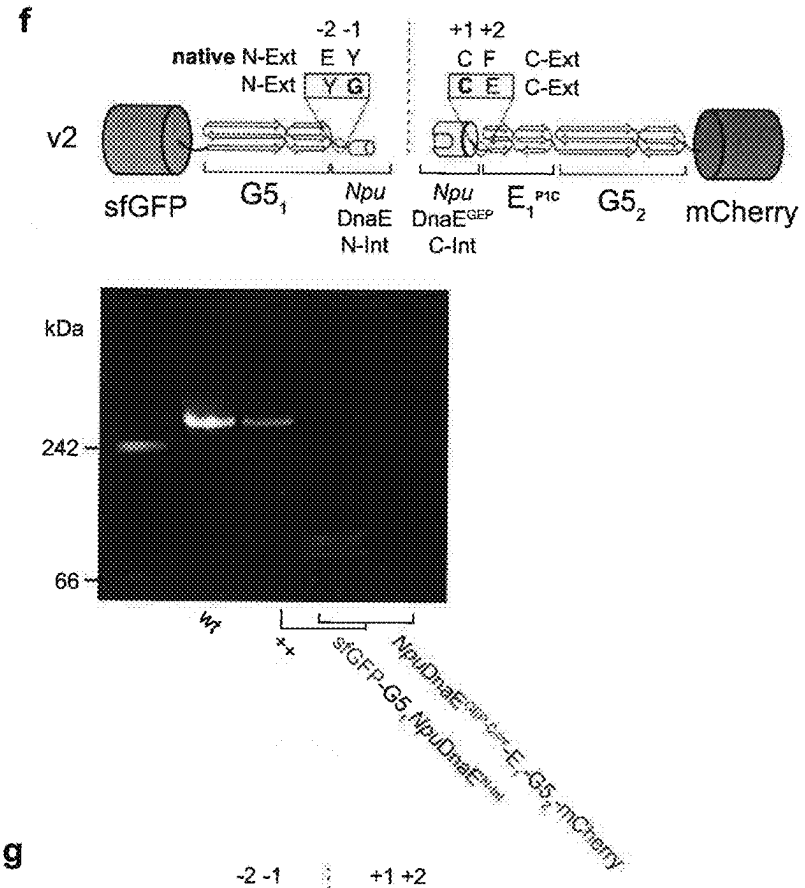
d



e

blocked MT3-QtEnc^FLAG
+SCNAR + 0.125 μM ionophore

Fig. 18 continued



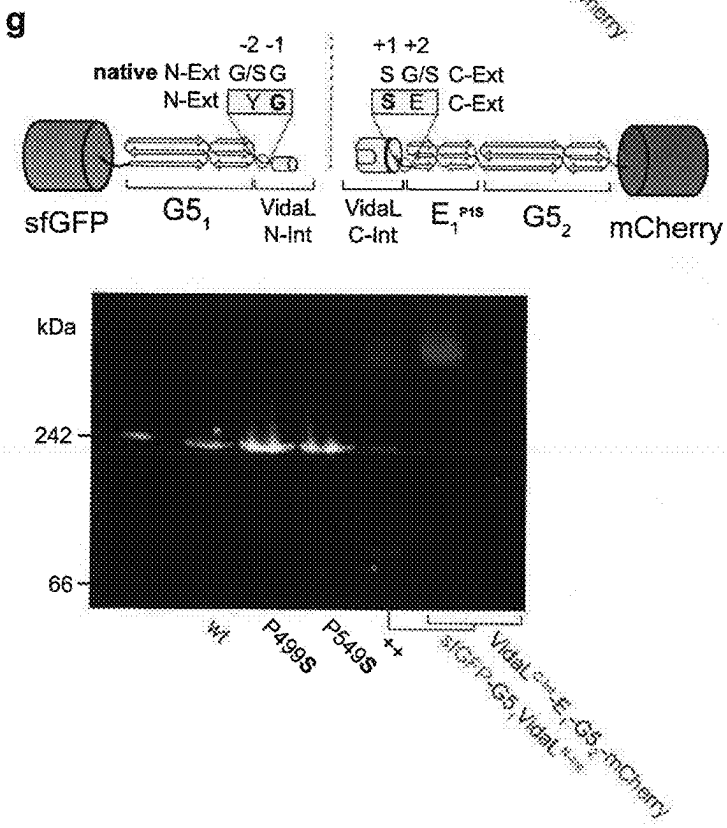
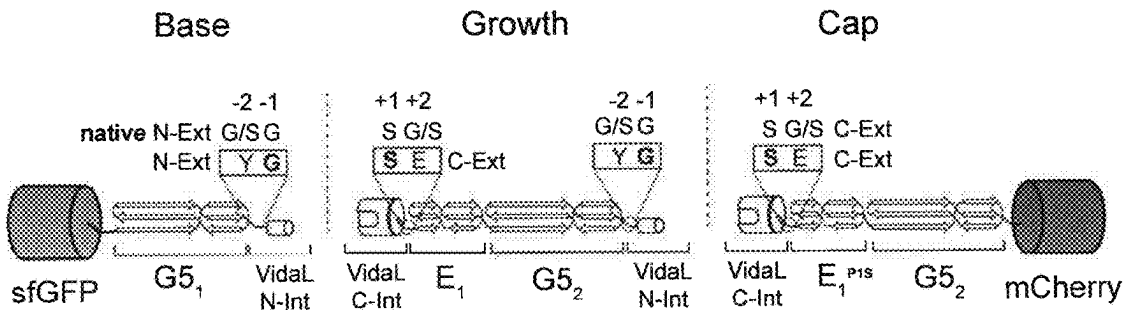
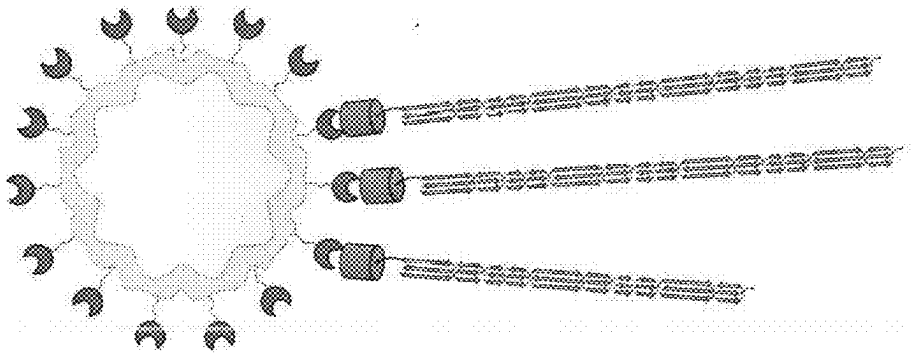


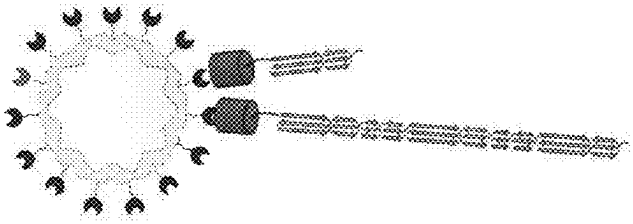
Fig. 18 continued

h



i





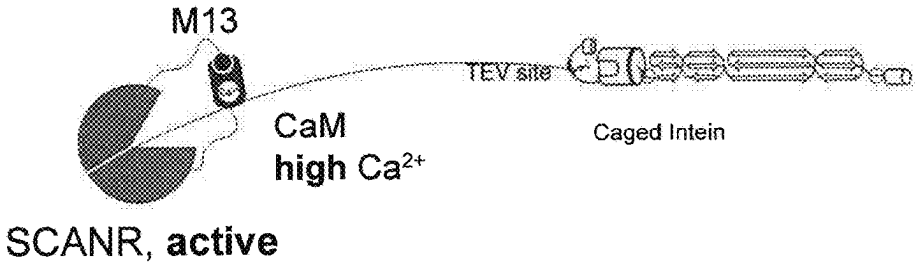
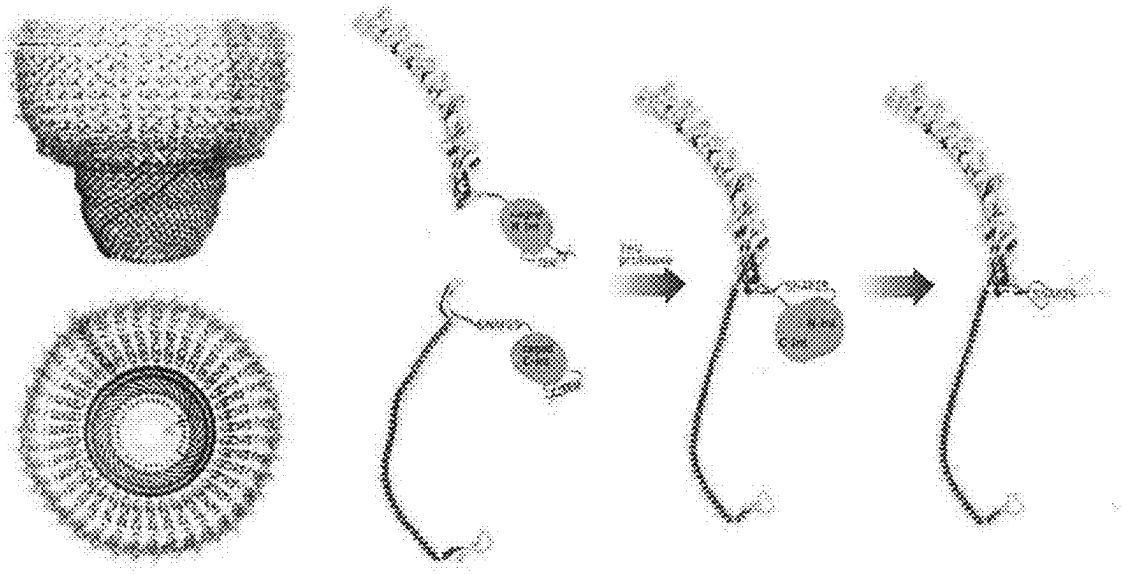


Fig. 18 continued

j



k

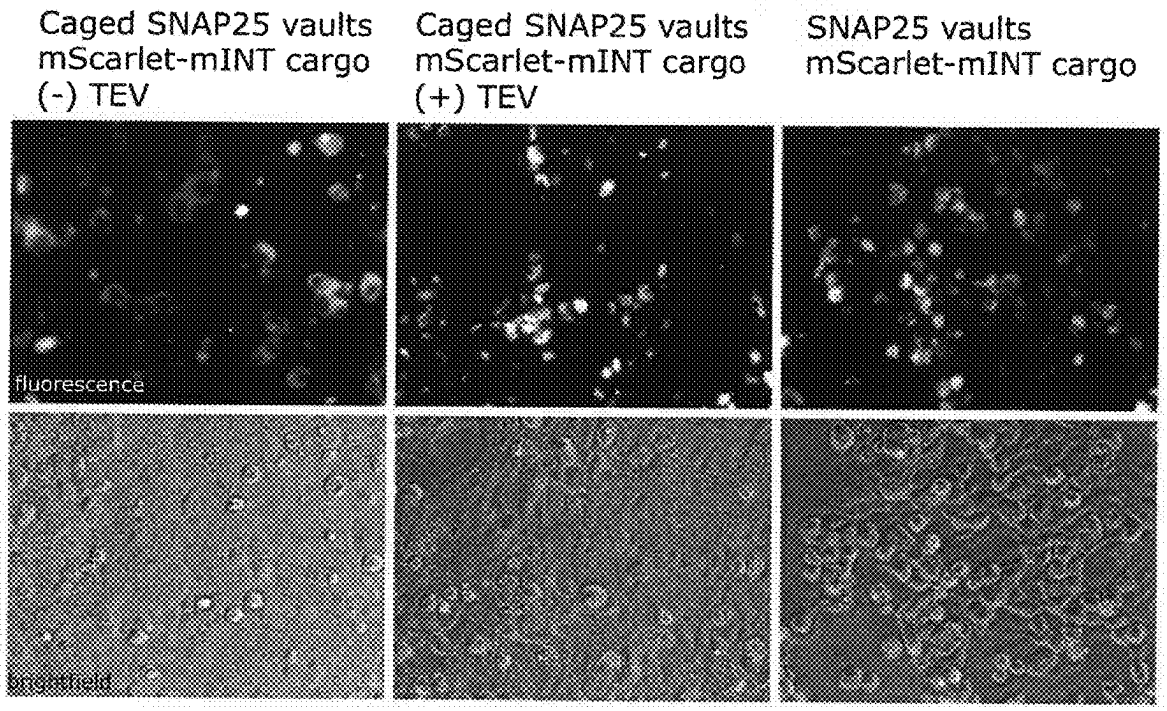


Fig. 18 continued

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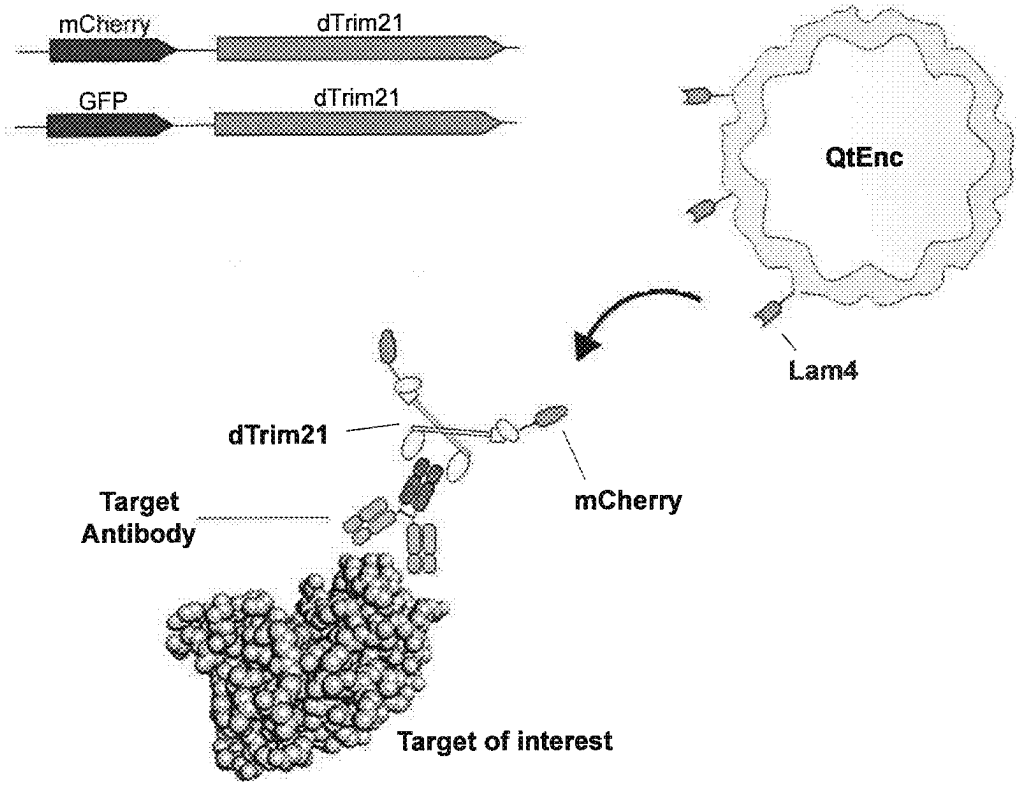
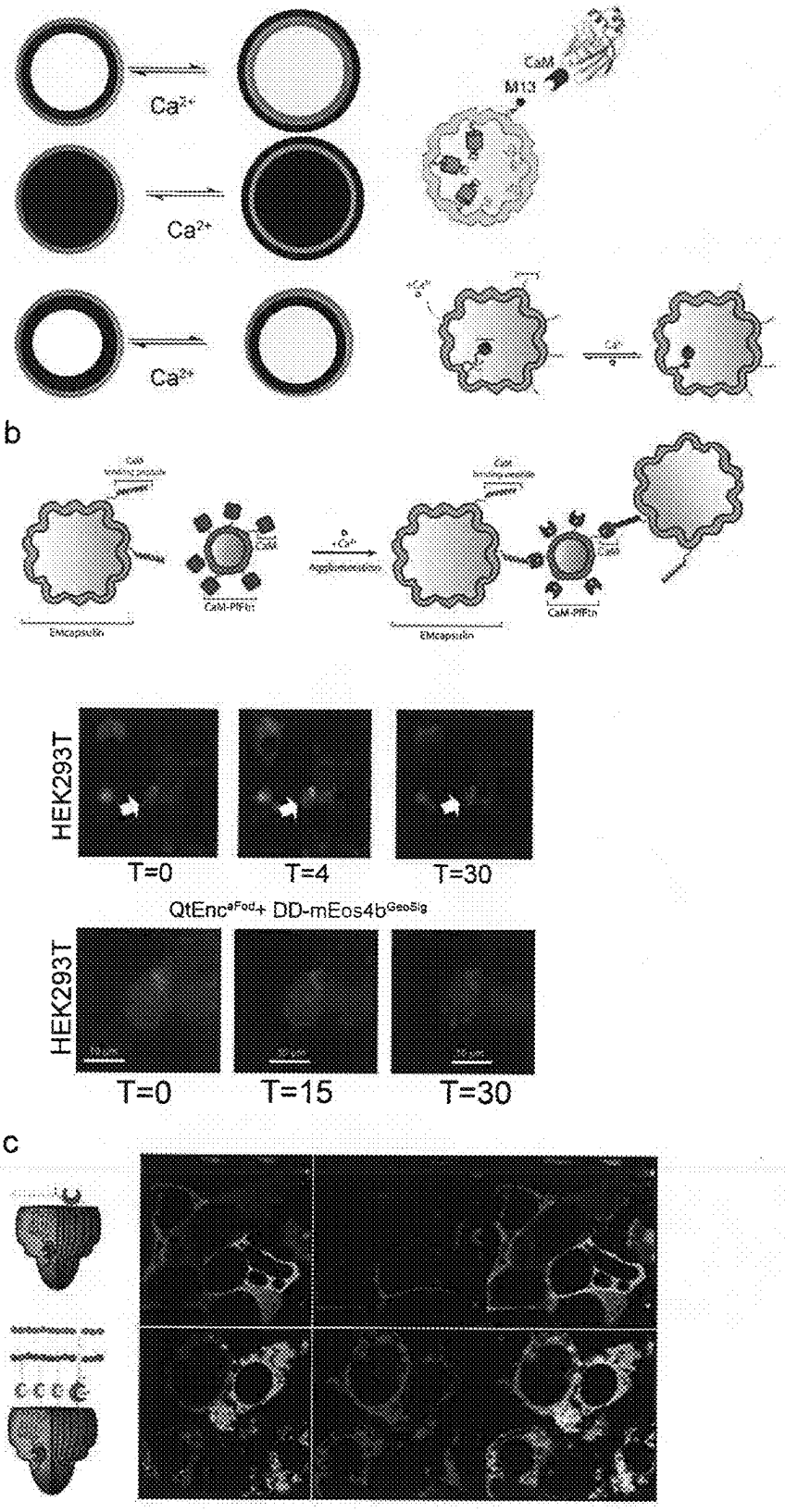


Fig. 19


Ca2+
Ca2+
Ca2+
CaM
M13
b
HEK293T
T=0
T=4
T=30
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HEK293T
T=0
T=15
T=30
c

Fig. 20

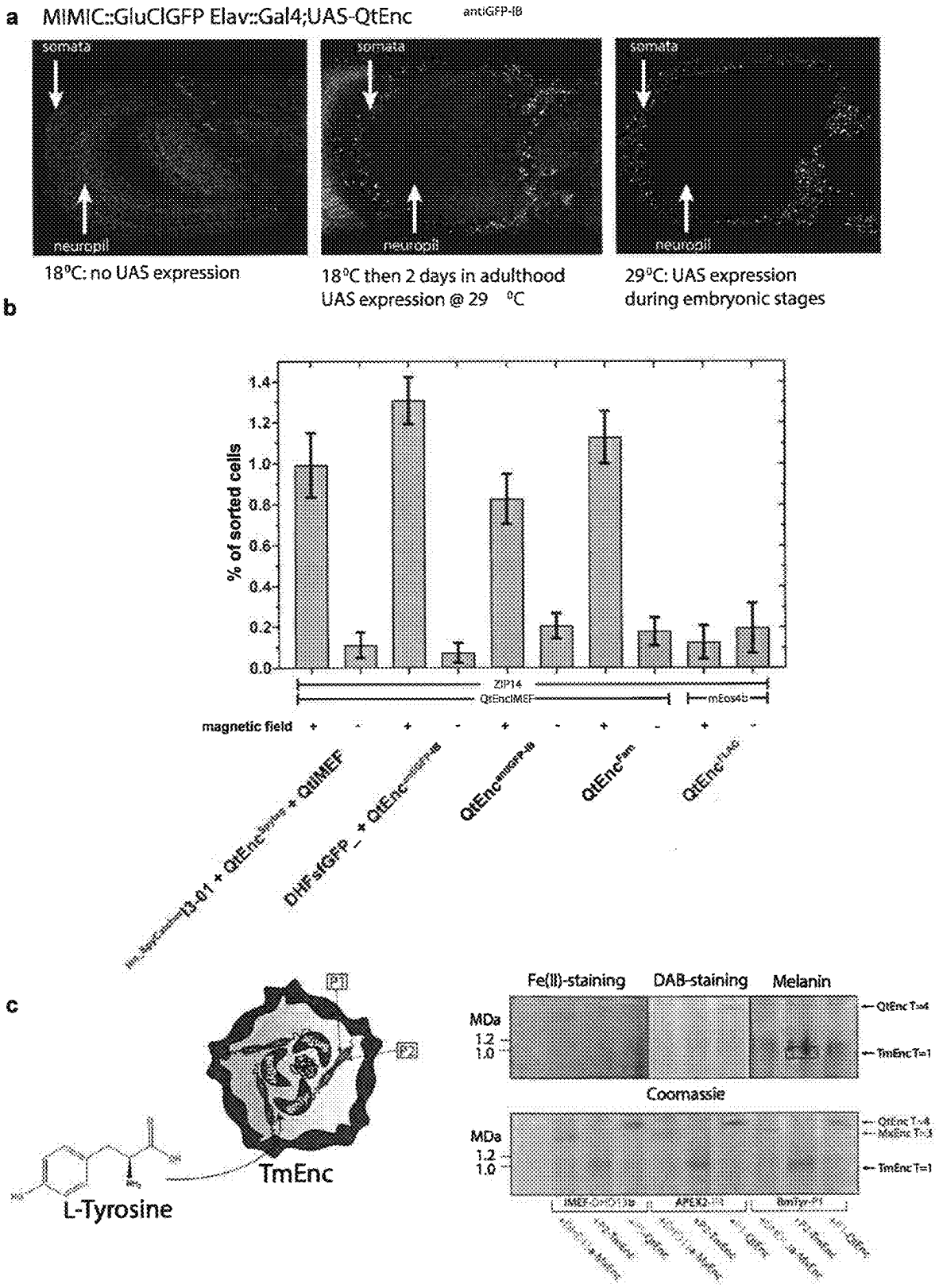

a
MIMIC::GluClGFP Elav::Gal4;UAS-QtEnc
antiGFP-IB
soma
neuropil
18°C: no UAS expression
18°C then 2 days in adulthood
UAS expression @ 29 °C
29°C: UAS expression
during embryonic stages
b
% of sorted cells
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
ZIP14
QtEncIMEF
mEos4b
magnetic field
+
-
QtEnc^antiGFP-IB
QtEnc^Fam
QtEnc^FLAG
DHFsfGFP_ + QtEnc^antiGFP-IB
c
P1
P2
TmEnc
L-Tyrosine
Fe(II)-staining
DAB-staining
Melanin
MDa
1.2
1.0
QtEnc T=4
TmEnc T=1
Coomassie
MxEnc T=3
APEX2
6mTyr-P1

Figure 21 | de-novo designed uranyl binding proteins.

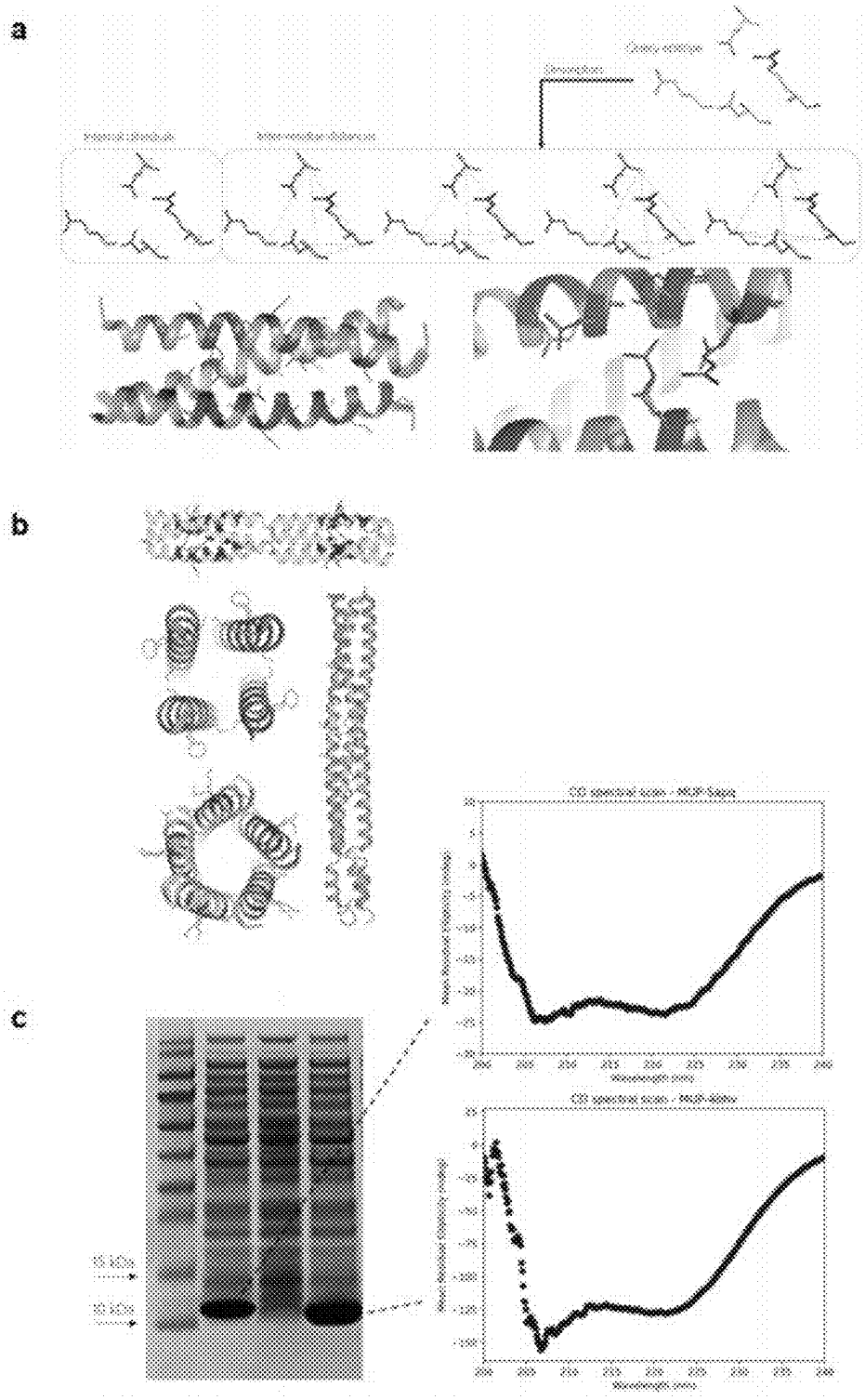
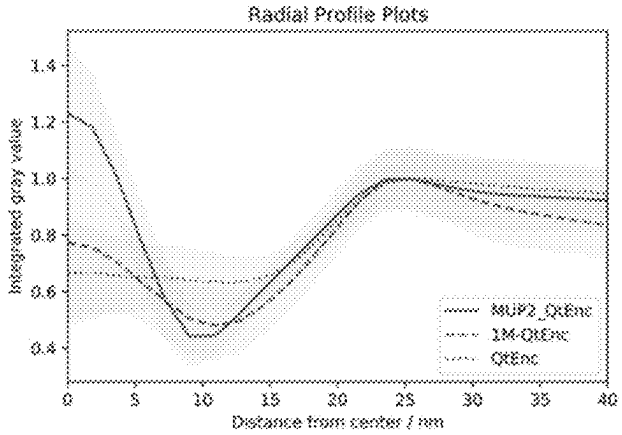


Figure 21 continued | de-novo designed uranyl binding proteins.

d



e

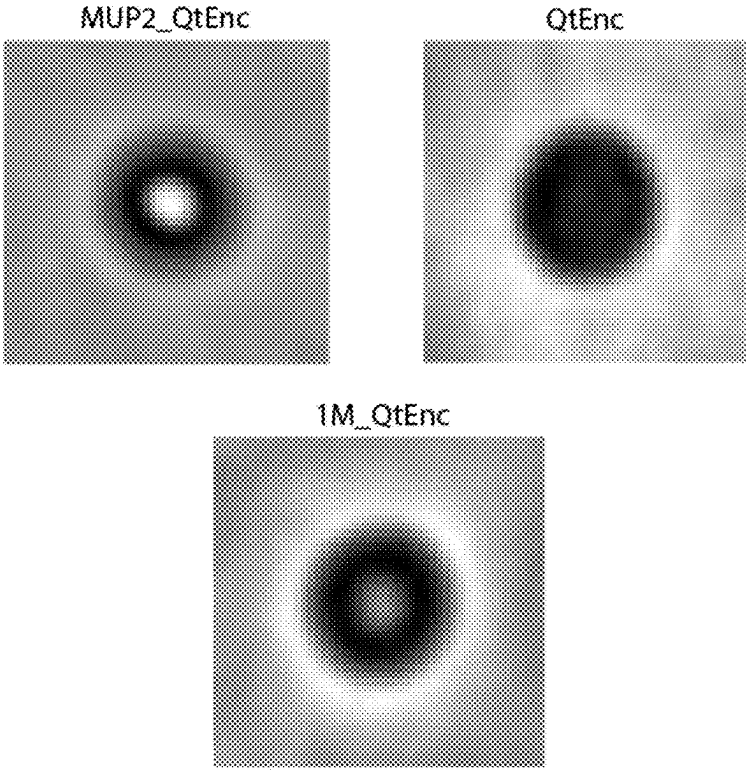


Figure 22 | Lipid-binding proteins as contrast-generating units (CGUs)

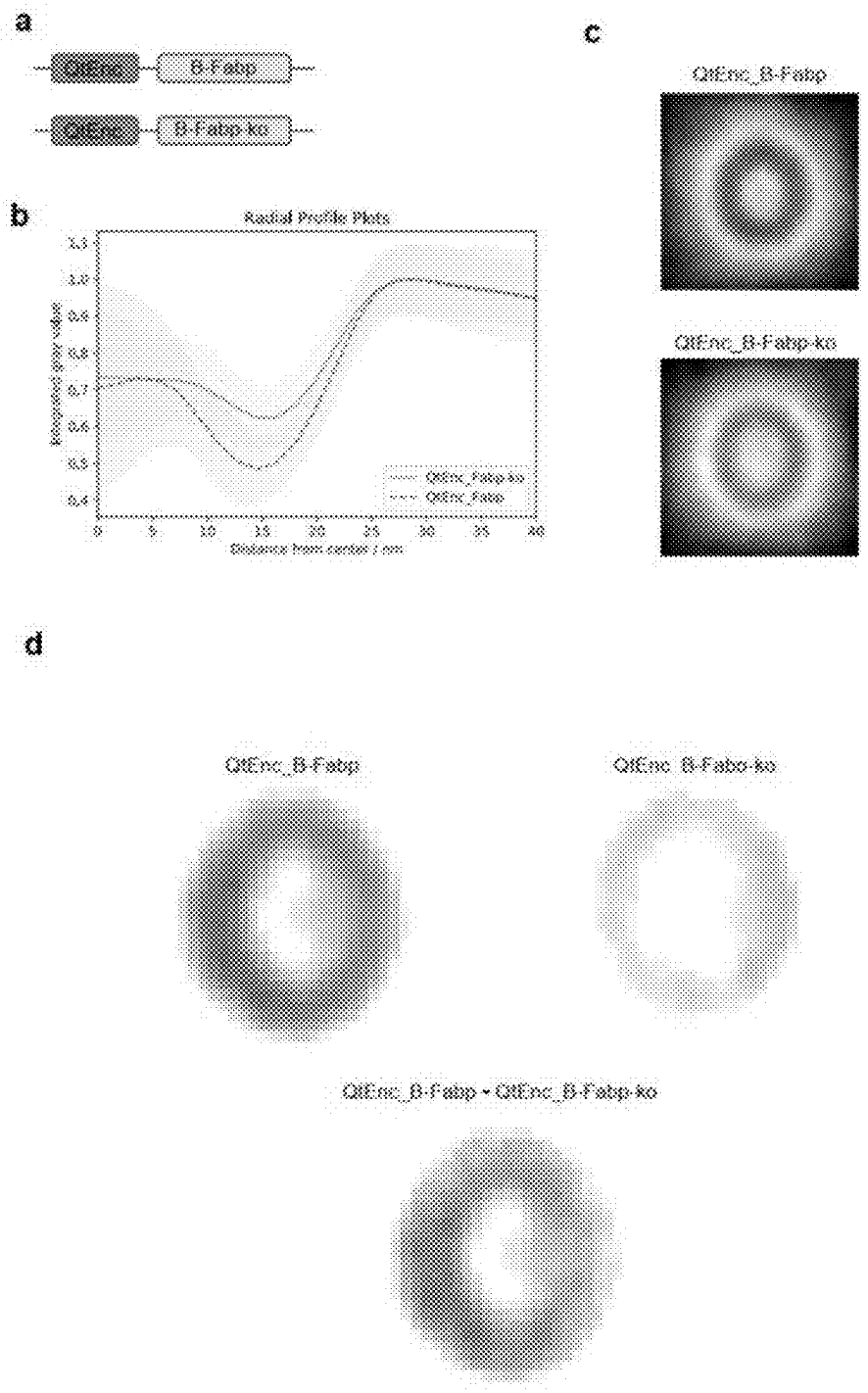
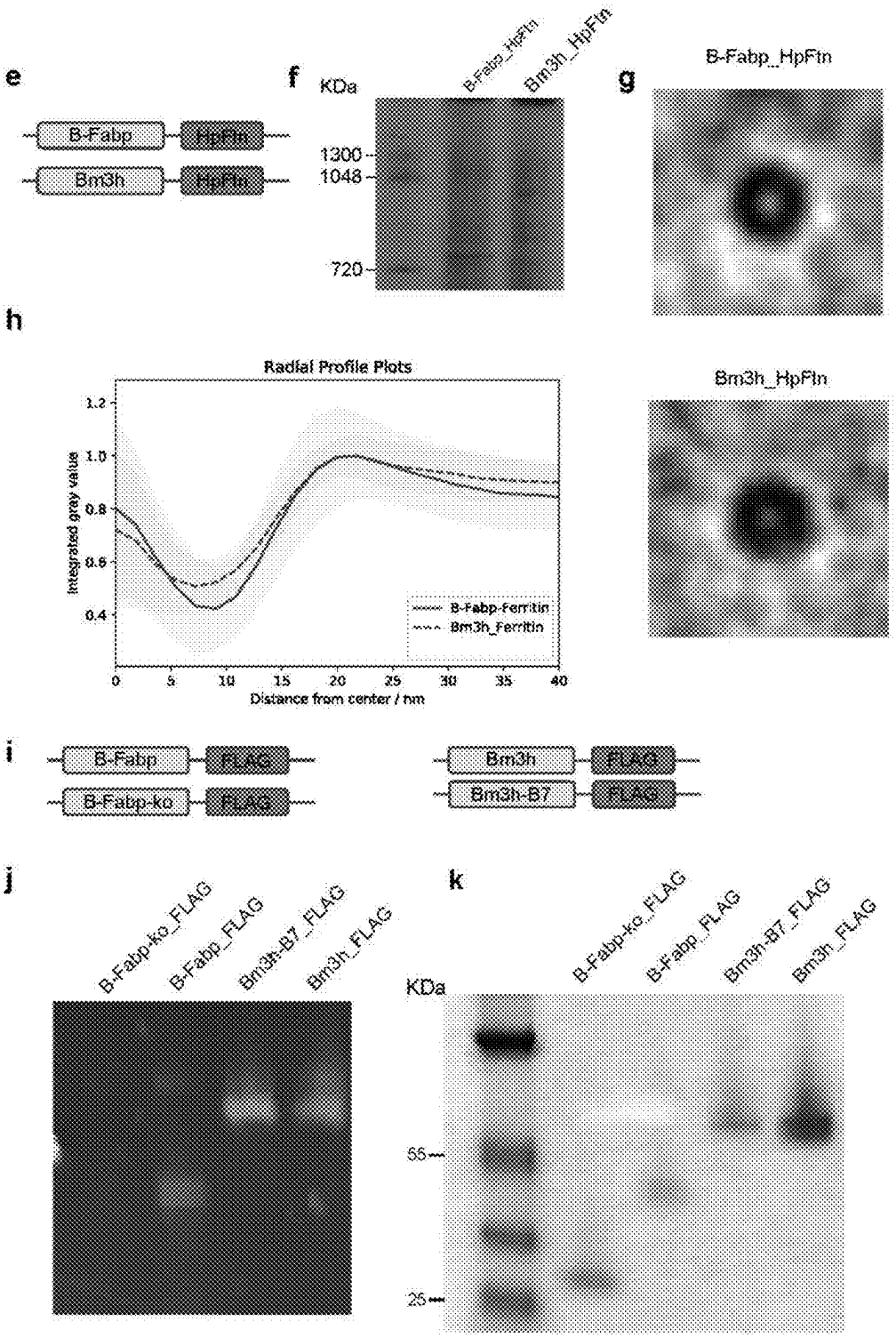


Figure 22 continued | Lipid-binding proteins as contrast-generating units (CGUs)



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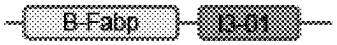
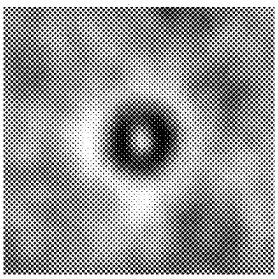


B-Fabp_I3-01



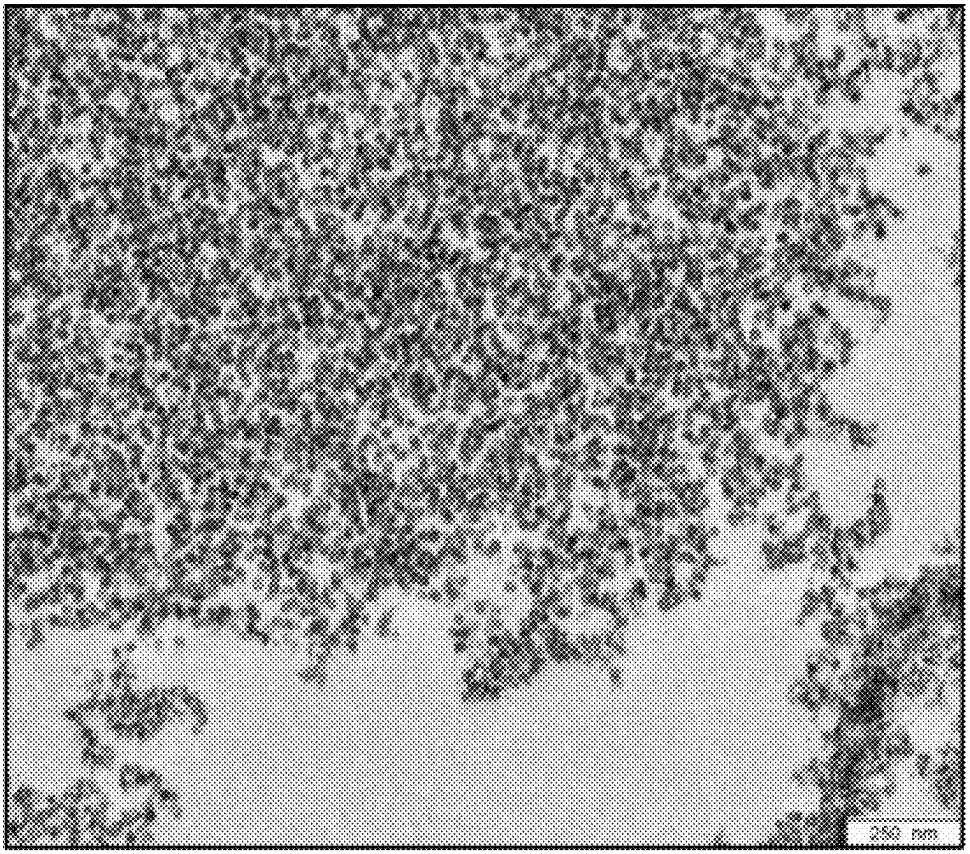


Figure 23 | Fluorescent encapsulins as high-contrast markers for CLEM.

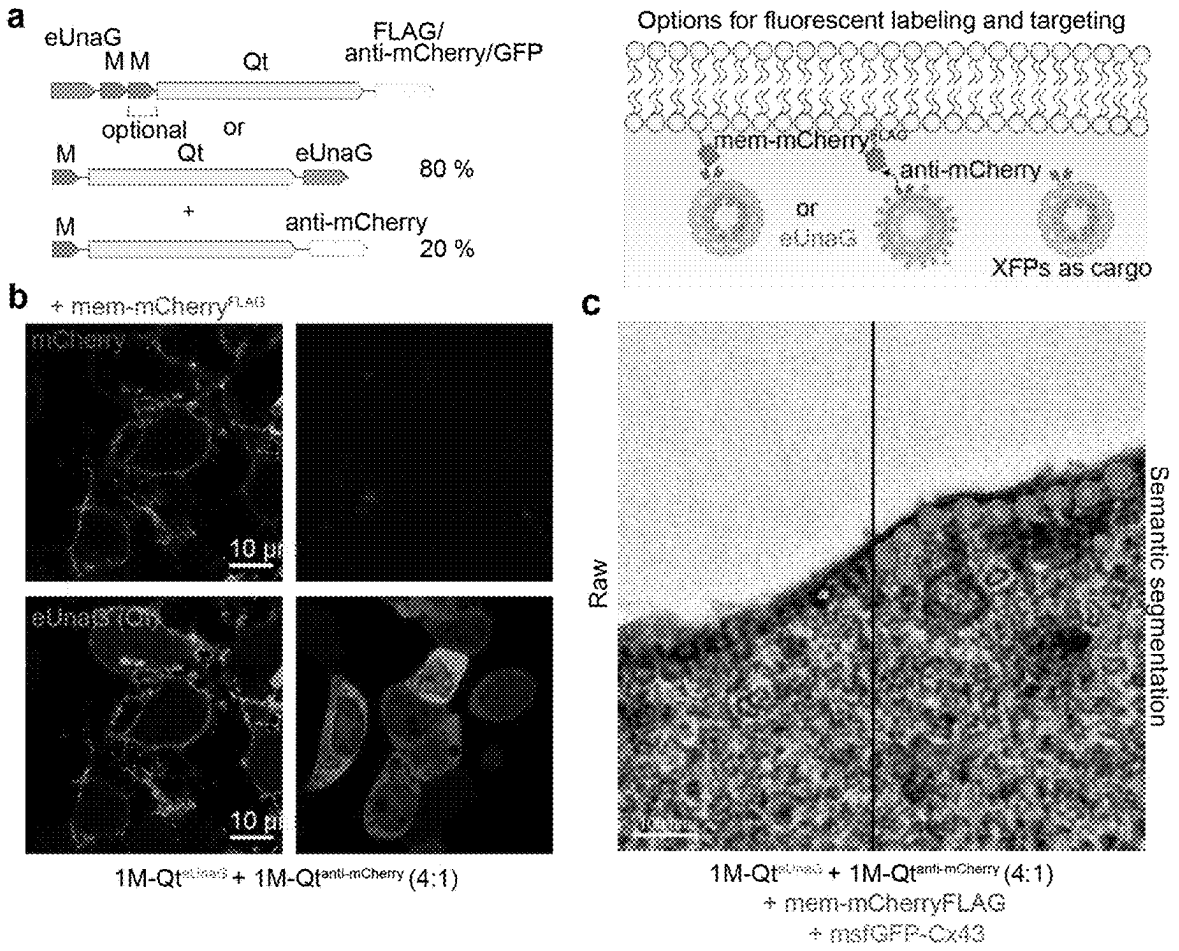


Figure 23 continued | Fluorescent encapsulins as high-contrast markers for CLEM.

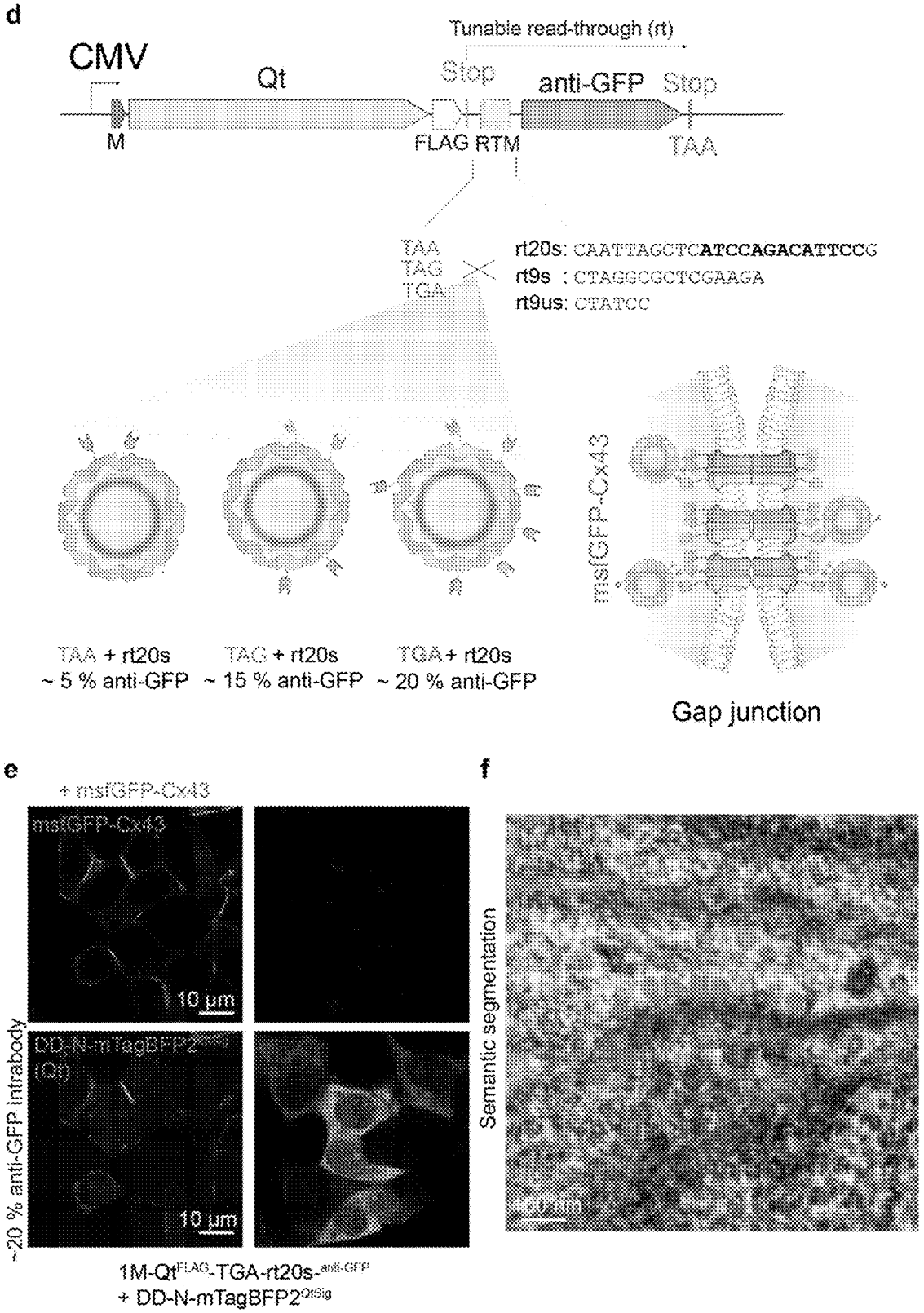
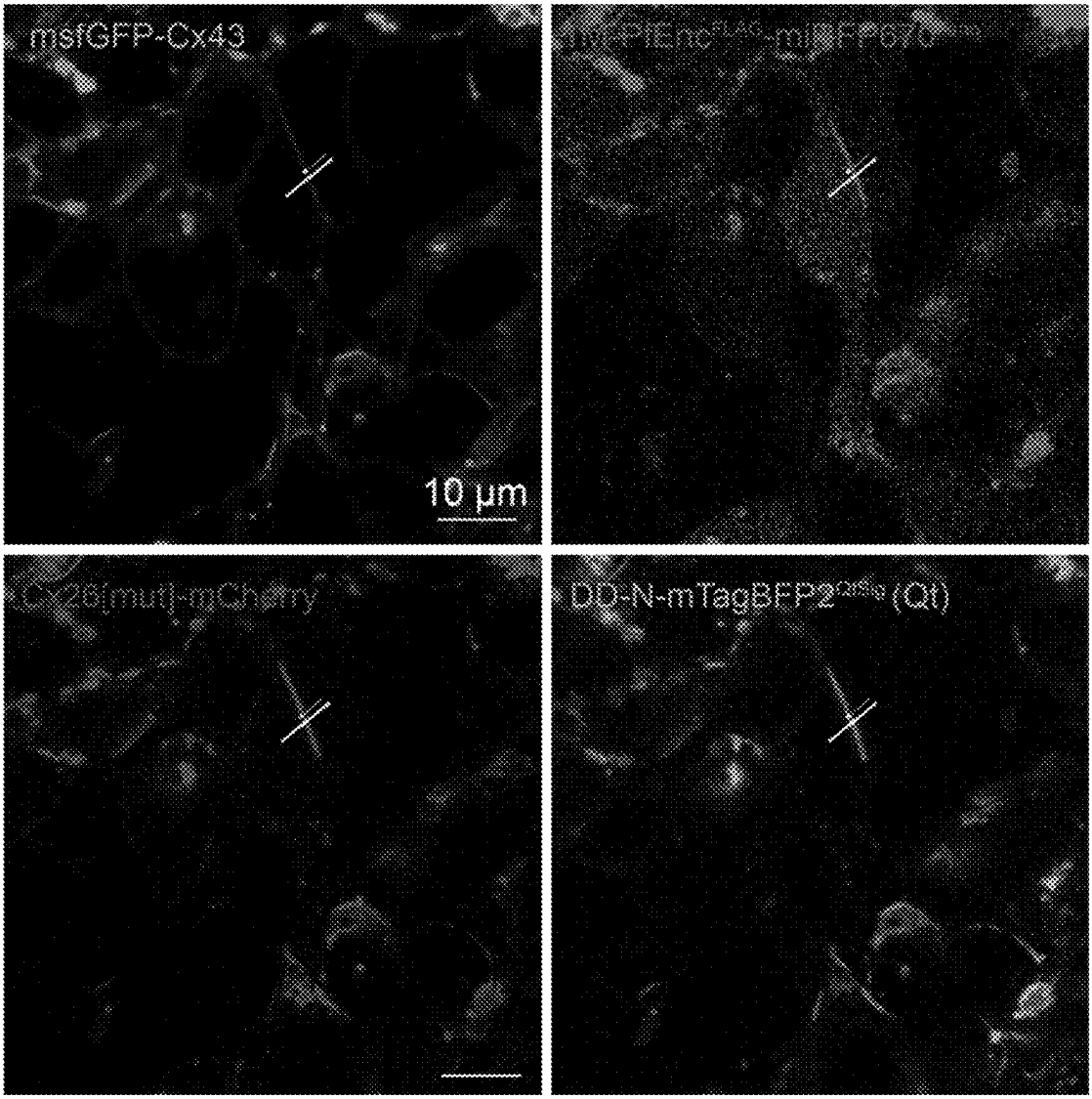


Figure 23 continued | Fluorescent encapsulins as high-contrast markers for CLEM.

g



connexin targets EMcapsulins

1M-Qt$^{anti\text{-}mCherry}$ + 1M-Qt^{FLAG}+ DD-N-mTagBFP2^{QtSi} + 1M-PfEnc^{FLAG}-miRFP670nano + 1 M-PfEnc^{FLAG}-anti-GFP + msfGFP-Cx43 + Cx26[mut]-mCherry

Figure 24 | Bioconjugation tags for exogenous synthetic fluorophores.

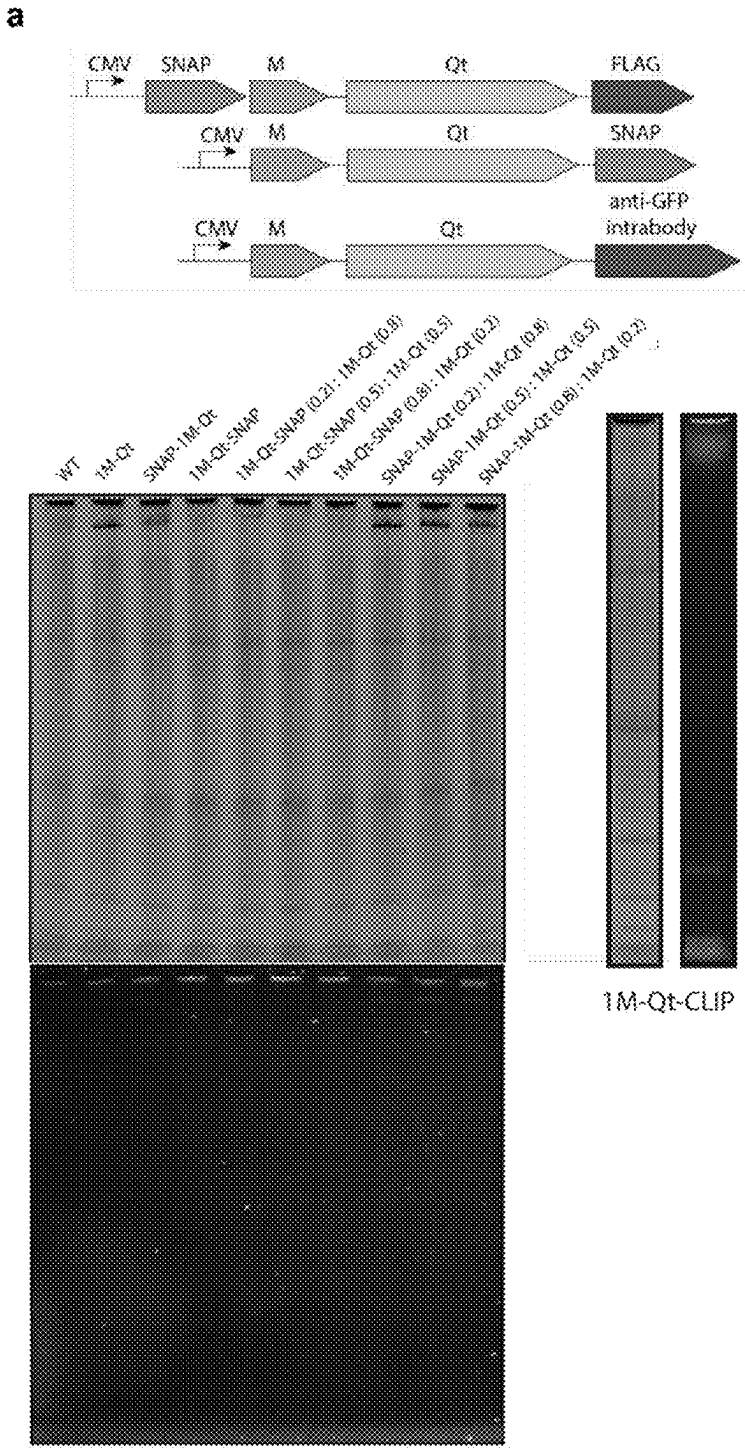


Figure 24 - continued | Bioconjugation tags for exogenous synthetic fluorophores.

b

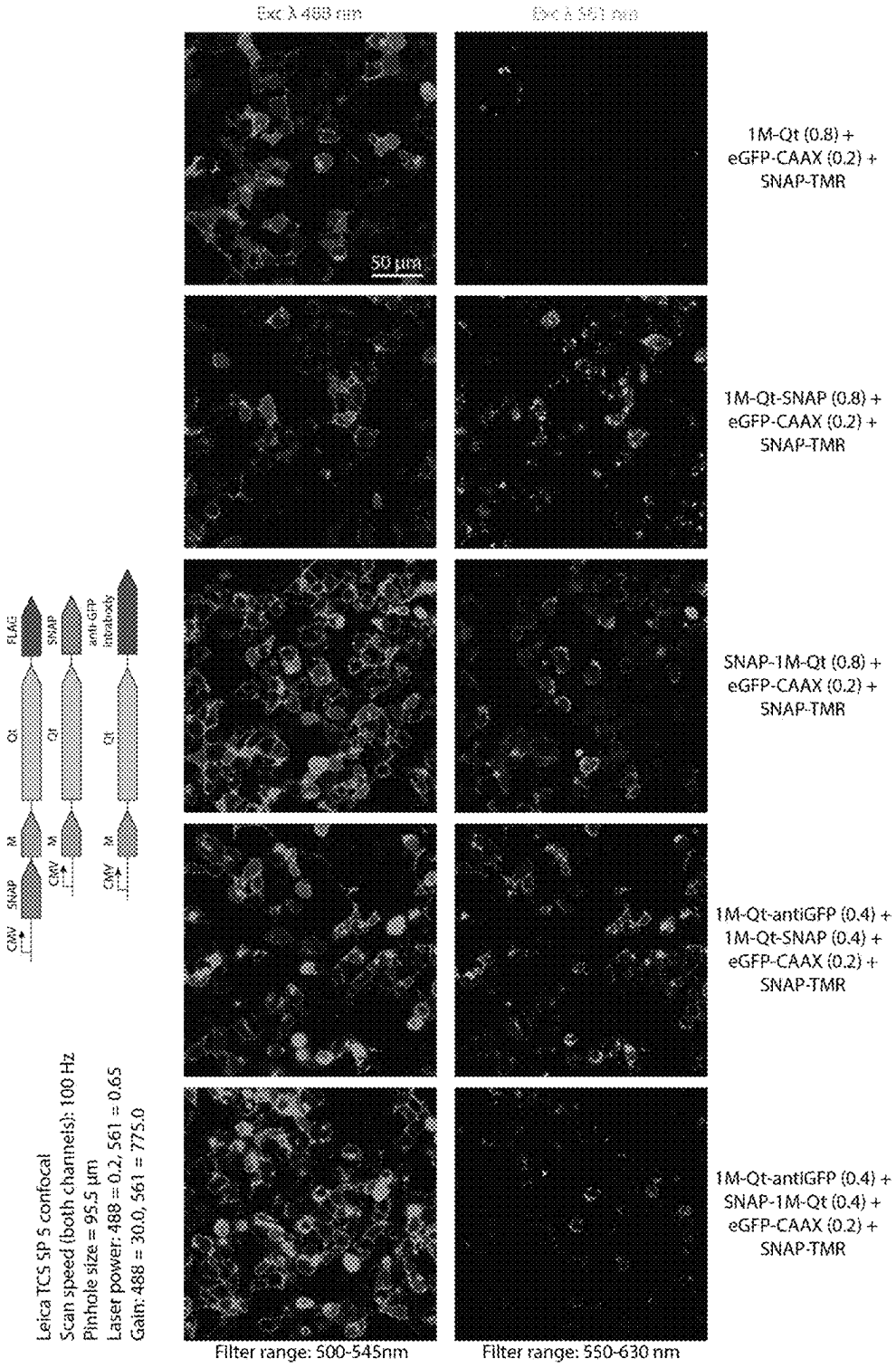


Figure 24 - continued | Bioconjugation tags for exogenous synthetic fluorophores.

C

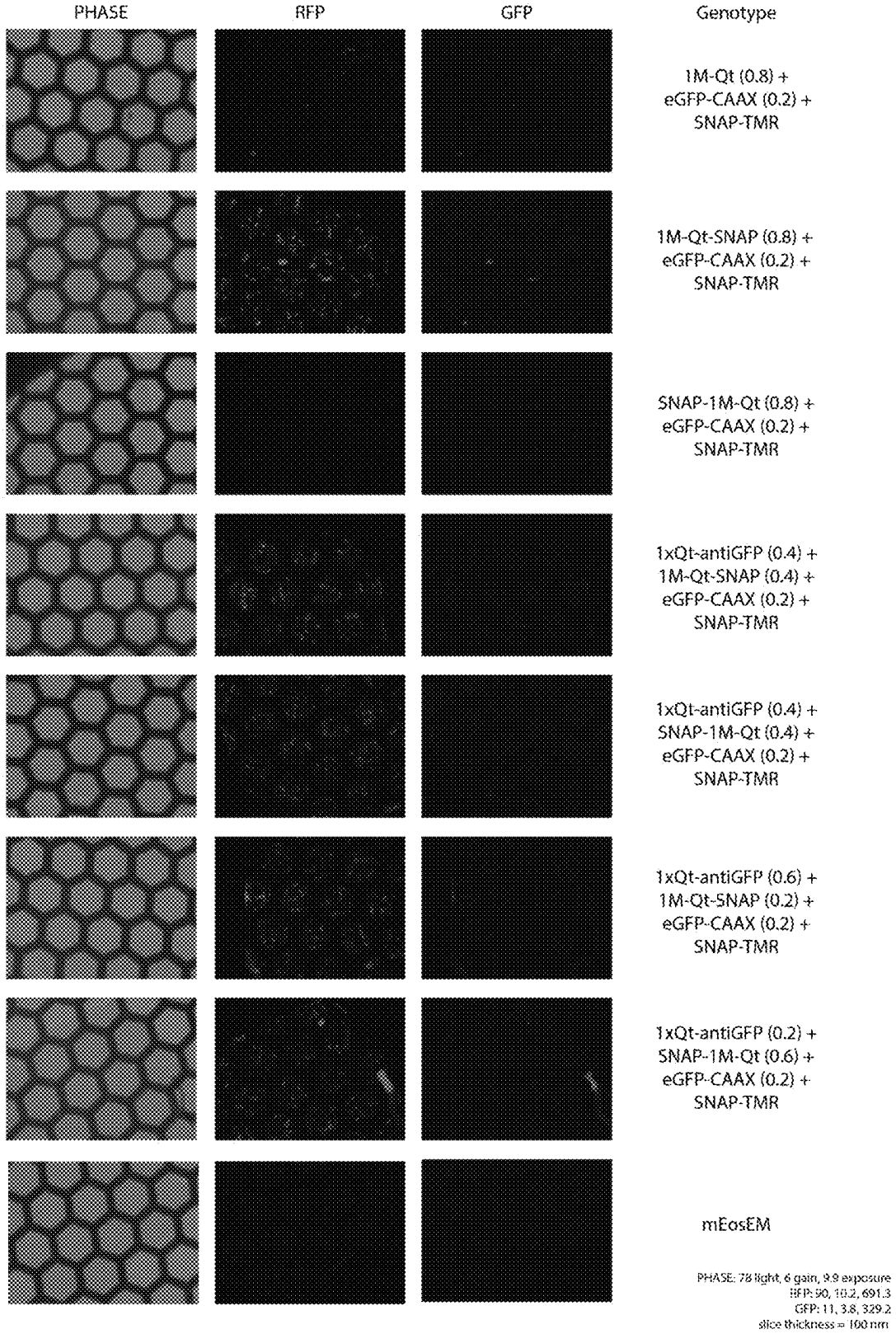


Figure 25 | Bioconjugation tags for exogenous synthetic fluorophores; fixation stable fluorescence contrast

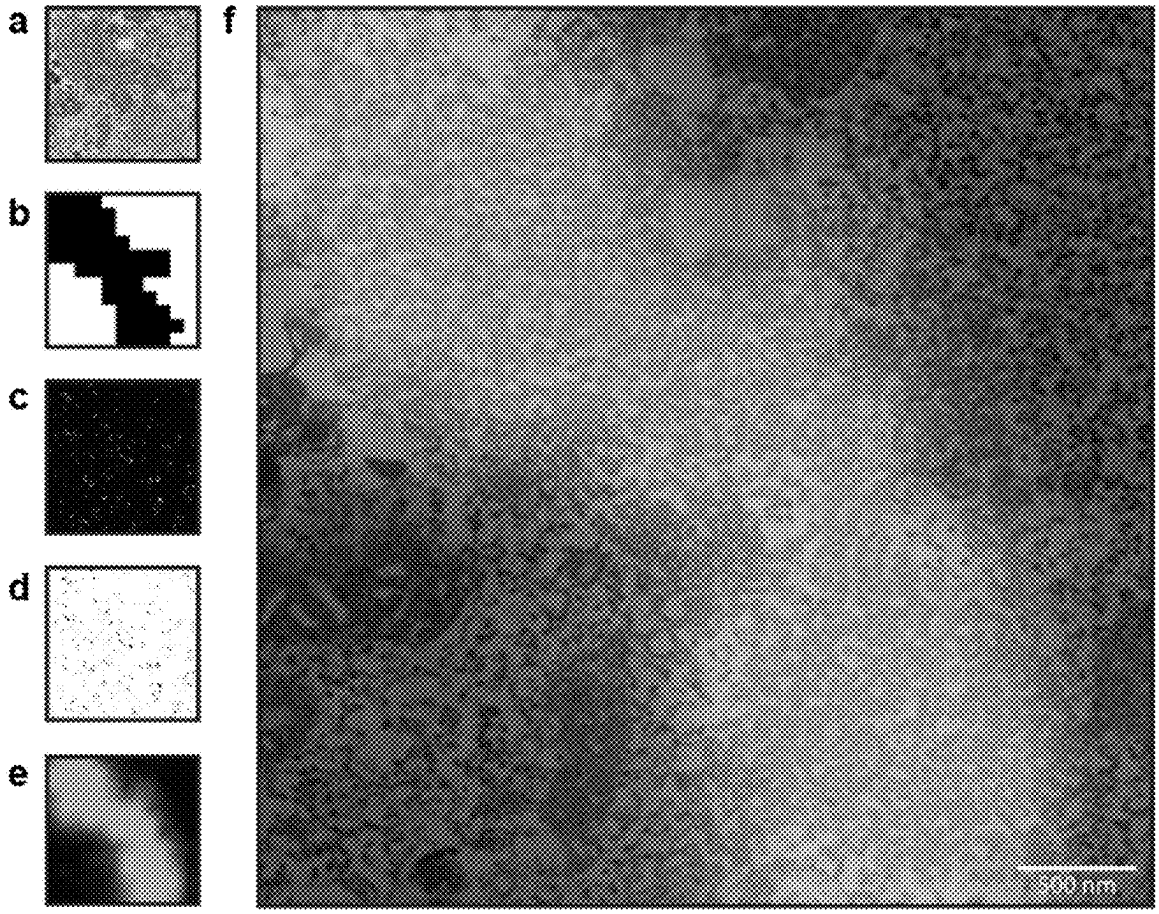
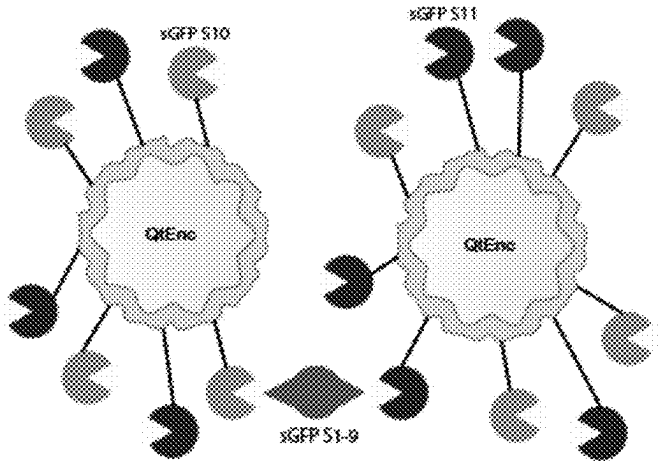


Figure 26 | Bimolecular Fluorescence Complementation (BiFC).

a



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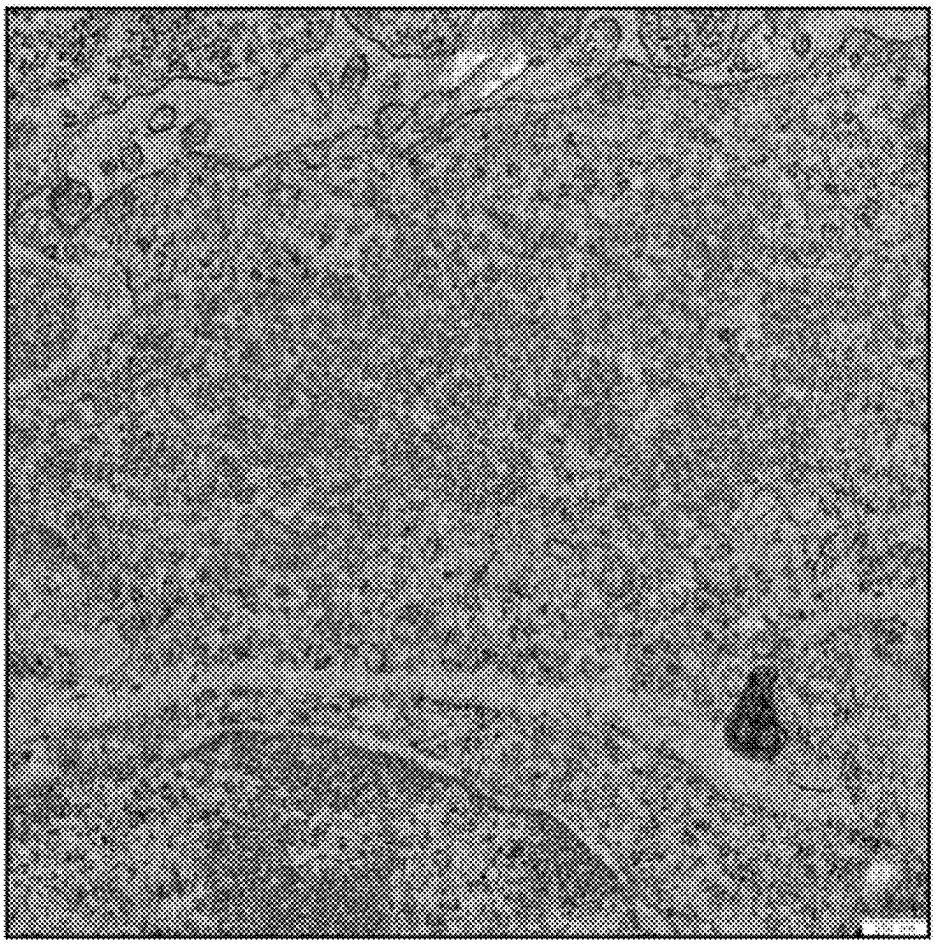
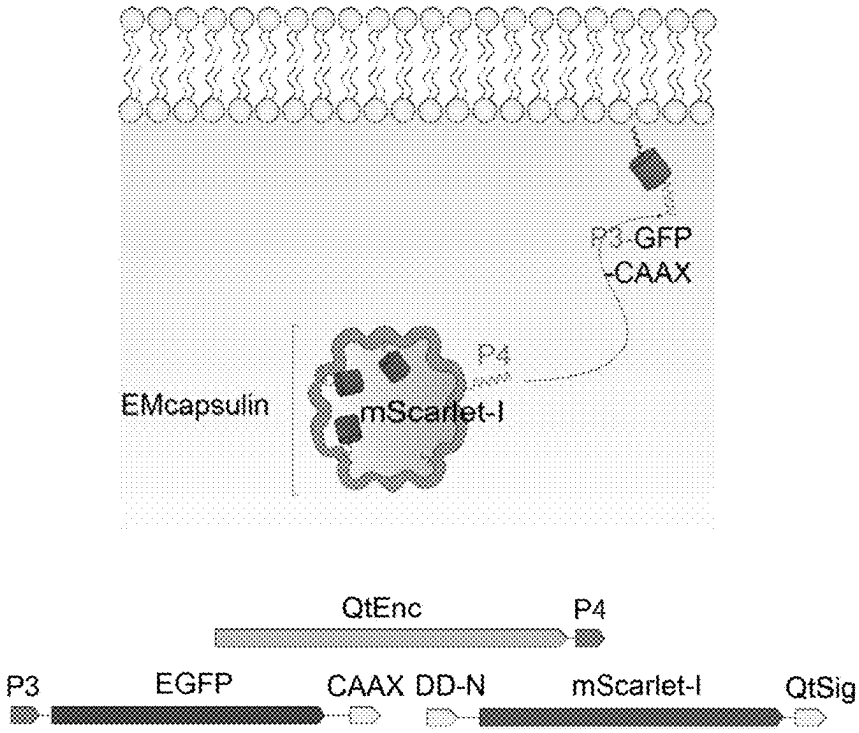


Figure 27 | Targeting of CLEM-compatible Enc variants via coiled-coil pairs.

a



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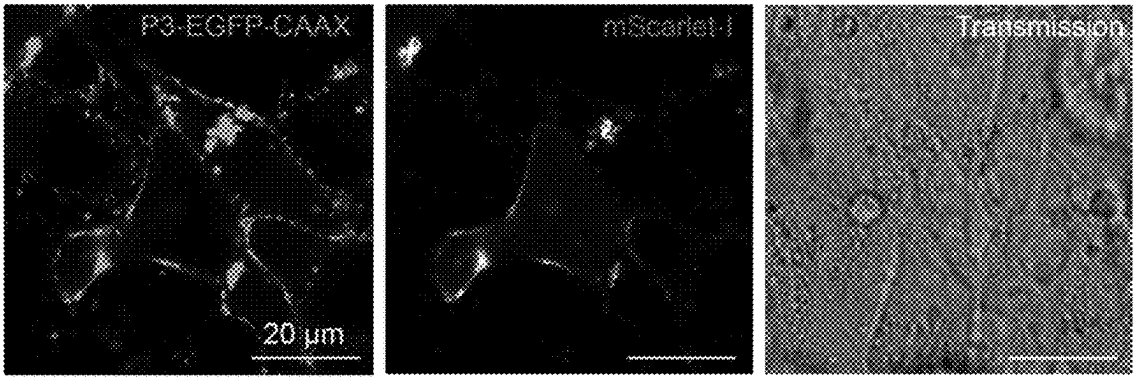


Figure 28 | Multiplexed EM contrast with different numbers of concatenated metallothioneins (as CGU) and encapsulins of different diameters (as structural elements)

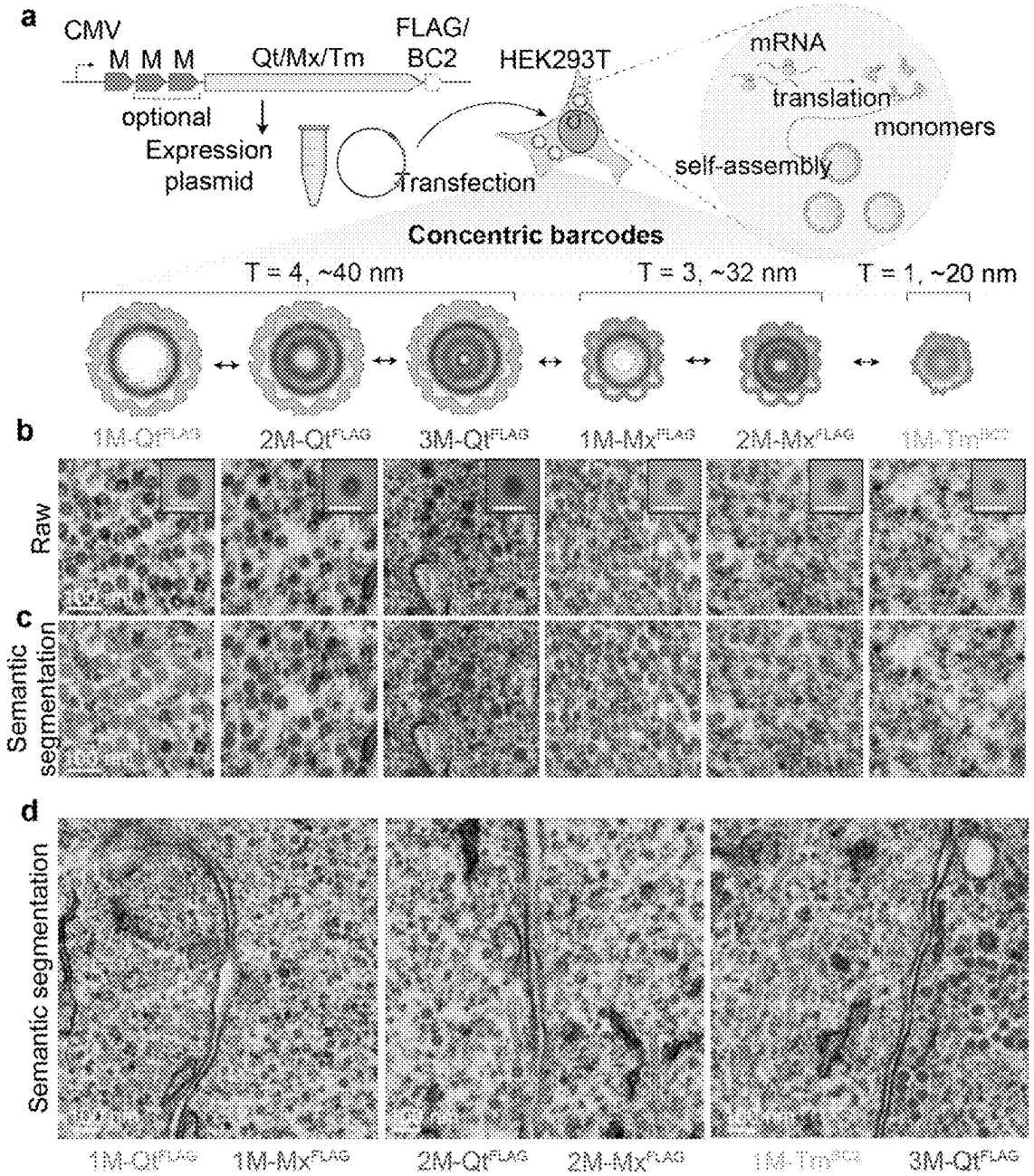


Figure 29 | In vivo expression of several encapsulins (as structural elements) and metallothioneins as contrast generating units (CGU) to generate concentric barcodes in TEM in vivo in Drosophila brain.

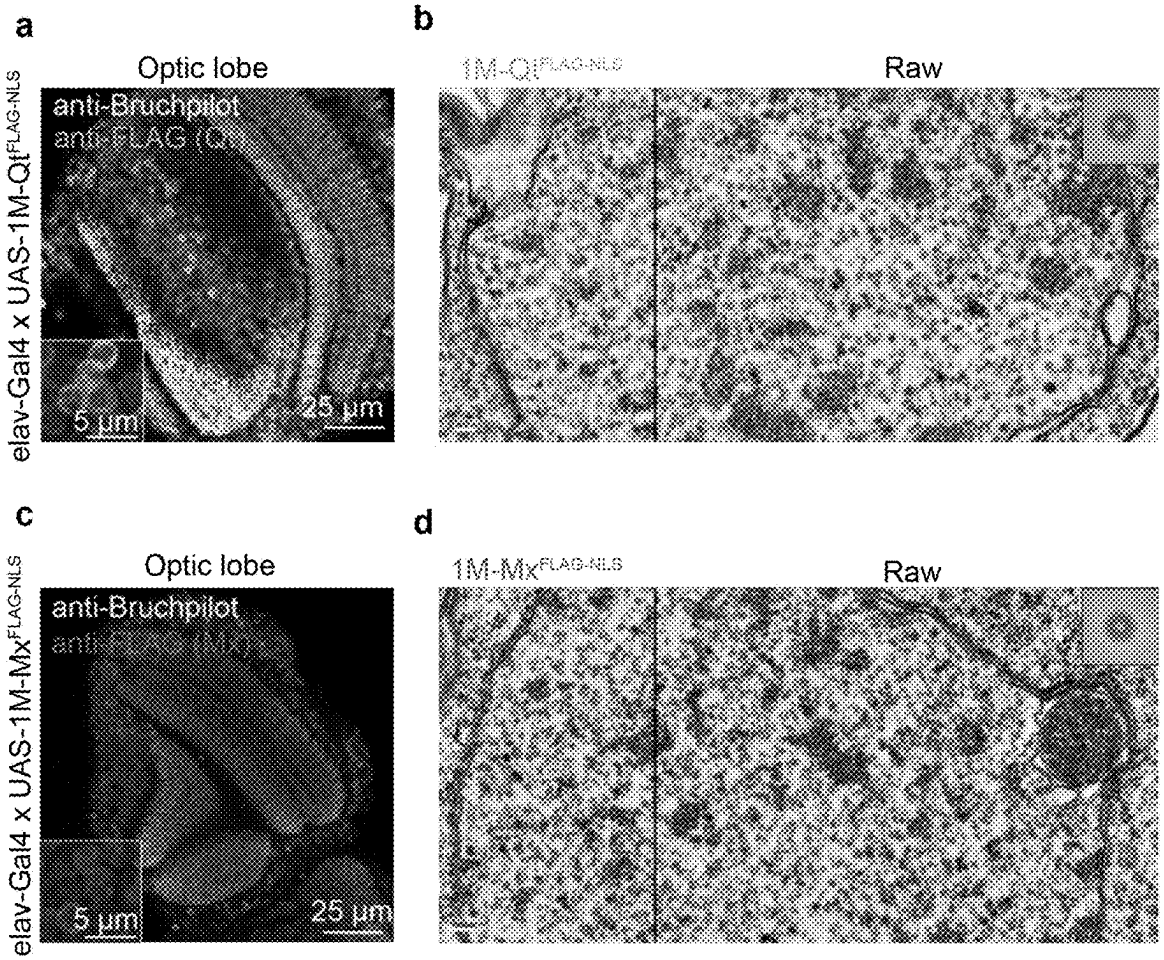


Figure 29 continued | *In vivo* expression of several encapsulins (as structural elements) and metallothioneins as contrast generating units (CGU) to generate concentric barcodes in TEM *in vivo* in *Drosophila* brain.

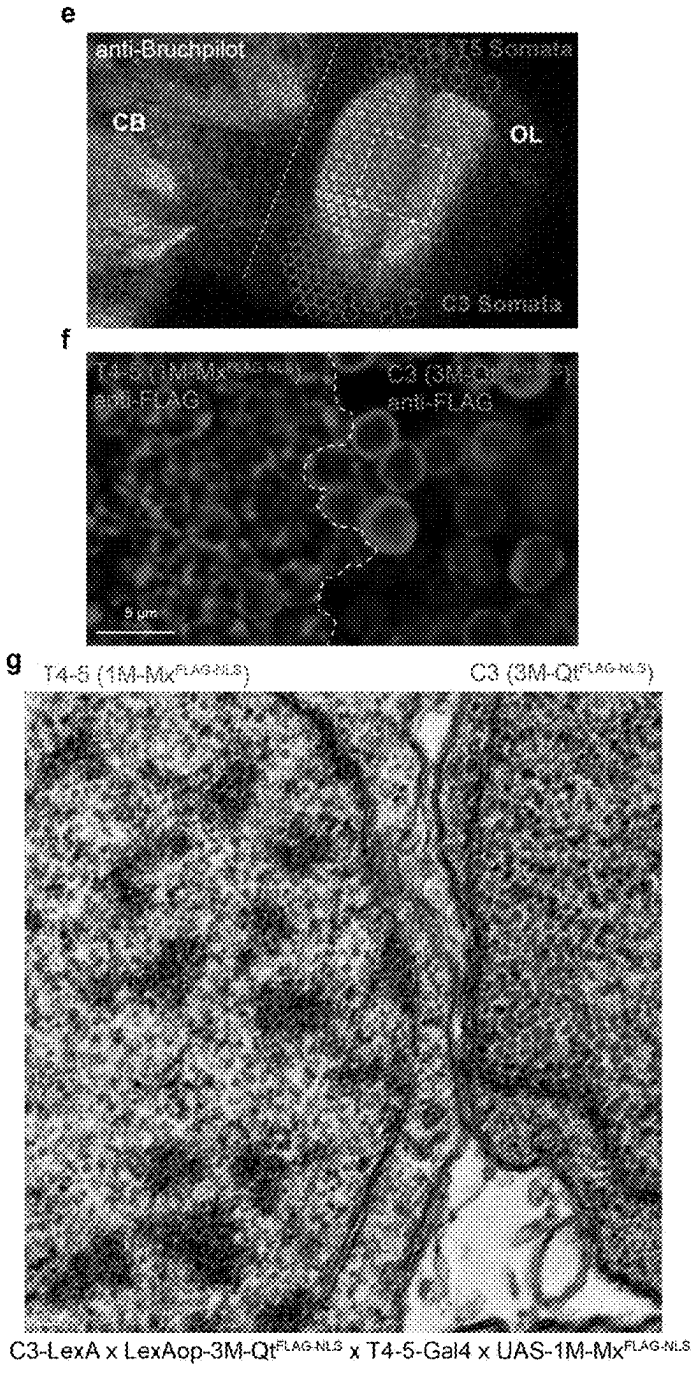


Figure 30 | Adeno-associated virus-encoded MT3-encapsulin fusion as genetically encoded EM marker in vivo in mouse brain.

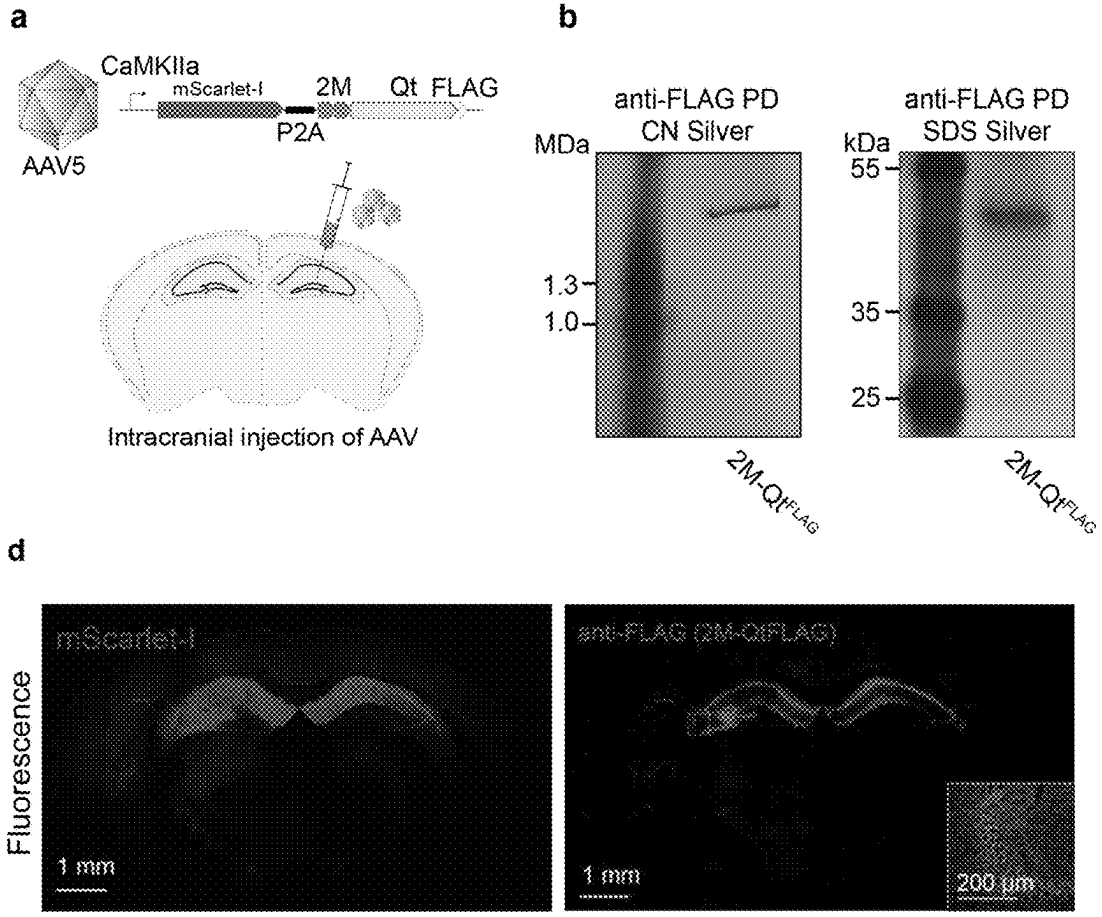


Figure 30 continued | Adeno-associated virus-encoded MT3-encapsulin fusion as genetically encoded EM marker in vivo in mouse brain.

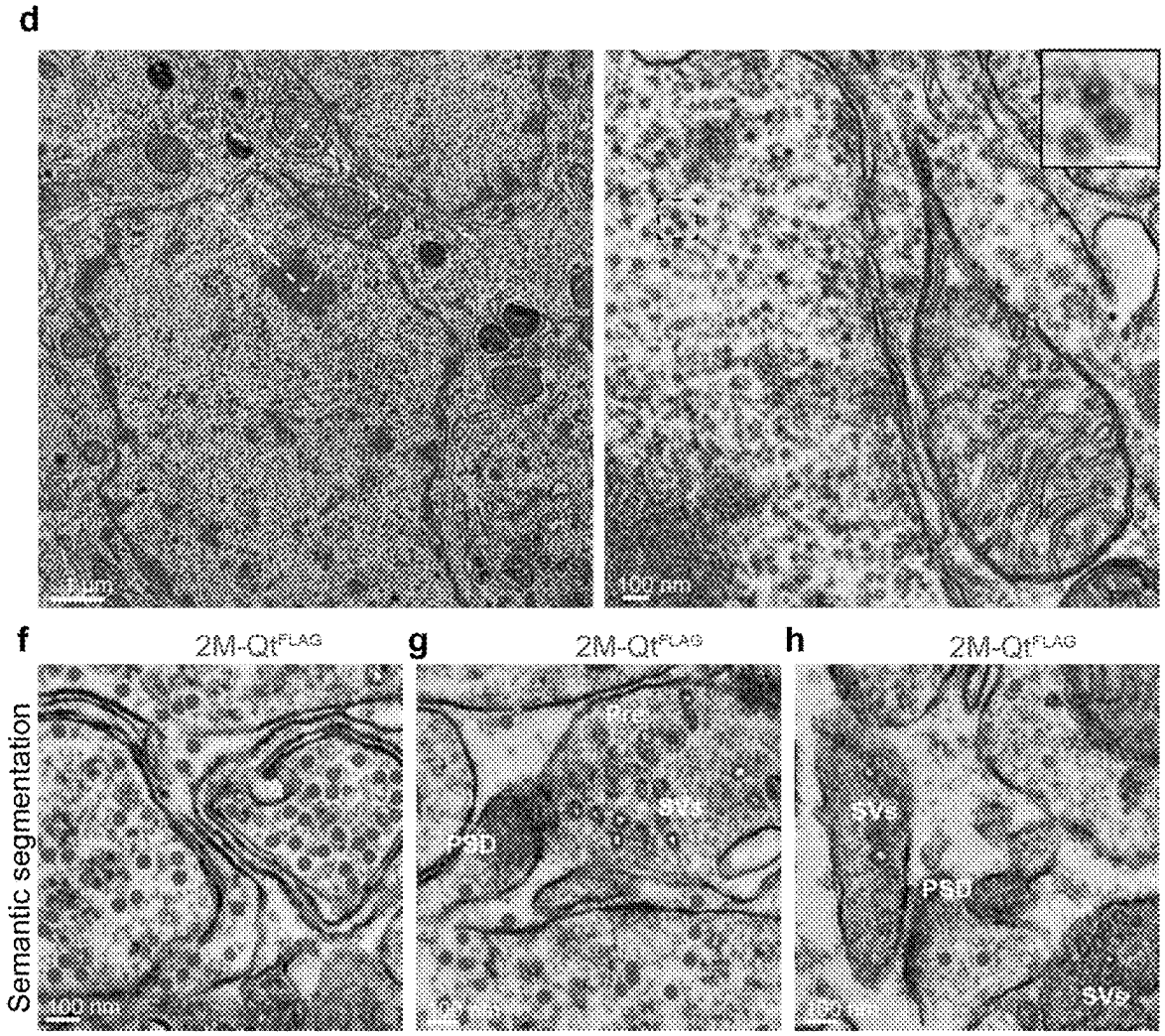


Figure 31 | Stabilized fluorescent RNA cargo targeted to self-assembling vaults as structural elements

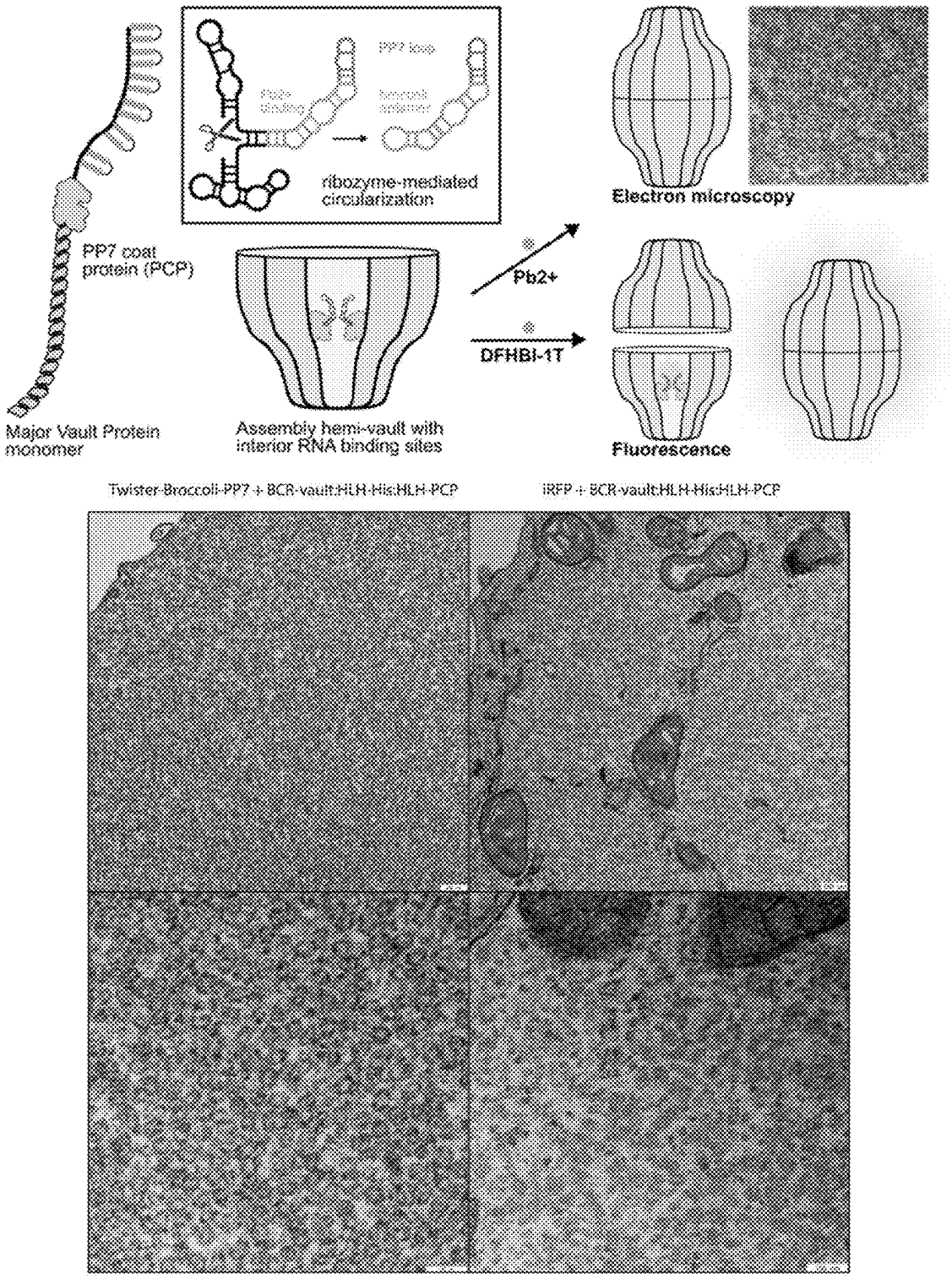


Figure 32 | Mono-to-polyvalent hubs as structural elements

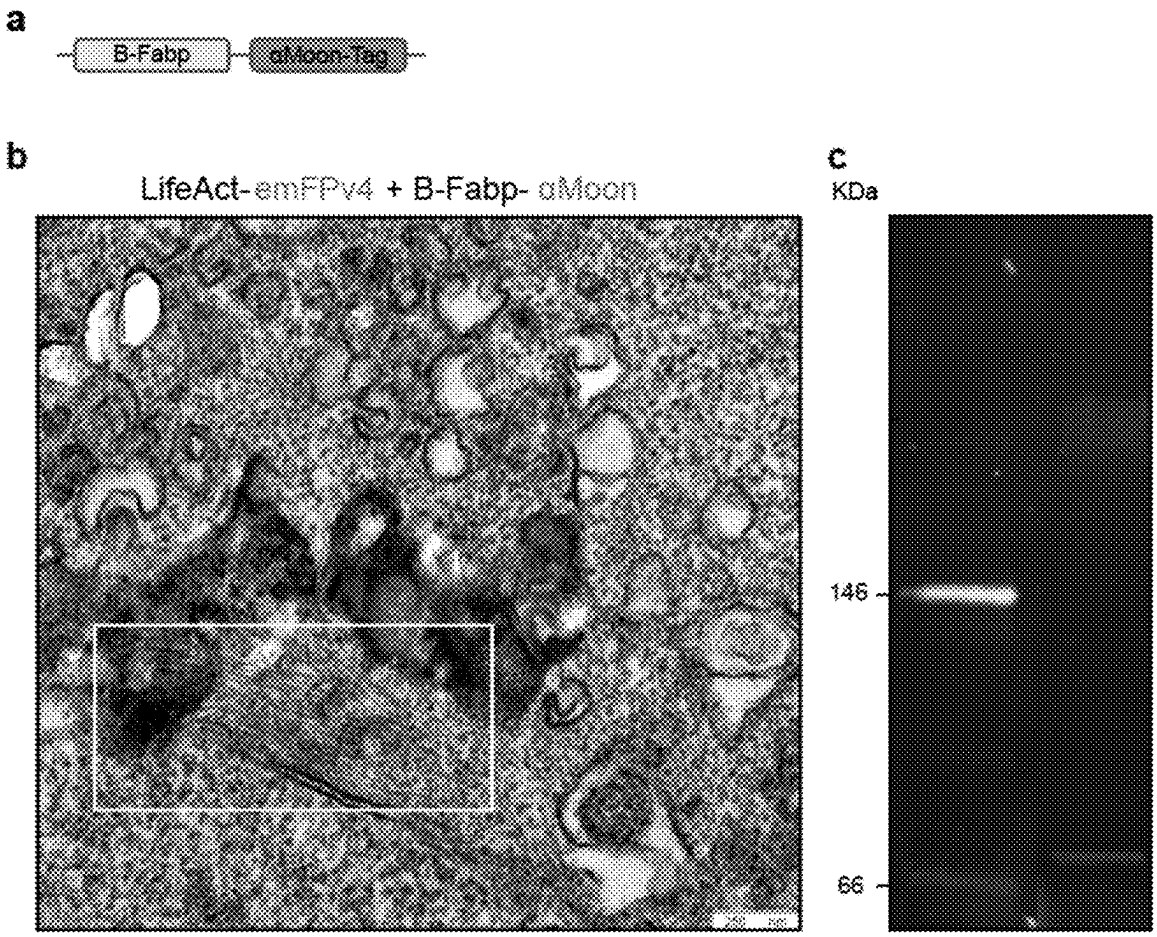


Figure 33 | Stoichiometry control.

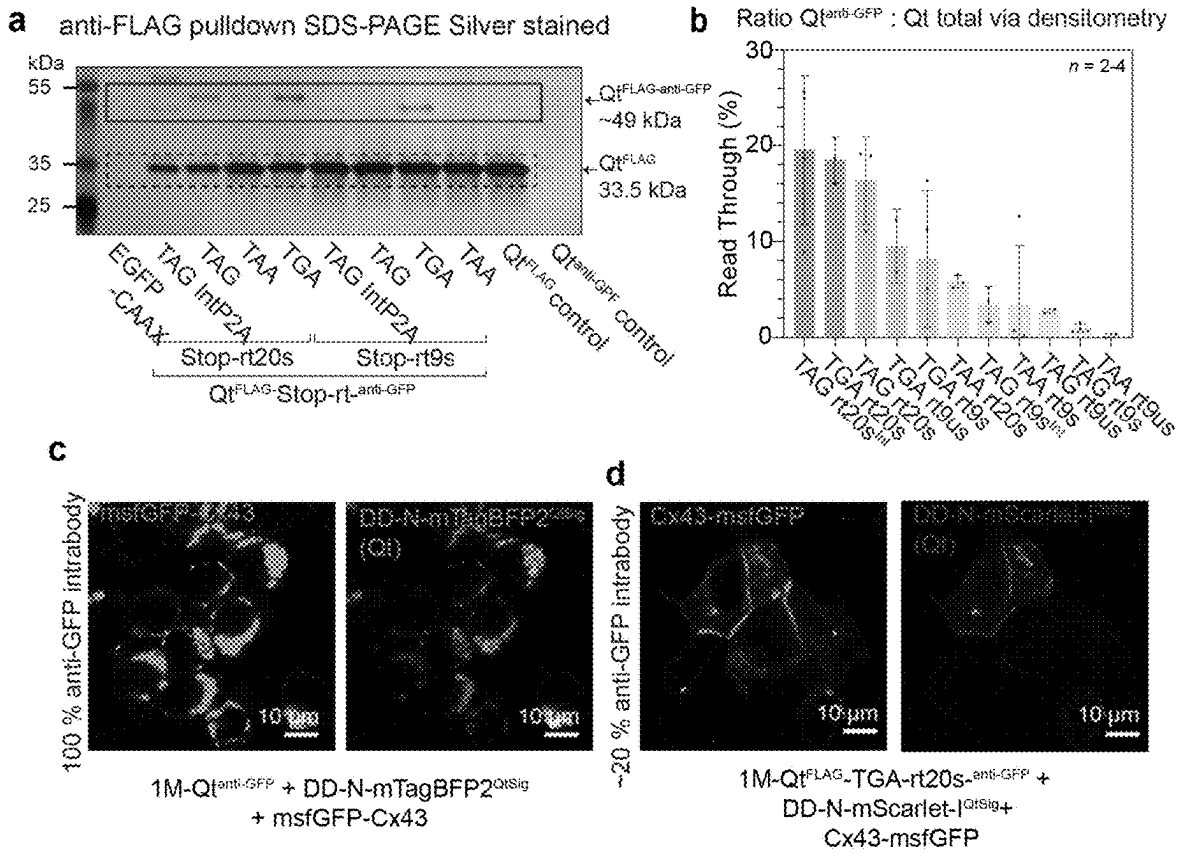


Figure 34 | Multiplexed patterning using hetero-bifunctional SasG concatemers and encapsulins.

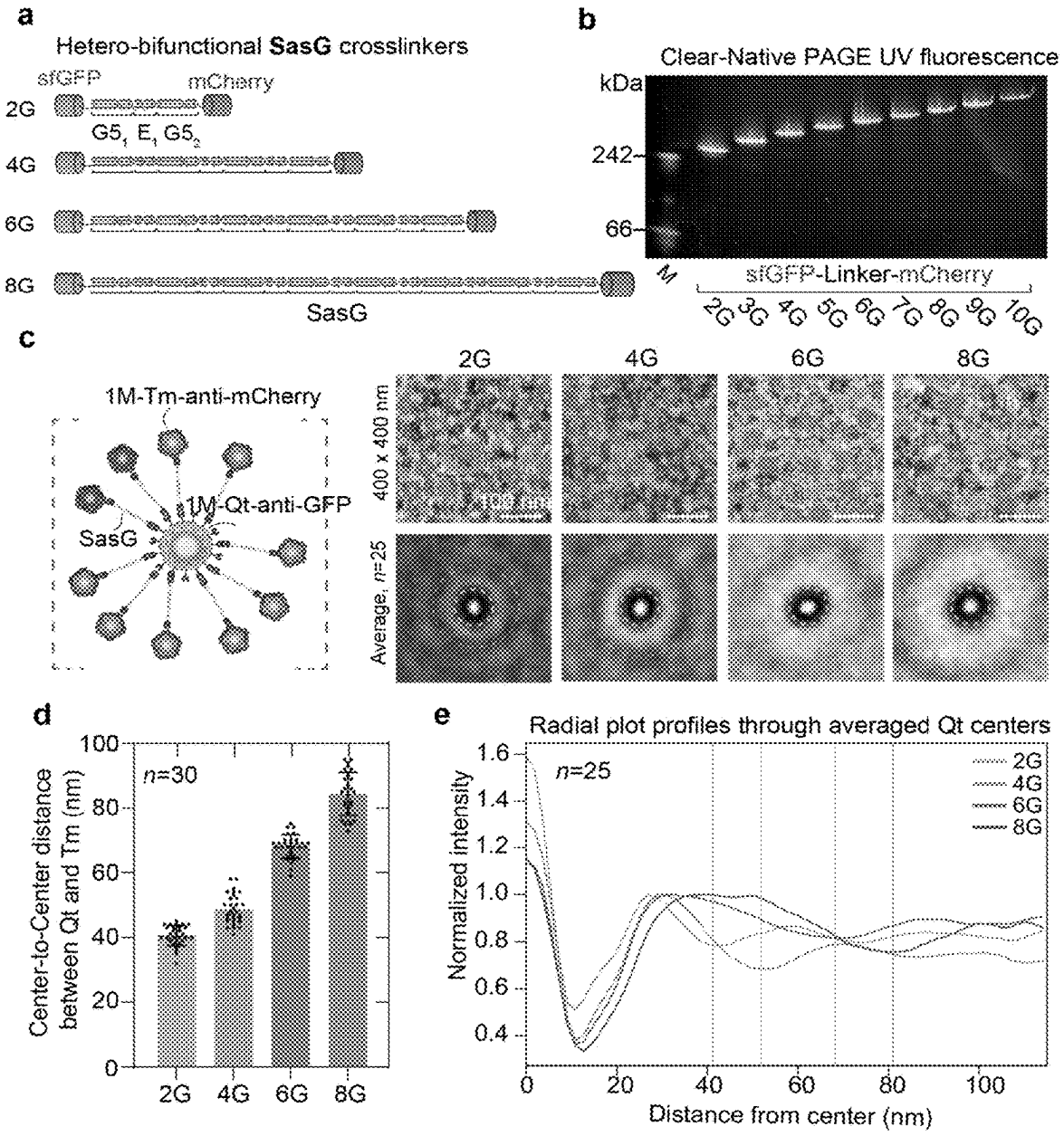


Figure 35 | Geometric sensing of Calcium via aggregation

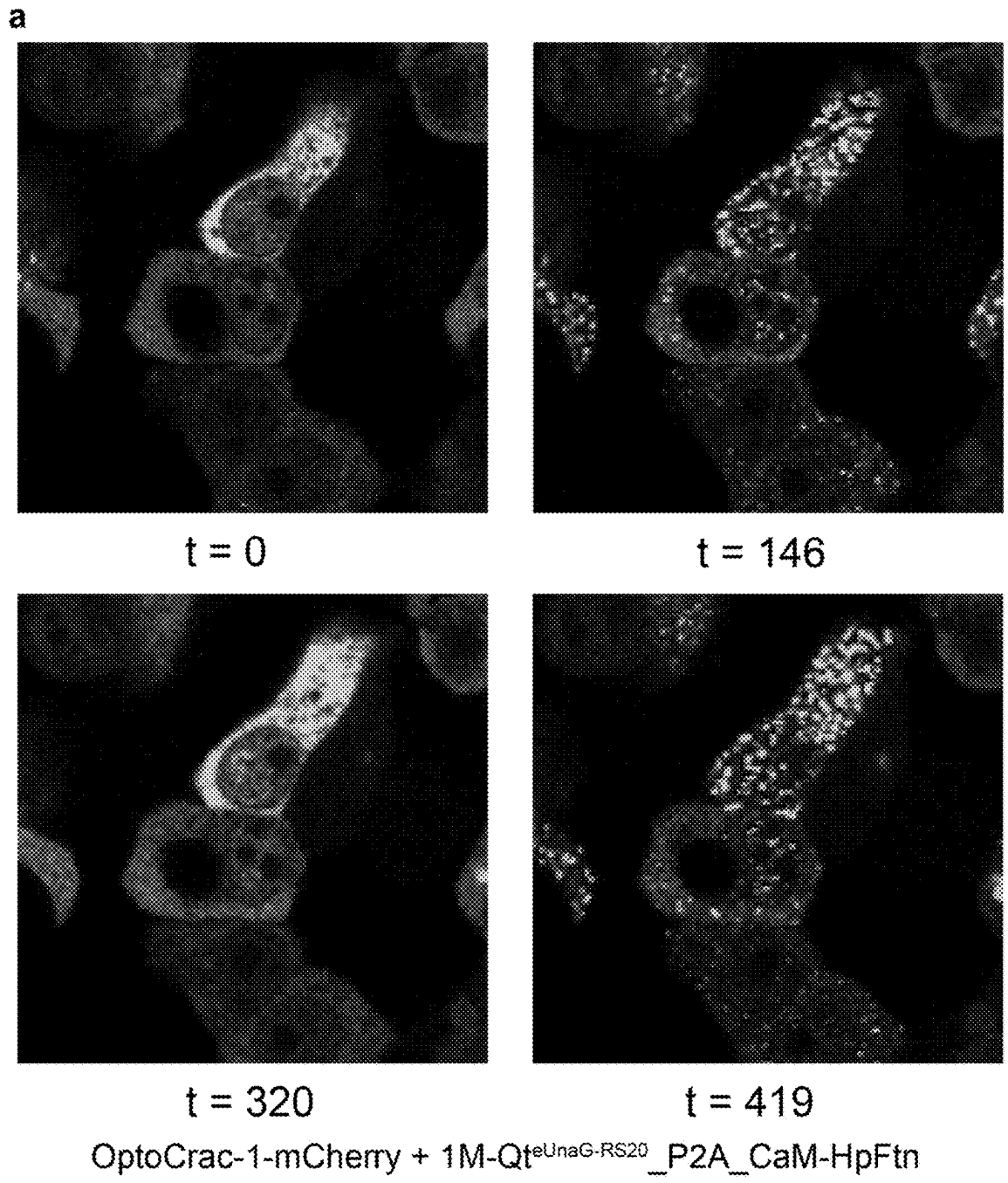


Figure 36 | Protein Designs for CLEM-GECI.

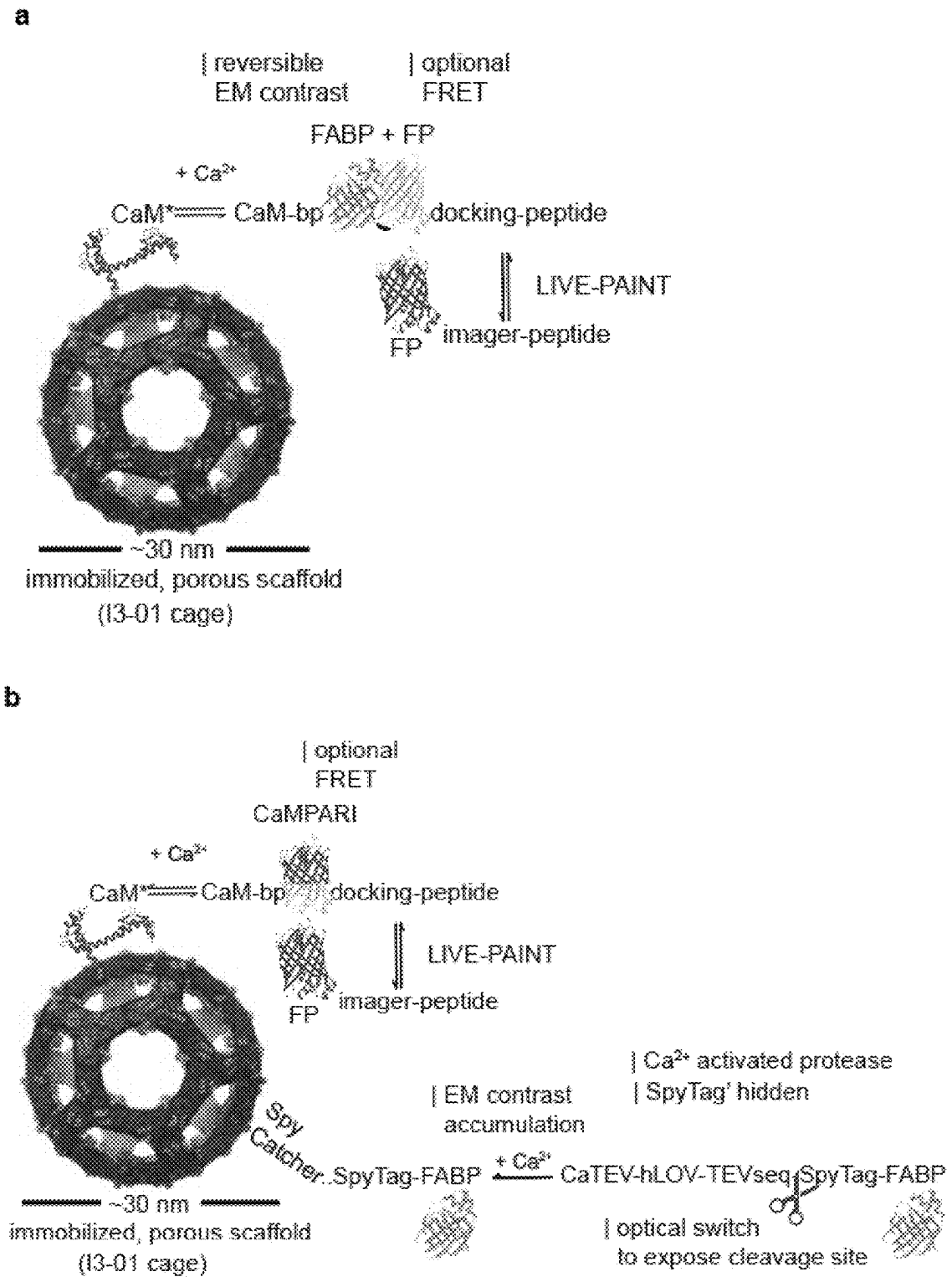


Figure 37 | Correlative bioluminescence-EM imaging.

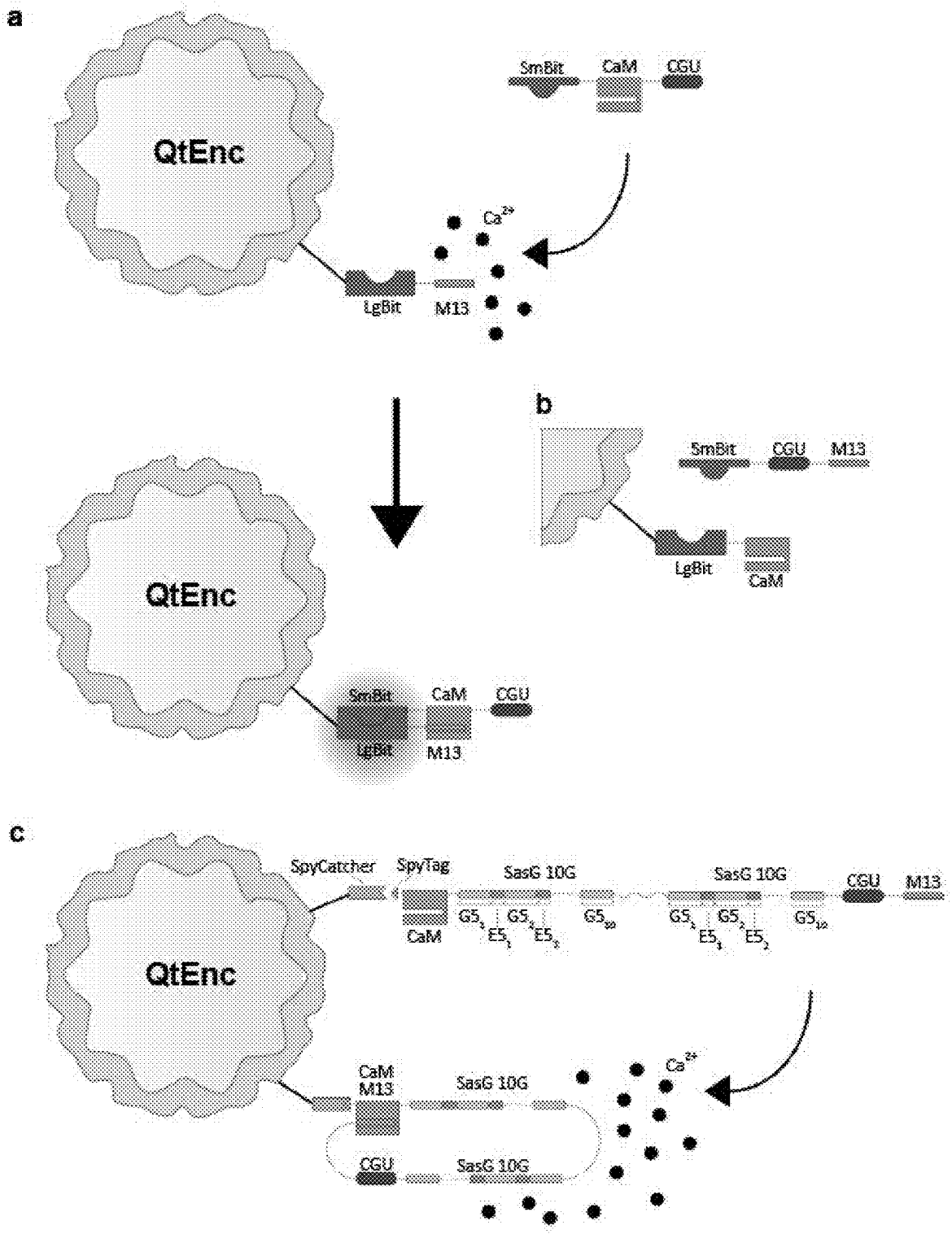


Figure 38 | Contrast from encapsulins as structural elements and metallothioneins as contrast-generating units in SEM and FIB-SEM of *Drosophila* neurons.

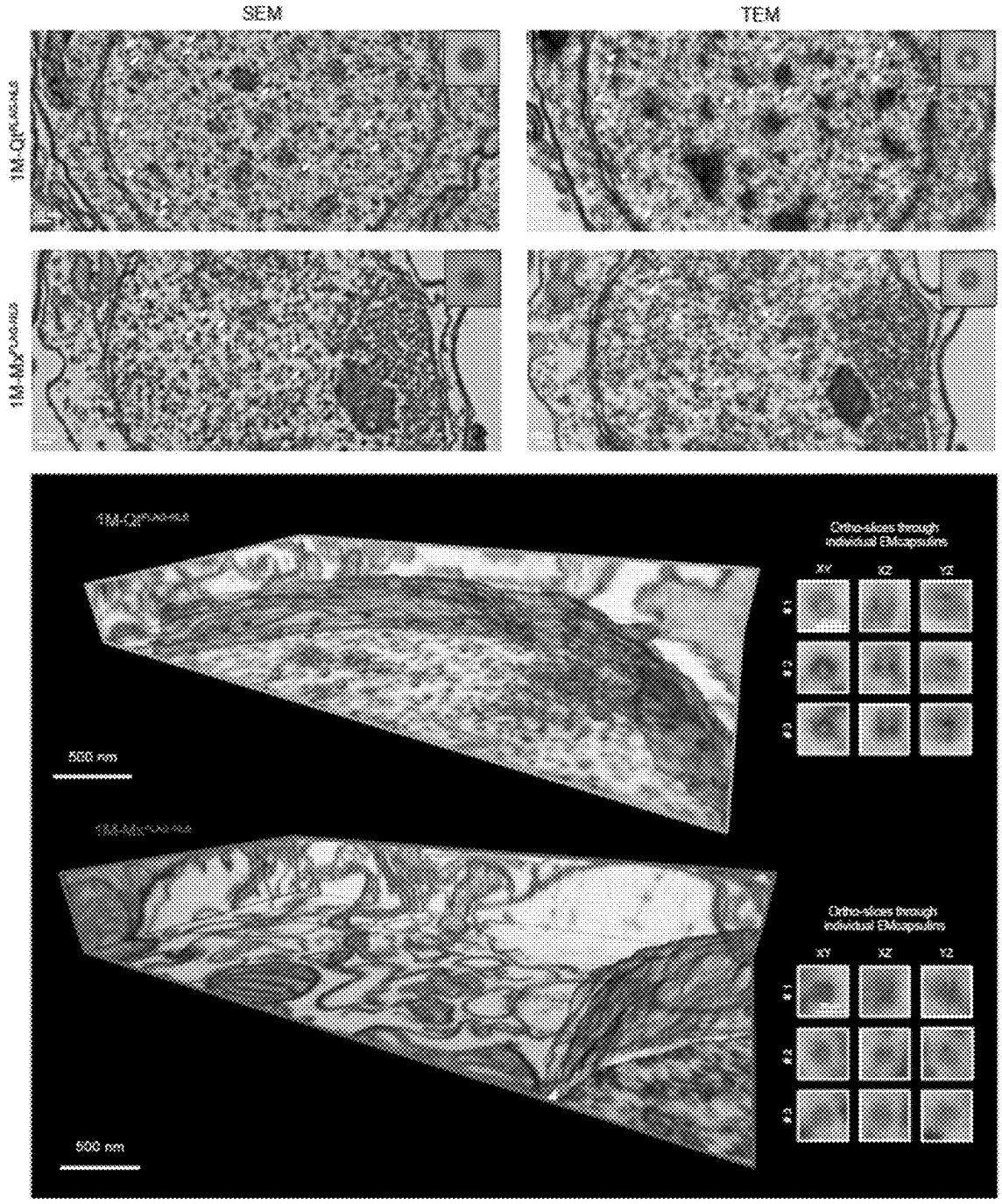


Figure 39 | High-res TEM micrographs of encapsulation-metallothioneins expressed in HEK293T.

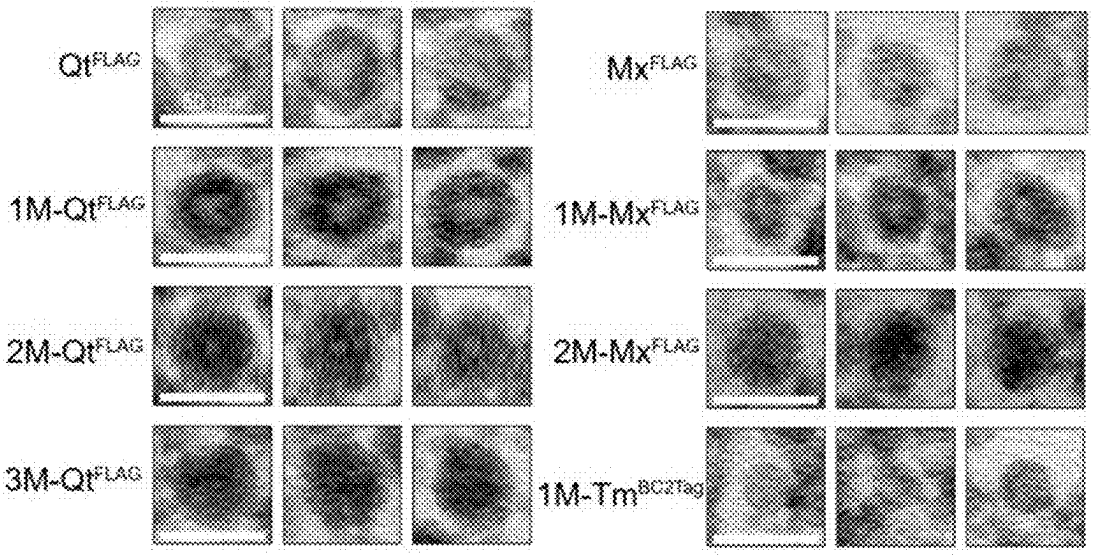
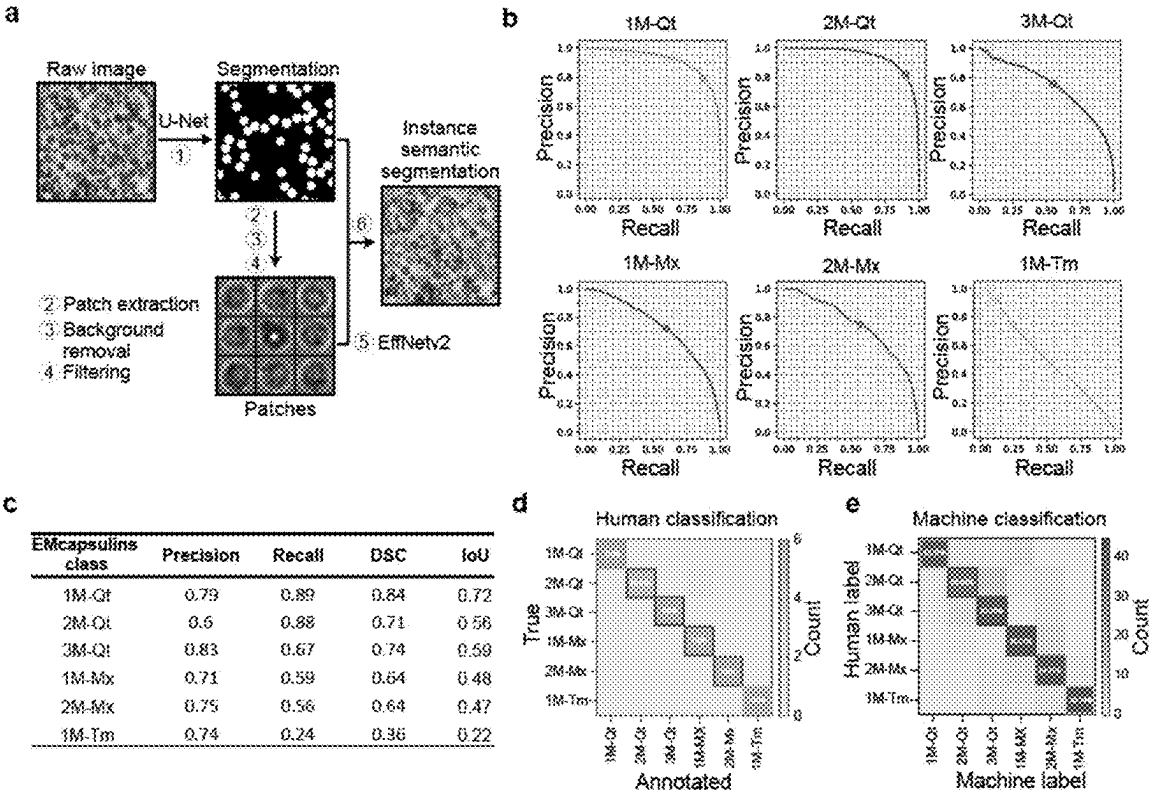


Figure 40 | Performance metrics of a sequential segmentation and classification pipeline.



EMcapsulins class	Precision	Recall	DSC	IoU
1M-Qt	0.79	0.89	0.84	0.72
2M-Qt	0.6	0.88	0.71	0.56
3M-Qt	0.83	0.67	0.74	0.59
1M-Mx	0.71	0.59	0.64	0.48
2M-Mx	0.75	0.56	0.64	0.47
1M-Tm	0.74	0.24	0.36	0.22

Figure 41 | Napari GUIs for interactive segmentation and classification of encapsulin-metallothionein particles.

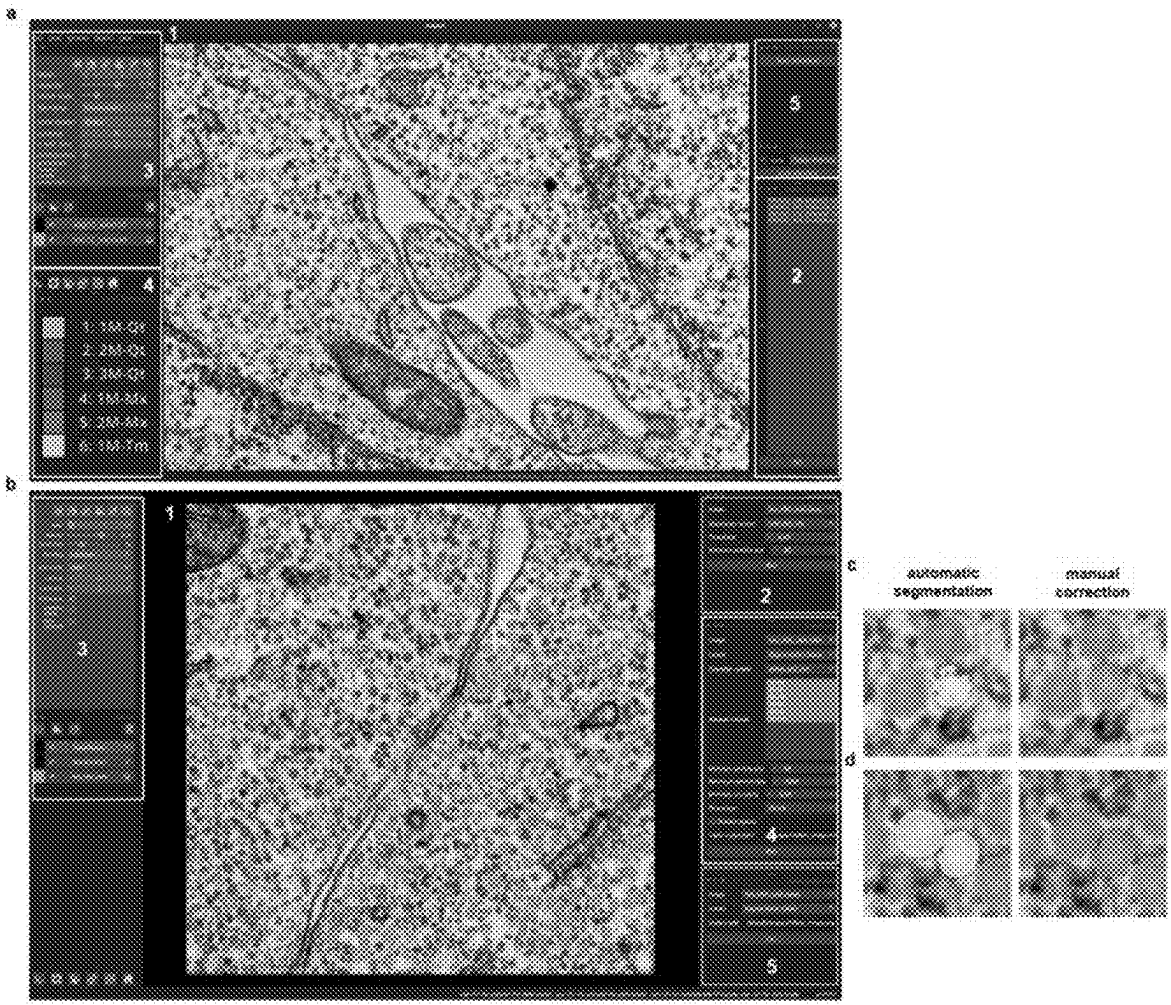


Figure 42 | Live microscopy experiments with targeted fluorescent encapsulin-metallothionein particles.

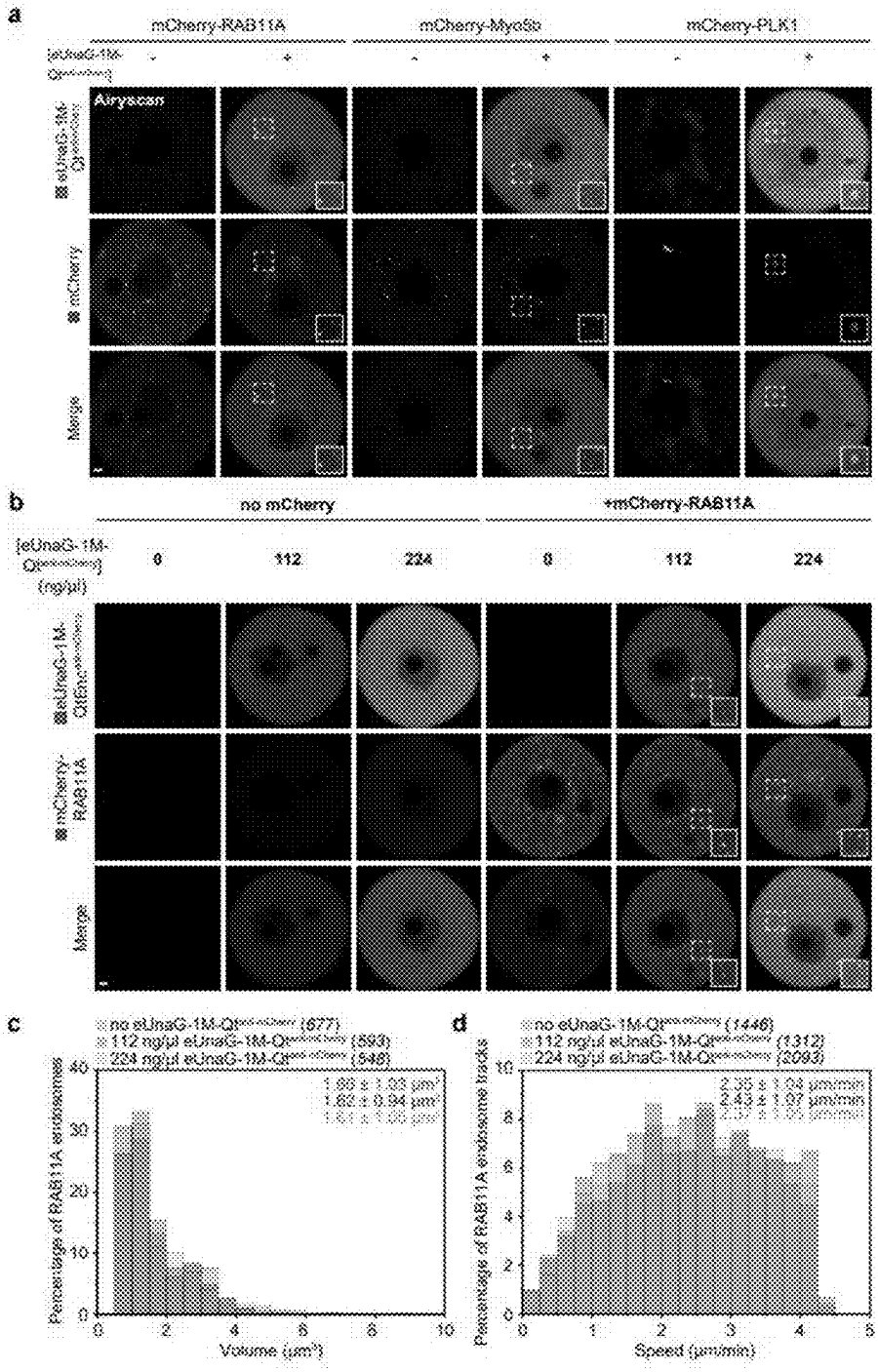


Figure 42 - continued | Live microscopy experiments with targeted fluorescent encapsulin-metallothionein particles.

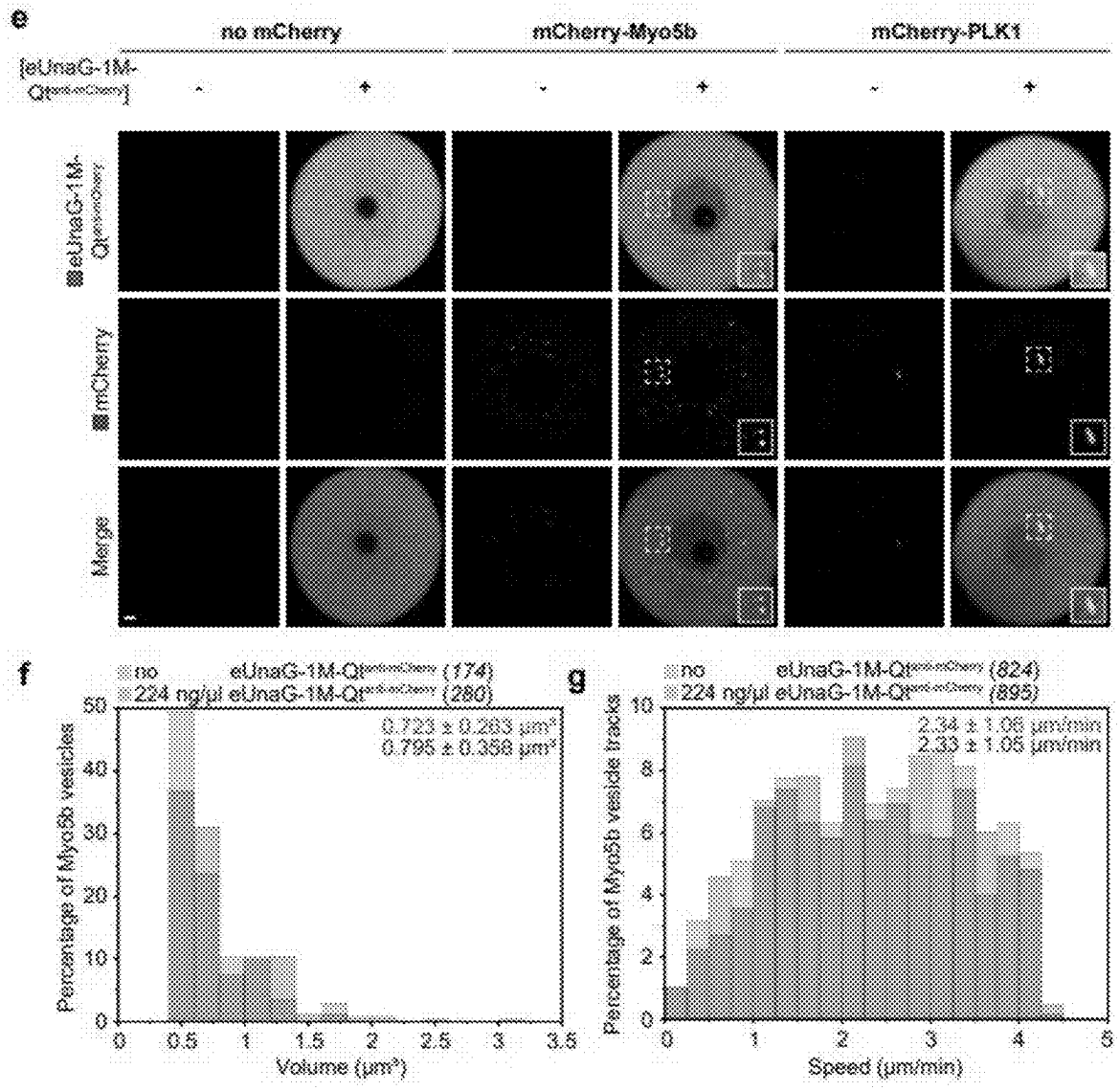


Figure 43 | Encapsulin-metallothionein particles targeted to subcellular compartments in mammalian cells and *Drosophila* cells.

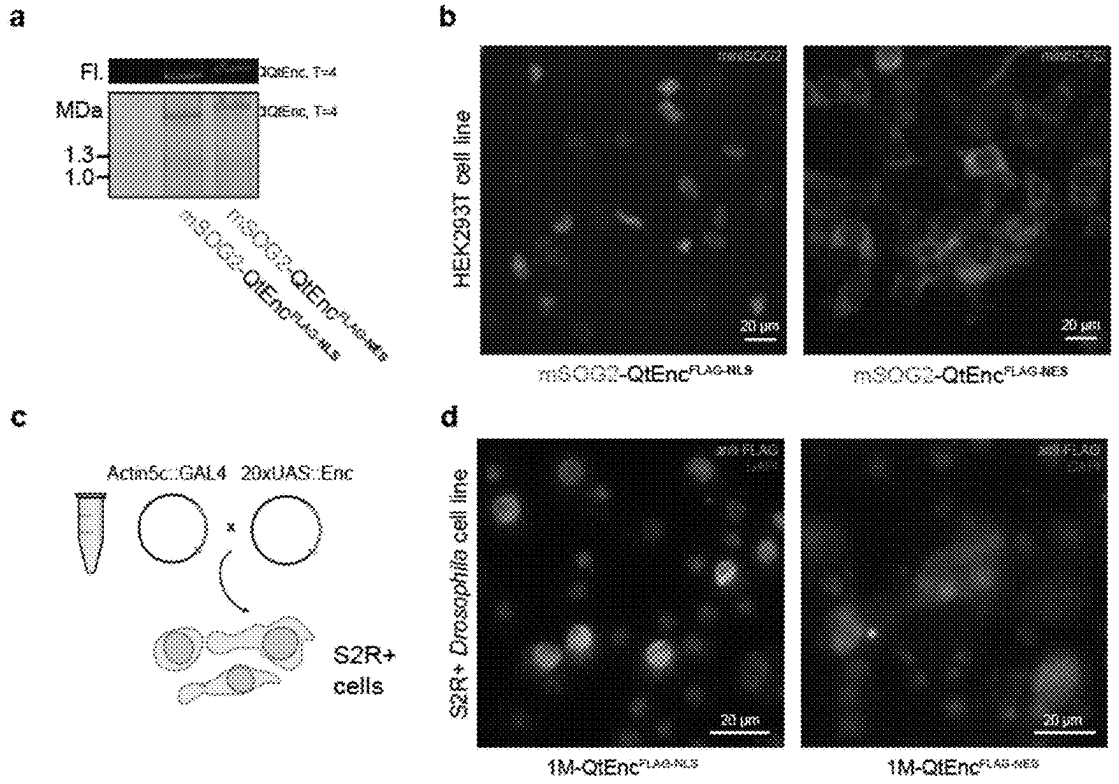


Figure 44 | Higher-magnification TEM micrographs of encapsulin-metallothionein particles expressed in *Drosophila* neurons.

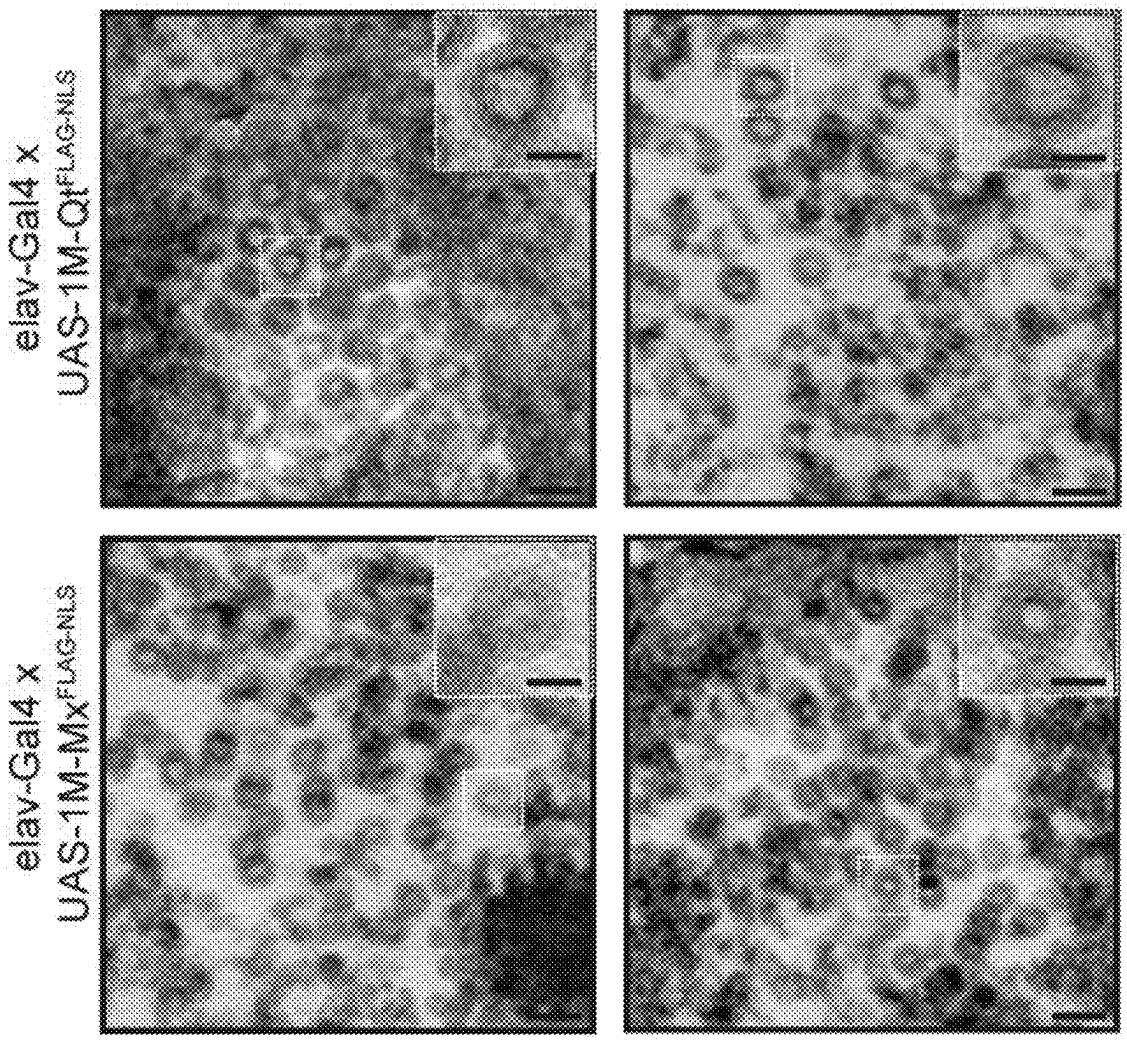
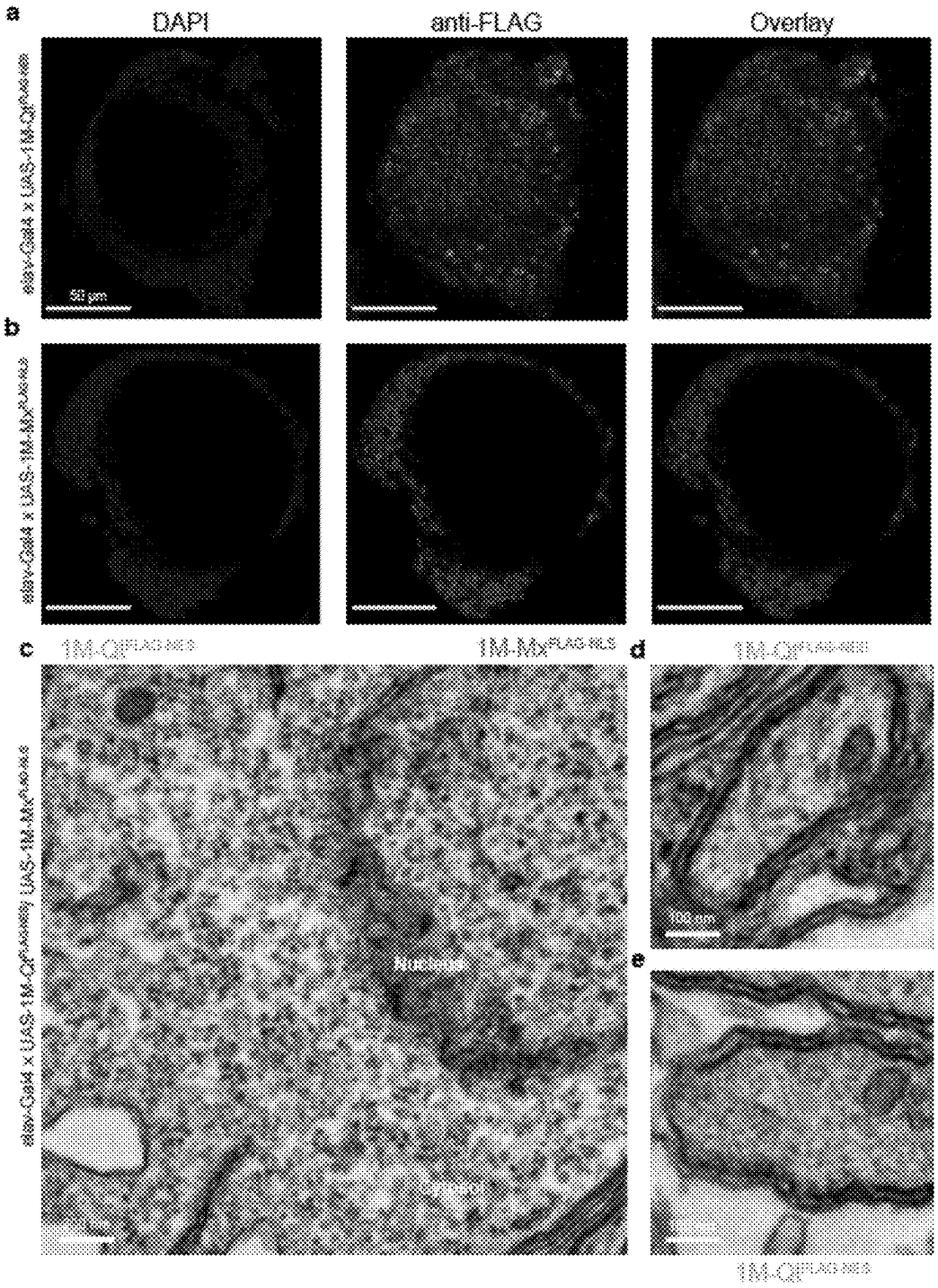


Figure 45 | Detection of encapsulin-metallothionein particles in the processes of *Drosophila* optic lobe neurons.



GENETICALLY CONTROLLED NANOSCOPY CONTRAST-GENERATING UNITS, GENETICALLY CONTROLLED STRUCTURAL ELEMENTS, GENETICALLY CONTROLLED SCAFFOLDS, NANOBIOMATERIAL BASED THEREON, AND USE THEREOF IN NANOSOCOPY METHODS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a national stage entry under 35 U.S.C. § 371 of International Patent Application PCT/EP2023/052908, filed Feb. 7, 2023 and published as International Patent Publication WO 2023/148392 A1 on Aug. 10, 2023, which claims the benefit of and priority to European Patent Application EP 22155466.0, filed on Feb. 7, 2022, the contents of each are hereby incorporated by reference.

REFERENCE TO A SEQUENCE LISTING

[0002] This application contains a Sequence Listing in computer readable form. The computer readable form is incorporated herein by reference.

FIELD OF THE INVENTION

[0003] The present invention relates to a genetically controlled nanoscopy contrast-generating unit comprising a metal interactor, wherein the metal interactor is compatible with nanoscopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols and wherein the metal interactor is a molecule to which metal ions can bind to or react with. The metal interactor is not a ferroxidase and is not an enzymatic product from an exogenous substrate. The present invention also relates to a genetically controlled structural element, wherein said genetically controlled structural element organizes the genetically controlled nanoscopy contrast-generating unit. The present invention also relates to a genetically controlled scaffold, wherein said genetically controlled scaffold spatially organizes the genetically controlled structural elements. The present invention also relates to the use of such genetically controlled nanoscopy contrast-generating unit, such genetically controlled structural element, and/or such genetically controlled scaffold for nanoscopy detection methods. The present invention also relates to a nanobiomaterial consisting of the isolated genetically controlled structural elements, and/or genetically controlled scaffolds. The present invention also relates to vectors comprising a nucleic acid encoding a genetically controlled nanoscopy contrast-generating unit, a genetically controlled structural element, and/or a genetically controlled scaffold.

INTRODUCTION

[0004] Biomedical research generates an increasing need for nanoscale mapping of cell-to-cell contacts as well as the intracellular distribution of organelles and biomolecules to decode, for example, structure-function relationships in tissue. Genetically-encodable fluorescent reporters have revolutionized biomedical research thanks to their ease of use and multi-color readout of cellular processes (Rodriguez et al., Trends in Biochemical Sciences, 2017). However, equivalent multiplexable genetic reporters for electron microscopy (EM) that are convenient to use while providing optimal resolution are not available yet.

[0005] Generally, it is desirable to achieve nanometer resolution to map, for example, cell-to-cell contacts. One example in which robust nanometer resolution is crucial is mapping cell-to-cell contacts of neuronal cells connected in neuronal networks. Here, the nanometer resolution has to be maintained over imaging volumes with edge lengths ranging from micro- to millimeters unequivocally disentangle intertwined neuronal processes.

[0006] Sparse labeling approaches range from silver-based stains used in conjunction with light microscopy (Pannese, Journal of the History of the Neurosciences, 1999) to fluorescent microscopy approaches such as transsynaptic viral tracing (Wickersham et al., Neuron, 2017) transsynaptic fluorescent protein complementation, and randomized combinatorial expression of fluorescent proteins. However, diffraction-limited fluorescence microscopy does not allow high-resolution imaging of, for example, the dense packing of neuronal processes in sub(-cortical) brain regions. Further sparse labeling approaches include super-resolution light microscopy (SRLM) and expansion microscopy (Schermelleh et al., Nature Cell Biology, 2019, Chen et al., Science 2015). SRLM can resolve synaptic contacts but involves detailed, cumbersome local analysis of selected structures labeled with dedicated fluorophores. Expansion microscopy can spatially separate selected molecular targets by pulling them apart via selective affinity handles connecting to an expanding polymer grid. This technology enables an effective sub-diffraction limit resolution with standard diffraction-limited microscopy. It thus allows high-throughput imaging with appropriate engineering solutions to automatize the clearance and isotropic expansion of the chosen targets, including membrane-bound targets to provide anatomical context.

[0007] In distinction to sparse labeling approaches, heavy metal stains for volumetric electron microscopy (Hua et al., Nature Communications, 2015) are used that densely label various biomolecules including lipids, proteins, and nucleic acids, which allows automated semantic segmentation of cellular membranes, organelles, protein complexes such as ribosomes, at nanometer-scale resolution over orders of magnitude larger volumes of interest in for example, brains of model organisms such as *C. elegans, Drosophila melanogaster, Danio rerio, Danionell translucida, Mus musculus*, as well as from human subjects. Established methods for volume electron microscopy include serial mechanical sectioning, collection, and arraying of individual slices, followed by either automated TEM or SEM/multi-SEM, or ion-based milling by either focused ion beam (FIB) or Gas Cluster prior to multiSEM. However, despite the rich anatomical information contained in the heavy-metal stained tissue, molecular information on the genetic identity and expression profile of cells of interest has to be filled-in via molecule-specific contrast, which is usually obtained via labor-intense correlation to antibody-targeted, or genetically expressed fluorophores. The 3D-distribution of these conventional markers can then be obtained via multiphoton microscopy pre-fixed tissue, followed by post-fixation, heavy-metal staining, and volume EM.

[0008] Antibody-coated gold nanoparticles have been used as non-genetic markers that work directly in EM without additional optical microscopy due to their precise site and strong EM contrast (Hainfeld, Science, 1987).

However, there are technical problems related to tissue penetration and biodistribution, artificial clustering, and epitope masking due to fixation. Locally triggered polymerization of 3,3'-Diaminobenzidine (DAB) with subsequent heavy metal binding has also been used to generate EM contrast. While this technology has been successfully used in, for example, proximity labeling, specialized protocols for diffusing a polymerizing substrate and an oxidant (3,3'-Diaminobenzidine (DAB), H_2O_2) are required, and the polymerization may lead to spatially unbounded contrast. Accumulating metals directly on genetically encoded proteins bearing tetracysteins, or metallothioneins have also been attempted, but these systems necessitate laborious workflows and incubation with toxic metals or gold nanoparticles.

[0009] Therefore, there is an increasing demand for providing robust EM contrast compatible with high-throughput fixation, staining, and acquisition protocols for volume EM of cells, organoids, and tissues. Ideally, said EM contrast is both genetically defined and geometric multiplexed EM and, in addition, also provides robust signals for light microscopy.

[0010] The inventors have previously shown that encapsulins can be robustly and non-toxically expressed in mammalian cells as self-assembling nanocompartments that can be visualized in EM, if the native ferroxidase (IMEF) is co-expressed, which oxidizes ferrous iron and leads to the formation of iron-oxide biominerals inside the encapsulin lumen. However, the contrast achievable in most cell types, tissues, or model organisms, such as *Drosophila melanogaster*, is insufficient. This is most likely the case because ferrous iron is limiting.

[0011] To obtain sufficiently strong EM contrast with standard fixation, post-fixation, and heavy-metal stain protocols, the inventors have surprisingly found genetically controlled nanoscopy contrast-generating units comprising fixation-stable metal interactors, which can be spatially organized by genetically controlled structural elements to yield unique shapes, in particular rotationally invariant concentric barcodes, which can themselves be spatially organized by genetically controlled scaffolds to produce distinct geometric patterns. The inventors demonstrate inter alia how these distinct contrast geometries can be used to augment anatomical EM maps with multiplexed genetically controlled information, to map the subcellular distribution of biomolecules of interest, to sense cellular activation states, and to actuate cellular states and processes biomechanically or biochemically, or via the deposition of electromagnetic energy or magnetic gradients under nanoscopy control in cell culture and biomedical organisms.

SUMMARY OF THE INVENTION

[0012] In one aspect, a genetically controlled nanoscopy contrast-generating unit comprising a metal interactor is claimed. The metal interactor is compatible with nanoscopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols, wherein the metal interactor is a molecule to which metal ions can bind to or react with. Such metal interactor is not a ferroxidase and not an enzymatic product from an exogenous substrate.

[0013] In one embodiment, the metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit comprises at least one of the following: a metal-interacting or metal-binding peptide or protein, a lipid-binding protein, an RNA-binding protein, a DNA or RNA molecule, a polymerizing or synthesizing enzyme, a biomineralizing enzyme, a bioconjugation tag, or a combination thereof.

[0014] In another embodiment, the metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit comprises at least one of the following: a metallothionein, osmiophilic amino acids, a lead binder, a lanthanide binder, a uranyl-binding protein, a vanadium binder, a copper and silver binder, a fatty-acid-binding protein, preferably FABP, a lipid-binding domain of a cytochrome P450, preferably the lipid- and heme-binding domain of the cytochrome p450 BM3h (BMh3), an RNA aptamer binder:RNA aptamer pair, a programmable RNA binding protein, a polymerizing kinase, a phytochelatine synthase, or a tyrosinase, or mixtures thereof.

[0015] In yet another embodiment, the genetically controlled nanoscopy contrast-generating unit further comprises a fluorophore or chromophore. The fluorophore is a fluorescent protein, a co-factor in a fluorescent protein, or an exogenous fluorophore. The chromophore is a chromoprotein, a co-factor in a chromoprotein, or an exogenous chromophore. The exogenous fluorophore or the exogenous chromophore can bind directly to the metal interactor.

[0016] In one embodiment, the metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit comprises at least one metallothionein, at least one fatty-acid binding protein, at least one lipid-binding domain, or at least one RNA molecule, and a fluorophore, wherein the fluorophore is a fluorescent protein.

[0017] In one embodiment, the genetically controlled nanoscopy contrast-generating unit comprises at least one attachment point. Said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners, bioconjugation-tags, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, and conformation-changing peptides including troponins, as well as combinations thereof.

[0018] In another aspect, a genetically controlled structural element is claimed, wherein said genetically controlled structural element spatially organizes the genetically controlled nanoscopy contrast-enhancing unit, wherein the genetically controlled structural element possesses a predetermined shape and pre-determined nanoscale size. Said genetically controlled structural element generates a shape that can be differentiated at the nanoscale, and said shape is optionally a barcode.

[0019] In one embodiment, the genetically controlled structural element comprises a member of the encapsulin family, a vault, an MS2 phage, a Qbeta bacteriophage, an AP205 phage, an engineered mono-to-polyvalent hub, a filament, a linker, or combinations or variants thereof.

[0020] In another embodiment, the genetically controlled structural element comprises at least one attachment point. Said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners, bioconjugation-tags, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, and conformation-changing peptides including troponins, as well as combinations thereof. In addition, the genetically-controlled nanoscopy contrast generating unit interacts or binds to the at least one attachment point.

[0021] In another embodiment, the genetically controlled structural element is an encapsulin and the genetically controlled contrast-generating units are selected from the group of metallothionein MT3, a series of different metallothionein species, fatty acid-binding proteins, preferably FABPs, and the lipid-binding domain of the cytochrome P450, or combinations thereof. In said embodiment, the lipid-binding domain of the cytochrome P450 is optionally the lipid- and heme-binding domain of the cytochrome P450 BM3 (BM3h). In said embodiment, one to three copies of the MT3 or one to three different metallothionein species are bound to the N-terminus of the encapsulin structural element. In addition, one or more MT3s, FABPs, or BM3hs are bound to the surface of the encapsulin structural element, optionally via a spacer, wherein the spacer is optionally a SasG of variable length. Such structural and spatial organization is configured to generate the distinct shape of a barcode, wherein the barcode is a concentric barcode differentiable at the nanoscale. Such concentric barcode may encode information on cellular states.

[0022] In yet another aspect, a genetically controlled scaffold is claimed. The genetically controlled scaffold comprises and spatially organizes the genetically controlled structural element(s), whereby said spatial organization generates distinct geometric patterns that can be differentiated at the nanoscale. Optionally, said distinct geometric patterns encode information on cellular states.

[0023] In another embodiment, the genetically controlled scaffold is selected from the group consisting of an endogenous cellular scaffold, a de novo designed scaffold, a SasG element, a CsgA element, an RNA or DNA structure, or combinations thereof.

[0024] In one embodiment, the genetically controlled scaffold comprises a SasG of variable length, one or more encapsulins as structural element, and at least one contrast generating unit selected from MT3 or a series of different metallothionein species. In such scaffold, the encapsulins are connected and spatially organized via SasG, and comprise the MT3, or the series of different metallothionein species.

[0025] In one embodiment, the genetically controlled nanoscopy contrast-generating unit, the genetically controlled structural element and/or the genetically controlled scaffold is compatible with intact cell systems, preferably with mammalian cells and organoids or biomedical model organisms.

[0026] In one further aspect, the present invention refers to the use of the genetically controlled structural elements and/or the genetically controlled scaffolds for nanoscopy detection, wherein nanoscopy detection comprises molecular mapping and/or geometric sensing.

[0027] In one embodiment, the nanoscopy detection is molecular mapping. Said molecular mapping provides information on the subcellular distribution of a molecule of interest within a cell or tissue via the binding of genetically controlled structural elements and/or genetically controlled scaffolds to a molecule of interest, which thus determines the subcellular localization of the genetically controlled structural elements and/or the genetically controlled scaffolds.

[0028] In another embodiment, the nanoscopy detection is geometric sensing. Said geometric sensing provides information on a specific cellular state, a cellular process, the presence or absence of an analyte or environmental parameter of interest within a cell or tissue, or the response to an external stimulus. The shape generated by the genetically controlled structural element(s) and/or the geometric pattern generated by the genetically controlled scaffold(s) changes in response to a pre-defined cellular state, a pre-defined cellular process, at least one analyte, or at least one environmental parameter, or an external stimulus.

[0029] In another embodiment, the nanoscopy detection comprising mapping and/or geometrical sensing further comprises geometric actuation. Said geometric actuation alters a cellular state or process by a biomechanical, and/or biochemical effect or via an external stimulus, or the deposition of external energy, electromagnetic radiation, mechanical energy, or magnetic gradients.

[0030] In another aspect, the invention relates a nanobiomaterial consisting of isolated genetically controlled structural element(s), and/or the genetically controlled scaffold (s). The genetically controlled structural element(s), and/or the genetically controlled scaffold(s) are thus isolatable from the source of origin, which is preferably a genetically modified cell or a cell-free system.

[0031] In yet another aspect, the invention relates to a vector comprising a nucleic acid encoding the genetically controlled nanoscopy contrast-generating unit, the genetically controlled structural element and/or the genetically controlled scaffold.

[0032] In one embodiment, the genetically controlled nanoscopy-generating unit according to any of the preceding embodiments comprises a metal interactor, wherein said metal interactor is one (SEQ ID NO: 1) or two murine metallothionein-3 (SEQ ID NO: 4), or wherein said metal interactor is a chimeric metallothionein sequence comprising three metallothionein sequences from three different species. In a preferred embodiment, the three metallothionein sequences from three different species are murine etallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5). In another equally preferred embodiment, the metal interactor is one (SEQ ID NO: 1) or two murine metallothionein-3 (SEQ ID NO: 4).

[0033] In another embodiment, the fluorescent protein of the genetically controlled nanoscopy contrast-generating unit according to the preceding embodiments is eUnaG, mScarlet-I, miniSog, or eUnaG and mCherry. In a preferred embodiment, the fluorescent protein is eUnaG. In one embodiment, eUnaG is N-terminally fused to one or two murine metallothionein-3. In an alternative embodiment, eUnaG is C-terminally fused to one or two murine metallothionein-3.

[0034] In yet another embodiment, the genetically controlled structural element according to any preceding embodiment comprise a member of the encapsulin family. In a preferred embodiment, the encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin. In one embodiment, the genetically controlled structural element is a member of the encapsulin family, and the genetically controlled contrast-generating unit is one (SEQ ID: NO: 1) or two murine metallothionein-3 (SEQ ID NO: 4). In a preferred embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin.

[0035] In another embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin and the genetically controlled contrast-generating unit is one (SEQ ID NO: 1) or two N-terminally fused murine metallothionein-3 (SEQ ID NO: 4), or genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5). In another embodiment, the one or two N-terminally fused murine metallothioneins, or the chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5) are located on the inner surface of the encapsulin. In another embodiment, a FLAG tag is C-terminally fused.

[0036] In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, wherein a FLAG tag is C-terminally fused (SEQ ID NO: 165). In yet another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is two N-terminally fused murine metallothionein-3, wherein a FLAG tag is C-terminally fused.

[0037] In yet another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag is C-terminally fused (SEQ ID NO: 169).

[0038] In even another embodiment, the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, wherein a FLAG tag is C-terminally fused (SEQ ID NO: 166).

[0039] In one embodiment, the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is two N-terminally fused murine metallothionein-3, and wherein a FLAG tag is C-terminally fused. In another embodiment, the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1), and wherein a FLAG tag is C-terminally fused. In yet another embodiment, the genetically controlled structural element is a *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, and wherein a FLAG tag is C-terminally fused. In yet another embodiment, the genetically controlled structural elementis a *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is two N-terminally fused murine metallothionein-3 (SEQ ID NO: 4), and wherein a FLAG tag is C-terminally fused. In one embodiment, the genetically controlled structural element is a *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag is C-terminally fused.

[0040] In one embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one (SEQ ID NO: 1) or two N-terminally fused murine metallothionein-3 (SEQ ID NO: 4), or wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused (SEQ ID NO: 168). In another preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused. In yet another embodiment, the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused (SEQ ID NO: 167). In even another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-enhancing unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag comprising a nuclear export signal is C-terminally fused.

[0041] In one aspect, a transgenic *Drosophila melanogaster* line expressing two genetically controlled structural elements is disclosed, wherein the first genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-

generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5),wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused and the genetically controlled structural element, and wherein the second genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused (SEQ ID NO: 167). In an alternative embodiment, the transgenic *Drosophila melanogaster* line expressing two genetically controlled structural elements is disclosed, wherein the first genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused (SEQ ID NO: 167), and wherein the second genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-enhancing unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag comprising a nuclear export signal is C-terminally fused. In one embodiment, said transgenic *Drosophila melanogaster* line expresses the genetically controlled structural element (*Quasibacillus thermotolerans* (Qt) encapsulin) comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused in C3 neurons and expresses the genetically controlled structural element (*Myxococcus xanthus* (Mx) encapsulin) comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag comprising a nuclear localization signal is C-terminally fused (SEQ ID NO: 167) in T4-5 neurons.

[0042] In another aspect, a nanoscopy method using the genetically controlled structural element according to any one of the preceding embodiments is disclosed. In one embodiment, the genetically controlled structural element does not interfere with cellular processes. In another embodiment, the nanoscopy method is electron microscopy. In one embodiment, the electron microscopy method is selected from the group consisting of scanning electron microscopy (SEM), transmission electron microscopy (TEM) and Focused Ion Beam Scanning Electron Microscopy (FIB-SEM). In another embodiment, no further incubation steps involving DAB and hydrogen peroxide or further exogenous substrates are required in the disclosed nanoscopy method.

[0043] In another embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one (SEQ ID NO: 1) or two murine metallothionein-3 (SEQ ID NO: 4), or wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein the genetically controlled structural element further comprises the fluorescent protein eUnaG. In one preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein a FLAG tag is C-terminally fused (SEQ ID NO: 155). In one embodiment, the genetically controlled structural element according to the preceeding embodiments and the following embodiments is compatible with both fluorescent microscopy and electron microscopy applications. In yet another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is two murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein a FLAG tag is C-terminally fused (SEQ ID NO: 156). In even another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is C-terminally fused (SEQ ID NO: 227). In one embodiment, the genetically controlled structural element further comprises at least one attachment point according to the preceding embodiments, wherein the at least one attachment point is an intrabody, wherein said intrabody is C-terminally fused. In one embodiment, the intrabody is an anti-mCherry intrabody, wherein said anti-mCherry intrabody is expressed on the outer surface of the encapsulin. In another embodiment, the genetically controlled structural element additionally comprises at least one further attachment point according to the preceding embodiments, wherein said attachment point is a coiled-coil domain. In an alternative embodiment, said attachment point is two coiled-coil domains. In another alternative embodiment, said attachment point is a SpyTag/SpyCatcher. In another embodiment, the genetically controlled structural element additionally comprises at least one further attachment point according to the preceding embodiments, wherein said attachment point is a SpyTag/SpyCatcher, wherein an intrabody is covalently attached to the SpyTag/SpyCatcher.

[0044] In one embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein mScarlet-I is encapsulated to the encapsulin lumen via an encapsulation signal. In another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein mScarlet-I is expressed as cargo protein in the encapsulin lumen. In yet another embodiment, the genetically controlled structural

element is a *Quasibacillus thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein APEX2 is expressed as cargo protein in the encapsulin lumen.

[0045] In one aspect, an electron microscopy method, wherein the genetically controlled structural element according to the preceding embodiment is used, wherein further incubation steps involving DAB and hydrogen peroxide are performed.

[0046] In another aspect, the two genetically controlled structutal elements are expressed in a ratio of approximately 4:1, wherein the first genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is C-terminally fused (SEQ ID NO: 227), wherein the second genetically controlled structural element further comprises at least one attachment point according to any of the preceding embodiment, wherein the at least one attachment point is an intrabody, wherein said intrabody is C-terminally fused. In another embodiment, said first and second genetically controlled structural elements are expressed in a ratio of approximately 4:1.

[0047] In another embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein the genetically controlled structural element comprises a programmable ribosomal read-through (rt) cassette, wherein said programmable ribosomal read-through cassette comprises a stop codon and a short read-through (rt) promoting motif at the end of the open-reading frame encoding the *Quasibacillus thermotolerans* (Qt) encapsulin. In a preferred embodiment, the stop codon is selected from the group consisting of TGA, TAA, TAG and the short read-through promoting motif is selected from the group consisting of rt20s (SEQ ID NO: 76), rt9s (SEQ ID NO: 74), rt9us (CTATCC). In an even more preferred embodiment, the stop codon is TGA, and the short read-through promoting motif is rt20s (SEQ ID NO: 76). In one embodiment, the genetically controlled structural element additionally comprises a C-terminally fused anti-GFP intrabody. In another embodiment, the genetically controlled structural element is co-expressed with Cx43-msfGFP or msfGFP-Cx43. In yet another embodiment, the genetically controlled structural element additionally comprises an anti-GFP intrabody.

[0048] In one aspect, a method of generating a distinct ratio of genetically controlled structural elements according to any of the preceding embodiments is disclosed, wherein said genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the Qt encapsulin comprises one N-terminally fused murine metallothionein-3,wherein at the end of the open-reading frame encoding the encapsulin *Quasibacillus thermotolerans* (Qt) the read-through motif rt20s (SEQ ID NO: 76) and the stop codon TGA are located, wherein the *Quasibacillus thermotolerans* (Qt) encapsulin comprises one C-terminally fused FLAG-tag, wherein said C-terminally fused FLAG tag is further extended by an anti-GFP intrabody upon ribosomal read-through, whereby the combination of the read-through motif rt20s (SEQ ID NO: 76) and the stop codon yields about 15% anti-GFB intrabodies, thereby serving as a surrogate marker for a translational read-through rate.

[0049] In another aspect, a cell line comprising the genetically controlled structural element of any of the preceding embodiments and the fusion protein msfGFP-Cx43 is disclosed.

[0050] In one embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt), *Myxococcus xanthus* (Mx) encapsulin or a *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein mScarlet-l. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused. In another preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is two murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused.

[0051] In one aspect, an AAV vector comprising the genetically controlled structural element of the previous embodiment is disclosed. In one embodiment, the AAV vector is selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9. In another embodiment, the AAV vector is pseudotyped. In a preferred embodiment, the AAV vector is AAV5. In another embodiment, the AAV vector comprising the genetically controlled structural element of the previous embodiment, wherein said genetically controlled structural element comprises m-Scarlet-1, wherein the AAV5 vector comprises a CAMKII promoter. In yet another embodiment, the AAV vector is for use in medicine. In even another embodiment, the AAV vector is for use in diagnostic imaging.

[0052] In another aspect, a fluorescence multichannel imaging method using the genetically controlled structural element according to the preceding embodiments is disclosed.

[0053] In yet another aspect, a method for monitoring organ, organoid or cells using the genetically controlled structural element according to the preceding embodiment is disclosed. In one embodiment, the cells are mammalian oocytes. In yet another embodiment, the mammalian oocytes are monitored. In even another embodiment, the mammalian oocytes are monitored prior to in vitro fertilization.

[0054] In one embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused.

[0055] In one aspect, a recycling endosome stain comprising the genetically controlled structural element according to the preceding embodiment is disclosed, wherein the anti-mCherry intrabody is targeted to mCherry-tagged RAB11A. In another aspect, a cargo vesicle stain comprising the genetically controlled structural element according to the preceding embodiment is disclosed, wherein the anti-mCherry intrabody is targeted to mCherry-tagged Myo5b. In yet another aspect, a centriolar microtubule-organizing stain comprising the genetically controlled structural element

according to the preceding embodiment is disclosed, wherein the anti-mCherry intrabody is targeted to mCherry-tagged PLK1.

[0056] In one aspect, a scanning electron microscopy imaging method or focused ion beam scanning electron microscopy imaging method using the genetically controlled structural element of any of the preceding embodiments is disclosed.

[0057] In one embodiment, a genetically controlled scaffold according to any of the preceding embodiments is disclosed, wherein said genetically controlled scaffold is a SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element, one or two murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) and *Thermotoga maritima* (Tm) as genetically controlled structural element, one or two murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In yet another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element, one or two murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In even another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) and *Thermotoga maritima* (Tm) as genetically controlled structural element, one murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In one embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, a *Quasibacillus thermotolerans* (Qt) encapsulin as genetically controlled structural element, one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein said Qt encapsulin has one or more anti-GFP intrabodies on its surface. In another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, a *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element, one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein said Tm encapsulin has one or more anti-mCherry intrabody on its surface. In yet another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, a *Quasibacillus thermotolerans* (Qt) encapsulin as genetically controlled structural element, one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein said Qt encapsulin has one or more anti-GFP intrabody on its surface, and a *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element, one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein the Tm encapsulin has one or more anti-mCherry intrabody on its surface. In another embodiment, the genetically controlled scaffold according to any of the preceding embodiments is disclosed, wherein the *Quasibacillus thermotolerans* (Qt) encapsulin having one or more anti-GFP intrabodies on its surface is linked to the matching anti-mCherry intrabody on the surface of the *Thermotoga maritima* (Tm) encapsulin. In yet another embodiment, the genetically controlled scaffold according to any of the preceding embodiments is disclosed, wherein the *Quasibacillus thermotolerans* (Qt) encapsulin having one or more anti-GFP intrabody on its surface results in an approximately 40 nm ring-shaped object, wherein the *Thermotoga maritima* (Tm) encapsulin having one or more matching anti-mCherry intrabody on the surface results in an approximately 25 nm spherical object, wherein said spherical object surrounds said ring-shaped object.

[0058] In one embodiment, the genetically controlled nanoscopy contrast-generating unit according to any one of the preceding embodiments is disclosed, wherein the metal interactor is a uranyl binder. In a preferred embodiment, the uranyl binder is MUP2 (SEQ ID NO: 45). In another embodiment, a genetically controlled structural element according to any of the preceding embodiments is disclosed, wherein the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is MUP2. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is MUP2 (SEQ ID NO: 148).

[0059] In another embodiment, the genetically controlled nanoscopy contrast-generating unit according to any one of the preceding embodiments is disclosed, wherein the metal interactor is a fatty acid-binding protein. In one embodiment, the fatty acid-binding protein is B-Fabp (SEQ ID NO: 36), B-Fabp-ko, (SEQ ID NO: 248) Bm3h (SEQ ID NO: 29), or Bm3h-B7 (SEQ ID NO: 247). In another embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is B-Fabp, B-Fabp-ko, Bm3h, or Bm3h-B7. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is B-Fabp, B-Fabp-ko, Bm3h, or Bm3h-B7.

[0060] In a further embodiment, the genetically controlled structural element is an engineered mono-to-polyvalent hub, wherein the genetically controlled contrast-generating unit is B-Fabp, B-Fabp-ko, Bm3h, or Bm3h-B7. In one embodiment, the engineered mono-to-polyvalent hub is one to ten anti-moon tags, wherein the genetically controlled contrast-generating unit is B-Fabp.

[0061] In another embodiment, the genetically controlled nanoscopy contrast-generating unit according to any one of the preceding embodiments is disclosed, wherein the metal interactor is a bioconjugation tag. In a preferred embodiment, the bionconjugation tag is SNAP or CLIP. In yet another embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is SNAP or CLIP. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is SNAP (SEQ ID NO: 260) or CLIP (SEQ ID NO: 261). In one embodiment, SNAP or CLIP is N-terminally or C-terminally fused.

[0062] In yet another embodiment, the genetically controlled structural element is an encapsulin selected from the group consisting of *Quasibacillus thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, and *Thermotoga maritima* (Tm) encapsulin, wherein the genetically controlled contrast-generating unit is one or two murine metallothionein-3, or wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein the genetically controlled contrast-generating unit comprises an attachment point, wherein said attachment point is a bioconjugation tag,

[0063] the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein the genetically controlled contrast-generating unit comprises an attachment point, wherein said attachment point is a bioconjugation tag, wherein said bioconjugation tag is SNAP or CLIP.

[0064] In even another embodiment, the genetically controlled nanoscopy contrast-generating unit according to any one of the preceding embodiments is disclosed, wherein the metal interactor is a metal-binding peptide/protein. In a preferred embodiment, the RNA aptamer-binder:RNA aptamer pair is the circularized Twister-Broccoli RNA aptamer.

[0065] In a further embodiment, a genetically controlled structural element according to any of the preceding embodiments is disclosed, wherein the genetically controlled structural element is a vault, wherein the genetically controlled contrast-generating unit is the circularized Twister-Broccoli RNA aptamer.

[0066] In one embodiment, the genetically controlled nanoscopy contrast-generating unit according to any one of the preceding embodiments is disclosed, wherein the metal interactor is a metal-binding peptide/protein. In a preferred embodiment, the metal-binding peptide/protein is *H. pylori* ferritin comprising at least one attachment point, and wherein said at least one attachment point is a calmodulin-binding peptide (SEQ ID NO: 134). In another embodiment, the genetically controlled structural element is *Quasibacillus thermotolerans* (Qt), wherein the genetically controlled contrast-generating unit is one murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein eUnaG, and wherein the genetically controlled structural element further comprises the synthetic calmodulin-binding peptide 20 (SEQ ID NO: 241). In one aspect, the genetically controlled contrast-generating unit of the preceding embodiment and the genetically controlled structural element of the preceding embodiment are for the use of any preceding embodiments. In one embodiment, the analyte for the use of any preceding embodiments is calcium.

BRIEF DESCRIPTION OF THE DRAWINGS

[0067] FIG. **1**: Metal-interacting domains and osmiophilic domains. FIG. **1**A: Exemplary 3D structure of yeast metallothionein (MT) (Protein data bank (PDB) accession number: 1AQS) bound to metal ions. Based on its high density in cysteines, MTs are osmiophilic. MTs are also reported to have a high affinity to lead (Pb), which is contained in standard EM stains. Exemplary sequences for these constructs are SEQ ID NO: 1-5 FIG. **1**B: Contrast-to-noise ratios of individual encapsulin particles as structural elements, which were either non-modified (QtEnc^{FLAG}; SEQ ID NO: 142), fused to a tandem MT3 metallothionein domain as a contrast-generating unit (2xMT3-QtEnc^{FLAG}; SEQ ID NO: 143, or filled with iron-oxides mineralized via a ferroxidase (IMEF) (QtEnc^{FLAG}+QtIMEF) (SEQ ID NOs: 142 and 52), as native cargo protein. FIG. **1**C: A strong contrast (with a certain shape) can be observed in TEM if the structural element QtEnc spatially organizes the genetically controlled nanoscopy contrast-generating unit comprising the metal-interacting protein MT3; left: TEM micrographs of HEK293T cells expressing QtEnc monomers, which assemble into structural elements N-terminally equipped with a tandem MT3 domain as a contrast-generating unit (2xMT3-QtEnc^{FLAG}); right: TEM micrographs of HEK293T cells expressing unmodified QtEnc structural elements, which form nanocompartments (QtEnc^{FLAG}). Scale bars are 100 nm. FIG. **1**D: Silver-stained SDS-PAGE loaded with material from an anti-FLAG pull-down experiment from HEK293T cells expressing MT3 or tandem MT3 (2xMT3) in the context of different encapsulin shell monomers, i.e., QtEnc, TmEnc, and MxEnc. The shift towards higher molecular weights indicates that MT domains are readily expressed as contrast generating units. Since the MT3-TmEnc sample has a BC2Tag (SEQ ID NO: 144) instead of a FLAG tag, no band is seen in the gel. FIG. **1**E: Schematic of genetic expression constructs for the methionine-rich protein from *Pinctada fucata* (30xMMKPDM; SEQ ID NO: 6) and the histidine-rich protein 2 (HRPII), which are expressed as fusion proteins to QtEnc or connected to a targeting moiety (QtSig; SEQ ID NO: 16) for QtEnc encapsulation. FIG. **1**F: Preferred proteins and protein motifs with high cysteine and/or histidine abundance as osmiophilic residues, identified by screening the Protein Data Bank (specific PDB accession number given) to achieve a high concentration of osmiophilic residues. Exemplary sequences for these constructs are SEQ ID NO: 6-11.

[0068] FIG. **2**: Metal-binding proteins. FIG. **2**A, FIG. **2**B: Selective examples for metal-binding domains, also called metal binders, which can coordinate heavy metals, such as uranyl, routinely contained in EM stains in the form of uranyl acetate. Shown are two domains into which metal binding sites were grafted, MUP2 (based on PDB:2AKF) SEQ ID NO: 45 and MUP5 (based on PDB:5APQ) SEQ ID NO: 46. The gels show a CN-PAGE (Clear Native Poly-

acrylamide Gel Electrophoresis) analysis of the expression of these domains as direct fusions to QtEnc encapsulin. FIG. **2**C: Example of a TEM micrograph from MUP2-QtEnc (SEQ ID NO: 148) showing ring-contrasts (specific shape of a concentric barcode) in the 2D projection of the spherical QtEnc used as a structural element. Scale bar is 50 nm. FIG. **2**D: BN-PAGE (Blue Native Polyacrylamide Gel Electrophoresis) analysis of encapsulin variants fused to lanthanide binding tags (LBT). The QtEnc variant fused to LBT15 yields a stable assembly (LBT15-QtEnc^{FLAG}; SEQ ID NO: 145). After adding terbium chloride, tryptophan-sensitized luminescence can be observed upon UV-illumination (UV-FL), demonstrating lanthanide binding to the structural element, also called nanosphere. This finding is supported by ICP-MS measurements (corresponding bar graph on bottom) showing Tb-enrichment in the LBT15 QtEnc variant compared to another variant (Twin-dLBT3; SEQ ID NO: 146) which worked less efficient and the empty encapsulin QtEnc^{FLAG}.

[0069] FIG. **3**: Fatty acid-/lipid binding proteins. FIG. **3**A: Antiparallel 1-barrel structures of L-FABP (PDB: 2LKK) and B-FABP (PDB: 1fdq) with an internal binding site that binds a fatty acid in an interior cavity. FIG. **3**B: TEM image of HEK cells co-expressing QtEnc-SpyTag003 (SEQ ID NO: 147) and B-FABP-SpyCatcher003 SEQ ID NO: 150, respectively, resulting in contrast enhancement (shape of concentric barcodes) depending on how many B-FABP molecules are bound to a given QtEnc. Two zoom-ins placed on the right show the localized contrast enhancement. Scale bars for the zoom-ins are 20 nm. FIG. **3**C: Schematic of the genetic constructs for a two-component system to fuse B-FABP via SpyCatcher003 as an attachment point to the encapsulin surface-functionalized with the corresponding SpyTag003 as attachment point (top). Clear-native PAGE gels (bottom left) showing the slowed-down native running behavior upon co-expression of both constructs vs. the expression of only encapsulin QtEnc as a control (bottom left). The corresponding Western Blot shows an additional band for the co-expression of both constructs (bottom right). FIG. **3**D: Another preferred embodiment of metal interactor comprised in the contrast-generating unit is the ligand-binding heme-domain of the cytochrome P450 BM3 (BM3h), which has been shown to selectively bind arachidonic acid (AA), a polyunsaturated fatty acid, which is a preferred interaction site for osmium tetroxide. FIG. **3**E: CN-PAGE (left) and (right) analysis of the co-expression of BM3h-SpyCatcher003 (SEQ ID NO: 151) with QtEnc decorated with SpyTags (SpyTag003) (SEQ ID NO: 147). FIG. **3**F: TEM images (and zoom-ins on the right) of HEK cells co-expressing the structural element QtEnc-SpyTag003 comprising SpyCatcher-Bm3h resulting in contrast enhancement depending on how many BM3h molecules, which are larger than FABPs, are bound to a given QtEnc. The ratio can be controlled by co-expressing structural element QtEnc without SpyTag, which can be achieved via transient expression or via read-through control (FIG. **15**) also in stable cell lines. Scale bars for the zoom-ins are 20 nm.

[0070] FIG. **4**: RNA, RNA aptamer —RNA aptamer-binding protein interactions FIG. **4**A: Shown is the RNA aptamer PP7 coat dimers (SEQ ID NO: 53), which interact with PP7 loops (SEQ ID NO: 56) attached to RNA aptamers. Other preferred aptamers are MS2 (SEQ ID NO: 152), which interacts with the protein MCP (SEQ ID NO: 100), or H23 (K-turn motif) (SEQ ID NO: 206), which interacts with the protein L7ae. (SEQ ID NO: 63). Here, the RNA-binding protein functions as a CGU. In other embodiments, the RNA aptamer-binding protein functions as a structural element. The aptamers, in this case, contain FIG. **4**B: PP7 stem-loop. For dual detection by EM and fluorescent microscopy, RNA aptamers such as FIG. **4**C: Spinach, SEQ ID NO: 55 FIG. **4**D: Dir2s, SEQ ID NO: 57 and FIG. **4**E: Rho-BAST SEQ ID NO: 59 may be chosen because they bind to differently colored fluorophores and also enable super-resolution SRLM. Aptamers may also contain multiple binding sites for small fluorophores. If necessary, the aptamers can be stabilized for mammalian expression via circularization. FIG. **4**F: Alternatively, or supportive to the use of RNA aptamer-binding proteins such as PCP as the CGU or structural element, protein motifs such as vertebrate RNA-recognition motif (RRM, PDB:3MDF; SEQ ID NO: 60), the very well conserved human K homology domain (KH, PDB:5WWX; SEQ ID NO: 61), or the Zinc Finger CCHC-type which binds RNA specifically (CCHC, PDB:2E5H; SEQ ID NO:62) are applied, which can bind RNA also unspecifically. FIG. **4**G: In addition to relying on the unspecific interaction of heavy metals with the phosphates of RNA, specific metal-binding sites such as the one shown here (see also Kanazawa and Kondo, Journal of Inorganic Biochemistry, (2017), 176:140-143) (SEQ ID NO: 58) can be used, also in combination with fluorophore-binding RNA aptamers such that co-localization upon formation of the antiparallel duplex can also be monitored via fluorescence imaging. Other metal-binding RNA motifs, including magnetic species such as nickel and cobalt, can be taken from metal-sensing ribozymes.

[0071] FIG. **5**: Polymerizing enzymes FIG. **5**A: 3D structure of the tetrameric polyphosphate kinase 2 (PPK2) of *F. tularensis* (PDB: 5LL0). PPKs can turn over the endogenously available substrates GTP or ATP to polymerize highly negatively-charged polyphosphate chains (polyP). FIG. **5**B: Schematic of DD-CgPPK2b-QtSig (SEQ ID NO: 47) targeted to/spatially organized in the structural element QtEnc lumen via the endogenous QtEnc encapsulation signal (QtSig). The QtSig encapsulation signal is "KGFTVGSLIQ" (SEQ ID NO: 16). It is the C-terminal fraction after the 2xGGGGS-Linker (SEQ ID NO: 153) in the sequence "DD-CgPPK2b-QtSig". Cg stands for the organism of origin *Corynebacterium glutamicum*. DD stands for a degron motif (SEQ ID NO: 154), leading to the degradation of the cargo protein (in this case, the PPK2 kinase) unless it is encapsulated in the lumen of encapsulin. ATP/GTP, endogenously present in cells, can enter via the pores of the structural element and is polymerized into a polyP chain, which is trapped inside the encapsulin lumen FIG. **5**C: Clear-Native PAGE analysis of lysates of HEK293T cells expressing QtEnc^{FLAG} (SEQ ID NO: 104) or MxEnc^{FLAG} (SEQ ID NO: 107) alone or co-expressing DD-CgPPK2b-QtSig. The gel was stained with DAPI, exhibiting a yellow shift upon binding to polyP. The UV fluorescence imaging of the gel (upper panel) reveals bands indicating intraluminal polyP accumulation. No UV fluorescent bands are observed when no cargo protein is co-expressed. FIG. **5**D: TEM micrograph of HEK293T cells expressing MxEnc^{FLAG}+DD-CgPPK2b-QtSig. Inside the ~32 nm encapsulins as structural elements, shapes generated by highly contrasted polyP cores can be observed. The scale bar is 100 nm. FIG. **5**E: TEM micrograph of HEK293T cells expressing QtEnc^{FLAG}+Phytochelatine-synthase 1 fused to

an encapsulation signal (AtPCS1-QtSig; SEQ ID NO: 49). "At" stands for the organism of origin *Arabidopsis thaliana*. The highly contrasted areas indicate heavy metal-binding to the intraluminal phytochelatins. The scale bar represents 100 nm. FIG. **5**F: Clear native PAGE loaded with lysates of HEK293T cells co-expressing TmEnc comprising the coiled-coil P2 (SEQ ID NO: 159) as a cargo adapter fused to a bacterial tyrosinase (BmTyr; SEQ ID NO: 51) via the encapsulation signal P1. Bm stands for *Bacillus megaterium* as the organism of origin of the tyrosinase. Please also see preferred coiled-coil pairs for the respective encapsulins, as shown in FIG. **8***c*. The gels were incubated with 100 μM copper chloride and 2 mM L-Tyrosine. The dark high molecular weight bands at 1.0 MDa represent melanin-loaded TmEnc nanospheres as structural elements that also attract heavy metal ions.

[0072] FIG. **6**: Biomineralizing enzyme Enzymatically generated biominerals such as iron-oxide are a resin to which heavy metals such as lead can bind to in order to intensify EM contrast. The stand-alone ferroxidase within the encapsulin system (IMEF; SEQ ID NO: 52) generates iron-oxide precipitates within the encapsulin nanocompartments as structural elements that are themselves already electron-dense and are thus also suitable for EM techniques that do not involve heavy-metal stains, such as cryo-ET. FIG. **6**A: 3D chart of a QtIMEF dimer. FIG. **6**B: Coomassie and Prussian-Blue stained BN-PAGE demonstrating QtEnc iron loading in mammalian cells upon supplementation of ferrous ammonium sulfate. FIG. **6**C: TEM micrograph of HEK293T cells showing contrasted shapes, generated by QtEnc as structural element with biomineralized iron oxide cores. FIG. **6**D: The metal biomineralization can be supported by co-expression of metal importers for ferrous iron (Zip14, SEQ ID NO:219) and manganese (DMT1, SEQ ID NO: 218) such that doping of iron biominerals with manganese can be obtained. FIG. **6**E: The ferroxidase activity of IMEF can here be supported by the multicopper oxidase Mnx (SEQ ID NOs: 222, 223, 224). FIG. **6**F: Alternatively, cystathionine-y-lyase (SEQ ID NO:220) can lead to the release of cysteines and subsequent formation of Sulfur clusters. Alkaline phosphatase (SEQ ID NO:221) can trigger the intraluminal formation of calcium-phosphate precipitates to which heavy metals can bind.

[0073] FIG. **7**: Dual-mode contrast-generating unit for EM and SRLM FIG. **7**A: Predicted 3D model of a fusion of the ultra-small engineered fluorescent protein eUnaG and MT3 yielding contrast for fluorescence techniques as well as EM. FIG. **7**B: Widefield fluorescence microscopy of HEK293T cells expressing eUnaG-MT3-QtEnc^{FLAG} (SEQ ID NO: 155). FIG. **7**C: CN PAGE analysis (upper blot) of lysates from HEK293 cells expressing either eUnaG-MT3-QtEnc or eUnaG-2xMT3-QtEnc^{FLAG} (SEQ ID NO: 156). The UV fluorescence image (lower blot) shows the bands corresponding to the assembled high-molecular weight encapsulin fusion emitting green light. FIG. **7**D: CN PAGE loaded with lysates of HEK293T cells expressing either mGreenLantern (SEQ ID NO: 157) or CaMPARI2-MT3-QtEnc (SEQ ID NO: 158) fusions. The UV fluorescent image shows green fluorescent bands corresponding to the assembled nano-compartments as structural elements. These data show that even larger fluorescent protein cargos can be placed upstream of the EM-contrast generating unit MT3. FIG. **7**E: TEM micrograph of HEK293T cells expressing eUnaG-MT3-QtEnc^{FLAG} showing highly contrasted shapes, i.e., ~40 nm spherical barcodes generated by the encapsulin with a distinct lumenal phenotype. A contrasted internal ring with a smaller diameter is visible, as well as a bright center spot (see, zoom-in). FIG. **7**F: TEM micrograph of HEK293T cells expressing eUnaG-2xMT3-QtEnc^{FLAG}. The presence of double the numbers of MT3 contrast generating units fills the lumen of the encapsulin structural element such that it can be distinguished from e) as a distinct concentric barcode. FIG. **7**G: While fusions of fluorescent proteins to the C-terminus of encapsulin monomers, facing to the outer surface of the structural element, are likely to prevent proper encapsulin assembly, the inventors could reconstitute tripartite split-GFP on the outer surface of encapsulin by co-expression of C-terminal fusions of GFP S10 (SEQ ID NO: 25) and GFP S11 (SEQ ID NO: 26) to QtEnc and co-expression (or alternatively also C-terminal fusion) of Split GFP1-9 (left scheme) (SEQ ID NOs: 23, 24 respectively). Correct assembly of the fusion constructs is shown via BN-PAGE, and reconstituted fluorescence is shown via epifluorescence microscopy only if all three components are expressed (on the right and bottom panels).

[0074] FIG. **8**: Modular targeting of host molecules Multiplexed targeting of guest molecules to the inside of structural elements can be achieved via bioorthogonal coiled-coil libraries. This modular targeting enables multi-modal detection in addition to EM contrast. FIG. **8**A: Shown here are coiled-coils targeting different fluorescent proteins selectively to the lumen of encapsulins (with different triangulation numbers: QtEnc (T=4), MxEn (T=3), TmEnc (T=1)) harboring the corresponding coiled-coil binding partner. The CN-PAGE panel on top shows the fluorescent signal of the cargo proteins encapsulated in either the T1, T3, or T4 encapsulins. FIG. **8**A demonstrates that the given fluorescent protein (FP) fused to a given coiled-coil will only be encapsulated if the encapsulin structural element carries the cognate coiled-coil (CC) partner. Best working CC-pairs to ensure bio-orthogonal targeting to the Tm, Mx, or Qt encapsulin species have been identified and described herein. This targeting strategy allows for bio-orthogonal targeting of fluorescent proteins, which is not possible with the promiscuous native encapsulation signal of encapsulins. Exemplary sequences for this construct is provided in SEQ ID NO: 159-164. FIG. **8**B: Corresponding fluorescent microscopy images show an enrichment and stabilization of the coil-coil-tagged fluorescent proteins inside the lumen of the encapsulin shells with the corresponding coiled-coil binding partners. Alternatively or in addition, the CCs can also be linked with an MT3 linker to enable EM and fluorescent detection (SEQ ID NO: 21 with an example for a cognate coiled-coil binding partner with SEQ ID NO: 22). Alternatively, exogenous fluorophores can be bioconjugated via SNAPtags or Halotags fused to the inner surface of encapsulins. Exemplary sequences (SEQ ID NO: 210, 211) FIG. **8**C: Independent demonstration of the highly selective binding of the selected pairs of coiled-coils inside the lumen of encapsulin, here measured by bioluminescent photon counts from a luciferase cargo. Coiled-coils were chosen from Lebar et al., Nat.Chem.Biol. (2020); Chen et al., Nature, (2019).

[0075] FIG. **9**: Encapsulins with different radii: FIG. **9**A: Schematic representation of encapsulin systems with different triangulation numbers, resulting in the following radii: *Q. thermotolerans* (Qt; T=4, 240 sub-units, 40 nm;), *M. xanthus* (Mx; T=3, 180 sub-units, 32 nm;), and *T. maritima*

(Tm; T=1, 60 sub-units, 20 nm;). FIG. **9**B-FIG. **9**D: Exemplary TEM micrographs of HEK293T cells expressing either MT3-QtEnc^{FLAG} (SEQ ID NO: 165), MT3-MxEnc^{FLAG} (SEQ ID NO: 166), or MT3-TmEnc^{BC2Tag} (SEQ ID NO: 144). The scale bar is 100 nm, and the scale bar in the zoom-ins is 20 nm. An exemplary sequence for this construct is provided in SEQ ID NO: 212. FIG. **9**E: Frequency distribution of diameters of the encapsulin nano-spheres as structural elements shown in b)-d). FIG. **9**F: CN-PAGE analysis of lysates of HEK293T cells expressing MT-fused encapsulin variants of varying radii. The MT-fused variants have the same electrophoretic mobility as the wild-type variants indicating that the MT domains (contrast-generating units) are lumenal and do not impair encapsulin assembly or change their geometric properties. FIG. **9**G: Mean image (left) of 100 manually segmented instances of TEM images of MT3-MxEnc and MT3-QtEnc expressed in HEK293 cells (shown right). Intensity profiles along the indicated on the mean images on the left (center panels), showing the distinct inner diameters of the white center and the outer black ring. Importantly, the geometrically distinct EM contrast can not only be detected in TEM, capable of high magnifications, but also in SEM compatible with high-throughput analysis by volume EM. FIG. **9**H: Higher-magnification TEM micrographs of *Drosophila* neurons in the optic lobe expressing MT3-QtEnc-FLAG-NLS (left) or MT3-Mx-FLAG-NLS (right). Scale bars are 50 nm (20 nm for inset). (Exemplary sequence for a fusion of the NLS to FLAG is provided in SEQ ID: 167). FIG. **9**I: juxtaposition of TEM and SEM images taken from brains of a *Drosophila melanogaster* line (elav-Gal4 x UAS-QtEnc^{FLAG}-NLS; SEQ ID NO: 168), which was fixed and stained with standard protocols. Ultrathin sections were then captured either on TEM grids or on silica wafers for subsequent analysis by SEM (inverted contrast), allowing for the analysis of the identical cell. FIG. **9**J: Same protocol as in h) but with MxEnc expressed in all neurons of the nervous system of *Drosophila melanogaster* (elav-Gal4 x UAS-MxEnc^{FLAG}-NLS; SEQ ID NO: 167). FIG. **9**K: MT3-QtEnc expressed in *Drosophila melanogaster* neurons. The tissue was fixed, embedded, stained, and prepared for FIB milling. FIB milling uses a focused ion beam to sequentially ablate material from a sample to enable volumetric imaging. After each milling step, an SEM image is acquired, and 3D information can be reconstructed from the resulting image series. An image volume of 3696 nm×1956 nm×204 nm (image width× image height×milling length) was acquired on a Crossbeam 550 FIB-SEM (Zeiss) with a voxel size of 4 nm using an InLens detector at 1.3 kV and a working distance of 5 mm. FIB beam settings: 30 kV/700 pA. Acquisition time: 67 minutes. The scale bar in the overview image represents 400 nm, the scale bar in the cropped image represents 50 nm. Inset: Ortho-slices through selected nanospheres.

[0076] FIG. **10**: Concentric barcodes Structural elements based on the concatenation of MT3 domains fused to Enc monomers produce differential concentric barcodes. FIG. **10**A: Scheme showing the single, double, or triple repeat MT-domains fused to the N-terminus of QtEnc, which provides increasingly more osmiophilic cysteine residues that also reach further into the lumen of the encapsulin shell. Note that for the triple repeat, a chimeric metallothionein series from multiple organisms was used to minimize redundant DNA sequences, which can be unstable (see, e.g., SEQ ID NOs: 5, 169). FIG. **10**B: TEM image of ultra-thin heavy metal-stained slices of HEK293T cells expressing MT3-QtEnc^{FLAG} resulting in an annular electron-dense ring with a bright center (left), 2xMT3-QtEnc^{FLAG} with a much smaller bright center, and 3xchimericMT3-QtEnc^{FLAG}, which adds an additional layer of contrast into the spherical structural element, i.e., an additional concentric ring in the 2D projection of the TEM, leaving no white center. FIG. **10**C: Corresponding barcode shapes for the MxEnc with smaller outer diameter. Singular or tandem MT-domains fused to the N-terminus of MxEnc. FIG. **10**D: Line plots through the center of an exemplary MT3-QtEnc^{FLAG} and 2xMT3-QtEnc^{FLAG} particle. Scale bar: 100 nm. FIG. **10**E: Schematic showing how additional contrast generating units (CGU), such as MT3 or FABP can be added to the outer surface of encapsulins (or other structural elements) via direct fusion, SpyTag/SpyCatcher interaction, or intrabody/XFP interaction (SEQ ID NOs: 191, 192). The spacing between such additional concentric barcodes can be controlled by a rigid spacer such as SasG. The rotational invariance of the concentric barcodes ensures a robust readout in nanoscopy even if an isotropic resolution cannot be obtained. In addition to encapsulins, the concentric assembly can also be achieved by other spherical structural elements such as ferritin or viral capsids, such as MS2 (SEQ ID NO: 100), *Acinetobacter* phage AP205, or Qbeta phages. FIG. **10**F Examples for outer contrast rings obtained by either binding the contrast-generating units MmMT3 (Mm stands for *Mus musculus*, SEQ ID NO: 1) or B-FABP (exemplary sequence SEQ ID NO: 36) to the outer surface of encapsulin via the isopeptide forming partners SpyTag/SpyCatcher. The construct comprising MmT3 is given as SEQ ID NO: 171. The construct comprising B-FABP is given as SEQ ID NO: 150. The TEM micrographs on the right show the corresponding concentric barcodes added to the outer surface of encapsulin, which can be modularly combined with intraluminal modifications with MT3.

[0077] FIG. **11**: Vault assemblies The claimed structural elements comprise vaults. Vaults consist of 2 hemi-vaults, each consisting of 78 sub-units of the major vault protein (PDB: 6BP7). FIG. **11**A: The schematic (left) and graphics (right) show several of the engineered vault constructs. The bimodal fluorescent and EM visible cargo (mEoS4b fused to APEX2; SEQ ID NO: 208) are connected to a targeting moiety (mINT, SEQ ID NO: 170), enabling cargo packaging into the vault compartment. In comparison to the wild-type vault, in which both termini face to the inside of the nanocompartment, an external attachment point is installed via insertion of palmitoylation sites contained within SNAP25 (SEQ ID NO: 78) via two helix-loop-helix motifs (antiparallel (AP) AP4 and P3 coils). Alternatively, an S-palmitoylation signal contained in Gap43 (SEQ ID NO: 209) is placed on the N-terminus to prevent the holo-vault assembly from two halves but instead target a hemi-vault to the membrane. FIG. **11**B: The corresponding fluorescent images show the distribution of mEos4b as destabilized cargo to the vault compartments. Whereas the distribution of mEos4b inside the wild-type holo-vaults is homogeneous inside the cytosol, the SNAP25-modified vaults show micrometer-sized green-fluorescent arrays, while the Gap43-modified variants SEQ ID NO: 209 show intracellular membraneous clusters. FIG. **11**C: TEM micrographs showing the large arrays of the SNAP25-modified vaults (left) (SEQ ID NO: 78). In comparison, the expression of vaults modified with APH peptides (using regular and trun-

cated antiparallel CCs from GA354 (SEQ ID NO: 79) and GA355 (APH) (SEQ ID NO: 80), on their surface results in clusters of different packing. FIG. **11**D: Comparison of distinct patterns generated in EM by vault constructs with external SNAP25 motif (left) and with IMEF as N-terminal fusion (right). FIG. **11**E: Fluorescence microscopy images of HEK293T cells expressing the major vault protein where a small fluorescent eUnaG (enhanced UnaG) protein was fused to the internal HLH domain, and the red fluorescent protein mScarlet was targeted to the lumen via an mINT motif. An exemplary sequence for this construct is provided in SEQ ID NOs: 77-85.

[0078] FIG. **12**: Nanofibrils and clusters Contrast-generating units such as MT3 can be added to naturally occurring or de novo designed fibrils or lattice-forming components to generate EM-contrasted structural elements. FIG. **12**A: AlphaFold prediction of the major curlin subunit CsgA from *E. coli*. This protein has been shown to form long amyloid-like fibers. FIG. **12**B: CsgA optimized for intracellular expression fused to a SpyTag was co-expressed with MT3 fused to the cognate SpyCatcher binding partner (SEQ ID NOs: 112, 171), yielding contrast-enhanced fibers. The TEM micrograph shows bundles of these highly contrasted fibers in the cytosol of HEK293T cells. As an alternative embodiment, de novo designed fibril forming proteins may be used for the generation of a structural element: FIG. **12**C: 3D image of a cutaway view of a de novo designed filament-forming protein (DHF119) (left). Confocal fluorescence microscopy of HEK293T cells expressing DHF119-sfGFP (right) (DHF119 published in Shen et al., Science (2018)). DAPI-stained nuclei are depicted blue, whereas the green signal shows the perinuclear DHF119 filaments. The scale bar is 20 μm. FIG. **12**D: Corresponding TEM micrograph of HEK293T cells expressing the contrast generating unit MT3 fused to DHF119_sfGFP filaments (SEQ ID NO: 110). FIG. **12**E: Two-component lattices (Di13b2 and Di13a, both published in Ben-Sasson et al., Nature (2021)) fused to GFP, which yield lattices as shown on the confocal fluorescent microscopy image. Scale bar is 20 μm. FIG. **12**F: Corresponding TEM micrograph in which MT3 is fused as a contrast-generating unit (SEQ ID NO: 1).

[0079] FIG. **13**: Concatenation of contrast generating units The contrast generating units can also be concatenated via short linkers to generate nanometer-sized contrast-generating units. FIG. **13**A: Shown here is the progression from a dimer, trimer, tetramer up to a decamer of FABP using its natural termini. One G-E-G repeat of SasG (~16 nm) is shown as a reference for scale (top of each image). Repeating sequences on the nucleotide level can be avoided by exploiting sequence differences between the subtypes from the large FABP family. Individual FABP contrast-generating elements can also be connected via MT3, serving as a flexible linker and, in addition, as a contrast-generating unit. Exemplary sequences for these constructs are given in SEQ ID NOs: 194, 195. FIG. **13**B: To increase the geometric diversity of the resulting structural elements, FABPs can be circularly permutated (cpFABP; SEQ ID NO: 193) to generate new termini between the alpha-helices. If those termini are fused between two cpFABPs to generate dimers, the angle can be controlled by the linker used for the fusion. FIG. **13**C: Via side-by-side concatenation of FABPs, cylindrical shapes can be generated that can be closed to toroidal shapes, which can be stabilized via hydrophobic moieties and further be spatially organized via, e.g., isopeptide bonds and inteins. An exemplary sequence for these constructs is given in SEQ ID NO: 196.

[0080] FIG. **14**: Mono-to-polyvalent hubs as structural elements While the substantial size that can be obtained with self-assembling nanostructures is an advantage for building nanoscopy-readable structures, it comes with the natural disadvantage that the resulting structure is symmetric and multivalent. Monovalent hubs or adapters to which several contrast-generating units can bind are thus beneficial. FIG. **14**A: (left) 3D image of an exemplary emFP (electron microscopy Fluorescent Protein) based on GFP showing the tag insertion points at the termini and an internal loop. (Right) Linear scheme showing the different emFP variants with the insertion points and a number of their respective intrabody-addressable tags. Exemplary sequences for these constructs are given in SEQ ID NOs: 92-99, 172-178. FIG. **14**B: Schematic of the contrast unit binding to the emFPs consisting of intracellularly-expressable intrabody or scFv fragment, the respective metal interacting unit (or a tandem thereof), GB-1 (to enhance solubility), a FLAG-epitope for detection, and a C-terminal RxxG degron for background suppression. Exemplary sequences for these constructs are given in SEQ ID NOs: 172-178. FIG. **14**C: Immunocytochemistry of HEK293 cells expressing LifeAct-emFPv4 (SEQ ID NO: 179) localizing to filamentous actin. The green signal (top) represents the emFPv4 (SEQ ID NO: 94) itself, whereas the red signal (bottom) corresponds to the FLAG-tag on the contrast unit, which colocalizes with the green signal indicating successful binding to the hub. FIG. **14**D: Anti-FLAG western blot of whole-cell lysates from HEK293T cells co-expressing LifeAct-emFPv4 (SEQ ID NO: 179) plus the respective metal binders. The bands correspond to the expressed contrast units demonstrating their successful expression in mammalian cells. FIG. **14**E: UV fluorescence clear native PAGE analysis of lysates from HEK293T cells co-expressing LifeAct emFPv4 and the respective contrast unit. The green signal at the bottom corresponds to non-bound emFPv4, whereas the higher molecular smears correspond to emFPv4 bound to several contrast units. FIG. **14**F:Furthermore, a few selected viral capsids break the symmetry with portal, tails, or accessory proteins as known for picorna-, parvo-, micro-, and leviviridae. A specific example would be the maturation protein of MS2, *Acinetobacter* AP205 phages, or the Allolevivirus Qbeta phage. The maturation protein is a specific component in the MS2 capsid, which represents a unique single attachment point. Based on the detailed structural information, a monomeric attachment of, e.g., MS2 capsids to F-pilus motifs can be designed via the maturation protein, while the MS2 RNA (or a subset thereof harboring the critical stem-loops) can provide EM contrast. The mammalian expression vectors are shown on the bottom (see also sequences of SEQ ID NOs: 100, 101, 102, 103). FIG. **14**G: A preferred instantiation for engineered mono-to-polyvalent adapters or hubs is based on coiled-coil-rich proteins such as the Anbu protease (left) (SEQ ID NO: 88) or toroid protein (right) (SEQ ID NO: 89), in which the external coiled-coils can be replaced by designed coiled-coils that have high-affinity binding partners. PDB entry numbers are given in FIG. **14**G. At the termini, all of these surface-exposed coiled-coils can be augmented by CCC-tags or Suntags. CCC-tags are a linear concatenation of coiled-coils. Suntag allows for recruiting up to 24 copies via a single-chain variable frag-

ment (scFv) antibody to which a contrast-generating unit as described above can be attached. FIG. **14**H: Other preferred examples of proteins with engineerable hypervariable loops that can be replaced with epitopes, coiled coils, or isopeptide-bonds are adhesins (left) (SEQ ID NOs: 89, 90) and fiber-knob domain proteins (right) (SEQ ID NO: 91). PDB entry numbers are given in FIG. **14**H.

[0081] FIG. **15**: Programmable stoichiometry control using read-through motifs FIG. **15**A: Structural elements can be equipped with genetically controlled internal and external attachment points to bind contrasting units, target the structures to molecules of interest, or generate geometric patterns. Protein domains might be directly fused to the termini or an internal region of the structural element. Protein cargos might be internally docked via endogenous targeting signals such as encapsulation signals in the case of encapsulin and mINT signals in the case of vaults. Furthermore, attachment points in the form of nanobodies, CC domains, SpyTag or SpyCatcher domains, SNAP/Clip-Tag domains, and Halo-Tag domains might be fused. FIG. **15**B: Since most structural elements are self-assembling and highly symmetrical, programmable translational read-through can be applied to regulate the stoichiometry of (surface) modifications. The schematic shows the genetic makeup of an exemplary programmable read-through (RT) cassette consisting of a QtEnc monomer gene with a C-terminal FLAG epitope followed by a stop codon and read-through promoting sequences (e.g., SEQ ID NO: 180, including a CTATCC DNA sequence after the stop codon, which promotes ribosomal (translational) read-through). When ribosomal read-through occurs, the ribosome skips the stop codon and continues to synthesize the nascent polypeptide chain. By using different RT motifs, different degrees of read-through can be obtained, yielding encapsulin nanostructures that consist of monomers with a C-terminal FLAG epitope (immediate stop, no RT) or with a FLAG with an additional intrabody domain (stop skipped, read-through occurred). The rate of read-through is determined by the stop codon and the respective RT motif (Exemplary SEQ ID NO: 74-76). The RT rate is defined as the number of monomers with the additional intrabody, which arise from the RT divided by the total number of monomers. Another variant of the RT cassette uses a fast-cleaving intein mutant (SspDnaE; SEQ ID NO: 181), followed by a P2A peptide to yield two fully independent, unfused, scarless polypeptide chains since the middle intein module splices on the N-terminus and downstream polypeptide will be liberated via the P2A peptide (SEQ ID NO: 182). Therefore, the RT system can be used to co-express two unrelated polypeptides at different ratios depending on the RT motif used. FIG. **15**C: Densitometric analysis of RT rates depending on different stop-codon RT motif combinations. The combination of stop codons with RT motifs allows for adjusting RT rates between ~1 and 20%. Another way of quantifying the RT rate is based on the complementation of a split NanoLuciferase. If RT occurs, a HiBit epitope will be translated downstream of the intrabody sequence. After cell lysis, purified LgBit protein is added, which reconstitutes a functional luciferase yielding a luminescence signal serving as a proxy for RT.

[0082] FIG. **16** Endogenous scaffolds FIG. **16**A: Structural elements can be spatially patterned via naturally occurring cellular scaffolds. The TEM micrograph of HEK293T cells expressing QtEnc modified with C-terminal farnesylation signal (SEQ ID NO: 40) shows the QtEnc capsids targeted to cellular membranes. FIG. **16**B: Structural elements can also be arranged on the cytoskeleton. The confocal fluorescence microscopy images show HEK293T cells expressing mScarlet-I-loaded QtEnc C-terminally modified with a KinTag peptide (Cross et al., Cell Chemical Biology (2021); SEQ ID NO: 113) mimicking a cargo adaptor connecting to endogenous motor proteins. The fluorescent signal represents the location of the encapsulins nanocompartments as structural elements within the cell, which can be seen as dotted signals in the perinuclear region and the periphery. FIG. **16**C: TEM micrograph of HEK293T cells co-expressing 2xMT3-QtEnc^{antiGFPIB} (SEQ ID NO: 183) and the lysosomal marker LAMP1-GFP, which presents GFP on the outside of the lysosomes. The micrograph shows that highly contrasted QtEnc nanostructures co-localize with the lysosomes. FIG. **16**D: In this example, the membrane is used as a scaffold via expressing membrane-localized GFP (GFP-CAAX) to which the anti-GFP intrabody on the surface of QtEnc binds to (left). In the control condition, GFP-CAAX is again expressed, but the intrabody is replaced with a FLAG tag (right). The contrast in both examples is provided by co-expression of the metal importer Zip14 and the ferroxidase IMEF targeted to the encapsulin via an encapsulation signal.

[0083] FIG. **17** Genetically controlled scaffolds for barcodes readable by nanoscopy FIG. **17**A: (top) Schematic of the use of the microbial filamentous protein SasG, a rigid hetero-bifunctional scaffold from *S. aureus*, to enable nanoscopically visible shapes, preferably barcodes. Of note, SasG consists of a repeating pattern of G5 and E units. G5_1-G5_2 is an exemplary representation of the length, wherein G5_1 and G5_2 are connected via E(1). G5_1-E(1)-G5_2, for instance, yields 16 nm. G5_1-G5_4 means G5_1-E(1)G5_2-E(2)-G5_3-E(3)-G5_4 yields 30 nm. Exemplary sequences for these constructs are given in SEQ ID NOs: 114-123. The termini are fused to sfGFP (SEQ ID NO: 184) and mCherry (SEQ ID NO: 18, respectively, which can be addressed with structural elements, in this case, with QtEnc modified with an antiGFP intrabody and TmEnc with an anti-mCherry intrabody (LaM-4) (SEQ ID NOs: 186, 187). Of note, SasG is here used as a genetically controlled scaffold. (bottom) Schematic representation of modular make-up of SasG filaments consisting of alternating G5 and E units yielding different sizes. sfGFP-G51-G54-mCherry (SEQ ID NO: 188) yields a length of approximately 30 nm. FIG. **17**B: Clear native PAGE analysis of lysates from HEK293T cells expressing different sfGFP-SasG-mCherry variants yielding different lengths. The CN-PAGE gel shows an sfGFP-mCherry tandem as well as different lengths of SasG as a spacer between sfGFP and mCherry. FIG. **17**C: Live wide-field fluorescence microscopy imaging of HEK293T cells expressing sfGFP-SasG_G51-G52-mCherry+MT3-QtEnc^{antiGFPIB}+P2-TmEnc^{antimcherryIB} (LaM-4) (SEQ ID NOs: 114, 189, 109). The red and green fluorescent channels demonstrate the expression of the heterobifunctional scaffold. Clusters are visible, which indicates the interaction between the scaffold and the polyvalent encapsulins serving as structural elements. FIG. **17**D: Corresponding TEM micrographs of HEK293T cells co-expressing sfGFP-SasG_G51-G52-mCherry+MT3-QtEnc^{antiGFPib}+P2-TmEnc^{antimcherryIB} (LaM-4). Clusters of 40 nm QtEnc structures surrounded by TmEnc capsules can be observed. The zoom-in shows the distinct spacing

between the patterning of QtEnc and TmEnc, which can be used to encode multiplexed information in an analogy to a QR barcode. FIG. **17**E: In distinction to d), a longer SasG with 4 G5 units (SasG-G51-G54) was co-expressed here. FIG. **17**F: Here, clusters containing sfGFP-SasG_G51-G52-mCherry linkers (~16 nm) and clusters containing sfGFP-SasG_G51-G54-mCherry (~30 nm length) are juxtaposed for comparison. FIG. **17**G: In addition to linear scaffolds, the rigidity of SasG also allows for more complex scaffolds. Depicted here is an example with triangular shapes in which isopeptide bonds (SpyTag/SpyCatcher, SnoopTag/SnoopCather) or inteins (SEQ ID NOs: 115-117) were used as unique connectors between the edges. The fluorescent proteins sfGFP, mCherry, and mTurquoise are also positioned at the edges to serve as binding sites for structural elements. FIG. **17**H: CN-PAGE analysis of lysates from HEK293T cells expressing different combinations of the components shown in g Under fluorescence illumination, the CN-PAGE gel demonstrates the expected combination of individual elements (color-coded). The bio-orthogonal reaction of the components is apparent from the mass shifts in the gels and the color mixing (not apparent in a black/white copy of this FIG. **17**H). The last lane (1+2+3) shows a high molecular weight band (dashed box) corresponding to the assembled triangle. The fluorescent proteins positioned at the vertices can be replaced by emFPs (SEQ ID NOs: 92-97) or other hubs (see, FIG. **15**) or contrast generating units. FIG. **17**I: Alternatively, unbounded clusters can be generated by linking together structural elements such as shown for encapsulins and multivalent de novo cages. The TEM micrograph shows HEK293T cells co-expressing iron-mineralizing QtEnc C-terminally modified with a SpyTag, which covalently clusters with 13-01 (Hsia et al., Nature (2016)), a de novo designed icosahedron, presenting 60 cognate SpyCatcher binding partners. FIG. **17**J: As an alternative to the proteinaceous scaffold exemplified by SasG, RNA scaffolds can be designed via ROAD (Geary et al., Nat. Chem., (2021)) can be used but using L7ae and BIV-tat (SEQ ID NOs: 63, 64) instead of MCP and PCP as attachment points and incorporating fluorescent aptamers such as Spinach (SEQ ID NO: 55) and Dir2s (SEQ ID NO: 57).

[0084] FIG. **18** Geometric sensing via proteolytic unmasking and molecular mapping Assembly of structural elements can be controlled via proteolytic de-blocking of monomeric subunits. FIG. **18**A: Schematic of calcium-dependent proteolytic unmasking of sterically blocked QtEnc monomers. The scheme shows the different genetic components, including the blocked monomer with a TEV cleavage site (3xLBT15-TEVsite-QtEnc-FLAG; SEQ ID NO: 128), the two calcium-dependent Split TEV parts (SCANR; published in O'Neil et al, ACS Chemical Biology, (2018)), a degron-tagged NanoLuc-cargo; SEQ ID NOs: 129, 130), which serves as a reporter for assembly because it will be protected upon proteolytic de-blocking, and a regular TEV protease. Upon elevated Ca^{2+} levels, the SCANR parts will be reconstituted, the re-complemented TEV protease will cleave off the sterical 3xLBT block, the encapsulin nanocompartment will assemble and encapsulate the Luciferase cargo enzyme such that it is protected from degradation and give bioluminescent signal. FIG. **18**B: In this example, QtEnc monomers are blocked with a triple LBT15 domain but can be unblocked via a bio-orthogonal protease such as TEV (TEVp), which leads to the assembly of the encapsulin nanospheres as shown by CN-PAGE. The protease may be expressed constitutively, under control of a promoter of interest, or can be made responsive to a second messenger such as calcium by using an engineered calcium-sensitive protease such as SCANR. Upon co-expression of SCANR, encapsulin assembly gradually increases with calcium, as can be seen by the increasingly stronger bands for the encapsulin on CN PAGE as well as an increasing luminescence signal obtained from the gel from a co-expressed NLuc cargo, which is destabilized unless it gets encapsulated inside the encapsulin shell. FIG. **18**C: SDS-PAGE of material from a FLAG pull-down from cells expressing the conditions in b). The molecular weight shift indicates calcium-dependent cleavage of the blocking domain when either TEVp or SCANR+ionophore are present. FIG. **18**D: Bulk luminescence reading of the experiment described in b). FIG. **18**E: TEM micrograph of HEK293T cells expressing the blocked monomer+SCNAR 24 h post ionophore treatment. Assembled MT3-QtEnc^{FLAG} nanocompartments (structural elements) are visible throughout the cytosol. FIG. **18**F; and FIG. **18**G: SasG filaments can also be engineered to increase in length upon a cellular signal or state. This can be achieved by using engineered split intein domains, which can be fused to fragments of SasG to reconstitute SasG filaments of different lengths. In this example, sfGFP-SasG_G51 units are reconnected to SasG_E1_G52_mCherry units via different split intein systems (VidaL in f) and Npu DnaE in g); SEQ ID NOs: 121-123 and 118-120). The reconstitution of the fragments is indicated by the yellow band running above 242 kDa on CN-PAGE, which has the same electrophoretic mobility as the sfGFP_SasG-G51_E1_G52_mCherry construct. FIG. **18**H: SasG filaments can also grow conditionally by using a self-growing EG fragment that has split-intein domains on either side of the building block (SEQ ID NOs: 120, 123). The growth can then be capped off by a capping unit (SEQ ID NOs: 119, 122). FIG. **18**I: This conditional growth can be made directional by using QtEnc^{antiGFPIB} as a scaffold, in which a calcium-dependent TEV (SCANR) would un-cage a caged split-intein (Gramespacher et al., 2017) and initiate growth. Upon a certain cellular signal of interest, the growth can be capped off by expressing the capping unit. FIG. **18**J: Proteolytically triggered nanostructure assembly can also be realized with vaults. The schematic shows a split vault monomer, in which each half is blocked by split intein that can be activated via proteolytical cut by, e.g., TEV, thus leading to the intein-mediated (supported by a coiled-coil motif) fusion of an intact vault monomer, exposing a SNAP25 motif. FIG. **18**K: The fluorescence images show the TEV-dependent agglomeration of a fluorescent cargo (mScarlet docking via the mINT binding site) compared to the condition in which non-split vault monomers are used (right column). FIG. **18**L:To complement molecular mapping via direct binding to the target biomolecule of interest, a deactivated version of Trim21 (dTrim21, SEQ ID NOs: 138, 139), incapable of auto-ubiquitinylation, can be co-delivered to cells (or expressed) together with standard antibodies to a target of interest, to act as an adapter to a structural element or scaffold. Shown here is a preferred instantiation, in which a fusion of mCherry or GFP to dTrim21 is used in combination with an encapsulin as a structural element harboring an anti-mCherry (Lam4) (SEQ ID NOs: 186, 187) or anti-GFP intrabody on the surface.

[0085] FIG. **19**: Geometric sensing via a change in the concentric barcode or patterning FIG. **19**A: Geometric sens-

ing can be conducted via recruitment of contrast generating units to the surface of structural elements. Shown here is the specific case of FABPs recruited via the interaction of calmodulin and calmodulin-binding peptides to encapsulins (SEQ ID NOs: 197, 198), which alters the contrast contour of the concentric barcode. Please note that this mode is the same as in FIG. **10**E and FIG. **10**F, except that the addition of the external concentric barcode is dependent on the calcium-driven binding of calmodulin to calmodulin-binding peptides. Bottom: In the encapsulin lumen, concentric barcodes can also be modified by using contractile elements such as engineered contractile elements from troponin that will shorten the distance to the protein shell upon binding of calcium (SEQ ID NOs: 136, 137). FIG. **19**B: In another preferred embodiment, the agglomeration state of structural elements such as encapsulin can be changed via calcium-mediated interactions of calmodulin and calmodulin-binding peptides. As another polydentate kernel for agglomeration, ferritin such as *Helicobacter pylori* can be used as a fusion to calmodulin (SEQ ID NO: 134). The data show the formation of fluorescent clusters of encapsulins loaded with fluorescent cargo and equipped with respective calcium-binding motives after adding 10 μM calcium ionophore. An analogous system can be built for phosphorylatable peptides (e.g. SEQ ID NO 239) and phosphopetide-binding proteins such as SEQ-ID NO: 206. FIG. **19**C: Alternatively, a calcium integrator by patterning can also be achieved by changing the subcellular localization of the nanostructure as a function of calcium concentration. Shown here is a preferred embodiment in which an N-myristoylation signal contained within recoverin (PDB: 1jsa; SEQ ID NO: 238) is fused to the N-terminus to enable calcium-dependent relocalization. As known for recoverin, this membrane anchor swings out in the presence of calcium, causing relocalization to membranes. As shown by the green fluorescent mEOS4b signal, the resultant protein complexes are homogeneously distributed in the cytosol (top) unless calcium influx is triggered, leading to the generation of clusters, similar to the constitutively available S-palmitoylation signal (bottom) (SEQ ID NO:209).

[0086] FIG. **20**: Geometrically precise actuation via biomechanical actuation and/or deposition of local energy FIG. **20**A: The genetically controlled structural elements and scaffolds can exert biomechanical forces by polyvalent interactions with their surfaces while providing monitoring of the manipulations via nanoscopy. Shown here is the clustering of endogenous glutamate receptors in *Drosophila* neurons via multivalent encapsulins surface-functionalized with intrabodies against GFP, which co-cluster GFP-tagged receptors. The control (left) shows the regular distribution of GluCl receptors labeled with GFP in *Drosophila* brains when encapsulins, surface-decorated with anti-GFP intrabodies, were not expressed via a temperature-sensitive promoter. When expression of MT3-QtEnc^{antiGFPintrabody} was permitted at 29° C. (using the established system with a temperature-sensitive allele of GAL80) either after sparing early developmental phases (middle panel) or during development (right panel), mild or strong clustering of GluCl receptors in the somata was observed (McGuire et al, Science, (2003). Thanks to the controllable spatial arrangement of polyvalent binders by scaffolds such as SasG, more complex spatial manipulations can be systematically optimized via the nanoscopy readout. FIG. **20**B: Geometrically defined actuation can also be achieved via local deposition of energy through magnetic gradient fields. Shown here is the magnetic cell sorting (MACS) of HEK293 cells overexpressing encapsulins with the ferroxidase QtEnc_IMEF encapsulated as a host enzyme (and the iron importer Zip14, or mEos4b as control), which leads to the biomineralization of biomagnetic iron-oxide species. In addition, the iron-oxide-filled encapsulins are surface-functionalized with different attachment points (SpyTag, anti-GFP intrabody) to spatially organized via different co-expressed scaffolds, including the de novo cage 13_01 functionalized with a SpyCatcher (see FIG. **17***i*)), the filament DHF functionalized with GFP (see FIGS. **12**C and **12**D). In addition, a farnesylation tag (see FIG. **16***a*)) is used to target the encapsulins to the membrane. A FLAG tag serves as control. After expression in HEK293 cells (grown with ferrous ammonium sulfate), the cells were dissociated and passed over a commercial magnetic column (Miltenyi) placed either inside the magnetic field or outside as a control. The data (mean with SEM) show that magnetic gradients exert sufficient mechanical forces to retain entire cells that are expressing the geometrically organized magnetic and EM-visible geometric patterns. FIG. **20**C: Similar to magnetic gradients, encapsulins can also be equipped with photoabsorbers such as biosynthetic pigments, which allow for energy deposition via visible or infrared electromagnetic radiation. Shown here as an example are encapsulins that have the enzyme tyrosinase encapsulated via coiled-coil pairs (P1/P2 in the case of TmEnc (SEQ ID NOs: 159, 190), other combinations are given in FIG. **20**C), which generate the strongly absorbing polymer melanin from the endogenously available amino acid tyrosine. This polymerization reaction occurs inside the lumen of the nanocompartment, which prevents the product melanin from diffusing out, while the substrate tyrosine can diffuse into the lumen through the encapsulin pores. Spatially organized patterns of these photoabsorbing encapsulin species can be used to photoablate cellular structures. Monitoring can also be achieved via photoacoustic imaging, which picks up photoabsorption.

[0087] FIG. **21**: de-novo designed uranyl binding proteins. FIG. **21**A: A starting epitope of disjoint residues can be mapped by its backbone (i.e., sequence-agnostic) features. Inter-residue atomic distance matrices and internal dihedrals can serve as canonical fingerprints for epitope matching. Starting from a query epitope of a high-affinity uranyl-binding site, several binding sites could be identified on a compact coiled-coil miniprotein with backbone RMSD <0.3. The uranyl binding residues can thus be engrafted in place of the template's residues to create a single-domain protein with multiple binding sites. FIG. **21**B: Top scoring hits all exhibited a high level of symmetry and a strong local shape similarity to the uranyl-binding epitope. C3-, C4-, C5-symmetric hits were dominant among top hits, given the number of sites/atom constraints. FIG. **21**C: Three design templates were highly expressed in *E. coli* and showed helical spectra. Results are shown for 4bhv, and 5apq oligomeric variants as analyzed by SDS/PAGE and circular dichroism. FIG. **21**D: Average radial profile plot showing a comparison between MUP2_QtEnc (n=100) and 1M_QtEnc (n=100) integrated gray value from the center of the encapsulins outwards. FIG. **21**E: Normalized average particle for both MUP2_QtEnc (n=100) and 1M_QtEnc (n=100).

[0088] FIG. **22**: Lipid-binding proteins as contrast-generating units (CGUs). FIG. **22**A: Schematic representation of QtEncapsulin (QtEnc) fused to brain-derived Fatty Acid-

Binding protein (B-Fabp) B-Fabp and a mutant of B-Fabp with ablated lipid binding (B-Fabp-ko). FIG. **22**B: Average radial profile showing a comparison between QtEnc_B-Fabp and QtEnc_B-Fabp-ko integrated gray values from the center of the encapsulins outwards (n=50). FIG. **22**C: Normalized average particle for both QtEnc_B-Fabp (n=50) and QtEnc_B-Fabp-ko (n=50). FIG. **22**D: Background-subtracted average particles for both QtEnc_B-Fabp (n=50) and QtEnc_B-Fabp-ko (n=50) highlighting the contrast of the encapsulin shells, B-Fabp and B-Fabp-ko. The average image on the button shows the differential contrast due to lipid binding (i.e., the contrast from B-Fabp-ko subtracted from the contrast from Bfabp). FIG. **22**E: Schematic representation of *H. pylori* ferritin fused to B-Fabp and Bm3h. FIG. **22**F: Clear-Native Page with Coomassie Staining confirming the assembly of both constructs FIG. **22**G: Normalized average particle for both HpFtn_B-Fabp (n=200) and HpFtn_Bm3h (n=200). FIG. **22**H: Average radial profile plot showing a comparison between HpFtn_B-Fabp and HpFtn_Bm3h integrated gray values from the center of the encapsulins outwards (n=200). FIG. **22**I: Schematic representations of B-Fabp, B-Fabp-ko, Bm3h, and Bm3h-B7, a Bm3h mutant which should inhibit lipid binding, fused to the FLAG peptide. FIG. **22**J, FIG. **22**K: Purified (anti-Flag tag) lipid-binding proteins were incubated for 15' with 1 μM BODIPY™ FL C16 (Invitrogen). Fluorescence of the protein-bound phospholipids was detected on a 12% Tris-Glycine Gel run under native conditions with either UV illumination (left) or Coomassie Staining (right). A Fluorescent band can be seen on the UV-illuminated gel for B-Fabp_FLAG at double than expected MW, indicating the presence of a dimer. A band can be seen for both Bm3h and Bm3h-B7 at the expected MW, indicating that both have bound the BODIPY™ FL C16. FIG. **22**L Genetic construct, TEM contrast of an average particle (n=200), and overview TEM contrast obtained from B-FABP-fused C-terminally onto the de-novo cage 13-01.

[0089] FIG. **23**: Fluorescent encapsulins as high-contrast markers for CLEM. FIG. **23**A: Targeted fluorescent encapsulins can be generated by N-terminal attachment of the small monomeric fluorescent protein (eUnaG) to 1M- and 2M-Qt harboring surface-exposed anti-mCherry intrabodies. Alternatively, encapsulin monomers fused with outwardly directed eUnaG can be co-expressed with encapsulin monomers, a portion of which can harbor an intrabody. FIG. **23**B: Confocal laser scanning microscopy of fluorescent encapsulin composed of 1M-QteUnaG monomers co-expressed in a 4:1 ratio with monomers bearing anti-mCherry intrabodies (1M-Qtanti-mCherry) with and without co-expression of membrane-bound mCherry (mem-mCherryFLAG). The scale is 10 μm. FIG. **23**C: Corresponding TEM micrograph of mem-mCherry-targeted 1M-Qtanti-mCherry+1M-Qtanti-mCherry (4:1). Scale bars represent 100 nm. FIG. **23**D: Control over the ratios of the different encapsulin monomers can be achieved via tunable ribosomal read-through cassettes (rt) encoded on a single cistron. To this end, different combinations of stop codons and short rt-promoting motifs are combined at the end of the ORF encoding 1M-Qt. If rt occurs, the C-terminus of 1M-QtFLAG is further extended by an anti-GFP intrabody. FIG. **23**E: Confocal fluorescence microscopy of HEK293T expressing the gap junction-forming protein msfGFP-Cx43 together with the 1M-QtFLAGrt20santi-GFP, resulting in ~20% anti-GFP intrabodies on the encapsulin surface. The encapsulins variants are also rendered fluorescent by co-expression of mTagBFP2 as cargo proteins with the Qt encapsulation signal (QtSig) and an N-terminal degron (DD-N), leading to degradation of the non-encapsulated fluorescent proteins. Scale bars represent 10 μm. FIG. **23**F Corresponding TEM micrograph showing 1M-Qt (with ~20% anti-GFP intrabody) labeling a gap junction. (Scale bar represents 100 nm) FIG. **23**G Confocal microscopy images showing multiplexed tagging of heterologous gap-junctions consisting of msfGFP-Cx43 and Cx26[mut]-mCherry with encapsulin assemblies consisting of 1M-PfEncFLAG-miRFP670nano/1M-PfEncFLAG-anti-GFP (Ratio 4:1) and 1M-QtFLAG+1M-Qtanti-mCherry (Ratio 4:1)+DD-N-mTagBFP2-QtSig, respectively. The scale bars represent 10 μm.

[0090] FIG. **24**: Bioconjugation tags for exogenous synthetic fluorophores. FIG. **24**A: SNAP-tag (New England Biolabs) was N-terminally or C-terminally appended to 1M-Q, expressed at varying ratios with unmodified 1M-Qt in HEK293T cells and loaded as native lysates on CN-PAGE (left) to ensure the assembly of encapsulins. The fluorescent SNAPtag substrate TMR star (New England Biolabs) was added to the gel for visualization of fluorescence to confirm the functionality of SNAPtag. Notice that a combination of SNAPtag-fused monomers with non-SNAPtag-fused encapsulin monomers is necessary to enable encapsulin assembly, which can be stably expressed via the read-through motifs described below. Right panel: Fluorescence from CN-PAGE derived from CLIPtag and substrate instead of SNAPtag. Instead of CLIPtag also biotin-binding avidins can be used. FIG. **24**B: Combinations of SNAPtag-labeled encapsulins (as indicated in the figure) were expressed either untargeted or targeted to GFP-fused to the membrane (CAAX motif) via an anti-GFP intrabody also presented on the encapsulin surface. c) Fluorescence from TMR-star bound to SNAPtag-surface-presenting encapsulins is maintained after fixation with glutaraldehyde, 0.1% OSO_4, uranyl-acetate, dehydration over an ethanol series, and epon (Epon 812) embedding at 4 degrees celsius.

[0091] FIG. **25** Bioconjugation tags for exogenous synthetic fluorophores; fixation stable fluorescence contrast FIG. **25**A: Correlative light-electron microscopy signals from 1M-QtEnc-SNAP construct expressed in HEK cells fixed, heavy-metal-stained and embedded in resin. Encapsulins were identified in the SEM image with a pixel size of 2 nm. FIG. **25**B: The acquired SEM image was used to generate a binary mask of encapsulins, scaled to the FIG. **25**C: wide-field fluorescence microscopy images used to identify the SNAP-TMR dye fluorescence bound to the SNAP-tag on the surface of the encapsulins. FIG. **25**D: The fluorescence image was converted to a binary mask. FIG. **25**E: A template-matching algorithm was used to identify the areas with the highest correlation of both masks in the fluorescence modality. FIG. **25**F: The identified area was scaled to match the dimensions of the SEM image and overlaid on the top of the SEM image.

[0092] FIG. **26**: Bimolecular Fluorescence Complementation (BiFC). Green fluorescence protein was re-complemented from a tripartite split with the two smaller components fused to encapuslins. Upon co-expression of the complementary beta-barrel sfGFP1-9, an agglomeration of fluorescent encapsulin assemblies can be obtained. FIG. **26**A: Representation of Co-expressed QtEnc_sfGFPS10, QtEnc_sfGFPS11 and sfGFP1-9. Coexpression of QtEnc_sfGFPS10 and QtEnc_sfGFPS11 leads to the assembly of

mixed capsids displaying both fusions on the surface. Reconstitutions of full sfGFP can happen in between the S10 and S11 strands fused to different encapsulins, leading to aggregation of fluorescent encapsulin assemblies FIG. **26**B: TEM Micrograph showing the aforementioned aggregation. Scale bar is 250 nm.

[0093] FIG. **27**: Targeting of CLEM-compatible Enc variants via coiled-coil pairs. FIG. **27**A: Schematic showing of CLEM-compatible encapsulins via orthogonal coiled-coil (CC) pairs to a surrogate membrane target, including schemes of the genetic constructs. Co-targeting of mScarlet-I with an encapsulation signal is used to render encapsulin fluorescent in this experiment. FIG. **27**B: Confocal fluorescence microscopy experiment showing encapsulin targeting to the membrane as depicted in a. The scale bar represents 20 μm.

[0094] FIG. **28**: Multiplexed EM contrast with different numbers of concatenated metallothioneins (as CGU) and encapsulins of different diameters (as structural elements): FIG. **28**A: Schematic representation of the expression in mammals of modular constructs encoding self-assembling encapsulin monomers with N-terminal fusions of metallothioneins (M) and C-terminal surface modifications for targeting (encapsulins). Expression of the encapsulin variants results in self-assembly of hollow protein nanospheres with different triangulation numbers (T), different diameters, and 1-3 concatenated copies of M facing the lumen of the porous protein envelopes. FIG. **28**B: TEM micrographs (8× magnification, 0.5525 pixels/nm) following the standard protocol for fixation and heavy metal staining of HEK293T cells expressing the different encapsulin variants from a. Scale bars indicate 100 nm. The insets show the average values of the manually segmented image sections (n=1000, except n=900 for 1M-TmBC2Tag) for each condition (side length of insets: 89.2 nm (49 pixels), scale bars: 50 nm). FIG. **28**C: Multiclass semantic segmentation from end-to-end U-network architecture. FIG. **28**D: Multiplexed detection of different encapsulin class combinations in neighboring HEK293T cells with overlaid semantic segmentation masks. Scale bars represent 100 nm.

[0095] FIG. **29**: In vivo expression of several encapsulins (as structural elements) and metallothioneins as contrast generating units (CGU) to generate concentric barcodes in TEM in vivo in *Drosophila* brain. Overview confocal fluorescence microscopy images of the optic nerve head (OL) of a *Drosophila* line with pan-neuronal expression of FIG. **29**A: 1M-QtFLAG-NLS, or FIG. **29**C: 1M-MxFLAG-NLS containing a nuclear localization signal (NLS). FLAG epitopes on the outer surface of encapsulins (anti-FLAG, cyan for 1M-QtFLAG-NLS and red for 1M-MxFLAG-NLS) are colocalized with cell nuclei (with DAPI in blue, scale bar 5 μm) but do not show cytoplasmic expression (anti-Bruchpilot, gray). Scale bar is 25 μm. FIG. **29**B, FIG. **29**D: Corresponding TEM images with semantic segmentation maps as overlays. The scale bar is 100 nm. The insets show the average of the respective encapsulin class identified in the validation dataset (n=132, bounding box: 89.2×89.2 nm), FIG. **29**E: Overview image of confocal fluorescence microscopy of the central brain (CB) and optic nerve head (OL) and FIG. **29**F: zoom on *Drosophila* optic nerve head, which contains both T4-T5 and C3 somata and expresses 1M-MxFLAG-NLS and 3M-QtFLAG-NLS encapsulins, and FIG. **29**G: corresponding TEM micrograph with superimposed multiclass semantic segmentation masks, color-coded as in FIG. **28**. The scale is 100 nm.

[0096] FIG. **30**: Adeno-associated virus-encoded MT3-encapsulin fusion as genetically encoded EM marker in vivo in mouse brain. FIG. **30**A: Schematic representation of the genetic construct for expression of 2M-QtFLAG together with mScarlet-I via AAV transduction and intracranial injection of AAVs into mouse hippocampus. FIG. **30**B: Native (CN) and corresponding SDS gels after silver staining confirming assembly of 2M-QtFLAG after pull-down (PD) from the excised hippocampus. FIG. **30**C: Confocal fluorescence images of a coronal section through mouse brain one month after AAV transduction, showing direct mScarlet I fluorescence in red and encapsulin expression in cyan (anti-FLAG, FITC). Scale bars are 1 mm and 200 μm for the inset, respectively. The inset shows a magnified region in the hippocampus. FIG. **30**D: TEM overview image and FIG. **30**E: magnification of the region bounded by the white dashed lines in d. Inset shows further magnification on the 3 encapsulins located within the bounding box (black dashed lines). Scale bars for the respective magnifications are 1 μm, 100 nm, and 50 nm. FIG. **30**F, FIG. **30**G, FIG. **30**H: Instances of encapsulins in neuronal processes, color-coded semantic segmentations as defined in FIG. **28**. ÷ denotes membrane interruptions. Scale bars represent 100 nm.

[0097] FIG. **31**: Stabilized fluorescent RNA cargo targeted to self-assembling vaults as structural elements FIG. **31**A: Schematic showing the circularized Twister-Broccoli RNA aptamer(DOI: 10.1038/s41587-019-0090-6) equipped with a PP7 aptamer. The variant shows the circularized spinach Pb2+-binding aptamer (DOI: 10.1039/c5cc01526j) FIG. **31**B: TEM micrograph showing vaults with Twister-Broccoli (left column) and without (right column).

[0098] FIG. **32**: Mono-to-polyvalent hubs as structural elements FIG. **32**A: Schematic representation of B-Fabp fused to Anti-Moon-Tag, binding to up to 10 Moon-Tags that are present on LifeAct-emFPv4. FIG. **32**B: TEM micrograph of Hek293T cells coexpressing LifeAct-emFPv4 and B-Fabp Anti-Moon-Tag showing contrasted actin filaments. FIG. **32**C: Clear Native page showing the binding of B-Fabp_Anti-Moon-Tag to LifeAct_emFPv4. The higher MW smear corresponds to varying copies of Bfabp-Anti-Moon-Tag binding the up to 10 motifs on LifeAct_emFPv4. At a lower MW the band corresponding to unbound B-Fabp_Anti-Moon-Tag is visible.

[0099] FIG. **33**: Stoichiometry control. FIG. **33**A: Example densitometric quantification of fractional read-through across different combinations of stop codons and read-through motifs. Read-through resulted in the extension of the FLAG tag with an anti-GFP intrabody (higher molecular weight band). The heterotypic encapsulins were pulled down over the FLAG tag. Note that the example SDS-PAGE shown here does not include stop codon combinations with RT9us. The more complex banding pattern in the case of TAG IntP2A indicates intein splicing patterns. The lower band can be explained by correct splicing, resulting in a 46.9 kDa band (Qtanti-GFP). The higher band can be explained by incorrect splicing, resulting in Qt-anti-GFP fused to IntP2A with a size of 68.5 kDa. FIG. **33**B: Percent read-through (rt) determined from densitometric analysis of the respective SDS-PAGE bands (QtFLAG-linker-anti-GFP/QtFLAG*100), (Bars represent mean±SD). FIG. **33**C: Control condition in which 100% of the anti-GFP intrabody, ie, 240 copies per encapsulin were expressed, resulting in

agglomeration of msfGFP-Cx43 at encapsulin binding. The scale is 10 μm. FIG. **33**D: Alternative labeling of Cx43 with C-terminal fusion of Cx43-msGFP (as opposed to N-terminal fusion as in FIG. **3***e*) and corresponding confocal fluorescence microscopy images. encapsulins were made fluorescent by co-expression of mScarlet-I as cargo proteins. Scale bars correspond to 10 μm.

[0100] FIG. **34**: Multiplexed patterning using hetero-bifunctional SasG concatemers and encapsulins. FIG. **34**A: A rigid hetero-bifunctional cross-linker was constructed from SasG capped off with sfGFP and mCherry. Different linker lengths were obtained by increasing the number of G5 domains connected by E domains (sfGFP-2G-mCherry up to sfGFP-10G-mCherry). FIG. **34**B: Clear-Native (CN) PAGE under UV illumination loaded with lysates from HEK293T cells expressing sfGFP-SasG-mCherry hetero-bifunctional linkers (2-10G units) yielded discrete yellow fluorescent bands. FIG. **34**C: Co-expression of 1M-Qtanti-GFP and 1M-Tmanti-mCherry with indicated crosslinkers, or no cross-linker (0G) as control, resulted in distinct encapsulin patterns with ~40 nm ring-shaped centers from 1M-Qt surrounded by a corona of ~25 nm spherical objects (1M-Tm) in TEM micrographs. The upper panel shows 400×400 nm exemplary regions showing the concentric, programmable encapsulin patterns with overlaid semantic segmentation results from the end-to-end network (8k× magnification, 0.5525 pixels/nm). Scale bars represent 50 nm. The lower panel shows averages around selected Qt centers surrounded by a layer of Tm (n=25). The bounding box represents 165 nm. FIG. **34**D: Distances between the centers of 1M-Qtanti-GFP and the centers of surrounding 1M-Tmanti-mCherry for the indicated cross-linker lengths (n=30). FIG. **34**E: Average radial profile plots from the center of each 1M-Qtanti-GFP (n=25) outwards via the crosslinkers towards the surrounding ring of 1M-Tmanti-mCherry color-coded for crosslinker length. The vertical lines represent contrast minima generated by the surrounding 1M-Tmanti-mCherry.

[0101] FIG. **35**: Geometric sensing of Calcium via aggregation. FIG. **35**A: Confocal fluorescence microscopy experiment of HEK293T cells co-expressing 1M-QteUnaG-RS20, CaM-HpFtn (see FIG. **19***b*) and a blue-light inducible optogenetic tool (OptoCracl-mCherry), where Calcium influx is stimulated via OptoCrac (doi:10.7554/eLife.10024). The panels show different time points of two consecutive stimulation cycles where 1M-QteUnaG-RS20 and CaM-HpFtn aggregate upon stimulation and disaggregate when the blue light stimulation is off.

[0102] FIG. **36**: Protein Designs for CLEM-GECI. FIG. **36**A: Schematic depiction of the genetically encoded components of the correlative super-resolution light microscopy (SRLM) EM calcium indicator (CLEM-GECI). The underlying molecular mechanism is calcium-dependent recruitment of metal-binding proteins (TEM contrast) and exchange sites for reversibly binding fluorescent proteins (PAINT contrast) to monodisperse, cytoskeleton-associated nano-scaffolds genetically expressed in cells of interest. LIVE-PAINT (Oi et al, Commun Biol, 2020) is enabled by a docking- and an imager-peptide pair. To accelerate PAINT imaging by expressing relatively high concentrations of imager-peptide-FPs while minimizing the fluorescent background from unbound imager-peptide-FPs, we will use a protein FRET pair based on the previous publication (Auer et al, Nano Letters, 2017). Specifically, the FP for recruitment to the scaffold via the CaM-binding peptide will be a FRET acceptor (such as TagRFP or stagRFP35) to elicit FRET only upon reversible binding of a FRET donor (e.g., TagGFP2) to the docking peptide. GCaMP as the FRET donor such that fluorescence background signals in the absence of calcium are further suppressed can also be used. In this mode, the donor fluorescence can be simultaneously detected to provide diffraction-limited calcium-dependent fluorescence at the full frame rate in pixels that will not be clustered via the localization events. b, CLEM-GECI variant that integrates the EM contrast under optical control by proteolytic unmasking of FABPs in a calcium-dependent fashion, such that it can bind to the scaffold. Specifically, the established scFLARE (Sanchez et al, PNAS, 2020) system containing the calcium-activated protease TEV (CaTEV) is adapted such that it cleaves a fused consensus protease site (TEVsite) but only when the light-dependent hLOV domain is extended under illumination with blue light. Since the subsequent SpyCatcher/SpyTag binding is irreversible, each nano-scaffold thus accumulates EM contrast as a function of calcium activity. The design adds optical control over an integration interval during which calcium-dependent accumulation of the EM contrast can occur. This contrast integration is accomplished by adapting the established scFLARE2 system, based on the proteolytic release of a transcription factor via a calcium-activated and selective protease (CaTEV) if the protease cleavage site (TEVsite) is exposed by illumination with 470 nm. Since SpyTag/SpyCatcher00338 form irreversible isopeptide bonds, the EM contrast accumulates on the scaffold within the photocontrolled time interval. PAINT contrast can be simultaneously localized in a separate channel by a red FP, such as stagRFP fused to the imager-peptide, which can also be a FRET acceptor for a green donor (e.g., TagGFP2).

[0103] FIG. **37**: Correlative bioluminescence-EM imaging. FIG. **37**A: Schematic representation of the genetically encoded components for a dual-modality (bioluminescence and EM) calcium indicator. The system is based on the strong affinity of calmodulin (CaM) for the synthetic peptide M13. In the presence of calcium ions, the conformational change of CaM enables high-affinity binding to the M13 peptide. Also fused to M13 is the large bit (LgBit) of a split nano-luciferase, which, when complemented with the small bit (SmBit) of said split nano-luciferase, for which it has very weak affinity, restores active luciferase. While the fused LgBit and M13 peptide are fused to QtEnc or another EM-appropriate scaffold, the fused SmBit and CaM are also fused to a contrasting entity for EM. When calcium ions are present, CaM binds the M13 peptide, reconstituting both luciferase halves for bioluminescence. At the same time, the CGU (e.g. FABP) is recruited to the structural element (e.g., encapsulins, ferritin, I3_01) for EM imaging. FIG. **37**B: The M13 can alternatively be fused on the protein to be recruited to the structural element and CaM fused to the structural element. LgBit and SmBit, parts of the split Nanoluciferase, are optional if only EM contrast is desired. FIG. **37**C: Alternative system in which all components are assembled (preferentially via an isopeptide bond via SpyCatcher/SpyTag) such that the calcium-dependent calmodulin-M13 interaction occurs within the same protein complex. Consequently, all binding partners are present at high local concentrations and at fixed maximal distances, which increases the response time of the sensor. Specifically, CaM and M13 are separated by two SasG filaments containing 10 G-do-

main repeats, wherein the two rigid SasG filaments are connected by a flexible linker as a joint, which can be held in the folded position in the presence of calcium. Note that the sensor mechanism depicted here can be generalized to any protein-peptide or protein-protein interactions that are modified via a cellular process of interest, e.g., based on phospho-peptide binding domains (FHA2) to sense kinase activity.

[0104] FIG. **38**: Contrast from encapsulins as structural elements and metallothioneins as contrast-generating units in SEM and FIB-SEM of *Drosophila* neurons. SEM and corresponding TEM images of the identical sample of a *Drosophila* line with panneuronal expression of either FIG. **38**A: 1M-QtFLAG-NLS or FIG. **38**B: 1M-MxFLAG-NLS following a standard fixation and staining protocol. Ultrathin sections were imaged on either TEM grids or silica wafers for subsequent analysis by TEM and SEM (reverse contrast) so that similar sections through the same cell could be analyzed by both techniques. SEM images were acquired using a Zeiss GeminiSEM with sense BSD, tandem decel at 1.5 kV. Corresponding TEM images were acquired with a Zeiss Libra120 at 120 kV, 13 μA, 100 μrad. Insets show average values (n=30) of respective particles from manual segmentation. White arrowheads indicate the presence of encapsulin-metallothionein particles within the nucleus. FIG. **38**C, FIG. **38**D: Isotropic FIB-SEM image volumes (4 nm voxel size) of *Drosophila* brains expressing c, 1M-Qt-FLAG-NLS (cyan) and d, 1M-MxFLAG-NLS (red) targeted to the nucleus. Encapsulin-metallothioneins and nuclear membranes were manually segmented and rendered within the FIB-SEM volume bounded by the ortho-disks. The magnifications (right) show ortho-disks through three Encapsulin-metallothioneins. Volume acquisition was performed with an SEM beam voltage of 1.3 kV, a working distance of 5 mm, and a nominal voxel size of 4 nm using an InLens detector. The FIB Ga beam was accelerated with a voltage of 30 kV and a current of 700 μA. The scale bars in the overview and zoom-ins represent 500 nm and 50 nm, respectively.

[0105] FIG. **39**: High-res TEM micrographs of encapsulation-metallothioneins expressed in HEK293T. All six classes of concentric barcodes, resulting from the distinct combination of encapsulin shells and metallothioneins, as well as wild-type controls (QtFLAG, MxFLAG), were acquired at a target image pixel size of 0.23 nm and an illumination angle of 0.800 mrad. The scale bars are 50 nm.

[0106] FIG. **40**: Performance metrics of a sequential segmentation and classification pipeline. FIG. **40**A: Flowchart describing the two-step semantic instance segmentation pipeline consisting of segmentation of encapsulin-metallothionein particles and background subtraction, followed by classification of the encapsulation-metallothionein instances. FIG. **40**B Pixel-level Precision-recall (PR) curves for all 6 classes. FIG. **40**C table showing the performance metrics. FIG. **40**D:Confusion matrix of a human classification experiment where 3 blinded human evaluators classified 12 patches of TEM micrographs from HEK293T cells (400×400 pixels, 2 examples per class) to one of the six different encapsulin-metallothionein particle classes (average accuracy: 97.22%). FIG. **40**E Confusion matrix for the classification results of the EfficientNetV2 on the segmented encapsulin-metallothionein particles.

[0107] FIG. **41**: Napari GUIs for interactive segmentation and classification of encapsulin-metallothionein particles. FIG. **41**A: Screenshot of the Napari GUI for the end-to-end semantic segmentation network, which allows for interactive label curation and interfacing with the U-net model (github.com/HelmholtzAI-Consultants-Munich/EMcapsulins_segmentation). (1) Napari image viewer, (2) import widget for loading all images as segmentation results in a selected folder, (3) napari tools for manual annotation, (4) color-code for the encapsulin-metallothionein particle classes, (5) export widget for the curated masks. FIG. **41**B: Screenshot of the napari GUI for the sequential segmentation-classification pipeline (github.com/StructuralNeurobiologyLab/emcaps): (1) napari image viewer, (2) segmentation widget (3) napari tools for manual annotation (4) classification widget (5), export widget for exporting a semantic segmentation overlay. FIG. **41**C:, FIG. **41**D: Examples of possible automated segmentation results flagged for not meeting the imposed criteria (linear pixel size range and circularity). Manual curation of incomplete or artificially fused segmentation instances (middle panel) allows for an improved class assignment (right).

[0108] FIG. **42**: Live microscopy experiments with targeted fluorescent encapsulin-metallothionein particles. FIG. **42**A: Individual frames from live-cell microscopy (Airyscan LSM880) of mammalian oocytes co-expressing mCherry-RAB11A, Myo5b-mCherry, or mCherry-PLK1 without or with eUnaG-1M-Qtanti-mCherry. Insets are magnifications of regions outlined by dashed boxes. The scale bar represents 5 μm. FIG. **42**B: Confocal images of live mouse oocytes microinjected with different concentrations of eUnaG-1M-Qtanti-mCherry mRNA in the absence and presence of mCherry-RAB11A. FIG. **42**C, FIG. **42**D: Quantification of volume (c) and speed (d) of RAB11A-positive recycling endosomes in mCherry-RAB11A-expressing mouse oocytes microinjected with different concentrations of eUnaG-1M-Qtanti-mCherry mRNA. The number of particles or tracks analyzed is specified in italics.

[0109] FIG. **43**: Encapsulin-metallothionein particles targeted to subcellular compartments in mammalian cells and *Drosophila* cells. FIG. **43**A: UV-fluorescence and Coomassie-stained BN-PAGE of lysates from HEK293T cells expressing QtEnc N-terminally fused to the small fluorescent protein miniSOG2, and C-terminally fused to a FLAG-epitope followed by an NLS (cMyc) or an NES (HIV). The bands apparent above 1.3 MDa correspond to the native assembled nanocompartments. The bands also show fluorescence, indicating that the N-terminally appended miniSOG2 was functional and did not comprise the assembly. FIG. **43**B: Corresponding live-cell fluorescence microscopy showing miniSOG2-QtFLAG-NLS predominantly localized in the nucleus and miniSOG2-QFLAG-NES predominantly localized in the cytosol. FIG. **43**C: The functionality of NLS constructs was confirmed in the S2R+ *Drosophila* cell line by co-expressing either UAS-1M-Qt-FLAG-NLS or UAS-1M-QtFLAG with Actin5c-Gal4. d) Widefield fluorescence microscopy showed that encapsulin-metallothionein particles with the NLS downstream of the FLAG-epitope (anti-FLAG, green signal) readily co-localized with the nucleus (DAPI, blue signal), whereas the variant without NLS was distributed throughout the cytosol.

[0110] FIG. **44**: Higher-magnification TEM micrographs of encapsulin-metallothionein particles expressed in *Drosophila* neurons. Neurons in the optic lobe expressing 1M-Qt-FLAG-NLS (top) or 1M-MxFLAG-NLS (down). Scale bars are 50 nm (20 nm for inset).

[0111] FIG. **45**: Detection of encapsulin-metallothionein particles in the processes of *Drosophila* optic lobe neurons. FIG. **45**A, FIG. **45**B: IHC of the optic lobe (OL) of *Drosophila* brains with pan-neuronal expression of either 1M-Qt-FLAG-NES (a) or 1M-MxFLAG-NLS (b). Anti-FLAG (Alexa 568, cyan for 1M-QtFLAG-NES and red for 1M-MxFLAG-NLS) and DAPI (blue) to show the distribution of the neuronal nuclei. Note that there is a substantial anti-FLAG signal in the neuropil only if the nuclear export signal (NES) but not the nuclear localization signal (NLS) is expressed. The scale bars represent 50 μm. FIG. **45**C TEM micrograph of the optic lobe of *Drosophila* pan-neuronally co-expressing 1M-QtFLAG-NES and 1M-MxFLAG-NLS with the multi-class semantic segmentation results overlaid according to the color scheme in main FIG. **1**. 1M-MxFLAG-NLS encapsulins are predominantly found in the nucleus. 1M-QtFLAG-NES encapsulins can be detected in the cytosol as well as in projections FIG. **45**D, FIG. **45**E: Scale bar in sub-panel c represents 200 nm. The scale bars in d and e represent 100 nm.

DEFINITIONS

[0112] Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the present invention belongs.

[0113] The singular forms "a", "an", and "the" include references to the plural unless explicitly stated otherwise in the context.

[0114] The term "comprising" means "including" as well as "consisting", e.g., a composition "comprising" X may consist exclusively of X or may include something additional, e.g., X+Y.

[0115] "Genetically controlled" means that at least one element is a genetically encoded biomolecule, such as DNA, RNA, or protein, which may interact with non-genetically encoded molecules such as, for example, certain metal-interactors or metal-binders or substrates for enzymatic activity. Genetically controlled is therefore not limited to genetic material that has been artificially introduced into the cell but comprises endogenous genetic material expressed by the cell as well. Artificially introduced (generic) material is herein described as "exogenous" material.

[0116] "Nanoscopy" refers to imaging-based methods that resolve structures with nanometer spatial resolution, such as electron microscopy (EM), super-resolution-light microscopy (SRLM), or absorbance-based methods such as optoacoustics. Preferred are high-throughput nanoscopy methods that allow for volume nanoscopy of tissue.

[0117] "Metal interactor" is a molecule to which metal ions can bind to or with which they can react.

[0118] A "metal-interacting peptide", for instance, includes molecules, which can reversibly bind to metals or react with a metal. Osmium, for instance, reacts with osmiophilic residues. Metal-binding (metal chelation) may still occur. As an example, MT3 is osmiophilic but may still be able to bind to lead after osmium tetroxide treatment.

[0119] A "metal-binding peptide", for instance, a lead binder, or a lanthanide binder is a molecule that (reversibly) binds to (instead of reacts with) metals.

[0120] "Exogenous" means not genetically controlled from within the biological system, e.g., a cell, but added to the biological system, e.g., the cell, from the outside as a compound or material.

[0121] "Genetically controlled nanoscopy contrast-generating unit" refers to a genetically controlled molecule which alters the interaction of electrons with matter, e.g., by the local enrichment of electron-dense elements, such as metals, for example, heavy-metals, such that contrast in electron microscopy is generated, and/or genetically encoded chromophores or fluorophores such that photons are absorbed and optionally emitted to generate a localized signal at the nanoscale, or a genetically controlled molecule that determines the local enrichment of a cofactor for a chromophore or fluorophore, or an exogenous chromophore or fluorophore, for the use in super-resolution light-microscopy methods (SRLM) or absorbance based super-resolution methods, e.g., based on optoacoustics.

[0122] "Fluorophore" refers to any type of fluorescent molecule.

[0123] "Chromophore" refers to, for example, a protein binding a chromophore as a cofactor, such as biliverdin or phycocyanobilin, or an enzymatically generated polymer such as melanin. Chromophores such as biliverdin are also comprised as well as light-absorbing, light-refracting, light-scattering, or light-reflecting parts within a molecule, which are responsible for its color.

[0124] "Genetically controlled structural element" refers to a structural element with geometrically precise nanometer-sized features, that spatially organizes contrast-generating units to sufficiently large nanoscale size, such that their spatial distribution is discernable as a distinct geometric shape by nanoscopy, e.g., EM or super-resolution-light-microscopy (SRLM).

[0125] "Spatially organized" means that the elements are arranged in a specific manner to create specific shapes or patterns.

[0126] A "geometric shape" is generated when genetically controlled nanoscopy contrast-generating units are spatially organized by a structural element.

[0127] A "barcode" or "nanoscopy-readable barcode" refers to a distinct spatial distribution of contrast, in particular via a series of contrast-rich and contrast-poor regions with defined spatial intervals, such as a series of high-contrast parallel bars with defined width and defined low-contrast intervals.

[0128] A "concentric barcode" refers to a series of contrast-rich or contrast-poor concentric spheres or rings. In nanoscopy, concentric barcodes can be read as the cross-section or intensity projection of certain spherical structural elements. A concentric barcode can be rotationally invariant and can intrinsically also encode directionality since it has a defined center and a surround such an inside-out or outside-in directionality can be defined.

[0129] "Genetically controlled scaffold" refers to a structure that can spatially organize structural elements to generate distinct geometric patterns discernable by nanoscopy.

[0130] A "geometric pattern" is a nanoscale pattern distinguishable in nanoscopy detection methods. Such geometric patterns are generated when genetically controlled structural elements are spatially organized by a scaffold.

[0131] An "attachment point" refers to a motif on a contrast-generating unit, a structural element, or a scaffold that enables specific binding between those elements or to a cellular structure or biomolecule of interest.

[0132] "Geometric multiplexing" refers to the parallel encoding of distinct pieces of information via multiple and distinct geometric shapes or patterns.

[0133] "Molecular mapping" refers to the nanoscopic visualization of the biodistribution of a molecule or molecules of interest with a genetically controlled structural element or scaffold.

[0134] "Geometric sensing" refers to the detection of an analyte or environmental parameter of interest (e.g., temperature, pH) via a change of the geometric shape or geometric pattern. Geometric sensing can also refer to the detection of multiple analytes or environmental parameters of the physiological or pathophysiological state of a cell, such as the response of a cell, ion flux in a cell, a response of the cell, a therapeutic response of the cell, an activation of the cell, or external stimulus to the cell, or combinations thereof.

[0135] "Geometric actuation" refers to the manipulation of cellular structures or processes by geometrically distinct patterns of biomolecules organized by structural elements and/or scaffold, which are also readable/visible by nanoscopy. The actuation may occur biomechanically, biochemically, and/or via deposition of external energy, e.g., via electromagnetic radiation (e.g., photoabsorption, or radiofrequency absorption), or mechanical energy (e.g., ultrasound energy), and/or magnetic gradients.

[0136] "Nanobiomaterial" refers to a nanoscale biomaterial, which is produced in an isolatable form from a biological cell or a cell-free system and comprises nanoscale genetically controlled geometric features, based on structural elements, scaffolds, attachment points, and comprising biominerals, biopolymers, or enzymatic products for use in downstream applications. A nanobiomaterial can be used to, for example, treat, strengthen or substitute a part, such as a tissue, organ, or function of a living system. Alternatively, a part of a non-living system can be strengthened or substituted, such as, for example, a prosthesis.

[0137] The term "vector" as used in this disclosure comprises the nucleic acid encoding the genetically controlled nanoscale contrast-enhancing unit, the genetically controlled structural element, and/or the genetically controlled scaffold under control of a target cell-specific promoter. Such vector is suitable to transfer the nucleic acid encoding the genetically controlled nanoscale contrast-enhancing unit, the genetically controlled structural element and/or the genetically controlled scaffold to a target cell or target tissue. Such vector may be a viral vector, a plasmid, an agrobacterium, an exosome or a virus or virus-like particle, or any other vector known in the art and suitable for the transfection of a specific target cell.

[0138] As used herein, a "eukaryotic cell", organ or organism may be yeast, fungus, protozoa, plant, higher plant, and insect, or amphibian cells, organs or organisms, such as the brain of *Drosophila melanogaster*, or "mammalian cells" such as HEK293 cultured cells (in vitro), graft cells and primary cell culture (in vitro and ex vivo), and in vivo cells, and also mammalian cells including human, which are commonly used in the art, without limitation.

[0139] "SEQ ID NO." refers to the number of the respective sequence in the sequence listing. Comprised by this invention are also sequences having 80%, 90% or 95% sequence identity to the respective sequences given in the sequence listing.

DETAILED DESCRIPTION

Genetically Controlled Nanoscopy Contrast-Generating Unit (CGU)

[0140] In one aspect, the invention relates to a genetically controlled nanoscopy contrast-generating unit comprising a metal interactor. The metal interactor is compatible with nanoscopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols. Moreover, the metal interactor is a molecule to which metal ions can bind to or react with, wherein the metal interactor is not a ferroxidase and not an enzymatic product from an exogenous substrate, such as 3,3'-diaminobenzidine that is turned over by an enzyme such as HRP, APEX, or APEX2, or by a light-triggered reaction mediated by miniSOG variants to generate a polymer as a product with which heavy metals can interact with.

[0141] The nanoscopopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols are preferably electron microscopy fixation protocols, electron microscopy post-fixation protocols and electron microscopy metal staining protocols, respectively. Thus, the genetically controlled nanoscopy contrast-generating unit is compatible with, for example, aldehydes such as formaldehyde, glutaraldehyde and mixtures thereof, which are commonly used in electron microscopy fixation protocols. The genetically controlled nanoscopy contrast-generating unit is also compatible with, for example, osmium tetroxide and tannic acid which are commonly used in electron microscopy post-fixation protocols. Furthermore, in preferred embodiments, the genetically controlled nanoscopy contrast-generating unit is also compatible with heavy metals, for example, uranium and lead which are commonly used in electron microscopy heavy metal staining protocols, as well as with lanthanides, which may be used as an alternative stain. In yet another embodiment, the genetically controlled nanoscopy contrast-generating unit mainly provides contrast by interaction with osmium tetroxide and partly by binding of a heavy-metal such as lead, after post-fixation.

[0142] Without being bound by theory, the inventors assume that osmium interferes with numerous metal-coordination sites. Thus, the genetically controlled nanoscopy contrast-generating units comprise metal interactors. Said metal-interactors interact with, for example, osmium tetroxide. It is assumed that the metal interactor provides contrast by osmiophilicity and metal binding, inter alia. For example, the metal interactor comprises one or more osmiophilic protein domains or peptides, thereby providing the desired contrast. Alternatively, a lipid-binding protein provides the desired contrast by interacting with, for example, osmium tetroxide. One example of a lipid-binding protein according to the invention is a fatty acid-binding protein. Thus, in one embodiment the metal interactor may react with osmium tetroxide such that osmium accumulates locally, whereby said locally accumulated osmium provides further interaction or binding sites for other metals. In another embodiment, the metal-interactor does not react with osmium tetroxide such that the metal-binding site provides further interaction or binding sites with heavy metals.

[0143] The metal-interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one metal-interacting peptide or a metal-interacting protein. In an embodiment, the metal-interacting peptide is a metallothionein, preferably MT3 or a series of different

metallothionein species. In a preferred embodiment, the metal interactor is a metallothionein, for example a murine metallothionein. In a preferred embodiment, the metallothionein is MT3, even more preferred a eukaryotic MT3 domain, or preferably a mammalian MT3 domain. The MT3 domain may comprise one, two (tandem MT3), or three MT3 molecules. In a specific embodiment, the MT3 domain is a mouse MT3 domain, wherein the mouse MT3 domain is a single or tandem domain, in other words, comprises one (SEQ ID NO: 1) or two (SEQ ID NO: 4) mouse MT3s. In another specific embodiment, a series of three MT molecules are chosen from different species to avoid redundant sequences on the DNA level which interfere with genetic stability (e.g., SEQ ID NO: 5). An exemplary MT3 is MmMT3 having SEQ ID NO: 1. Exemplary sequence IDs for a series of MT3 molecules are SEQ ID NOs: 1-5.

[0144] In another embodiment, the metal-interacting protein may comprise a high abundance of osmiophilic amino acids. The metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit may thus comprise at least one osmiophilic amino acid or one or more osmiophilic proteins, rich in cysteines, methionines, and/or tryptophanes. In a preferred embodiment, the osmiophilic amino acid/protein comprises one or more cysteine residue. An exemplary osmiophilic protein is MT3 (SEQ ID NO: 1), HRPII (e.g., SEQ ID NO: 17 fused to the encapsulation signal), or MMKPDM (SEQ ID 6). Alternatively, the metal-interacting peptide/protein may be selected from PDB entries 2m17, 4n18, 2jyt, 51ah, 3hcu.

[0145] The metal-interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one metal-binding peptide or metal-binding protein. In an embodiment, the metal-binding protein is a lead binder, such as MT3 having SEQ ID NO: 1. In an embodiment, the metal interactor is a lanthanide binder, such as lanmodulin (SEQ ID NO: 18). In another embodiment, the metal-binding protein is a uranyl binder, such as MUP2, or MUP5, having SEQ ID NOs: 45 and 46. In a preferred embodiment, the metal interactor is a super-uranyl-binding protein (SUP), a de novo designed protein having the sequence set forth in SEQ ID NO: 225. In another embodiment, the metal-binding protein is a vanadium binder, such as vanabin 2 (SEQ ID NO: 14). In another embodiment, the metal-binding protein is a copper and/or silver binder. In one embodiment, the metal interactor is one or more copper-binding peptide, such as CusF (SEQ ID NO: 15). In another embodiment, the metal interactor is one or more silver binding peptide, such as AG4 (SEQ ID NO: 199). In even another embodiment, the metal interactor is one or more copper and silver binding peptide, such as AG4 (SEQ ID NO:199).

[0146] Therefore, the difference between a metal-reacting and a metal-binding peptide/protein is that the metal-binding does not irreversibly modify the peptide/protein, i.e, it can also unbind/dissociate again.

[0147] The metal-interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one lipid-binding peptide or a lipid-binding protein. The bound lipid interacts with, for example, a heavy-metal stain. In an embodiment, such lipid-binding protein is a member of the family of fatty acid-binding proteins (FABPs). Given that lipids/fatty acids are a primary target for heavy metals, in particular, the EM post-fixative and contrast agent osmium tetroxide, the inventors identified fatty acid-binding proteins (FABPs) as a class of proteins that can generate genetically controlled and spatially confined EM contrast-generating units. FABPs are a family of proteins (liver (L-), intestinal (I-), heart (H-), adipocyte (A-), epidermal (E-), ileal (II-), brain (B-), myelin (M-) and testis (T-) that share very similar three-dimensional structures (PRINTS database pattern FATTYACIDBP; accession number PR00178), containing an antiparallel p-barrel structure with an internal binding site that holds the fatty acid in an interior cavity. Exemplary sequences are given in SEQ ID NOs: 30-39, such as for brain (B-)-FABP (SEQ ID NO: 36). Variants that preferentially bind polyunsaturated fatty acids, such as PDB-lfdq and PDB-2LKK (FIG. **3***a*), are preferred embodiments. In a preferred embodiment, the fatty acid-binding protein is PDB: 1fdq (SEQ ID NO: 36), a protein that binds polyunsaturated fatty acids, such as arachidonic acid, known to interact with osmium tetroxide. In yet another embodiment, such lipid-binding protein is the lipid-binding domain of a cytochrome P450, such as BM3. Preferably the lipid- and heme-binding domain of the cytochrome P450 BM3 (BM3h; SEQ ID NO:29) or variants thereof, such as Bm3h-B7. Alternatively, the lipid-binding peptide/protein may be selected from the list comprising farnesylation, prenylation, and myristoylation motifs with exemplary SEQ ID NOs: 40-43. In a preferred embodiment, the lipid-binding protein is B-FABP, B-FABP-ko, Bm3h, or Bm3h-B7.

[0148] The metal interactor of the genetically-controlled nanoscopy contrast-generating unit may comprise at least one RNA or a DNA molecule. Nucleic acids interact with heavy metals that are used in EM stains. The metal interactor of the genetically-controlled nanoscopy contrast-generating unit may comprise an RNA-binding protein bound to such RNA via an RNA aptamer. Preferably, the metal interactor is an RNA aptamer-binding protein bound to RNA which is modified with aptamer motifs. RNA aptamer binder: RNA aptamer pair interaction is preferably taken from viruses. The bound RNA interacts with the heavy-metal stain. In one embodiment, the RNA-binding protein is at least one RNA-binding protein, wherein the RNA-binding protein preferably binds RNA, which comprises an RNA aptamer. A pair of an RNA aptamer: RNA aptamer-binding protein is thus preferred. In a preferred embodiment, a pair of an RNA aptamer: RNA aptamer-binding protein is, for example, PP7: PCP (SEQ ID NO: 56 and 53, 54), MS2: MCP (SEQ ID NO: 152 and 100), H23:L7ae (SEQ ID NO:206 and 63), K-turn motif:L7kk (SEQ ID NO: 206 and 63). In another embodiment, the RNA-binding protein comprises a programmable RNA-binding protein, such as dCas13 (e.g., the dCas13 of *Prevotella* sp, SEQ ID NO: 200), or PUF proteins/pumilios (e.g., human pumilio homology domain, SEQ ID NO: 201), or polyA-binding protein (Kuehn et al, Biochimica et Biophysica Acta (BBA, 2004). In a preferred embodiment, said bound RNA comprises a secondary structure, preferably a geometrically distinct secondary structure. In another embodiment, the RNA aptamer is selected from RNA aptamers that bind fluorophores, such as Spinach, Dir2s, and RhoBAST (SEQ ID NOs: 55, 57, 59). In another preferred embodiment, the RNA contains an engineered metal-binding with an exemplary sequence given in SEQ ID NO: 58. In another preferred embodiment, the RNA aptamer-binder: RNA aptamer pair circularized is twister-broccoli RNA aptamer.

[0149] The metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one polymerizing or synthesizing enzyme, by which a product is formed which in turn interacts with, for example, a heavy-metal stain. In one embodiment, the polymerizing or synthesizing enzyme comprises a kinase, a tyrosinase, a synthase, an RNA-dependent RNA polymerase transcriptase, an RNA-dependent DNA polymerase such as reverse transcriptase, a DNA polymerase, or a lipid synthetase. In a preferred embodiment, the polymerizing or synthesizing enzyme is a kinase or a tyrosinase. In one embodiment, the polymerizing enzyme may be a polymerizing kinase that can turn over, for example, GTP or ATP under the formation of highly negative-charged polyphosphate chains. In a preferred embodiment, the kinase is tetrameric polyphosphate kinase 2 (PPK2b), preferably having SEQ ID NO: 48. In a particularly preferred embodiment, the kinase is tetrameric polyphosphate kinase 2 (PPK2) of *F. tularensis* (PDB: 5LL0). In one embodiment, the synthesizing enzyme may be a tyrosinase. In a preferred embodiment, the tyrosinase is a bacterial tyrosinase that generates the strongly absorbing polymer melanin from the endogenously available amino acid tyrosine. Therefore, the tyrosinase may form melanin which may interact with, for example, a heavy-metal stain. In an even more preferred embodiment, the tyrosinase is a *Bacillus megaterium* tyrosinase (BmTyr), preferably having SEQ ID NO: 51. In yet another embodiment, the synthesizing enzyme is a phytochelatin synthase. In a preferred embodiment, the phytochelatin synthase is phytochelatin synthase 1 (AtPCS1), preferably having SEQ ID NO: 49.

[0150] The metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one biomineralizing enzyme. The resulting biomineral itself is electron-dense, or interacts with other electron-dense materials. In one embodiment, the biomineralizing enzyme comprises iron-oxide biominerals. In another embodiment, the biomineralizing enzyme comprises ferroxidase. In yet another embodiment, the biomineralizing enzyme is an iron-oxide biomineral such as a ferroxidase. In another embodiment, the biomineralizing enzyme is a ferroxidase from the Iron-Mineralizing Encapsulin-Associated Firmicute (IMEF, SEQ ID NO: 52) or Ferritin (PfFt, SEQ ID NO: 213, or *H. pylori* ferritin). In another embodiment, the biomineralizing enzyme is complemented by the iron importer Zip14 (SEQ ID NO: 219) and the manganese importer DMT1 (SEQ ID NO: 218), such as to achieve doping of the produced iron oxide biomineral with manganese. In another embodiment, the enzyme is alkaline phosphatase, in a preferred embodiment not membrane-bound (SEQ ID NO: 221), which can lead to calcium-phosphate formation. In another embodiment, the enzyme is cystathionine-y-lyase with an exemplary sequence (SEQ ID NO: 220).

[0151] The metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise at least one bioconjugation tag. In one alternative embodiment, the genetically controlled nanoscopy contrast-generating unit is at least one bioconjugation tag. Without being bound by theory, the bioconjugation tag provides contrast by conjugation to metal complexes and/or exogenous fluorophores or chromophores. In one embodiment, the bioconjugation tag is, for example, SpyTag/SnoopTag-Catcher, SNAP, Clip, Halo, coiled coils, or inteins. In a preferred embodiment, an exogenous compound binding and/or reacting with the bionconjugation tag is, for example, a chromophore and/or fluorophore or a tag-compatible metal-chelator such as macrocyclic compounds, i.e., a DOTA, DO3A, DOTAM, DTPA, NOTA, NODAGA derivative or a ring or linear polymers such as dendronized polymers. In another preferred embodiment, the bioconjugation tag is a pair of coiled coils. In yet another preferred embodiment, the bionconjugation tag is SNAP. In another embodiment, the bioconjugation tags are coiled coils, and said coiled coils are utilized to generate super-resolution contrast by PAINT (points accumulation for imaging in nanoscale topography). In yet another embodiment, a low concentration of bioconjugation tags is used. A low concentration of bioconjugation tags depends on various parameters inter alia, such as the type of bioconjugation tag utilized and the type of genetically controlled contrast-enhancing unit, inter alia.

[0152] The metal interactor comprised in the genetically controlled nanoscopy contrast-generating unit may comprise a combination of at least two of said metal-interacting peptide/protein, metal-binding peptide/protein, lipid-binding protein, RNA-binding protein, RNA or DNA molecule, polymerizing or synthesizing enzyme, or bioconjugation tag. This means that all of the above-listed contrast-providing genetically controlled nanoscopy contrast-generating units can be combined.

[0153] Without being bound by theory, the metal-interactor provides contrast by osmiophilicity and metal-binding, inter alia. Furthermore, all of the contrast-generating units of the invention generate not only contrast in electron microscopy but may also be detected by fluorescence, bioluminescence, absorbance, magnetic measurements such as NMR, MRI, NanoSIMS, nitrogen-vacancy magnetometry, mass spectrometry imaging, and/or ultrasound. In one embodiment, the genetically controlled nanoscopy contrast-generating unit is detectable by both electron microscopy and fluorescence microscopy or optoacoustic microscopy techniques. In yet another embodiment, the genetically controlled nanoscopy contrast-generating unit is compatible with both electron microscopy and fluorescence microscopy techniques.

[0154] Therefore, in one preferred embodiment, the genetically controlled nanoscopy contrast-generating unit comprises a metal interactor, and further comprises a fluorophore or a chromophore. The fluorophore is, for example, a fluorescent protein, a co-factor in a fluorescent protein, or an exogenous fluorophore such as an Alexa dye or an indocyanine derivative. The fluorophore may also be a fluorophore-binding RNA aptamer. In one embodiment, the fluorescent protein is for example UnaG, preferable eUnaG (SEQ ID NO: 202), mGreenLantern (e.g, SEQ ID NO: 203), emFP (e.g, SEQ ID NO: 92-99), CaMPARI2 (e.g, SEQ ID NO: 204), mCherry (e.g, SEQ ID NO:185) or mRFP (e.g, SEQ ID NO: 205). Any other fluorescent protein known in the art and suitable for this purpose is encompassed in this embodiment. In another embodiment, the fluorescent protein is eUnaG, mScarlet, miniSog, or eUnaG and mCherry. In even another embodiment, the fluorophore-binding RNA aptamers are, for example, spinach (SEQ ID NO: 55) and/or DIR2s (SEQ ID NO: 57).

[0155] In one preferred embodiment, the genetically controlled nanoscopy contrast-generating unit comprises a metal interactor, wherein the metal interactor comprises at least one metallothionein, at least one fatty acid-binding

protein, at least one lipid-binding domain or at least one RNA molecule and further comprises a fluorophore, wherein the fluorophore is a fluorescent protein.

[0156] In one embodiment, the metal interactor is an MT3 domain and the fluorophore is GreenLantern, CaMPARI2, mEos4b (SEQ ID NO:214), or mEosEM (SEQ ID NO:215); in other words, the genetically controlled nanoscopy contrast-generating unit is a GreenLantern-MT3 or a CaMPARI2-MT3, mEos4b-MT3, mEosEM-MT3 fusion protein. In another embodiment, the metal is an MT3 domain and the fluorophore is UnaG, preferably enhanced UnaG (eUnaG) (SEQ ID NO: 202); in other words, the genetically controlled nanoscopy contrast-generating unit is a eUnaG-MT3 fusion protein. In another embodiment, the MT3 domain are two MT3 domains or in other words, a tandem domain and eUnaG is N-terminally fused, resulting in a eUnaG-2xMT3 fusion protein.

[0157] In another embodiment, the metal interactor is an RNA-binding protein bound to RNA via aptamers. The RNA aptamers may be spinach, which may further bind to exogenous fluorophores. Said RNA aptamers thus allow dual detection by both electron microscopy and fluorescence microscopy.

[0158] In another embodiment, the genetically controlled nanoscopy contrast-generating unit comprises a metal interactor and a chromophore. The chromophore may be a chromoprotein, a co-factor in a chromoprotein, or an exogenous chromophore such as a dark quencher. The chromoprotein is, for example, any fluorescent protein, a protein binding a chromophore as a co-factor, such as biliverdin (SEQ ID NO: 216) or phycocyanobilin (SEQ ID NO: 217), or an enzymatically generated polymer such as melanin, or light-absorbing, light-refracting, light-scattering, or light-reflecting parts within a molecule which are responsible for its color. For instance, the genetically controlled nanoscopy contrast-generating unit comprises a eUnaG-MT3 fusion protein, wherein eUnaG binds the endogenous ligand bilirubin.

[0159] Alternatively, the genetically controlled nanoscopy contrast-generating unit comprises a metal interactor and further comprises a bioluminescent protein, for example firefly luciferase, nanoluciferase, renilla luciferase, or AkaLuc.

[0160] The genetically controlled nanoscopy contrast-generating unit may comprise at least one attachment point. Said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In one embodiment, the genetically controlled contrast-generating unit is *H. pylori* ferritin comprising at least one attachment point, wherein said at least one attachment point is a calmodulin binding peptide (SEQ ID NO. 134). In one embodiment, the genetically controlled nanoscopy contrast-generating unit comprises internal attachment points. Said internal attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In another embodiment, the genetically controlled nanoscopy contrast-generating unit comprises external attachment points. Said external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins (Thestrup et al., Nature Methods, 2014), as well as combinations thereof. In yet another embodiment, the genetically controlled nanoscopy contrast-generating unit comprises internal attachment points and external attachment points. Said internal and external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof.

[0161] In a preferred embodiment, the genetically controlled nanoscopy contrast-generating unit comprises MT3, FABP, or BM3h as the metal interactor as either direct fusions or via attachment points chosen from coiled-coils, isopeptide forming pairs or inteins, wherein via the attachment point the CGU can be attached to structural elements such as encapsulins, vaults, emFP, or SasG.

Genetically Controlled Structural Elements (SEs)

[0162] In one aspect, the invention relates to a genetically controlled structural element (SE). The genetically controlled structural element comprises and spatially organizes at least one genetically controlled nanoscopy contrast-enhancing unit. The genetically controlled structural element interacts or binds to the genetically controlled nanoscopy contrast-enhancing unit and therefore, organizes the genetically controlled nanoscopy contrast-enhancing unit. In general, the genetically controlled structural element has to be of a sufficient size that is detectable by, for example, in high-throughput EM using, e.g., a pixel size of 1 to 4 nanometers. The genetically controlled structural element possesses a pre-determined shape and pre-determined nanoscale size and generates a shape that can be differentiated at the nanoscale, i.e., it can be detected and distinguished from shapes of other SEs or other (cell) structures in EM and other nanoscale detection methods. Such a distinct shape is preferably a barcode, even more preferably a concentric barcode.

[0163] The distinct shape is a function of the 3D distribution of the genetically controlled nanoscopy contrast-generating units within the genetically controlled structural element. In other words, the geometrically distinct shape is generated by the interaction of the structurally organized genetically controlled nanoscopy contrast-generating units and the genetically controlled structural element. In standard EM methods, these 3D distributions are commonly detected or presented as 2D cross-sections or projections onto a plane.

[0164] If such a shape generates a distinct spatial distribution of contrast, in particular, a series of contrast-rich and contrast-poor regions with defined spatial intervals, such as a series of high-contrast parallel bars with defined width and defined low-contrast intervals, the shape is called a "barcode". In a preferred embodiment, the distinct shapes are concentric rings, i.e., an annular shape, which in the limit converges to a disc shape. In one embodiment, the distinct shape is, for example, a ring, a disc, a rectangle, a triangle etc.

[0165] In another preferred embodiment, concatenated MT3 domains fused to encapsulin monomers produce an annular or disc shape. In one embodiment, single or tandem MT3 domains are fused to the N-terminus of QtEnc. In another embodiment, tandem MT3 domains provide twice the number of osmiophilic residues which reach further into the lumen of the encapsulin. More contrast is generated, and thus the diameter of the "inner circle" of the ring shape decreases, resulting in a disc. If three MT3 domains are fused to an encapsulin, the shape is a completely "dark" disc (see, FIG. **10***b*). In one embodiment, MT3-QtEnc^{FLAG} is a ring. In other words, one MT3 is fused to the interior of an encapsulin, resulting in a ring shape. In said embodiment, the ring is an annular electron-dense ring with a bright center. In another embodiment, 2xMT3-QtEnc^{FLAG} is a disc. In other words, two MT3s are fused to the interior of an encapsulin, resulting in a disc shape. Said disc has a darker appearance than the MT3-QtEnc^{FLAG} ring. In an alternative embodiment, 3xMT3-QtEnc^{FLAG} adds another layer of contrast to the lumen, which appears as a disc. In other words, three MTs from different species (3xchimericMT, SEQ ID NO: 169) are fused to the interior of an encapsulin, resulting in a disc shape. All three shapes are called "concentric barcodes," which can be complemented by additional shapes generated by adding more layers of contrast to the outer surface of the spherical nanostructure (FIGS. **10***e*, **10***f*).

[0166] The genetically controlled structural element is preferably a self-assembling structure. A self-assembling structure has the advantage of consisting of only a few building blocks while having the disadvantage of being polyvalent, thus making it challenging to include sparse attachment points that can be used to bind to a target of interest or attach to a scaffold to generate a precise geometric pattern. In one embodiment, the genetically controlled structural element is not self-assembling. In another embodiment, the genetically controlled structural element is self-assembling. In one embodiment, the genetically controlled structural element is not symmetrical. In another embodiment, the genetically controlled structural element is symmetrical. In one embodiment, the genetically controlled structural element is not self-assembling and not symmetrical. In another embodiment, the genetically controlled structural element is self-assembling and symmetrical. An encapsulin is an example of a genetically controlled structural element, which is self-assembling, symmetrical, and spherical. A vault is an example of a genetically controlled structural element that is self-assembling and symmetrical in one axis but is not a sphere. Obtaining a low valency, let alone a single valency on the outer surface, is very challenging if a self-assembling and symmetrical structure is used. A low valency is preferred such that cross-linking of, for example, the target is avoided.

[0167] A solution to the problem is provided by genetically controlling the stoichiometry of self-assembling building blocks with or without distinct attachment points. This objective can be achieved via changing the concentration of plasmids or viruses encoding the respective genetically encoded building blocks in transient transfection or transduction systems. For a stable genetic modification, a solution is provided by a translational read-through system (FIG. **15**), which uses several variants of termination codons to regulate the probability of ribosomes passing through the termination codon to prolong the translated peptide, e.g. by a terminal attachment point.

[0168] In one embodiment, the stoichiometry of surface modifications of the self-assembling and symmetrical genetically controlled structural element can thus be regulated. In one embodiment, said regulation takes place by programmable translational read-through. In a preferred embodiment, programmable translational read-through entails a programmable RT cassette comprising a structural element with a stop codon and a read-through promoting sequences. In another preferred embodiment, the programmable RT cassettes comprise a QtEnc monomer gene with a C-terminal FLAG epitope followed by a stop codon and read-through promoting sequences. In one embodiment, the programmable translational read-through is determined by the stop codon and the respective read-through motif. In one embodiment, the stop codon is selected from the group consisting of UAG, UAA, and UGA (TAG, TAA; TGA). In a preferred embodiment, the stop codon is TGA. In one embodiment, the read-through motif is selected from the group consisting of 3 SEQ ID NOs: 74-76. In one embodiment, the combination of the stop codon and read-through motif allows for adjusting read-through rates between about 1 and 20%. In one embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating units is one murine metallothionein-3, wherein the genetically controlled structural element comprises a programmable read-through cassette, wherein said programmable read-through cassette comprises distinct combinations of stop codons and short read-through promoting motifs at the end of the open-reading frame encoding the encapsulin *Quasibacillius thermotolerans* (Qt). In one embodiment, the stop codon is selected from the group consisting of TGA, TAA, TAG and wherein the short read-through promoting motif is selected from the group consisting of rt20s (SEQ ID NO: 76), rt9s (SEQ ID NO: 74), rt9us (CTATCC). In a preferred embodiment, the stop codon is TGA and the read-through promoting motif is rt20 (SEQ ID NO: 76). In another embodiment, the genetically controlled structural element additionally comprises a C-terminally fused anti-GFP intrabody. In yet another embodiment, the genetically controlled structural element is co-expressed with Cx43-msfGFP. In even another embodiment, the genetically controlled structural element is co-expressed with msfGFP-Cx43. In another embodiment, the genetically controlled structural element is co-expressed with a C-terminally fused Cx43-msfGFP. In an alternative embodiment, the genetically controlled structural element is co-expressed with a C-terminally fused msfGFP-Cx43. In even another embodiment, the genetically controlled structural element additionally comprises a N-terminally, or C-terminally fused anti-GFP intrabody. In a preferred embodiment, the additionally fused anti-GFP intrabody faces the exterior, i.e. not the lumen. In one aspect, a method of generating a distinct ratio of genetically controlled structural elements is dis-

closed. In one embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, wherein said *Quasibacillius thermotolerans* (Qt) encapsulin comprises one N-terminally fused murine metallothionein-3, wherein at the end of the open-reading frame encoding the encapsulin *Quasibacillius thermotolerans* (Qt) the read-through motif rt20s (SEQ ID NO: 76) and the stop codon TGA are located, wherein the *Quasibacillius thermotolerans* (Qt) encapsulin comprises one C-terminally fused FLAG-tag, wherein said C-terminally fused FLAG tag is further extended by an anti-GFP intrabody upon ribosomal read-through, whereby the combination of the read-through motif rt20s (SEQ ID NO: 76) and the stop codon yields about 15% anti-GFP intrabodies, thereby serving as a surrogate marker for a translational read-through rate. In one embodiment, distinct combinations of a read-through motif and a stop codon yield about 5%, or about 20% anti-GFP intrabodies, i.e. a read-through rate of about 5% or 20%. Thus, in another embodiment a method for the detection of translational read-through rates is also provided. In a further aspect, a cell line comprising the genetically controlled structural element and the C-terminally fused Cx43-msfGFP is provided.

[0169] In an embodiment, the genetically controlled structural element is self-assembling, symmetrical, and rotationally invariant. A member of the encapsulin family is an example of a genetically controlled structural element that is self-assembling, symmetrical, and rotationally invariant. Taking the example of encapsulins, a maximum number of internal attachment points is desirable to maximize the density of contrast-generating units.

[0170] In one embodiment, the genetically controlled structural element comprises a member of the encapsulin family, a vault, an MS2 phage, a Qbeta phage, an AP205 phage, an engineered mono-to-polyvalent hub, a filament, or a linker, or combinations or variants thereof.

[0171] The genetically controlled structural element may comprise a member of the encapsulin family. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably from the species *Q. thermotolerans* (QtEnc; T=4, 40 nm in diameter), *M. xanthus* (MxEnc; T=3, 32 nm in diameter), and *T. maritima* (TmEnc; T=1, 20 nm in diameter). In another embodiment, the encapsulin has a triangulation number of four, three, or one. In even another embodiment, the encapsulin has a size of between about 20 to 45 nm, about 35 to 45 nm, about 27 to 37 nm, or about 15 to about 25 nm in diameter. In a preferred embodiment, the encapsulin has a size of about 40 nm, 30 nm or 20 nm in diameter. In another preferred embodiment, the encapsulin has a triangulation number of four and a size of about 40 nm, a triangulation number of three and a size of about 30 nm, a triangulation number of 1, and a size of about 20 nm all in diameter.

[0172] In another embodiment, the genetically controlled structural element comprises an encapsulin and at least one genetically controlled nanoscopy contrast-generating unit comprising a metal interactor wherein the encapsulin spatially organizes the genetically controlled nanoscopy contrast-generating unit. In another embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein. In a preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising an encapsulin and at least one metal interactor. In one embodiment, the metal interactor is a uranyl binder. In a preferred embodiment, the uranyl binder is MUP2 (SEQ ID NO:45), MUP5 (SEQ ID NO: 46), SUP (SEQ ID NO: 225), des_7bau (SEQ ID NO: 268), des_2akf_3bs (SEQ ID NO: 269), des_2akf_6bs (SEQ ID NO: 270), or des_5apq_6bs (SEQ ID NO: 271). In a particularly preferred embodiment, the uranyl binder is MUP2 (SEQ ID NO:45) and the genetically controlled structural element is an encapsulin selected from *Quasibacillius thermotolerans* (Qt), *Myxococcus xanthus* (Mx), and *Thermotoga maritima* (Tm). In a preferred embodiment, the uranyl binder is MUP2 and the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin (SEQ ID NO: 148). In a preferred embodiment, the at least one metal interactor is a metallothionein, preferably MT3. In one embodiment, said MT3 is murine MT3. In another preferred embodiment, the encapsulin is fused with a tandem MT3 domain, in other words, comprises two MT3 domains. In one embodiment, an encapsulin is N-terminally fused to a tandem mouse MT3 domain. In another preferred embodiment, the fusion protein is MT3-QtEnc (SEQ ID NO: 165), MT3-MxEnc (SEQ ID NO: 166), or MT3-TmEnc, or in other words, a genetically controlled structural element comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3 (MmT3). In one embodiment, the one murine metallothionein is located on the inner surface of the encapsulin. In another embodiment, the fusion protein is 2xMT3-QtEnc, 2xMT3-MxEnc, or 3xMT3-TmEnc, or in other words, a genetically controlled structural element comprising *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsuin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is two N-terminally fused murine metallothionein. In one embodiment, the two murine metallothioneine are located on the inner surface of the encapsulin. In yet another embodiment, the fusion protein is 3x MT3-QtEnc, 3xMT3-MxEnc, or 3xMT3-TmEnc, or in other words, a genetically controlled structural element comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating uni is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5). In one embodiment, the three N-terminally chimeric fused metallothioneins are located on the inner surface of the encapsulin.

[0173] In another embodiment, the genetically controlled structural element, comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin and a metallothionein according to the preceding embodiments undergoes sequential segmentation and classification, wherein the sequential segmentation and classification comprises the steps of (i) segmentation, (ii) background sub-

traction, (iii) classification. Table 1 below displays tabulated segmentation metrics for all 6 classes. Overall average model precision is 82.2%, recall 74.6%, DSC 0.78, and IoU 0.64.:

TABLE 1

Sequential segmentation and classification of *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin comprising one (1M) or two murine metallothioneins (2M) or the chimeric metallothionein sequence having three metallothioneins (3M):

EMcapsulins class	Precision	Recall	DSC	IoU
1M-Qt	0.79	0.89	0.84	0.72
~~2M-Qt~~	~~0.6~~	~~0.88~~	~~0.71~~	~~0.56~~
3M-Qt	0.83	0.67	0.74	0.59
1M-Mx	0.71	0.59	0.64	0.48
2M-Mx	0.75	0.56	0.64	0.47
1M-Tm	0.74	0.24	0.36	0.22

[0174] In yet another preferred embodiment, the fusion protein is MT3-QtEnc-FLAG, MT3-MxEnc-FLAG, or MT3-TmEnc-BC2Tag. In still another embodiment, the fusion protein is MT3-TmEnc-FLAG. Put differently, a genetically controlled structural element comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3 (MmT3), wherein a FLAG tag is C-terminally fused is disclosed. In one embodiment, the one murine metallothionein is located on the inner surface of the encapsulin. In another embodiment, the fusion protein is 2xMT3-QtEnc-FLAG, 2xMT3-MxEnc-FLAG, or 3xMT3-TmEnc-FLAG, or in put differently, a genetically controlled structural element comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is two N-terminally fused murine metallothionein, wherein a FLAG-tag is C-terminally fused. In one embodiment, the two murine metallothioneine are located on the inner surface of the encapsulin. In yet another embodiment, the fusion protein is 3xMT3-QtEnc-FLAG (SEQ ID NO: 169), 3xMT3-MxEnc-FLAG, or 3xMT3-TmEnc-FLAG, or in other words, a genetically controlled structural element comprising a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin), further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5)., wherein a FLAG-tag is C-terminally fused. In one embodiment, the three N-terminally chimeric fused metallothioneins are located on the inner surface of the encapsulin.

[0175] In even another embodiment, the genetically controlled structural element additionally comprises apart from a C-terminally fused FLAG-tag also a nuclear localization signal (NLS). In one embodiment, said NLS can be fused to said FLAG-tag via cMyc. Consequently, in one embodiment, the genetically controlled structural element is *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, comprising a genetically controlled contrast-generating unit having one, or two N-terminally fused murine metallothionein-3, or wherein the genetically controlled contrast-generating units is chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag with a nuclear localization signal is C-terminally fused. In another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapuslin, wherein the genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, or wherein a FLAG tag with a nuclear localization signal is C-terminally fused. In even another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapuslin, comprising a genetically controlled contrast-generating unit having three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein a FLAG tag with a nuclear localization signal is C-terminally fused.

[0176] In another preferred embodiment, the genetically controlled structural element is an encapsulin, and the at least one metal interactor is RNA.

[0177] In yet another preferred embodiment, the genetically controlled structural element is an encapsulin, and the at least one metal interactor is an RNA-binding protein.

[0178] In even another preferred embodiment, the genetically controlled structural element is an encapsulin, and the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein.

[0179] In one embodiment, the genetically controlled structural element is an encapsulin, the at least one metal interactor is RNA and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, with co-expression of ZIP14, DMT1, or a tyrosinase.

[0180] In yet another preferred embodiment, the genetically controlled structural element is an encapsulin, the at least one metal interactor is an RNA-binding protein and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase.

[0181] In even another preferred embodiment, the genetically controlled structural element is an encapsulin, the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase.

[0182] In a preferred embodiment, the genetically controlled nanoscopy contrast-generating unit is the synthetic enzyme tyrosinase and the structural element is an encapsulin comprising the tyrosinase. Melanin is generated in the encapsulin lumen by the tyrosinase (an exemplary tyrosinase is BmTyr having SEQ ID NO: 51). In one embodiment, melanin binds to heavy metals. In another embodiment, the melanin is contrasted without binding to heavy metals in EM.

[0183] In another embodiment, the genetically controlled nanoscopy contrast-generating unit is the polymerizing enzyme kinase and the structural element is an encapsulin comprising the kinase, preferably PPK2. ATP or GTP enters the genetically controlled structural element via its pores, where it is polymerized into a polyphosphate chain trapped inside the encapsulin lumen. The result is highly contrasted polyphosphate pores. In this particular embodiment, the resulting structures are from about 25 to 33 nm, preferably about 32 nm, and comprise MxEnc^{FLAG}+DD-CgPPK2b-QtSig (SEQ ID NOs: 107, 47).

[0184] In another embodiment, the encapsulin comprises mineralized iron oxide via its native IMEF cargo protein. In yet another embodiment, an IMEF dimer is docked into the encapsulin shell, where ferrous ion enters through the pore in the encapsulin shell and is subsequently bio-mineralized. The resulting encapsulin is, for example, QtEnc+QtIMEF, which is a spherical structure of about 40 nm.

[0185] In another embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising an encapsulin, at least one metal interactor, and a fluorophore. In a preferred embodiment, the fusion protein is eUnaG-MT3-QtEnc (SEQ ID NO: 155), or put differently a genetically controlled structural element, wherein the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, comprising a genetically controlled contrast-generating units having one murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein eUnaG. In a preferred embodiment, the genetically controlled structural element is *Quasibacillius thermotolerans* (Qt) encapsulin. In another preferred embodiment, eUnaG is N-terminally fused. In another embodiment, the genetically controlled structural element additionally comprises a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-MT3-QtEnc^{FLAG}. In one aspect, a fluorescence multichannel imaging method is provided, using the genetically controlled structural element additionally comprising a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-MT3-QtEnc^{FLAG}. In another aspect, a method for monitoring organ, organoid or cells is provided, using the genetically controlled structural element additionally comprising a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-MT3-QtEnc^{FLAG}. In another embodiment, eUnaG is C-terminally fused. Therefore, in one embodiment, the fusion protein is MT3-QtEnc^{eUnaG}. In another aspect, the genetically controlled structural element according to the preceding embodiments is compatible with both fluorescent microscopy and electron microscopy applications. In a preferred embodiment, the genetically controlled structural element according to the preceding embodiments is used for sequential analysis, first by fluorescent microscopy, followed by electron microscopy. In another embodiment, the genetically controlled structural element further comprises at least one attachment point, wherein the at least one attachment point is an intrabody, wherein said intrabody is C-terminally fused. In one embodiment, the intrabody is an anti-mCherry intrabody. In another embodiment, the anti-mCherry intrabody is expressed on the outer surface of the encapsulin. Thus, in one embodiment, the fusion protein is MT3-QtEnc-^{an}ti-^{mcherry}. In another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused. Hence, the fusion protein according to the preceding embodiment is eUnaG-MT3-QtEnc$^{anti\text{-}mcherry}$. In one aspect, a fluorescence imaging method using the genetically controlled structural element, wherein the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused, or in other words, the fusion protein eUnaG-MT3-QtEnc$^{anti\text{-}mcherry}$ is provided. In another aspect, a method for monitoring organ, organoid or cells using the genetically controlled structural element according to the preceding embodiment is provided. In one embodiment, the monitored cells are mammalian oocytes. In a preferred embodiment, the oocytes are murine oocytes. In another preferred embodiment, the oocytes are human oocytes. In another embodiment, the mammalian oocytes according to the preceding embodiments are monitored prior to in vitro fertilization. In one aspect, a recycling endosome stain comprising a *Quasibacillius thermotolerans* (Qt) encapsulin as genetically controlled structural element, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused, wherein the anti-mCherry intrabody is targeted to RAB11A is provided. In another aspect, a cargo vesicle stain comprising a *Quasibacillius thermotolerans* (Qt) encapsulin as genetically controlled structural element, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused, wherein the anti-mCherry intrabody is targeted to Myo5b is provided. In yet another aspect, an acentriolar microtubule-organizing stain comprising the genetically controlled structural comprising a *Quasibacillius thermotolerans* (Qt) encapsulin as genetically controlled structural element, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein eUnaG is N-terminally fused, wherein an anti-mCherry intrabody is C-terminally fused, wherein the anti-mCherry intrabody is targeted to PLK1 is provided.

[0186] In one embodiment, MT3-QtEnc^{eUnaG} is co-expressed with MT3-QtEnc$^{-anti\text{-}mcherry}$. In a preferred embodiment, MT3-QtEnc^{eUnaG} is co-expressed with MT3-QtEnc$^{-anti\text{-}mcherry}$ in a ratio of approximately 4:1. In one aspect, a subcellular labelling method is provided wherein MT3-QtEnc^{eUnaG} is co-expressed with MT3-QtEnc$^{-anti\text{-}mcherry}$. In a preferred embodiment, MT3-QtEnc^{eUnaG} is co-expressed with MT3-QtEnc$^{-anti\text{-}mcherry}$ in a ratio of approximately 4:1. In another embodiment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a coiled-coil domain. In a preferred embodiment, the attachment point is two coiled-coil domains. In yet another embodi-

ment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a SpyTag/SpyCatcher.

[0187] In a particularly preferred embodiment, the fusion protein is eUnaG-MT3-QtEnc or eUnaG-2xMT3-QtEnc, or in other words, a genetically controlled structural element, wherein the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, comprising a genetically controlled contrast-generating units having two murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein eUnaG. In a preferred embodiment, the genetically controlled structural element is *Quasibacillius thermotolerans* (Qt) encapsulin. In another preferred embodiment, eUnaG is N-terminally fused. In another embodiment, the genetically controlled structural element additionally comprises a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-2xMT3-QtEnc-^{F}LAG. In one aspect, a fluorescence multichannel imaging method is provided, using the genetically controlled structural element additionally comprising a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-2xMT3-QtEnc^{FLAG}. In another aspect, a method for monitoring organ, organoid or cells is provided, using the genetically controlled structural element additionally comprising a C-terminally fused FLAG tag, such that the fusion protein is eUnaG-2xMT3-QtEnc^{FLAG}. In another embodiment, eUnaG is C-terminally fused. In another embodiment, the genetically controlled structural element further comprises at least one attachment point, wherein the at least one attachment point is an intrabody, wherein said intrabody is C-terminally fused. In one embodiment, the intrabody is an anti-mCherry intrabody. In another embodiment, the anti-mCherry intrabody is expressed on the outer surface of the encapsulin. In another embodiment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a coiled-coil domain. In a preferred embodiment, the attachment point is two coiled-coil domains. In yet another embodiment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a SpyTag/SpyCatcher.

[0188] In even another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein eUnaG, and wherein the genetically controlled structural element further comprises synthetic calmodulin-binding peptide 20 (SEQ ID NO: 241). In one embodiment, the genetically controlled structural element according to the preceding embodiment and a genetically controlled nanoscopy contrast-generating unit, wherein said genetically controlled nanoscopy contrast-generating unit comprises the metal-binding peptide/protein is *H. pylori* ferritin, comprising at least one attachment point, and wherein said at least one attachment point is a calmodulin-binding peptide (SEQ ID NO: 134) are used for nanoscopy detection, wherein nanoscopy detection comprises molecular mapping and/or geometric sensing. In another embodiment, the genetically controlled structural embodiment further comprising the synthetic calmodulin-binding peptide 20 (SEQ ID NO: 241), the genetically controlled contrast-generating unit of SEQ ID NO: 31 and additionally OptoCracl-mCherry are used for nanoscopy detection, wherein nanoscopy detection comprises molecular mapping and/or geometric sensing. OptoCracl-mCherry is a blue-light inducible optogenetic tool and calcium influx is stimulated via OptoCrac1 (doi:10.7754/eLife.10024). In a preferred embodiment, said molecular mapping provides information on the subcellular distribution of a molecule of interest within a cell or tissue via the binding of the genetically controlled structural element and the genetically controlled constast-generating unit according to the preceding embodiment to a molecule of interest, which thus determines the subcellular localization of the genetically controlled structural elements and the genetically controlled constast-generating unit.

[0189] In yet another embodiment, the nanoscopy detection is geometric sensing, and wherein said geometric sensing provides information on a specific cellular state, a cellular process, or the presence or absence of an analyte or environmental parameter of interest within a cell or tissue, or the response to an external stimulus, and wherein the shape generated by the genetically controlled structural element and the genetically controlled contrast-generating unit changes in response to a pre-defined cellular state, a pre-defined cellular process, at least one analyte, or at least one environmental parameter, or an external stimulus. In a preferred embodiment, the at least one analyte is calcium.

[0190] In even another embodiment, the nanoscopy detection comprises mapping and/or the geometrical sensing further comprises geometric actuation, wherein said geometric actuation alters a cellular state or process by an external stimulus. In a preferred embodiment, the external stimulus is calcium.

[0191] In one embodiment, eUnaG-MT3-QtEnc generates concentric barcodes of about 35-45 nm in diameter, preferably about 40 nm. In one embodiment, said spherical structures harbor a distinct lumenal phenotype showing a contrasted internal ring as well as a bright center spot. In one embodiment, eUnaG-MT3 is localized to the encapsulin lumen. In yet another embodiment, the fusion protein is eUnaG-2xMT3-QtEnc, and the lumen is homogeneously contrasted.

[0192] In one embodiment, UnaG-MT3-QtEnc is localized to the cytosol. In another embodiment, UnaG-2xMT3-QtEnc is localized to the cytosol.

[0193] In yet another embodiment, the fusion protein is MT3-MxEnc^{FLAG}-cMyc-NLS. In one embodiment, MT3-MxEnc-FLAG-cMyc-NLS is expressed pan-neuronally in *Drosophila melanogaster*. In yet another embodiment, MT3-MxEnc^{FLAG}-cMyc-NLS is expressed pan-neuronally in the optical lobe in *Drosophila melanogaster*. In a preferred embodiment, MT3-MxEnc^{FLAG}-cMyc-NLS is expressed in T4-T5 neurons in *Drosophila melanogaster*, or in other words, a genetically controlled structural element, wherein the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, and wherein a FLAG tag with a nuclear localization signal is C-terminally fused via cMyc. In another aspect, a transgenic *Drosophila melanogaster* line is disclosed. In one embodiment, the transgenic *Drosophila melanogaster* line expresses MT3-

MxEnc^{FLAG}-cMyc-NLS. In one aspect, MT3-MxEnc^{FLAG}-cMyc-NLS, or in other words, a genetically controlled structural element, wherein the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one N-terminally fused murine metallothionein-3, and wherein a FLAG tag with a nuclear localization signal is C-terminally fused via cMyc is used in a nanoscopy method. In one embodiment, the genetically controlled structural element does not interfere with cellular processes. In another embodiment, the nanoscopy method is electron microscopy. In yet another embodiment, the electron microscopy method is selected from the group consisting of scanning electron microscopy (SEM), transmission electron microscopy (TEM) and Focused Ion Beam Scanning Electron Microscopy (FIB-SEM). In even another embodiment, the electron microscopy method does not require further incubation steps involving DAB and hydrogen peroxide or further exogenous substrates.

[0194] In even another embodiment, the fusion protein is 3xMT3-QtEnc_^{FLAG}-cMyc-NLS. In one embodiment, 3xMT3-QtEnc_^{FLAG}-cMyc-NLS expressed pan-neuronally in *Drosophila melanogaster*. In a preferred embodiment, 3xMT3-QtEnc_^{FLAG}-cMyc-NLS is expressed in C3 neurons in *Drosophila melanogaster*, or in other words, a gentetically controlled structural element, wherein the genetically controlled structural element is a *Quasibacillus thermotolerans* (Qt) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is three N-terminally fused chimeric metallothionein-3, and wherein a FLAG tag with a nuclear localization signal is C-terminally fused via cMyc. In another aspect, a transgenic *Drosophila melanogaster* line is disclosed. In one embodiment, the transgenic *Drosophila melanogaster* line expresses 3xMT3-QtEnc_^{FLAG}-cMyc-NLS. In a preferred embodiment, the transgenic *Drosophila melanogaster* line expresses 3xMT3-QtEnc_^{FLAG}-cMyc-NLS and MT3-MxEnc^{FLAG}-cMyc-NLS. In another preferred embodiment, the transgenic *Drosophila melanogaster* line expressed MT3-MxEnc^{FLAG}-cMyc-NLS in T4-T5 neurons and 3xMT3-QtEnc_^{FLAG}-cMyc-NLS in C3 neurons. In one aspect, 3xMT3-QtEnc_^{FLAG}-cMyc-NLS, or in other words, a genetically controlled structural element, wherein the genetically controlled structural element is a *Myxococcus xanthus* (Mx) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is three N-terminally fused chimeric metallothionein-3, and wherein a FLAG tag with a nuclear localization signal is C-terminally fused via cMyc is used in a nanoscopy method. In one embodiment, the genetically controlled structural element does not interfere with cellular processes. In another embodiment, the nanoscopy method is electron microscopy. In yet another embodiment, the electron microscopy method is selected from the group consisting of scanning electron microscopy (SEM), transmission electron microscopy (TEM) and Focused Ion Beam Scanning Electron Microscopy (FIB-SEM). In even another embodiment, the electron microscopy method does not require further incubation steps involving DAB and hydrogen peroxide or further exogenous substrates.

[0195] In a preferred embodiment, MmMT3-QtEnc is from about 35 to 45 nm in diameter, preferably about 39.24±3.51 nm, most preferably about 39 nm. In one embodiment, MmMT3-MxEnc is from about 25 to 35 nm in diameter, preferably about 29.94±2.61 nm, most preferably about 30 nm. In one embodiment, MmMT3-TmEnc is from about 15 to 25 nm in diameter, preferably about 21.2±2.54 nm, most preferably about 21 nm.

[0196] In another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein mScarlet-l. In a preferred embodiment, the genetically controlled structural element, is a *Quasibacillius thermotolerans* (Qt) encapuslin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused. In another preferred embodiment, the genetically controlled structural element, is a *Quasibacillius thermotolerans* (Qt) encapuslin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is two murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused.

[0197] In a specifically preferred embodiment, the genetically controlled structural element is an encapsulin and the genetically controlled nanoscopy contrast-generating unit comprises a metal interactor selected from the group of metallothionein, preferably MT3 or a series of different metallothionein species, fatty acid-binding proteins (FABPs), and the lipid-binding domain of the cytochrome P450, preferably the lipid- and heme-binding domain of the cytochrome P450 BM3 (BM3h) or a combination of these metal interactors (SEQ ID NO: 229, 230, 231). Therefore, the genetically controlled structural element according to this embodiment is an encapsulin selected from the group consisting of *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin and the genetically contrast-generating unit is B-FABP, B-FABP-ko, Bm3h, or Bm3h-B7. In a preferred embodiment, the encapsulin is a *Quasibacillius thermotolerans* encapsulin (Qt). In this embodiment, if the metal interactor is one or more metallothionein, one to three copies of the MT3 or one to three different metallothionein species are bound to the N-terminus of the encapsulin. In an alternative embodiment, the genetically contrast-generating unit is the lipid-binding protein, i.e. no metallothionein is present. Moreover, one or more MT3, FABP, or BM3h are bound to the surface of the encapsulin, optionally via a spacer, wherein the spacer is optionally a SasG element of variable length. Such organized structural element is configured to generate a distinct shape of a barcode, wherein the barcode is a concentric barcode differentiable at the nanoscale (SEQ ID NO: 228, 232, 233, 234, 235, 236). Such concentric barcode may encode information about the cellular state.

[0198] In yet another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin and the genetically

contrast-generating unit is a bionconjugation tag. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, *Myxococcus xanthus* (Mx) encapsulin, or *Thermotoga maritima* (Tm) encapsulin and the genetically controlled contrast-generating unit is the bioconjugation tag SNAP. In a preferred embodiment, the genetically controlled structural element is an *Quasibacillius thermotolerans* (Qt) encapsulin and the genetically controlled contrast-generating unit is SNAP. In one embodiment, SNAP is either N-terminally or C-terminally fused.

[0199] The genetically controlled structural element may comprise a vault. In an embodiment, the vault comprises two hemi-vaults, each comprising 39 subunits of the major vault protein. In yet another embodiment, the vault protein comprises at least one fluorophore, preferably a fluorescent protein. In a preferred embodiment, the vault protein comprises a small fluorescent protein. In a more preferred embodiment, the small fluorescent protein is eUnaG, and the fluorescent protein is mScarlet. In another preferred embodiment, the small fluorescent protein is fused covalently to the artificially introduced internal HLH domain of the vault protein and/or the fluorescent protein is targeted non-covalently via a minimal interaction (mINT) motif. In yet another preferred embodiment, the vault comprises a SNAP25 palmitoylation motif. In a preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising a vault and at least one metal interactor. In yet another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor comprises at least one metallothionein. In yet another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor is at least one murine metallothionein. In even another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor is tandem MT3. In another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor is RNA. In yet another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor is an RNA-binding protein. In another embodiment, the genetically controlled structural element is a vault and the genetically controlled constrast-gerating unit is a RNA aptamer-binder: RNA aptamer pair. In said embodiment, the RNA aptamer-binder: RNA aptamer pair is preferably the circularized twister-broccoli aptamer. In even another preferred embodiment, the genetically controlled structural element is a vault, and the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein. In one embodiment, the genetically controlled structural element is a vault, the at least one metal interactor is RNA and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase. In yet another preferred embodiment, the genetically controlled structural element is a vault, the at least one metal interactor is an RNA-binding protein and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase. In even another preferred embodiment, the genetically controlled structural element is a vault, the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase.

[0200] The genetically controlled structural element may comprise a bacteriophage, in other words, prokaryotic (bacterial and archaeal) viruses. In an embodiment, the genetically controlled structural element comprises a bacteriophage and at least one genetically controlled nanoscopy contrast-generating unit comprising a metal interactor wherein genetically controlled nanoscopy contrast-generating unit is spatially organized by the structural element. In a preferred embodiment, the genetically controlled structural element is selected from the group consisting of MS2 phage (SEQ ID NO: 100), Qbeta phage (SEQ ID NO: 102), AP205 phage (SEQ ID NO: 207). In yet another preferred embodiment, the genetically controlled structural element is a self-assembling and thus, symmetric and multivalent genetically controlled structural element such as for example, MS2 phage and Qbeta phage. In a preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising a bacteriophage and at least one metal interactor. In a preferred embodiment, the at least one metal interactor is MT3. In yet another preferred embodiment, the genetically controlled structural element is a bacteriophage and the at least one metal interactor comprises at least one metallothionein. In yet another preferred embodiment, the genetically controlled structural element is a bacteriophage and the at least one metal interactor is at least one murine metallothionein. In even another preferred embodiment, the genetically controlled structural element is a bacteriophage, and the at least one metal interactor is tandem MT3. In another preferred embodiment, the genetically controlled structural element is a bacteriophage, and the at least one metal interactor is RNA. In yet another preferred embodiment, the genetically controlled structural element is a bacteriophage and the at least one metal interactor is an RNA-binding protein. In even another preferred embodiment, the genetically controlled structural element is a bacteriophage and the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein. In one embodiment, the genetically controlled structural element is a bacteriophage, the at least one metal interactor is RNA and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF or a tyrosinase. In yet another preferred embodiment, the genetically controlled structural element is a bacteriophage, the at least one metal interactor is an RNA-binding protein and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase. In even another preferred embodiment, the genetically controlled structural element is a bacteriophage, the at least one metal interactor is a lipid-binding protein, preferably a fatty-acid binding protein, and the genetically controlled nanoscopy contrast-generating unit additionally comprises a kinase, IMEF, or a tyrosinase.

[0201] The genetically controlled structural element may comprise an engineered mono-to-multivalent hub. Such engineered mono-to-multivalent hub is, for instance, a SunTag, an anti-moon tag, or CCC-tag, preferably an emFP (SEQ ID NOs: 92-99). In one embodiment, the genetically controlled structural element is an engineered mono-to-multivalent hub. In another embodiment, the genetically controlled structural element is an engineered mono-to-

multivalent hub further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is B-FABP (SEQ ID NO: 36), B-FABP-ko (SEQ ID NO: 248), Bm3H (SEQ ID NO: 29), or Bm3H-B7 (SEQ ID NO: 247). In a preferred embodiment, the genetically controlled structural element is an anti-moon tag, preferably one to twenty anti-moon tags, more preferably one to fifteen anti-moon tags, more preferably one to ten anti-moon tags. In another embodiment, the genetically controlled structural element is one to ten anti-moon tags and the genetically controlled structural element further comprises a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is B-FABP. In a preferred embodiment, the genetically controlled structural element is one anti-moon tags and the genetically controlled structural element further comprises a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is B-FABP In (SEQ ID NO: 259). In yet another embodiment, the genetically controlled structural element comprises at least one mono-to-multivalent hub and at least one metal interactor by the organization of the genetically controlled nanoscopy contrast-generating unit.

[0202] The genetically controlled structural element may comprise one or more filaments. In a preferred embodiment, the one or more filament is DHF 119. In another preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising at least one filament and at least one metal interactor. In a preferred embodiment, the metal interactor is MT3.

[0203] The minimal structural element can thus be constructed from just linkers, such as a GGSG linker (SEQ ID NO:237) that connect individual CGUs such as FABPs (FIG. **13**).

[0204] The genetically controlled structural element may comprise at least one or more fibers. In a preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fiber. In a preferred embodiment, the at least one or more fibers is an amyloid-like fiber. In an even more preferred embodiment, the amyloid-like fiber is functional amyloid. In a preferred embodiment, the functional amyloid is CsgA, preferably *E. coli* CsgA. In another preferred embodiment, the CsgA is optimized for intracellular expression, i.e., the CsgA is codon-optimized for mammalian cells. In another embodiment, the fiber is contrast-enhanced by fusing the fiber with, e.g., to a SpyTag. In a preferred embodiment, the genetically controlled structural element organizing the genetically controlled nanoscopy contrast-generating unit is a fusion protein comprising a fiber and at least one metal interactor. In a preferred embodiment, the metal interactor is MT3, a lipid-binding protein, or RNA. In another preferred embodiment, MT3 is fused to the cognate SpyCatcher binding partner.

[0205] In another embodiment, the genetically controlled structural element is spaghetti monster fluorescent proteins and variants thereof such as emFPs (SEQ ID NOs: 92-99) into which amino acid sequences are introduced that in turn can be bound by the set of attachment points conjugated to the genetically controlled nanoscopy contrast generating units such as MT3, FABPS, BM3h, RNA, RNA aptamers, metal binders.

[0206] The genetically controlled structural element may be the rigid rod-like protein SasG (SEQ ID NO: 207). In a preferred embodiment, SasG comprises a linear structure composed of concatenated SasG elements. In one preferred embodiment, SasG may contain mono-to-polyvalent hubs such as emFPs SEQ ID NOs: 92-99 instead of the fluorescent proteins, e.g. sfGFP, mTurquoise2, or mCherry (in FIG. **17**); alternatively, CGUs such as FABPs directly replace the fluorescent proteins (SEQ ID NO: 30-39). In one embodiment, said concatenable elements provide attachment points to genetically controlled nanoscopy contrast-generating units according to the invention. For example, in one embodiment, the genetically controlled nanoscopy contrast-generating units comprise a metallothionein, a lipid-binding protein, or RNA, and at least one RNA-binding protein.

[0207] The genetically controlled structural element may further comprise at least one attachment point. Said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. The genetically controlled nanoscopy contrast-generating unit binds to and/or interacts with the structural element via at least one attachment point. In one embodiment, the genetically controlled structural element is an encapsulin from *Quasibacillius thermotolerans* (Qt), *Myxococcus xanthus* (Mx), or *Thermotoga maritima* (Tm), wherein the genetically controlled contrast-generating unit is one or two murine methallothionein, or wherein the genetically controlled contrast-generating unit is a chimeric metallothionein sequence comprising three N-terminally fused metallothioneins comprising murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5), wherein the genetically controlled contrast-generating unit comprises an attachment point, wherein said attachment point is a bionjungation tag, wherein said bioconjugation tag is SNAP. In a preferred embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, wherein the genetically controlled contrast-generating unit is one murine metallothionein, wherein the genetically controlled contrast-generating unit comprises an attachment point, wherein said attachment point is a bionjungation tag, wherein said bioconjugation tag is SNAP. As laid out above, in other embodiments the fussion protein is eUnaG-MT3-QtEnc^{FLAG} or eUnaG-2xMT3-QtEnc^{FLAG} and the genetically controlled structural element further comprises at least one attachment point, wherein the at least one attachment point is an intrabody, wherein said intrabody is C-terminally fused. In one embodiment, the intrabody is an anti-mCherry intrabody. In another embodiment, the anti-mCherry intrabody is expressed on the outer surface of the encapsulin. In another embodiment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a coiled-coil domain. In a preferred embodiment, the attachment point is two coiled-coil domains. In yet another embodiment, the genetically controlled contrast-generating unit additionally comprises at least one further attachment point, wherein said attachment point is a SpyTag/SpyCatcher.

[0208] In one embodiment, the genetically controlled structural element comprises internal attachment points. Said internal attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, SpyTag or SpyCatcher domains, SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In another embodiment, the genetically controlled structural element comprises external attachment points. Said external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In yet another embodiment, the genetically controlled structural element comprises internal attachment points and external attachment points. Said internal and external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In one embodiment, the genetically controlled nanoscopy contrast-generating unit interacts or binds to at least one external attachment point. In yet another embodiment, the genetically controlled nanoscopy contrast-generating unit can interact or bind to internal and/or external attachment points, whereby the interaction or binding leads to a distinct, pre-defined shape.

[0209] In one embodiment, the genetically controlled nanoscopy contrast-generating unit is N-terminally and/or C-terminally fused to the genetically controlled structural element. In a preferred embodiment, the genetically controlled nanoscopy contrast-generating unit is N-terminally fused to the genetically controlled structural element. In an even more preferred embodiment, the genetically controlled nanoscopy contrast-generating unit is MT3 and is N-terminally fused to an encapsulin. In an equally preferred embodiment, MT3 is N-terminally fused to an encapsulin, and an epitope tag is fused to the C-terminus of encapsulin. In one embodiment, the C-terminal epitope tag is a FLAG tag, or BC2 tag.

[0210] In one embodiment, the genetically controlled structural element comprises a small fluorescent protein, which provides both high contrast in EM applications and super-resolution in fluorescence applications. In another embodiment, a small fluorescent protein is N-terminally or C-terminally appended to the genetically controlled structural element. In another embodiment, a small fluorescent protein is N-terminally appended to the genetically controlled structural element. In yet another embodiment, the genetically controlled structural element is n=1, 2, 3, 4, 5, 6, 7, 8, 9, or more. In a preferred embodiment, the small fluorescent protein is UnaG, and UnaG is N-terminally appended to the genetically controlled structural element. In another preferred embodiment, the genetically controlled structural element is an encapsulin. In an even more preferred embodiment, UnaG is N-terminally appended to 1x MT3-QtEnc, resulting in UnaG-1xMT3-QtEnc. In an equally preferred embodiment, UnaG is N-terminally appended to 2xMT3-QtEnc, resulting in UnaG-2xMT3-QtEnc.

[0211] In one embodiment, the genetically controlled structural element is loaded with protein cargo. In another preferred embodiment, the genetically controlled structural element is loaded with protein cargo and targeted to an intracellular protein target by an intrabody. In a preferred embodiment, the protein cargo is mScarlet. Therefore, in one embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein mScarlet-I is encapsulated to the encapsulin lumen via an encapsulation signal. In another embodiment, the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein mScarlet-I is expressed as cargo protein in the encapsulin lumen. In another embodiment, the protein cargo is APEX2 and APEX2 is expressed as cargo protein in the encapsulin lumen by encapsulating APEX2 via an encapsulation signal. In one aspect, an electron microscopy method is provided, wherein the genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, or *Thermotoga maritima* (Tm) encapsulin further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein APEX2 is expressed as cargo protein in the encapsulin lumen and further incubation steps involving DAB and hydrogen peroxide are performed.

[0212] In one embodiment, the intrabody is directly fused to the C-terminus of the genetically controlled structural element. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably QtEnc. In an equally preferred embodiment, the intrabody is covalently attached to the genetically controlled structural element by SpyTag-SpyCatcher chemistry, wherein the SpyTag is presented on the exterior of the genetically controlled structural element, and the intrabody is fused to a SpyCatcher domain. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably QtEnc. In another preferred embodiment, the intracellular protein target is membrane localized EGFP (EGFP-CAAX) and the intrabody is an anti-GFP intrabody. In yet another preferred embodiment, a cognate coiled-coil (CC) pair is fused to the exterior of the genetically controlled structural element; the cognate CC part P3 is N-terminally appended to the intracellular protein target. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably QEnc; the cognate CC part P3 is N-terminally appended to the membrane-localized EGFP (EGFP-CAAX).

[0213] In one embodiment, the genetically controlled structural element is detectable by both electron microscopy and fluorescence microscopy techniques. In yet another embodiment, the genetically controlled structural element is compatible with both electron microscopy and fluorescence microscopy techniques.

[0214] In one embodiment, the genetically controlled structural element is expressed in a cell of a given tissue.

Said tissue is captured on TEM grids or on silica wafers for subsequent analysis by TEM or SEM, allowing the detection of said genetically structural element in the identical cell. In a preferred embodiment, the genetically controlled structural element is QtEnc-FLAG-NLS. In another preferred embodiment, the genetically controlled structural element can be detected by both TEM and SEM.

[0215] In another embodiment, the genetically controlled structural element is detected by FIB-SEM (focused ion beam scanning electron microscopy). In yet another embodiment, MT3-QtEnc is detected by FIB-SEM. In a preferred embodiment, MT3-QtEnc is expressed in *Drosophila melanogaster* neurons and detected by FIB-SEM. In another preferred embodiment, the genetically controlled structural element can be detected by TEM, SEM including FIB-SEM, and fluorescence microscopy.

[0216] In one embodiment, the genetically controlled structural element can be directed to the nucleus. In another embodiment, the genetically controlled structural element can be directed to the cytosol. In one embodiment, the genetically controlled structural element is an encapsulin. In a preferred embodiment, the encapsulin is QtEnc. In a preferred embodiment, the genetically controlled structural element is QtEnc N-terminally fused to a fluorescent protein. In an even more preferred embodiment, the genetically controlled structural element is QtEnc, and the N-terminally fused fluorescent protein is miniSOG2. In an equally preferred embodiment, QtEnc is N-terminally fused to miniSOG2, and C-terminally fused to a FLAG epitope, followed by a mammalian NLS (c-myc) or a NES (HIV). In another embodiment, the N-terminally fused fluorescent protein does not compromise the assembly of the genetically controlled structural element. In a preferred embodiment, the N-terminally fused miniSOG2 does not compromise the assembly of QtEnc.

[0217] Another preferred embodiment is the CC-MT3-QtEnc construct, for which an exemplary sequence is given in SEQ ID NO: 21, with a CC-binding partner given in SEQ ID NO: 22.

[0218] The genetically controlled structural element may be of any combination of the above listed structural elements in any combination with any genetically controlled nanoscopy contrast generating unit disclosed herein. The structural element may comprise one or more contrast generating units comprising one or more of a metal-interacting polypeptide/protein, metal-binding peptide/protein, lipid-binding protein, RNA-binding protein, RNA or DNA molecule, polymerizing or synthesizing enzyme, or bioconjugation tag. This means, all of the above-listed contrast-providing genetically controlled nanoscopy contrast-generating units, can be combined with each other and can be spatially organized in any one or more of the above-listed structural elements. The genetically controlled structural elements and the genetically controlled nanoscopy contrast-generating units disclosed herein are thus to be seen as modules that may be combinable in form of modular combinatorics.

Genetically Controlled Scaffolds

[0219] In yet another aspect, the invention refers to a genetically controlled scaffold. The genetically controlled scaffold comprises and spatially organizes one or more genetically controlled structural elements. Such spatial organization generates distinct geometric patterns that can be distinguished at the nanoscale. Preferably, such distinct geometric patterns encode information on cellular states.

[0220] Such generated geometric patterns include vaults arrayed via SNAP25 (FIG. **11**), APH or N-terminal IMEF, encapsulins bound to the membrane via farnesylation tags, or via membrane-localized GPF targets (FIG. **16**), which can also be used to localize encapsulins to other organelles such as lysosome, multiple encapuslins organized via SasG or RNA as scaffolds (FIG. **17**).

[0221] In one embodiment, the information on cellular states is information in relation to external stimuli, for example, environmental parameters such as pH, temperature, or, influx, or efflux of ions such as calcium, response to ions such as calcium, proteolytic activity, conformational changes, or receptor densities. In another embodiment, the information on cellular states can for example identify a normal, i.e., healthy cell from a diseased cell in a pathological state. In yet another embodiment, the information on cellular states can identify diseases such as neurological diseases or cancer.

[0222] The genetically controlled scaffold may be selected from the group consisting of an endogenous cellular scaffold, a de novo designed scaffold, one or more SasG elements (SEQ ID NO: 112), CsgA (SEQ ID NO: 112), RNA or DNA structures, or combinations thereof.

[0223] The genetically controlled scaffold interacts or binds to the genetically controlled structural elements and, therefore, organizes the structural element. In one embodiment, the genetically controlled structural element comprises a member of the encapsulin family, a vault, MS2 phage, Qbeta phage, AP205 phage, mono-to-multivalent hubs, a filament, a linker, or combinations or variants thereof. In a preferred embodiment, the genetically controlled structural element is modified at the C- or N-terminus, suitable modifications are, for example, myristoylation, palmitoylation, isoprenylation, or prenylation such as farnesylation and gernaylgeranylation, or glypation. In another preferred embodiment, the genetically controlled structural element is modified by C-terminal farnesylation. By said C-terminal farnesylation the genetically controlled structural element is targeted to the membranes of endogenous, i.e., cellular scaffolds.

[0224] In an embodiment, the genetically controlled scaffolds are endogenous cellular scaffolds, such as cellular membranes of organelles, i.e., the nucleus, endoplasmic reticulum, Golgi apparatus, mitochondria, plastids, lysosomes, the inner cell membrane, and vacuoles. In yet another embodiment, the endogenous cellular scaffold is the cytoskeleton, i.e, actin filaments and/or microtubuli.

[0225] In another embodiment, the genetically controlled scaffold is an exogenous scaffold, such as a de novo designed scaffold. In one embodiment, the de novo designed scaffold is selected from the group consisting of, for example, filaments such as DHF or designed RNA structures. In a preferred embodiment, the de novo designed scaffold is DHF or 13-01, a de novo designed icosahedron comprising 60 cognate SpyCatcher binding partners.

[0226] In one preferred embodiment, the targeted controlled structural element is an encapsulin. In a preferred embodiment, the encapsulin is QtEnc, MxEnc, or TmEnc. In an even more preferred embodiment, the genetically controlled structural element is an iron-mineralizing QtEnc C-terminally modified with a SpyTag, wherein said iron-mineralizing QtEnc is C-terminally modified with a SpyTag

covalently clustered with 13-01. The iron-mineralized C-terminally modified QtEnc with a SpyTag that is covalently clustered with 13-01 leads to unbounded clusters. In said embodiment, the genetically controlled scaffold is geometrically unbounded. In a preferred embodiment, the genetically controlled scaffold arranges or organizes an encapsulin, even more preferably QtEnc, even more preferably a modified QtEnc comprising an antiGFP antibody and/or TmEnc with an anti-mCherry intrabody. In said embodiment, the genetically controlled scaffold is geometrically unbounded.

[0227] In yet another embodiment, the scaffold is a linear scaffold, such as a linear protein structure such as SasG. In even another embodiment, the scaffold is a concatenable linear protein. In a preferred embodiment, the linear scaffold is a bacterial surface protein, even more preferred SasG from *S. aureus* (SEQ ID NO: 207). In another embodiment, the SasG C-terminus and N-terminus of the genetically controlled structural element are fused to fluorescent proteins, wherein the C-terminus and N-terminus are fused to sfGFR and mCherry, respectively, or wherein the N-terminus and C-terminus are fused sfGFR and mCherry.

[0228] The spatial organization of the genetically controlled structural elements by the genetically controlled scaffold yields distinct patterns. In one embodiment, the genetically controlled scaffold yielding distinct patterns is SasG. In a preferred embodiment, the genetically controlled scaffold yielding patterns is concatenated SasG. In another embodiment, a pattern is formed by distinct pre-defined spacers and attachment points within SasG. In another embodiment, the SasG spaces and attachment points are fully controllable such that the resulting SasG pattern is a fully-genetically defined linear barcode, i.e., each genetic element on the DNA and RNA has its corresponding linear element on the protein level, whereby a geometrically defined pattern is formed. In yet another embodiment, the geometrical pattern is bounded. In one embodiment, the genetically controlled structural element is an encapsulin, or ferritin (iron-mineralizing QtEnc C-terminally modified with a SpyTag, wherein in said iron-mineralizing QtEnc is C-terminally modified with a SpyTag covalently clustered with SasG) and the genetically controlled scaffold is SasG. In another embodiment, a pattern is formed by SasG in a linear assembly, i.e., without one or more structural elements.

[0229] In a specifically preferred embodiment, the genetically controlled scaffold is SasG of variable lengths, wherein the SasG comprises and spatially organizes encapsulins as structural elements, wherein the encapsulins comprise and spatially organize a genetically controlled nanoscale contrast-generating unit comprising one or more MT3 domains or a series of different metallothionein species (SEQ ID NO: 169) as the metal interactor. In one embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, one encapsulin from *Quasibacillius thermotolerans* (Qt), *Myxococcus xanthus* (Mx), or *Thermotoga maritima* (Tm) as genetically controlled structural element, and one or more murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In another embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, an encapsulin selected from the group consisting of *Quasibacillius thermotolerans* (Qt), *Myxococcus xanthus* (Mx), or *Thermotoga maritima* (Tm) as genetically controlled structural element, and one or two murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In yet another embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, one encapsulin from *Quasibacillius thermotolerans* (Qt), *Myxococcus xanthus* (Mx), or *Thermotoga maritima* (Tm) as genetically controlled structural element, and one or two murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit. In even another embodiment, the genetically controlled scaffold comprises a SasG having 2, 3, 4, 5, 6, 7, 8, 9 or 10 G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, one encapsulin selected from the group consisting of *Quasibacillius thermotolerans* (Qt) or *Thermotoga maritima* (Tm) as genetically controlled structural element, and one murine metallothionein-3 as genetically controlled nanoscopy contrast-generating unit.

[0230] In another embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, one *Quasibacillius thermotolerans* (Qt) encapsulin as genetically controlled structural element having one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein said Qt encapsulin has one or more anti-GFP intrabody on its surface. In a further embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, one *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element having one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein the Tm encapsulin has one or more anti-mCherry intrabodies on its surface.

[0231] In a further embodiment, the genetically controlled scaffold comprises SasG having 2, 3, 4, 5, 6, 7, 8, or more G5 domains connected by E domains, said SasG having N-terminally fused sfGFP and C-terminally fused mCherry, one *Quasibacillius thermotolerans* (Qt) encapsulin as genetically controlled structural element having one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein said Qt encapsulin has one or more anti-GFP intrabody on its surface, and one *Thermotoga maritima* (Tm) encapsulin as genetically controlled structural element having one murine metallothionein as genetically controlled nanoscopy contrast-generating unit, wherein the Tm encapsulin has one or more anti-mCherry intrabody on its surface. In one embodiment, the Qt encapsulin having one or more anti-GFP intrabody on its surface is linked to the matching anti-mCherry intrabody on the surface of the Tm encapsulin. In another embodiment, said Qt encapsulin having one or more anti-GFP intrabody on its surface results in an approximately 40 nm ring-shaped object, wherein the Tm encapsulin having one or more matching anti-mCherry intrabody on the surface results in an approximately 25 nm spherical object, wherein said spherical object surrounds said ring-shaped object.

[0232] In an embodiment, the genetically controlled scaffold is formed by amyloid curly fibrils such as CsgA from *E. coli* providing attachment points.

[0233] In another embodiment, the genetically controlled scaffold is designed from RNA origami structures that folds into rigid assemblies that can span tens of nanometers. In a preferred embodiment, said RNA origami structures contain aptamer loops such as PP7 or MS2 to which proteinaceous contrast-generating units can be attached. In another preferred embodiment, said RNA origami structures contain aptamers for exogenous fluorophores, such as Spinach. In another preferred embodiment, the aptamer structures are circularized via ligase RtcB via the Tornado system to stabilize them in mammalian cells.

[0234] In one embodiment, the genetically controlled scaffold comprises at least one attachment point. Said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In one embodiment, the genetically controlled scaffold comprises internal attachment points. Said internal attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In another embodiment, the genetically controlled scaffold comprises external attachment points. Said external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags for covalent protein labeling such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In yet another embodiment, the genetically controlled scaffold comprises internal attachment points and external attachment points. Said internal and external attachment points are selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags for covalent protein labeling such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In one embodiment, the genetically controlled scaffold interacts or binds to at least one external attachment point of a structural element.

[0235] In one embodiment, the genetically controlled structural elements comprise external attachment points. In a preferred embodiment, the external attachment points are monovalent. In one embodiment, the genetically controlled scaffold is SasG and the genetically controlled structural element is an encapsulin and comprises at least one attachment point, wherein the attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners such as SpyTag or SpyCatcher domains, SnoopTag/SnoopCatcher, DogTag/DogCatcher, bioconjugation tags for covalent protein labeling such as SNAP/Clip-Tag domains, and/or Halo-Tag domains, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides such as troponins, as well as combinations thereof. In one preferred embodiment, the genetically controlled scaffold is SasG, and the genetically controlled structural element is an encapsulin and comprises at least one fluorescent molecule. In another embodiment, the genetically controlled scaffold is SasG, and the genetically controlled structural element is an encapsulin and comprises two fluorescent molecules such as sfGFP and mCherry. In another embodiment, the genetically controlled scaffold, the genetically controlled structural element, and the two fluorescent molecules are detectable by both electron microscopy and fluorescence microscopy techniques. In yet another embodiment, the genetically controlled scaffold, the genetically controlled structural element, and the two fluorescent molecules are compatible with both electron microscopy and fluorescence microscopy techniques. In one embodiment, SasG fusion proteins, such as sfGFP-SasG-mCherry to which structural elements can bind via bioorthogonal intrabodies to the fluorescent proteins. In a preferred embodiment, the SasG proteins form geometric patterns by connecting the structural elements QtEnc of about 40 nm in diameter with the structural elements TmEnc of about 20 nm diameter. The resulting pattern comprises QtEnc surrounded by TmEnc, wherein the low-contrast space between both structural elements is determined by the length of the rigid SasG linker. In another embodiment, the fusion proteins $QtEnc^{antiGFPib}$ and TmEnc-LaM-4 are disclosed, also resulting in distinct patterns.

[0236] In a preferred embodiment, the SasG-organized patterns of multiple encapsulins as structural elements are modularly combined with the concentric barcodes generated inside the lumen of each structural element.

[0237] The genetically controlled scaffold may be of any combination of the above-listed scaffolds in any combination with any genetically controlled structural element and any genetically controlled nanoscopy contrast generating unit disclosed herein. The scaffold may comprise at least one structural element, wherein each structural element may comprise one or more contrast generating units comprising one or more of a metal-interacting polypeptide/protein, metal-binding peptide/protein, lipid-binding protein, RNA-binding protein, RNA or DNA molecule, polymerizing or synthesizing enzyme, or bioconjugation tag. This means, all of the above-listed contrast-providing genetically controlled nanoscopy contrast-generating units, can be combined with each other and can be spatially organized in any one or more of the above listed structural elements, wherein all such combined structural elements can be combined with each other and spatially organized by any of the disclosed scaffolds. The genetically controlled scaffolds, genetically controlled structural elements, and genetically controlled nanoscopy contrast-generating units disclosed herein are thus to be seen as modules, which may be combinable in form of modular combinatorics.

Use of the Invention

[0238] In another aspect, the present invention relates to the use of a genetically controlled structural element, and/or a genetically controlled scaffold for nanoscopy detection, wherein nanoscopy detection comprises molecular mapping

and/or geometric sensing. In certain embodiments, the nanoscopy detection further comprises geometric actuation.

[0239] Molecular mapping and/or geometric sensing is preferably performed in cells, organoids, tissue, or model organisms. In one embodiment, the cell is an animal cell selected from the group consisting of the genera Homo, *Rattus, Mus, Sus, Bos, Danio, Canis, Felis, Equus, Salmo, Oncorhynchus, Gallus, Meleagris, Drosophila*, or *Caenorhabditis*. In a preferred embodiment, the animal cell can be of the species *Homo sapiens, Rattus norvegicus, Mus musculus, Sus scrofa, Bos taurus, Danio rerio, Danionella translucida, Salmo salar, Canis lupus, Felis catus, Equus caballus, Oncorhynchus mykiss, Gallus, Meleagris gallopavo, Drosophila melanogaster* or *Caenorhabditis elegans*. The animal cell can be from a cow, pig, sheep, goat, bison, horse, donkey, mule, rabbit, chicken, duck, goose, turkey, or pigeon. In a particularly preferred embodiment, the animal cell is a mammalian cell and is selected from the group consisting of neuronal cells, glial cells, cardiomyocytes, glucose-responsive insulin-secreting pancreatic beta cells, hepatocytes, astrocytes, oligodendrocytes, chondrocytes, osteoblasts, retinal pigment epithelial cells, fibroblasts, keratinocytes, dendritic cells, hair follicle cells, renal duct epithelial cells, vascular endothelial cells, testicular progenitors, smooth and skeletal muscle cells, hematopoietic cells, cartilage cells or epidermal cells as well as insulin-secreting p-cells, embryonic stem cells, and mesenchymal cells. In an even more preferred embodiment, the mammalian cell is a human cell and is selected from the group consisting of neuronal cells, glial cells, cardiomyocytes, glucose-responsive insulin-secreting pancreatic beta cells, hepatocytes, astrocytes, oligodendrocytes, chondrocytes, osteoblasts, retinal pigment epithelial cells, fibroblasts, keratinocytes, dendritic cells, hair follicle cells, renal duct epithelial cells, vascular endothelial cells, testicular progenitors, smooth and skeletal muscle cells, hematopoietic cells, cartilage cells or epidermal cells as well as insulin-secreting p-cells, embryonic stem cells, and mesenchymal cells.

[0240] In another embodiment, the mapping and/or sensing is performed in organoids or tissues. In yet another embodiment, the mapping and/or sensing is performed in model organisms. In one embodiment, the model organism is, for example, *C. elegans, Drosophila melanogaster, Danio rerio, Danionella translucida, Mus musculus, Taeniopygia guttata.*

[0241] The genetically controlled structural element, and/or a genetically controlled scaffold may be used for nanoscopy detection to read-out multiplexed information on the promoter activity and gene expression state of cells. The genetically controlled structural element, and/or a genetically controlled scaffold may furthermore provide information about diffusion constants in different cells and tissues. The genetically controlled structural element, and/or a genetically controlled scaffold may furthermore be used as fiducial markers, throughout entire cells to improve alignment of tilt series, perform drift corrections, or serve as geometrically defined reference markers for image quality assessment, such as point-spread functions or contrast-to-noise-ratios.

[0242] The genetically controlled structural element, and/or a genetically controlled scaffold may be used for nanoscopy detection, wherein nanoscopy detection comprises molecular mapping. In this case, the molecular mapping provides information on the subcellular distribution of a molecule of interest within a cell or tissue via the binding of genetically controlled structural elements and/or genetically controlled scaffolds to a molecule of interest which thus determines the subcellular localization of the genetically controlled structural element and/or the genetically controlled scaffolds. In some embodiments, the nanoscopy detection is electron microscopy detection, such as scanning electron microscopy (SEM), transmission electron microscopy (TEM) and Focused Ion Beam Scanning Electron Microscopy (FIB-SEM). In one embodiment, no further incubations teps involving DAB and hydrogen peroxide or further exogenous substrates are required. In an alternative embodiment, further incubation steps involving DAB and hydrogen peroxide can be used, if for example, APEX2 is used as a cargo protein inside the lumen of the genetically controlled structural element such as an encapsulin.

[0243] In another embodiment, the information on the subcellular distribution of a molecule of interest within a cell or tissue is provided by the binding to a molecule of interest by the genetically controlled structural element comprising at least one genetically controlled nanoscopy contrast-generating unit, and/or the genetically controlled scaffolds. The molecule of interest may be localized in the lysosomes and endosomes, mitochondria, nucleus, plasma membrane, endoplasmatic reticulum, Golgi apparatus, and/or cytosol. In one embodiment, the genetically controlled structural element and/or the genetically controlled scaffold are targeted to one or more of the subcellular compartments. In another embodiment, the molecule of interest within a cell or a tissue is, for example, a protein, lipid, or carbohydrate. In a preferred embodiment, the molecule of interest is a functionally relevant epitope on organelles, a receptor or channel in a membrane.

[0244] In one embodiment, the genetically controlled structural element and/or the genetically controlled scaffold is targeted to an intracellular or extracellular protein target. In a preferred embodiment, the genetically controlled structural element is targeted to an intracellular protein target. In one embodiment, the genetically controlled structural element is targeted to the intracellular protein target by an intrabody. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably QtEnc. In one embodiment, the intrabody is directly fused to the C-terminus of encapsulin as the genetically controlled structural element. In another preferred embodiment, the intracellular protein target is membrane localized EGFP (EGFP-CAAX) and the intrabody is an anti-GFP intrabody. In an equally preferred embodiment, the intrabody is covalently attached to the genetically controlled structural element by SpyTag-SpyCatcher chemistry, wherein the SpyTag is presented on the exterior of the genetically controlled structural element, and the intrabody is fused to a SpyCatcher domain. In a preferred embodiment, the genetically controlled structural element is an encapsulin, preferably QtEnc. In yet another equally preferred embodiment, a cognate coiled-coil pair is fused to the genetically controlled structural element and the respective cellular target. In a preferred embodiment, the genetically controlled structural element is an encapsulin, and the cellular target is an intracellular protein target. In one particularly preferred embodiment, the cognate coiled-coil pair is fused to the exterior of QtEnc; the cognate CC part P3 is N-terminally appended to the membrane-localized EGFP (EGFP-CAAX).

[0245] In another preferred embodiment, molecular mapping occurs via a heterobifunctional adapter made from inactivated Trim21 (dTrim21) fused to a fluorescent protein to which intrabodies fused to encapsulins as structural elements can bind (see, e.g., FIG. **18**).

[0246] Alternatively, or in addition to the molecular mapping, the genetically controlled structural element, and/or a genetically controlled scaffold may be used for nanoscopy detection, wherein nanoscopy detection comprises geometric sensing. In this case, geometric sensing provides information on a specific cellular state, a cellular process, or the presence or absence of an analyte or environmental parameter of interest within a cell or tissue, or the response to an external stimulus. Such sensing is achieved in that the distinct shape generated by the genetically controlled structural element, and/or the geometric pattern generated by the genetically controlled scaffold changes in response to a pre-defined cellular state, a pre-defined cellular process, at least one analyte or at least one environmental parameter, or an external stimulus. Alternatively, a change in a distinct shape and/or distinct pattern is only generated if such analyte, environmental parameter, or external stimulus is present in sufficient strength, or only in response to specific cellular states or processes.

[0247] The change in shape occurs by a spatial rearrangement of the contrast-generating units on a structural element or via the rearrangement of the structural elements on a scaffold. This may occur by a conformational change in the scaffold, the structural element, or the contrast-generating unit.

[0248] A specific cellular state is, for instance, a specific constellation of promoter activities, the influx or efflux of ions such as calcium, response to ions such as calcium, proteolytic activity, conformational changes, or receptor densities, a response of a cell, a therapeutic response of the cell and activation of the cell. A specific cellular process is, for instance, protein expression and transport, or mitochondrial fusion or fission. An exemplary analyte is, for instance, calcium or cAMP. An external stimulus is, for instance, a depolarization or the application of electromagnetic or mechanical energy or magnetic gradients. In another embodiment, the at least one environmental parameter is for example, pH, temperature.

[0249] In one embodiment, shape change is brought about by an analyte-triggered assembly of a structural element via proteolytic unblocking of a sterically hindered precursor. In one embodiment, the structural elements are blocked, preferably with a triple LBT15 domain. In another embodiment, the blocking domain is cleaved in a calcium-dependent manner. In yet another embodiment, the blocking domain is cleaved when either TEVp or SCANR and ionophore are present. In one embodiment, the genetically controlled structural element assembles following calcium-dependent cleavage of the blocking domain in the presence of either TEVp or SCNAR and ionophore. In even another embodiment, the structural elements assemble upon proteolytic cleavage by a protease. In one embodiment, a degron destabilized NLuc cargo is co-expressed. In another embodiment, the co-expressed cargo serves as a read-out measure. In another preferred instantiation, proteolytic unmasking, which can be triggered by calcium, leads to the concatenation and thus stepwise growth of the scaffold SasG, capped off with distinct fluorescent proteins. In another preferred instantiation, proteolysis unblocks inteins to re-complement split vault monomers.

[0250] In another preferred embodiment, a change in the concentric barcode is obtained by the calcium-driven binding of calmodulin, fused to a contrast generating unit FABP, to calmodulin-binding peptides presented on the surface of encapsulins as structural elements.

[0251] In another preferred embodiment, the agglomeration state of structural elements such as encapsulin can be changed via calcium-mediated interactions of calmodulin and calmodulin-binding peptides.

[0252] In yet another preferred embodiment, a change in patterning can also be achieved by relocalization of structural elements to the membrane via calcium-dependent myristoyl-switch proteins.

[0253] In addition to the molecular mapping and geometric sensing, the genetically controlled structural element, and/or a genetically controlled scaffold may be used for nanoscopy detection, wherein nanoscopy detection further comprises geometric actuation. Geometric actuation alters a cellular state or process by a biomechanical and/or biochemical effect or via an external stimulus, ore the deposition of external energy, electromagnetic radiation, mechanical energy, or magnetic gradients.

[0254] An example for a biomechanical effect is clustering of a receptor via a multidentate structural element or scaffold, such that cellular signaling is modified. Electromagnetic radiation is, for instance, visible or near-infrared light. Mechanical energy is, for instance, mechanical waves covering the ultrasound frequency range.

[0255] Such genetically controlled structural element, and/or the genetically controlled scaffold preferably exerts a biomagnetic, biomechanical, and/or biochemical effect on a biological or non-biological structure.

[0256] In one embodiment, genetically controlled structural elements and scaffolds exert biomechanical forces by polyvalent interactions with their surfaces, such as clustering of endogenous receptors in model organisms, which can be monitored by nanoscopy.

[0257] In another embodiment, the genetically controlled structural element, and/or the genetically controlled scaffold exerts a biomagnetic effect on a biological or non-biological structure. In one preferred embodiment, encapsulins such as QtEnc are rendered magnetic by co-expression of the ferroxidase IMEF and optionally multicopper oxidase Mnx. The expressing cells can thus be magnetically sorted via Magnetic-activated cell sorting (MACS) and subsequently brought back in culture. In addition, or alternatively, the magnetic encapsulins can be bound to intracellular structures such as organelles to manipulate their subcellular localization via magnetic gradients.

[0258] In one embodiment, the biomagnetic effect causes specific (re)-arrangements or (re)-organization and for example, a physiological response. In another embodiment, the genetically controlled structural element, and/or the genetically controlled scaffold exerts a biomechanical effect on a biological or non-biological structure.

[0259] The geometric actuation can be combined with geometric sensing in that an analyte or parameter that causes a change in a geometric pattern for geometric sensing (e.g. an agglomeration) may then be the condition for effective geometric actuation (e.g. via magnetic gradient fields, which exert more forces on the agglomerated pattern than the

monodisperse structural elements). Furthermore, geometric actuation can be monitored via molecular mapping and geometric sensing.

Detection of the Inventive Patterns and Shapes

[0260] In another embodiment, the geometric pattern is defined by pre-determined shapes of the pre-determined nanoscale-sized genetically controlled structural elements comprising at least one genetically controlled nanoscopy contrast-generating unit.

[0261] In one embodiment, element-specific methods built into EM instruments such as for example, EDX, EELS, or nanoSIMS can detect the specific metal localized by the metal interactor an orthogonal dimension for multiplexing, in addition to the geometric shape and pattern. In one preferred embodiment, the pre-determined shape is, for instance, an encapsulin or a vault. In one embodiment, the concatenation of the genetically controlled nanoscopy contrast-generating unit to a genetically controlled structural element produces a distinct shape. In another embodiment, the distinct shape is a function of the 3D distribution of the genetically controlled nanoscopy contrast-generating units within the genetically controlled structural element. In other words, the geometrically distinct shape is generated by the interaction of the genetically controlled nanoscopy contrast-generating units and the genetically controlled structural element. In another preferred embodiment, the same shape or pattern can be detected by EM techniques such as TEM, SEM, FIB-SEM and fluorescence of optoacoustics nanoscopy, preferentially with super-resolution techniques.

Nanobiomaterial

[0262] In one aspect, the invention relates to nanobiomaterial consisting of isolated genetically controlled structural elements and/or isolated genetically controlled scaffolds. This nanobiomaterial thus consists of the genetically controlled structural elements and/or genetically controlled scaffolds disclosed herein, which are all isolatable from their originating system, which is a genetically modified cell or a cell-free system.

[0263] "Genetically modified" means in this respect that its DNA has been altered by the deletion or addition of genetic material. A "cell-free system" refers to the in vitro synthesis of polypeptides in a reaction mix comprising biological extracts and/or defined reagents. The reaction mix will comprise a template for the production of the macromolecule, e.g. DNA, mRNA, etc.; monomers for the macromolecule to be synthesized, e.g. amino acids, nucleotides, etc.; and co-factors, enzymes and other reagents that are necessary for the synthesis, e.g. ribosomes, uncharged tRNAs, tRNAs charged with unnatural amino acids, polymerases, transcriptional factors, tRNA synthetases, etc.

[0264] In one embodiment, the nanobiomaterial is a genetically controlled structural element. In another embodiment, the nanobiomaterial is a genetically controlled structural element and a genetically controlled scaffold. In yet another embodiment, the nanobiomaterial is a genetically controlled scaffold.

[0265] Such nanobiomaterial can be used for any nanoscopy method such as TEM, SEM, SRLM, or optoacoustic superresolution microscopy as described herein, however in a two-step process which comprises the production of the nanobiomaterial, its isolation, and its subsequent use in a biological or non-biological system.

Vectors

[0266] The invention further relates to one or more vectors comprising the nucleic acid encoding the genetically controlled nanoscopy contrast-generating unit, the genetically controlled structural element, and/or the genetically controlled scaffold.

[0267] A vector comprising a nucleic acid encoding a genetically controlled structural element such as encapsulin and optionally a genetically controlled nanoscopy contrast-generating unit. In some embodiments, the genetically controlled nanoscopy contrast-generating unit is already present in the cell which is transduced with the vector comprising the structural element. In another embodiment, the vector comprises the nucleic acid encoding a genetically controlled scaffold. Such vector may comprise the nucleic acid encoding the scaffold, the structural element, and the contrast-generating unit. In another embodiment, one of the genetically controlled nanoscopy contrast-generating unit, the genetically controlled structural element, and the genetically controlled scaffold is already present in the cell into with the vector is to be transduced.

[0268] The vector may be any vector suitable for the transduction of nucleic acids into cells. The encoded elements may be expressed under the control of a cell-specific promoter. The encoded element may be codon-optimized for cellular expression. Such vector may be a viral vector, a plasmid, an exosome, or any other known vector. A viral vector may be a AAV vector. Suitable vectors or constructs according to the invention are disclosed in Table 2 below.

[0269] In one aspect of the invention, the AAV vector comprises any combination of the genetically controlled scaffolds, genetically controlled structural elements, and genetically controlled nanoscopy contrast-generating units disclosed herein. In one embodiment, the AAV vector comprises a genetically controlled structural element, wherein said genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one or two murine metallothionein-3, wherein the genetically controlled structural element further comprises the fluorescent protein mScarlet-1. In a preferred embodiment, the AAV vector comprises a genetically controlled structural element, wherein said genetically controlled structural element is an encapsulin from *Quasibacillius thermotolerans* (Qt), further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused. In another preferred embodiment, the AAV vector comprises the genetically controlled structural element, wherein said genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is two murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused. In another embodiment, m-Scarlet-I is fused to the two murine metallothionein-3 via P2A. In yet another embodiment, the AAV vector is a AAV5 vector and comprises a CaMKIIa promoter. In another preferred embodi-

ment, the AAV vector comprises a genetically controlled structural element, wherein said genetically controlled structural element is a *Quasibacillius thermotolerans* (Qt) encapsulin, further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is two murine metallothionein-3, wherein mScarlet-I is N-terminally fused, wherein a FLAG tag is C-terminally fused. In another embodiment, m-Scarlet-I is fused to the two murine metallothionein-3 via P2A. In yet another embodiment, the AAV vector is a AAV5 vector and comprises a CaMKIIa promoter. In another embodiment, an AAV5 vector comprises the genetically controlled structural element, wherein said genetically controlled structural element is an encapsulin from *Quasibacillius thermotolerans* (Qt), further comprising a genetically controlled contrast-generating unit, wherein said genetically controlled contrast-generating unit is one murine metallothionein-3, wherein mScarlet-I is N-terminally fused to one murine metallothionein-3 via P2A, wherein a FLAG tag is C-terminally fused, wherein the AAV5 vector is under control of a CaMKIIa promoter, or put differently, latter vector is AAV5-CaMKIIa-mScarlet-I-P2A-2M-QtFLAG

[0270] In a further embodiment, the AAV vector is selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9. In a preferred embodiment, the AAV vector is AAV5. In another embodiment, the AAV vector is pseudtotyped. In another embodiment, the AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, or AAV9 vector comprises a CAMKII promoter. In a preferred embodiment, the AAV5 vector comprises a CAMKII promoter.

[0271] In another aspect, the disclosed AAV vector is for use in medicine. In one embodiment, the disclosed AAV vector is for use in diagnostic imaging.

EXAMPLES

Example 1: Cell Expression and Specimen Preparation for Systematic Evaluation of Contrast-Generating Units for EM

[0272] We generated a library of constructs that could be suitable for a genetically controlled contrast-generating unit based on their ability to spatially control metal-interactors, which may also serve as binders for exogenous fluorophores or chromophores. To this end, we adapted naturally occurring proteins and/or de novo designed proteins. For the search of proteins with high content of osmiophilic residues (shown in FIG. **1**E, FIG. **1**F) we used a Python script, which reads protein sequences of an input database such as PDB and calculates the number of osmiophilic residues (C H M W) divided by the length of the protein.

[0273] We used standard plasmid lipofection techniques in HEK293 cells to express a library of constructs coding for metal-interactors to screen for sufficient contrast in TEM after standard fixation, post-fixation, and staining protocols (FIGS. **1**-**6**). All DNA constructs were either custom synthesized by IDT DNA Technologies or assembled from multiple fragments via HiFi assembly, traditional ligation cloning, or PCR-based mutagenesis methods and cloned into pcDNA 3.1 (+) Zeocin for mammalian expression.

[0274] Low passage number HEK293T cells (ECACC: 12022001, obtained via Sigma-Aldrich) were cultured in advanced DMEM with 10% FBS and penicillin-streptomycin at 100 μg/ml at 37° C. and 5% CO2. HEK293T cells were transfected using X-tremeGENE HP (Roche) transfection reagent according to the manufacturer's protocol (3:1 μl reagent:μg DNA). DNA amounts (ratio shell to cargos) were kept constant in all transient experiments to yield reproducible DNA-Lipoplex formation.

[0275] Expression was confirmed by native and SDS gel electrophoresis (12% BioRad TGX gels, run at 200 V for 40 min) (FIGS. **1**, **2**, **3**, **5**, **6**). Constructs resulting in robust, non-toxic expression were then subjected to EM sample preparation using standard EM fixation, post-fixation, and staining protocols compatible with protocols also used for tissue from model organisms.

[0276] For EM sample preparation, the staining method was adapted from Deerinck et al., Microsc. Microanal. (2010). HEK293 cells were harvested 36 hours post-transfection, using accutase treatment, and pelleted by centrifugation. The pellets were then fixed with 2.5% Glutaraldehyde in 0.1 M sodium cacodylate buffer (pH 6.7-7.0) for 20 min. For *Drosophila melanogaster* brains, the fixation duration varied between 20 minutes and 24 hours. After removal of fixative, the material was post-fixed using the 1:1 mixture of 4% OsO_4 with 0.3 M CB, containing 3% potassium hexacyanoferrate (II) for 20 minutes on ice. The post-fixative solution was removed, and the material was washed twice with 0.1 M sodium cacodylate buffer for 2 minutes, followed by 2×5 min Milli-Q washing steps. Milli-Qwater was removed, and the material was optionally treated with 1% tannic acid (10 min, RT). Then, tannic acid was decanted, and the material was washed 5 times for 5 minutes using Milli-Q water. The material was then treated with 1% uranyl acetate solution (30 min, RT), with subsequent 5 times 5 minutes washing steps with Milli-Q water. Afterward, the material was subjected to treatment with 3% lead aspartate (15 min, RT). Again, the material was washed (5×5 min in Milli-Q water) before proceeding to epoxy embedding. The epoxy embedding process was conducted over 2 days. On the first day, the material was incubated on ice with 75% EtOH for 10 minutes, followed by incubation in 90% EtOH for 10 minutes and 100% EtOH for 30 minutes, then 100% EtOH for 30 min on ice. The EtOH solution was replaced with pure propylene oxide and incubated for 5 minutes under RT. Next, the solution was discarded, and the material was incubated in 1:1 mixture of EPON and Propylene oxide for 30 minutes under RT. Subsequently, the material was sequentially incubated at room temperature in 100% EPON for 30 minutes and again with fresh EPON solution overnight. On the next day, the old epoxy was removed, the material was briefly rinsed in fresh 100% epoxy and left in newly-poured 100% epoxy for 72 hours under 60° C. The *Drosophila* m. brain prior to final EPOXY curation was oriented such that several optical lobes were located parallel to the block's slicing plane. The resulting blocks were subjected to trimming and slicing. For cellular material, the trimming of excess EPOXY from the block's surface was done using an EM TRIM milling system (Leica Microsystems, Germany). Using an UltraCut E microtome (Reichert/Leica, Germany) the prepared blocks were prepared with a histo-knife (DIATOME, Switzerland) and then sequentially cut with an ultra-knife (DIATOME, Switzerland) at a slice thickness of 70 nm, verified by the slices' interference pattern. The slices were deposited either on the surface of a 200 mesh copper grid or the polished side of a silicon wafer.

[0277] TEM images were acquired on a Libra120 TEM (Carl Zeiss GmbH, Germany), equipped with a CCD camera (TRÖNDLE Restlichtverstärkersysteme, Germany) using ImageSP software (SYSPROG, Belarus). Before image acquisition, all grid-supported specimens were pre-irradiated with 120 kV beam voltage, 13 μA beam current, 200 μrad illumination angle without insertion of apertures. The actual image acquisition took place with the activated BIO-AIS condenser aperture system and 60 μm objective aperture under the same beam conditions as used for pre-irradiation, except for the illumination angle that was specified to be equal to 100 μrad. The target magnification for the presented images was selected as 8000× in the microscope control software, exposure timing was set equal to 1000 s. Selection of regions of interest for computing contrast-to-noise-ratios (CNR) was performed using ImageJ.

Example 2: Complementation of Contrast-Generating Units with Light-Dependent Microscopy Methods

[0278] Constructs combing metal interactors and fluorophores were expressed in HEK293 cells as described in detail in Example 1.36 hours post-transfection, fluorescence microscopy was conducted on a confocal microscope (Leica SP5 using the 488 nm laser line, Leica Microsystems) or epifluorescence microscope (EVOS FL Auto Cell Imaging System (Thermo Fisher Scientific) (FIG. **7**). Fluorescence on-gel analysis was performed by illuminating the CN-PAGE gel by UV light and capturing the image on a standard CCD camera (FIG. **5***c* after incubation with DAPI, FIG. **7***c*, FIG. **7***d*, FIG. **8***a* direct fluorescence). Multimodal detection, complementing EM contrast, was also extended to bioluminescence detection, via a luciferase targeted to the inside of the encapsulin via bioorthogonal coiled-coil adapters. Luminescence measurements were taken after the addition of fumirazine on a luminometer (Berthold Centro LB 960 (Berthold Technologies) at 0.1 s acquisition time.) (FIG. **8***c*). In a similarly modular fashion, the enzyme tyrosinase was encapsulated inside the TmEnc, and the formation of melanin was confirmed on a native gel by photoabsorbance, which is also the basis of the photoacoustic signal (FIG. **20***c*). Alternatively, fluorophores can also be attached via SNAP or HaloTags or can also be presented on the outer surface (e.g., via C-terminal eUnaG fusion) of structural elements such as encapsulins, which leaves the lumen of encapsulins unaltered for organizing contrast-generating units for EM. Since entire fluorescent proteins fused to the outward-facing N-terminus of encapsulins tend to disrupt encapsulin assembly, we decided to reconstitute the smaller fragments of tripartite split-GFPnon the surface as explained in FIGS. **7***g*-**7***i* and verified assembly and fluorescence by BN-PAGE and fluorescent microscopy, respectively.

Example 3: Geometric Multiplexing with Concentric Barcodes Based on Spherical Structural Elements

[0279] We genetically concatenated multiple contrast-generating units from metallothionein 3 (MT3) spherical structural elements based on variants of encapsulins and expressed these structural elements in HEK293 cells (FIGS. **9***a*-**9***h*, see detailed protocol in Example 1), as well as in *Drosophila* neurons (FIGS. **9***i*-**9***k*). To this end, a vector was generated for transgenesis by cloning the respective constructs into pJFRC7-20XUAS-IVS or pJFRC19-13XL-exAop2-IVS and submitting those to a commercial *Drosophila* Embryo Injection Service for transgenesis. Sample preparation for TEM from HEK cells and freshly dissected *Drosophila* brains was performed as described in detail in Example 1. Histograms of the distribution of diameters were generated with the measurement tools implemented in ImageJ (FIG. **9***e*). Line profiles shown in FIG. **9***f* were computed by using ImageJ and custom-written python scripts.

[0280] We furthermore conducted comparative imaging via TEM and SEM of the identical nuclei of *Drosophila* neurons expressing MT3-QtEnc-Flag-NLS or MT3-MxEnc-Flag-NLS (FIGS. **9***h*-**9***j*). To this end, ultrathin sections were captured on either TEM grids or on silica wafers for imaging via TEM or SEM, respectively. SEM images were acquired with an SEM Gemini 360 (Carl Zeiss GmbH, Germany), equipped with a Bio-BSD detector (Carl Zeiss GmbH, Germany) using ATLAS software (Carl Zeiss GmbH, Germany). Silicon wafers supporting the samples were glued to the stage with silver glue (PLANO GmbH, Germany). Image acquisition parameters were: 6.5 kV beam voltage, 2 nm nominal pixel size with a 30 μm objective aperture at a working distance of 3.7 mm. The stage was subjected to a bias voltage of 5 kV.

[0281] Furthermore, the different encapsulin: metallothionein combinations can be detected via focused ion beam (FIB)-SEM as shown in FIG. **9***k*). To this end, FIB-SEM image acquisition was performed with the SEM Crossbeam 550 (Carl Zeiss GmbH, Germany), equipped with the InLens, BSE, SESI detectors (Carl Zeiss GmbH, Germany) running ATLAS software. The metal-sputtered block with the specimen of interest was positioned on the stage with silver glue (PLANO GmbH, Germany) to ensure the proper adhesion and discharging of the specimen. A guiding pad was deposited in the proximity of the ROI to meet the requirements of image capture alignment during the three-dimensional volume recording. The following settings were used for image acquisition: SEM beam voltage 1.3 kV, a working distance of 5 mm, 4 nm nominal voxel size. The FIB Ga beam, accelerated by 30 kV voltage and holding a current of 700 μA, was used for three-dimensional slicing of the block's volume.

[0282] As shown in FIG. **10**, by concatenating one or multiple metallothioneins, different concentric barcodes can be generated that provide rotational invariant contours also on non-isotropic imaging slices (i.e. in cross-sections or maximum intensity projections) defined by multiple rings of contrast in the lumen of encapsulins (line plots in FIG. **10***d* generated by ImageJ). Those concentric barcodes can be complemented by additional rings (FIG. **10***e*) using any of the contrast-generating units detailed in previous Examples and Figures, for instance, by FABPs targeted via an isopeptide bond formation. Shown in FIG. **10***f*) is the schematic of the genetic constructs for binding MT3 or FABP to the surface to the spherical QtEnc via SpyTag/SpyCatcher isopeptide formation (also compare FIG. **3***b*).

Example 4: Geometric Multiplexing with Non-Spherical Structural Elements

[0283] Different modifications of the major vault protein were assembled from synthesized DNA and expressed in HEK293 cells, as detailed in Example 1. Fluorescent cargo proteins fused to the enzyme APEX2 were co-expressed and

imaged via confocal fluorescence microscopy on an SP5 Imaging System, Confocal Microscope (Leica, Wetzlar, Germany). Histochemistry was performed using a standard protocol for APEX2, applying 3,3'-diaminobenzidine (DAB) and hydrogen peroxide (H_2O_2) (FIGS. **11***a*, **11***b*). TEM imaging was performed as described in detail in Example 1 (FIGS. **11***c*, **11***d*). Epifluorescence microscopy (EVOS FL Auto Cell Imaging system (Thermo Fisher Scientific) was performed to confirm the dual fluorescence labeling of the major vault protein by UnaG, fused to the internal HLH domain, and the red fluorescent protein mScarlet, targeted to the lumen via an mINT motif.

[0284] We furthermore generated non-spherical structural elements by fusing MT3 to auto-assembling Csga monomers (FIGS. **12***a*, **12***b*), fibril- or lattice-forming elements (FIGS. **12** *c*-**12***f*), which were evaluated by TEM as described in detail in Example 1. In addition, structural elements can be formed by the concatenation of the nanoscopy contrast-generating units based on FABPs connected via minimal linkers (as detailed in FIG. **13**).

Example 5: Monovalent-to-Polyvalent Hubs as Structural Elements and Control of Valency on Structural Elements

[0285] We constructed monovalent adapters to multiple contrast-generating units by constructing variants of spaghetti monster (emFP, FIGS. **14***a*-**14***e*) that harbor several epitopes for intrabodies or frankenbodies, which can be fused to the respective nanoscopy contrast-generating units as detailed in FIG. **14***b*). In order to test, whether those variants are still fluorescent, we expressed them in HEK293 cells as described in Example 1 and imaged them on an EVOS FL Auto Cell Imaging system (Thermo Fisher Scientific) (FIGS. **14***a*, **14***c*). Furthermore, we evaluated via combined fluorescence imaging and immunohistochemistry whether the emFPs could be targeted to subcellular structures and still provide the binding sites for the multiple binders. FIG. **14***c* shows emFPv4 yielding green fluorescence via mGreenLantern that partially overlaps with Cy-3 fluorescence indicating binding of the antiMoon-Tag intrabody. We furthermore demonstrated the successful interaction on the monovalent-to-polyvalent hub by using CN-PAGE, which shows higher-molecular band species under UV illumination corresponding to bound anti-moon intrabody fused to different metal-interactors (FIG. **14***i*). As an alternative to the use of monovalent-to-polyvalent hubs, we evaluated programmable translational read-through to control the stoichiometry of attachment points on the surface of encapsulins to systematically reduce the valency of the surface-presented attachment points (which would otherwise only be determined by the icosahedral symmetry). To this end, we expressed the genetic constructs depicted in FIGS. **15***a*, **15***b*, such that variable amounts of the bioluminescent tag HiBit were surface-expressed on QtEnc. We subsequently conducted a HiBit assay (Promega) following the protocols suggested by the commercial system using a standard luminometer.

Example 6: Geometric Multiplexing by Spatially Organizing Structural Elements on Cellular Scaffolds

[0286] Given the nanometer-scale resolution of electron microscopy and super-resolution microscopy techniques, multiplexed information can be readily encoded by modifying the subcellular localization of the structural elements detailed in previous figures via scaffolds expressed at distinct subcellular locations inside cells. We demonstrate several examples of this strategy by expressing in HEK293 cells—followed by TEM analysis—both as described in Example 1, either a membrane localization signal (farnesylation tag, FIG. **16***a*), a peptide from a cargo adaptor which binds to endogenous motor proteins (KinTag, FIG. **16***b*), or an anti-GFP intrabody targeted to lysosomal-localized GFP (FIG. **16***c*), or membrane-localized GFP (FIG. **16***d*, in the control condition on the right, a Flag epitope was expressed instead of the anti-GFP intrabody).

Example 7: Geometric Multiplexing by Designer Scaffolds

[0287] As an alternative to using endogenous scaffolds, we demonstrate the versatile application of the rigid hetero-bifunctional protein from *S.aureus* as an engineered scaffold, whose length can be systematically varied to present bio-orthogonal adapters at both ends (FIG. **17***a*). To demonstrate the precise linear extension of the designed SasG linker when expressed in mammalian cells, we expressed a version of variable length with the FRET pair sfGFP and mCherry on either end, expressed them in HEK293 cells (described in Example 1), and subjected the cell lysate to CN-PAGE under UV illumination. This analysis shows a FRET effect indicated by a yellow signal for only the direct fusion of sfGPF and mCherry. In distinction, the bands corresponding to the constructs with longer spacers between the fluorescent proteins give a green fluorescent signal indicating the absence of FRET and the isolated fluorescence from sfGFP (FIG. **17***b*). We furthermore validated the rigid hetero-bifunctional crosslinker SasG in combined fluorescence microscopy and TEM (FIG. **17***c, d*) based on the protocols described in detail in the previous examples. The results show distinct spatial patterns of two differently sized encapsulins (QtEnc and TmEnc), indicating that constraints from steric hindrance are sufficient to obtain distinct barcoding patterns from the combination of several structural elements and contrast-generating units (FIG. **17***e, f*). In addition to the use of a single SasG element, several of these linear connectors can be expressed to generate more complexly shaped structural elements such as triangles and other platonic shapes. By expressing 3 bio-orthogonal pairs of adapters chosen in this case from isopeptide-forming pairs and inteins, triangular shapes can be enforced upon co-expression of the respective components in HEK293 cells and using on-gel fluorescent analysis of the individual combinations of co-expressed components. The results also show a high-molecular species corresponding to the combination of all three elements (last lane in FIG. **17***h*). Alternatively, to proteinaceous scaffolds such as SasG, scaffolds can also be designed from RNA as shown in FIG. **17***g*, which may in parallel provide contrast based on the motifs detailed in FIG. **4**.

[0288] For completion, in addition to the geometrically precise and bounded scaffolds, one can also use simpler clustering of structural elements such as encapsulins surface-presenting SpyTags with multivalent crosslinkers (in this case SpyCatcher mounted to the de novo cage 13-01 (FIG. **17***i*). The EM contrast, in this case, is provided by the ferroxidase IMEF, resulting in a complete filling of the

encapsulin lumen. Alternatively, modular combinations with the concentric barcodes detailed in Example 3 can be used.

Example 8: Molecular Mapping and Geometric Sensing

[0289] For mapping the subcellular distribution of biomolecules of interest, structural elements or scaffolds can be targeted to the biomolecule of interest via a range of attachment points whose valency can be controlled via mono-to-polyvalent hubs, which allow for the attachment of several contrast-generating units or structural elements to a bioorthogonal attachment point to the biomolecule of interest (FIG. **14**) or via read-through control of the stoichiometries of the attachment points (FIG. **15**). Targeting of the target biomolecule of interest can also be achieved via the intracellular delivery of exogenous antibodies (via electroporation or microinjection) that can be connected to a structural element or scaffold via a deactivated Trim21 molecule (dTrim21), which can be fused to an attachment point such as a fluorescent protein (FIG. **18***l*). This "sandwich" arrangement allows binding of a structural element and additional mapping capabilities via fluorescence microscopy).

[0290] To demonstrate that the geometrically distinct structural elements can be made responsive to cellular states, we expressed sterically hindered variants of encapsulins as structural elements containing the contrast-generating unit MT3 (genetic constructs shown in FIG. **18***a*) that allow for proteolytic unmasking by the tobacco etch virus-derived (TEV) bio-orthogonal TEV protease, of which a calcium-dependent version has been generated that is termed SCANR. After expression in HEK293T cells and inducing calcium influx by addition of increasing concentrations of the calcium ionophore (Calcimycin A23187, Sigma-Aldrich), a higher molecular weight band appears on the CN-PAGE (FIG. **18***b*), corresponding to the accumulation of a band corresponding to the proteolytically cleaved protein on SDS-PAGE (FIG. **18***c*). In addition, we co-expressed degron-destabilized luciferase (NanoLuc) such that we could use a luciferase signal as an indicator for the amount of NanoLuc that was encapsulated inside the lumen of the encapsulins (via the appropriate encapsulation signal, QtSig). Thus, we could use simple bioluminescent detection with the luciferase-substrate fumirazine to quantify the calcium-dependent proteolytically triggered encapsulin assembly via the amount of luciferase that was protected inside the encapsulin lumen to give a bioluminescent signal (FIG. **18***d*). The corresponding TEM image shows the expected ring-shaped MT3-QtEncFlag structural elements after calcium influx (FIG. **18***e*).

[0291] As an extension to geometric sensing via changing the shape obtained from structural elements, we also demonstrate how the geometric pattern formed by several structural elements can be altered by altering the geometry of the scaffold as a function of an analyte of interest. FIGS. **18***f*-**18***i* show how SasG scaffolds can be concatenated via split-intein-mediated processes. These components thus realize a step-wise growing counter/timer mechanism, which can be triggered or stopped by using caged inteins, or modifying the concentration of unmasked Base or Cap modules (FIGS. **18***h*, **18***i*).

[0292] We furthermore show that the concept of the proteolytic unmasking of sterically-hindered precursors to structural elements can also be applied to non-spherical structural elements such as vaults. FIG. **18***j* shows a schematic demonstrating a split major vault protein that is modified by split-intein pairs blocked by masking peptide connected via a TEV-protease cleavage site (FIG. **18***j*). To show that vault auto-assembly occurs upon co-expression of TEV protease, we co-expressed the fluorescent protein mScarlet with an mINT targeting signal addressing it to the vault lumen and subjected the respective HEK293 cells to epifluorescence microscopy (EVOS FL Auto Cell Imaging system (Thermo Fisher Scientific)). The images show that a cytosolic accumulation of fluorescence signal occurs upon TEV co-expression, which is similar to the signal observed when non-sterically blocked vault monomers (right column) were expressed (FIG. **18***k*).

[0293] In addition to the mechanism of proteolytic unmasking of the building blocks of structural elements, concentric barcodes can be added to the outside of spherical structural elements via, for instance, the surface presentation of calmodulin-binding peptides such as M13 to which calmodulin (CaM) fused to contrast-generating units can bind (FIG. **19***a*) similar to the interaction of isopeptide-forming partners displayed in FIGS. **3***b*,**3** *c*. We have furthermore co-expressed QtEnc surface-modified with the CaM-binding peptide aFod and a multi-dentate cross-linker constructed from a ferritin variant from *Pyrococcus furiosus* surface-modified with CaM (FIG. **19***b*) and the degron-destabilized fluorescent protein mEos4b. We subsequently conducted epifluorescence microscopy and observed the formation of fluorescent intracellular clusters after minutes of triggering calcium influx via the calcium ionophore A23187 (Sigma-Aldrich). These data thus demonstrate the agglomeration of multi-dentate structural elements as a reporter mechanism. The analogous mechanism can be established for phosphorylatable peptides and phosphopeptide-binding proteins such as SEQ ID NOs: 239, 206. Similarly, relocalization of structural elements, demonstrated on the example of vaults in FIG. **19***c*, can be demonstrated by expressing a variant of vaults modified with a myristoyl-switch motif adapted from recoverin, which relocalizes to the membrane upon binding to calcium. The confocal microscopy images show the formation of fluorescent clusters upon pharmacological triggering of calcium influx (30 μM A23187), derived from the co-expressed vault-packaged mEos4b.

Example 9: Geometric Actuation

[0294] We have generated several *Drosophila* lines as described in Example 1 in which a multi-dentate QtEnc surface-modified with anti-GFP intrabodies (QtEncantiGFPIB) is expressed via a panneuronal promoter (Elav) in a standard temperature-dependent fashion via the Gal4:UAS system. When this line is crossed with a line expressing a GFP-tagged receptor GluCl in a transposon Minos-mediated integration cassette (MiMIC) (Venken et al., 2011), the intraneuronal localization of receptors can be controlled via biomechanical actuation through multi-dentate binding to the gradually expressed multi-dentate nanoscopy-visible structural element, which is detected by immunohistochemistry to the Flag-tag in FIG. **20***a*. Please note the temperature-dependent release (switch from 18° C. to 29° C., using the standard method to control the conventional GAL4-UAS system via a temperature-sensitive allele of GAL80) of the receptor to the neuropil of the respective *Drosophila* neurons.

[0295] In addition to the biomechanical manipulation of the subcellular distribution of biomolecules of interest, we demonstrate in FIG. **20***b* how cells can be magnetically sorted when they express encapsulins that are expressing the ferroxidase IMEF. The graph shows the selective retention of HEK293 cells expressing QtEnc and IMEF on commercially available columns (Miltenyi), demonstrating that the magnetic-field-dependent force is sufficient to retain entire cells on magnetic columns. Importantly, all examples here show biomagnetic encapsulins as structural elements, which are patterned by either de novo (the cage 13_01 or the filament DHF, FIG. **12***d*) or natural (farnesylation, FIG. **16***a*) scaffolds which can localize magnetic actuation in the cell while the precise patterns can be read out by nanoscopy, confirming the distinct geometry for the magnetically actuatable structures.

[0296] In addition to biomagnetic manipulation with EM-visible nanoscale patterns, we furthermore demonstrate in FIG. **20***c* that the strongly photoabsorbing and thus photoablatable polymer melanin, visible standard EM stains, can be formed inside the geometrically distinct structural element such as TmEnc. After the expression of the different genetic combinations of coiled-coil adapter pairs (e.g., P1/P2 for encapsulating *Bacillus megaterium* BmTyr-P1 to P2-TmEnc as specified in FIG. **20***c*, melanin formation could be demonstrated by color formation on CN-PAGE.

Example 10: Fixation-Stable, Nanoscale EM Contrast

[0297] Our first objective was to generate variants of encapsulins, which produce robust EM contrast with nanoscale precision (EMcapsulins) using standard EM fixation and staining protocols, and without additional incubation steps necessary to allow diffusion of DAB and H_2O_2 or other exogenous substrates. EMcapsulins are one exemplary genetically controlled structural element according to the invention.

[0298] Since murine Metallothionein-3 (M) has been demonstrated to be a potent lead binder and acidic stretches of other metallothionein domains have been shown to interact with uranyl ions, we reasoned that M might not only work in specialized EM procedures but also provide localized EM contrast organized by encapsulins and standard staining protocols. As laid out in the aspects and embodiments of the invention below, the genetically controlled structural element (here: EMcapsulin) comprises at least one contrast-generating unit. According to the invention and this example, the EM capsulins comprises one or two murine metallothionein-3 (SEQ ID NO: 1, SEQ ID NO: 4), or a chimeric metallothionein sequence comprising three metallothionein, i.e. murine metallothionein-3 (MmT3), *Synechococcus elongatus* (SmtA) metallothionein, and *Triticum aestivum* Ec-1 metallothionein (TaEC1) (SEQ ID NO: 5).

[0299] Given M's small size and flexibility, we thought it unlikely to disrupt encapsulin assembly. We thus generated direct fusions to the lumen-facing N-terminus of encapsulin monomers instead of encapsulating M as cargo protein to obtain better control over the stoichiometry and suppress background from non-encapsulated cargo (FIG. **30***a*).

[0300] When we expressed M as N-terminal fusions to encapsulins from *Quasibacillus thermotolerans* (Qt), *Myxococcus xanthus* (Mx), and *Thermotoga maritima* (Tm) in HEK293T, we could confirm by Clear Native (CN) PAGE that Qt^{FLAG} and Mx^{FLAG} variants showed the expected electrophoretic running behavior for T=4 and T=3 icosahedral assemblies under native conditions, irrespective of the N-terminal fusion of M (FIG. **30***a*). 1M-Tm^{BC2} showed similar electrophoretic mobility as the T=1 assembly of Mx^{FLAG}, which is known to occur when no cargo proteins are co-expressed.

[0301] Based on these promising biochemical data, we next expressed the 1M-Qt^{IIAG} fusion and wild-type encapsulin (QtFLAG) in HEK293T cells and subjected them to a standard EM sample preparation protocol, consisting of fixation with glutaraldehyde, post-fixation with OsO_4, followed by heavy metal staining with uranyl acetate and lead citrate, Epon embedding, microtome sectioning and imaging on TEM grids.

[0302] The resulting TEM micrographs showed annular contrast shapes with a brighter center spot outlined by a darker ring for 1M-Qt^{FLAG}.

Example 11: Concentric EM Barcodes

[0303] We next sought to evaluate whether concatenating multiple copies of M on the inner surface of EMcapsulins could add distinct layers of annular EM contrast (FIG. **28***a*). Indeed, in comparison to the TEM contrast of 1M-QtFLAG, we observed a broadening of the contrasted ring for 2M-QtFLAG and the vanishing of the bright spot in the center when a third metallothionein domain (3M-Qt^{FLAG}) was added (FIGS. **28***a*, **28***b*). Since a concatenation of 3 murine metallothionein sequences prevented EMcapsulin assembly, we constructed 3M from a chimeric sequence of three metallothionein domains from different species ($MmMT3^{20}$, $SeSmtA^{22}$, and $TaEC1^{25}$).

[0304] In the case of Mx^{FLAG}, the outer diameter of the contrasted edges was expectedly smaller than that of QtFLAG such that a single M (1M-Mx^{FLAG}) resulted in a bright center similar in diameter to that seen for 2M-Qt^{FLAG}. Adding a second M to Mx^{FLAG} (2M-Mx^{FLAG}) abolished the bright central spot. Complementarily, 1M-Tm^{BC2} exhibited the smallest outer diameter without a prominent bright center (FIG. **30***b*). Thus, the modular combination of metal interactors and different-sized protein shells led to well-separated outer diameters for the three types of spherical protein shells and distinct radial profiles for all six classes of EMcapsulins.

[0305] Higher TEM magnifications demonstrate that the layering of contrasted rings is in line with the location of M on the inner surface of the protein shell (FIG. **39**).

Example 12: Automatic Semantic Segmentation

[0306] To test how robustly the EMcapsulins can be identified and classified, we trained an end-to-end U-net for multi-class semantic segmentation of the 6 EMcapsulins classes on 250 TEM images obtained from all experimental categories reported here. Semantic segmentation results are shown as overlays in FIG. **28***d*, color-coded by class as defined in FIG. **28***a*. Segmentation metrics, such as the Dice similarity coefficients (DSC) per EMcapsulin class, are tabulated in Table 1, giving an average DSC score of 0.65 (validation set), 0.71 (test set 1) and 0.63 (test set 2).

[0307] We also report several object-detection metrics, such as an average recognition quality (harmonic mean of precision and recall) of 0.64, 0.70, and 0.61 for the validation set, test sets 1 and 2, respectively.

[0308] For comparison, we also implemented a sequential segmentation (U-net) followed by classification (EfficientNetV2-M) of the segmented image patches after background subtraction to ensure that the classification signal emerges from the EMcapsulins themselves (FIG. **40***a*). Segmentation and classification scores compared with human annotations are given in FIGS. **40** **40***b*, **40***d*, **40***e*).

[0309] When we then expressed combinations of two EMcapsulin classes in separate HEK cells, pooled in the same sample for multiplexed detection, we found that the end-to-end network (FIG. **28***d*) produced slightly better semantic segmentation results than the sequential segmentation-classification pipeline (FIGS. **42***e*, **42***f*).

[0310] For optimal usability, we also generated a napari graphical user interface (GUI) that allows for interactive curation of semantic segmentations using the publicly available pre-trained models.

Example 13: Programmable EMcapsulin Nanopatterns

[0311] We next aimed to further increase the encoding capacity of the multiplexed EM gene reporters by arranging multiple EMcapsulins into different patterns.

[0312] We thus generated a series of rigid heterobifunctional crosslinkers from the microbial filamentous protein SasG capped off with the fluorescent proteins superfolder GFP (sfGFP) and mCherry, for which bio-orthogonal intrabodies exist (FIG. **34***a*).

[0313] We obtained increasing linker lengths by concatenating G5 domains connected via E domains (2G-8G) that resulted in distinct protein species as shown by the sharp yellow fluorescent bands on CN-PAGE upon UV illumination (FIG. **34***b*). Only a direct fusion of the fluorescent proteins without SasG (sGFP-0G-mCherry) emitted at a red-shifted wavelength, indicating Forster resonance energy transfer (FRET).

[0314] When we then co-expressed the fluorescent linkers together with different EMcapsulins that were surface-modified with the matching intrabodies (1M-Qt$^{anti\text{-}GFP}$ and 1M-Tm$^{anti\text{-}mcherry}$), we observed distinct EMcapsulin patterns in TEM, in which the annular 1M-Qt shapes were surrounded by 1M-Tm at distinct interparticle distances dependent on the linker length (FIGS. **34** *c*-**34***e*).

Example 14: Dual EM and Fluorescent Gene Reporters

[0315] While direct fusions of fluorescent proteins of the GFP family tended to disrupt encapsulin assembly in our hands, we reasoned that the flexible M might function as a linker to a small fluorescent protein such as eUnaG to allow for proper assembly. The resulting dual-contrast EMcapsulins could be targeted to subcellular structures of interest for sequential analysis by fluorescent and electron microscopy (FIG. **23***a*).

[0316] Indeed, eUnaG-1M-Qt^{FLAG} migrated as a well-defined band on Clear-Native PAGE corresponding to an assembly with T=4 icosahedral symmetry. In comparison, a blurred band was detected for eUnaG-2M-Qt^{FLAG}, indicating more heterogeneous assemblies, possibly due to space limitations in the lumen of the nanospheres.

[0317] We thus investigated whether eUnaG is also tolerated on the outer surface of Qt, thus reserving the EMcapsulin lumen for variable copies of M (FIG. **23***a*). This variant indeed showed a sharp fluorescent band with decreased electrophoretic mobility as compared to eUnaG-1M-Qt^{FLAG} in agreement with the expected increase in the hydrodynamic diameter from adding proteins on the outer surface.

Example 15: Labeling of Subcellular Targets

[0318] Next, we wanted to test how well the dual-mode EMcapsulins could be directed to intracellular locations of interest. We, therefore, installed anti-mCherry-intrabodies on the outer surface of the fluorescent EMcapsulin (1M-Qt^{eUnaG}) by co-expressing 1M-Qt$^{anti\text{-}mcherry}$ in a ~4:1 ratio.

[0319] When we co-expressed membrane-targeted mCherry (mem-mCherry^{FLAG}), the fluorescent EMcapsulin co-localized to the membrane (FIG. **23***b*) (Manders' coefficient M1=0.870, Manders' M2=0.966, Costes P-value: 1.00), and the corresponding TEM images could resolve individual EMcapsulins lined up on the membrane (FIG. **23***c*).

[0320] To showcase the modularity of the labeling approaches, we tested the expression of SpyTag/SpyCatcher adapters or bioorthogonal coiled-coil pairs as targeting moieties and fluorescent proteins or APEX2 as cargo proteins.

[0321] Based on these promising results, we next chose connexins as a molecular target for fluorescent EMcapsulins. Connexins assemble into connexons forming gap-junctions that contribute to cell-to-cell communication in many biological systems, including in neuronal networks.

[0322] Connexins have also previously been fused to fluorescent proteins and modified with tetracysteine tags targeted by biarsenical fluorophores, including ReAsH. These were then used for photo-induced production of singlet oxygen to polymerize DAB, leading to electron-dense precipitates on the gap junctions, validated by immunogold labeling.

[0323] To gain control over the stoichiometry of our fully-genetic system from a single genetic construct, we developed a translational read-through (rt) system based on shortened variants of previously identified rt motifs (FIGS. **23** *d*-**23***f*), in which the nascent amino-acid chain of an EMcapsulin is released at a leaky stop codon in the majority of cases. In contrast, the ribosome continues translating over the adjacent rt motif in a tunable fraction of cases to also translate the fused C-terminal intrabody. By combining three stop codons with three shortened rt motifs (rt20s, rt9s and rt9us), we created a small library yielding rt efficiencies between ~1% and ~20% (FIG. **3***d*).

[0324] When co-expressing the rt cassette yielding ~20% translational read-through, i.e., ~50 intrabodies per EMcapsulin (1M-Qt^{FLAG}-TGA-rt20s-$^{anti\text{-}GFP}$) with msfGFP-Cx43, we found proper transport of Cx43 to the membrane (green channel) and adequate labeling by EMcapsulins (blue channel) on the membrane (FIG. **23***e*) (Manders' coefficient M1=0.989, Manders' coefficient M2=0.953, Costes P-value: 1.00), which was confirmed in the TEM micrographs from corresponding samples (FIGS. **23** *f*, **23***g*). The same rt cassette (TGA-rt20s) yielded similar connexin-labeling also for Cx43 with a C-terminally fused msfGFP (FIG. **32***c*), while a control condition without an rt cassette, i.e., an expression of 100% intrabodies per 1M-Qt (i.e., 240 copies on the surface) resulted in clustering of Cx43 in the ER and no cell surface signal as expected (FIG. **3***d*).

[0325] To further demonstrate the value of fluorescent EMcapsulins, we performed live-cell microscopy in mammalian oocytes co-expressing different mCherry-tagged tar-

gets with eUnaG-1M-Qt$^{anti\text{-}mcherry}$ (FIG. **42**). Green fluorescent EMcapsulin colocalized with mCherry-RAB11A on recycling endosomes (FIGS. **42***b*-**42***d*) or with mCherry-Myo5b on cargo vesicles (FIGS. **42***e*-**42***g*), in line with previously reported subcellular localizations. Automated segmentation and tracking analyses revealed no substantial difference in the volume and speed of labeled compartments in the absence or presence of EMcapsulins. In contrast, a homogenous background was observed in the absence of mCherry targets (FIGS. **42** *b*, **42***e*). In addition, we targeted mCherry-PLK1 to label relatively static acentriolar microtubule-organizing centers (FIG. **42***e*).

Example 16: Multiplexed EMcapsulin Contrast in *Drosophila* Neurons

[0326] We next sought to assess whether the EMcapsulin contrast in cell culture would also transfer to in vivo applications in neurons. We thus generated transgenic *Drosophila* lines with pan-neuronal expression of 1M-Qt-$^{FLAG\text{-}NLS}$ and 1M-Mx$^{FLAG\text{-}NLS}$ harboring a nuclear localization signal (NLS) (FIG. **29**), whose functionality was confirmed beforehand in cell culture (FIG. **43**) via immunohistochemical analyses (insets in FIGS. **29** a, **29***c*).

[0327] Higher TEM magnifications again showed increased contrast on the inner surface of the EMcapsulin protein shells, similar to what was observed in HEK cells (FIG. **44**).

[0328] To demonstrate multiplexed EMcapsulin detection in different neuronal types in the same animal, we generated a transgenic *Drosophila* line expressing 3M-Qt$^{FLAG\text{-}NLS}$ in C3 neurons and 1M-Mx$^{FLAG\text{-}NLS}$ in T4-5 neurons, whose somata are adjacent in the optic lobe, such that one can capture them in the same field-of-view in TEM (FIGS. **29***e*-**29***g*). Furthermore, we have co-expressed 1M-Qt with a nuclear export signal (1M-Qt$^{FLAG\text{-}NES}$) and 1M-Mx$^{FLAG\text{-}NLS}$ in the same neuronal type and observed substantial expression of 1M-Qt$^{NES\text{-}FLAG}$ in neuronal processes (FIG. **45**).

Example 17: EMcapsulin Contrast in Volume SEM

[0329] Since SEM is the other common mode for volume EM, we compared SEM and TEM contrast directly from adjacent ultramicrotome sections of the same *Drosophila* neurons. We found that similar image information can be obtained from EMcapsulins in TEM and SEM (FIG. **38**). The line profiles through the EMcapsulins in TEM and SEM show similar outer diameters based on the contrast edges, whereas the lumen of both nanospheres appears brighter in TEM than in SEM.

[0330] We also tested whether the EMcapsulin contrast is compatible with FIB-SEM tomography, which enables fully automated volume imaging with isotropic nanometer resolution. We chose a voxel size of 4 nm, a resolution informative for connectome analyses and could readily discern 1M-Qt$^{FLAG\text{-}NLS}$ (FIG. **38***c*) and 1M-Mx$^{FLAG\text{-}NLS}$ (FIG. **38***d*).

Example 18: EMcapsulin Expression in Mouse Brain

[0331] To assess EMcapsulin contrast in mammalian neurons, we co-expressed 2M-Qt^{FLAG} with m-Scarlet-I in mouse hippocampus via viral transduction. Native gel analysis verified EMcapsulin expression and assembly (FIG. **30***b*). Immunohistochemical fluorescence analysis confirmed EMcapsulin expression in CamKIIa-positive neurons in the hippocampus (FIG. **30***c*).

[0332] EM analysis revealed EMcapsulin expression in neuronal somata (FIG. **30***d*) and processes (FIGS. **30***f*-**30***g*), although some membrane discontinuities were observed in some regions, occasionally precluding a clear delineation of cellular boundaries. The narrow size distribution and sphericity of the rigid proteinaceous EMcapsulin shells produced concentric contrast edges at the inner and outer circumferences of the annular cross-sections. This appearance differentiated the EMcapsulins from synaptic vesicles, which exhibited more variable sizes and non-circular luminal and external borders consistent with their flexible lipid membranes.

[0333] Jointly, these imaging data show robust detection of barcoded EMcapsulins in different cell types and EM modalities.

Materials and Methods of Examples 10-18

Molecular Biology

[0334] All DNA constructs were custom-synthesized by IDT DNA Technologies or assembled from multiple fragments via HiFi assembly, traditional ligation cloning (using EcoRI and NotI sites), or PCR-based mutagenesis methods, and cloned into pcDNA 3.1(+) Zeocin for mammalian expression. The constructs are presented in Table 2 below.

Mammalian Cell Culture

[0335] Low passage number HEK293T cells (ECACC: 12022001, obtained via Sigma-Aldrich) were cultured in advanced DMEM with 10% FBS and penicillin-streptomycin at 100 μg/ml at 37° C. and 5% CO_2. HEK293T cells were transfected using X-tremeGENE HP (Roche) transfection reagent according to the manufacturer's protocol (3 μl reagent per μg of DNA).

Fly Husbandry and Strains

[0336] Flies were raised in the facilities at the Max Planck Institute for Biological Intelligence at 25° C. and 60% humidity on standard cornmeal agar medium at 12 h light/dark cycle. Only female brains were analyzed. The following driver lines were used: elavC155-Gal4 (pan-neuronal expression, Bloomington *Drosophila* Stock Center (BDSC) 458), R35A03-LexA (expression in C3 neurons, BDSC 54706) and R42F06-Ga/4 (T4-T5 neurons expression, BDSC 41253). The UAS-EMcapsulin (1M-Qt$^{FLAG\text{-}NLS}$ and 1M-Mx$^{FLAG\text{-}NLS}$) strains were generated as follows: The DNA cassette encoding the EMcapsulins was custom-synthesized and subsequently cloned into XhoI/XbaI sites of pJFRC7-20XUAS-IVS-mCD8::GFP (Addgene plasmid No. 26220), after removal of the mCD8::GFP cassette. The plasmids were injected into the attP2 landing site strain (Bloomington *Drosophila* Stock Center, no. 8622) for PhiC31 integrase-mediated transgenesis (BestGene Inc.). The LexAop-EMcapsulin ($_3$M-Qt$^{FLAG\text{-}NLS}$) strain was generated as follows: The DNA cassette encoding the EMcapsulin was custom-synthesized and subsequently cloned pJFRC19-13XLexAop2-IVS-myr::GFP (Addgene plasmid No. 26224) using XhoI/XbaI after removal of the myr::GFP cassette. For the expression of the 3M-QtFLAG-NLs and 1M-MxFLAG-NLS EMcapsulins in C3 and T4-T5 neurons, respectively, we used both the Gal4/UAS and LexA/LexAop

binary expression systems. The final genotype allowed for the simultaneous expression of LexAop-3M-Qt$^{FLAG-NLS}$ by the C3-neuronal driver 35A03-LexA and the expression of UAS-1M-Mx$^{FLAG-NLS}$ by the T4-T5-neuronal driver R42F06-Ga/4. In a separate experiment, we pan-neuronally (elavC155-Ga/4 driver) co-expressed UAS-1M-Qt$^{FLAG-NES}$ and UAS-1M-Mx$^{FLAG-NLS}$.

Experiments with Mice

[0337] All in vivo experiments in mice were approved by the government of Upper Bavaria. Experiments were carried out in three male C57BL/6N, 3 months old mice. Animals were housed in individually ventilated cages in specific pathogen-free conditions and a 12 h light/dark cycle. Water and food were provided ad libitum. Surgical preparations. Mice were administered 0.1 mg/kg buprenorphine (Temgesic, Indivior UK) intraperitoneally 30 minutes before the start of the surgery. Isoflurane was used for inhalation anesthesia: 5% for induction and 1.5-2% for maintenance. Anesthesia depth was checked by corneal and toe pinch reflexes, and the surgery started once these reflexes were absent. Body temperature was maintained around 36.5° C. with a heating mat, and corneal hydration was ensured using eye ointment (Bepanthen, Bayer). Viral injections. Mice were positioned in a stereotaxic frame, and the skin was disinfected with Betadine (Braunoderm, Braun). 20 μL lidocaine 2% (Braun) were injected subcutaneously for additional local skin and periosteum anesthesia. A 10 mm long scalp incision was made, and the fascia was gently pushed to the side. The skull was cleaned and allowed a few minutes to dry. A 400 μm in diameter burr hole was drilled while avoiding overheating or damage to the meninges. A 33 gauge stainless steel injection cannula was inserted about 1500 μm below the surface of the cortex, and one μL of AAV5-CaMKIIa-mScarlet-I-P2A-2M-Qt^{FLAG} (~1×10^{12} particles) solution was injected over a 10 min period using a syringe pump (PHD 22/2000, Harvard Apparatus). The cannula was held in position for 5 minutes after the injection to allow the viral solution to diffuse in the brain tissue and then slowly retracted. The incision was closed with tissue glue (Vetbond, 3M), and lidocaine 2% was applied to the skin to prevent postoperative pain. For postoperative analgesia, 5 mg/kg Meloxicam (Metacam 2 mg/ml, Boehringer Ingelheim) was injected subcutaneously, and the animals were kept on a heated mat until they woke up. 5 mg/kg Meloxicam was administered subcutaneously once a day for the two subsequent days to provide postoperative analgesia. Brain dissection. One month after the virus injection, mice were sacrificed with an overdose of Ketamine/Xylazine and perfused with PBS. The brains were dissected and stored in 4% PFA solution for further processing for immunohistochemical analysis or directly homogenized in MPER lysis buffer using a Dounce tissue homogenizer without fixation agent for pull-down experiments.

Gel Electrophoresis

[0338] Blue native (BN) and Clear Native (CN) PAGE analyses were performed using the NativePAGE Novex Bis-Tris Gel System (Invitrogen) according to the protocol of the manufacturer.

[0339] For CN-PAGE, the cathode buffer contained 0.05% of the anionic detergent sodium deoxycholate. Briefly, cell lysate volumes containing 100-500 ng of nanocompartments were loaded onto pre-cast NativePAGE™ 3 to 12% gels and run at 150 V for 2 h at room temperature. If fluorescent protein assemblies were separated on CN-PAGE, the apparatus was shielded from light to avoid bleaching. CN-PAGE gels were illuminated on a standard UV table and documented using a conventional cell phone camera to detect fluorescently-labeled protein assemblies. To stain for the total protein content in the cell lysates, we performed a Coomassie staining on the BN/CN-PAGE gels. For on-gel APEX2-mediated DAB-polymer formation, gels were treated with DAB and hydrogen peroxide using the SIGMAFAST™ DAB Kit (Sigma Aldrich, D0426). SDS-PAGE was performed using a Bio-Rad Mini-PROTEAN cell and pre-cast 12% Bio-Rad TGX gels (40 min at 200 V). Protein bands from pull-down experiments were visualized using SilverQuest™ Silver Staining Kit (Thermo Fisher). For pull-downs of FLAG-tagged EMcapsulins, anti-FLAG® M2 Magnetic Beads (Sigma-Aldrich, M8823) were used according to the manufacturer's protocol and eluted using 3× FLAG® Peptide (Sigma Aldrich, F4799). BC2-tagged EMcapsulins were pulled down with Spot-Trap Magnetic Agarose beads (Chromotek, 'etma') according to the manufacturer's protocol and eluted in the native state using an alkaline elution buffer.

Immunolabeling and Confocal Microscopy (*Drosophila*)

[0340] For immunolabeling, brains were dissected in cold PBS and fixed in 4% paraformaldehyde (containing 0.1% Triton X-100) at room temperature for 22 min. Afterward, the brains were washed three times with PBT (PBS containing 0.3% Triton X-100) and blocked with 10% normal goat serum in PBT at room temperature for 1 h. Brains were then incubated with primary antibodies diluted in PBT containing 5% normal goat serum for 24-48 h at 4° C.

[0341] After five wash steps with PBT, brains were incubated with secondary antibodies diluted in PBT containing 5% normal goat serum for 24-48 h at 4° C. Brains were subsequently washed five times with PBT and once with PBS before being mounted in SlowFade Gold Antifade Mountant (Thermo Fisher Scientific). Imaging was performed using a Leica SP8 laser scanning confocal microscope equipped with 488-, 561- and 633-nm lasers and a 63× objective. Image processing was performed with the ImageJ software package[52]. The following antibodies were used. Primary antibodies: rat anti-FLAG (1:200, Novus Biologicals, NBP-1-06712), rabbit anti-Sox102F (1:200[53]), and mouse anti-Bruchpilot (1:20, Developmental Studies Hybridoma Bank (DSHB), AB2314866). Secondary antibodies (used at 1:400): Alexa Fluor 568-conjugated goat anti-mouse (Invitrogen, A11004), Alexa Fluor 568-conjugated goat anti-rabbit (Invitrogen, A-11011), and Alexa Fluor 647-conjugated goat anti-rat (Invitrogen, A21247). DAPI (1:1000; Invitrogen) was applied for 5 min at the end of the immunolabeling protocol to stain nuclei, followed by extensive washing with PBT. The identity of adjacent C3 and T4-5 neurons in the IHC shown in main FIG. **4***f* was established based on the co-staining against Sox102f.

Mouse Brain IHC and Microscopy

[0342] Brain tissue was cut into 70 μm thick slices on a cryotome before incubation for 1 hour at room temperature in a 1% BSA and 0.2% Triton X-100 in PBS solution to ensure permeabilization/blocking. Next, tissue slices were incubated at room temperature for 2 hours with an anti-FLAG FITC (F4049, Sigma Aldrich) monoclonal antibody

conjugate diluted to a 2 μg/ml. Slices were washed 3 times for 5 min in PBS and incubated with 10 mM DAPI. Again, tissue was washed 3 times for 5 minutes with PBS, and brain slices were mounted on microscopy slides with Aqua Poly Mount (Polysciences, Warrington, PA). Imaging was performed on a Leica SP5 (Leica Microsystems) to acquire the FITC signal corresponding to 2M-Qt^{FLAG} EMcapsulins and the signal from co-expressed mScarlet-I and DAPI.

Fluorescence Microscopy on HEK Cells

[0343] Widefield fluorescence microscopy was performed on an EVOS fluorescence microscopy system (Invitrogen) equipped with filter cubes to image DAPI, GFP, and RFP. The GFP filter cube was used to image eUnaG. A Leica SP5 (Leica Microsystems) equipped with 405, 488, 561, and 633 nm laser lines were used for confocal microscopy imaging, shown in FIG. **3**. Colocalization analysis was performed with the Coloc2 plugin (release 3.0.5) for ImageJ (v1.53u). The region of interest was set around the prominent cells to exclude background. A PSF of 3.0px was assumed as a conservative estimation for standard confocal microscopes. Background subtraction was performed in ImageJ on both channels with a 50px rolling ball subtraction without smoothing. Costes P-value was calculated with 100 randomizations.

Live-Cell Microscopy on Mammalian Oocytes

[0344] Oocytes were isolated from the ovaries of 8- to 12-week-old FVB/N female mice. Fully grown oocytes of around 75 μm in diameter with a centered nucleus were arrested at prophase in homemade phenol red-free M2 supplemented with 250 μM dibutyryl cyclic AMP (db-cAMP) (Sigma-Aldrich) under paraffin oil (ACROS Organics) at 37° C. For eUnaG imaging, the medium was supplemented with 3 μm bilirubin (Sigma-Aldrich). eUnaG-1M-Qt$^{anti\text{-}mcherry}$, mCherry-Myo5b, mCherry-Plk1, and mCherry-RAB11A mRNAs were synthesized and quantified as previously described. Mouse oocytes were microinjected with 3.5 μl of mRNAs. eUnaG-1M-Qt$^{anti\text{-}mcherry}$ mRNA was microinjected at a needle concentration of 112 or 224 ng/μl, mCherry-Myo5b mRNA at 152.1 ng/μl, mCherry-PLK1 mRNA at 111.1 ng/μl, and mCherry-RAB11A mRNA at 84.1 ng/μl. Oocytes were allowed to express the mRNAs for 3 hours before confocal or Airyscan imaging on LSM880 (Zeiss).

[0345] Automated segmentations of RAB11A-positive recycling endosomes and Myo5b-positive vesicles were performed using the Machine Learning Trainer function of Vision4D (Arivis). Segmented objects were tracked using the Tracking function. Specific parameters used were: Brownian Motion (Centroid) for motion type, 1 μm for max. distance, Center of Geometry for centroid, no fusions or divisions, none for continue tracks, 2 for max. time gap and none for weighting. The volumes and speeds of RAB11A-positive recycling endosomes and Myo5b-positive vesicles were then exported into Excel (Microsoft) and OriginPro (OriginLab).

EM Sample Preparation

[0346] For EM sample preparation, the staining method was adapted from Briggman et al., Nature (2011) and used for both HEK cells and freshly dissected *Drosophila* brains. HEK293T cells were harvested with Accutase (Sigma-Aldrich) 36 hours post-transfection and pelleted by centrifugation. As an initial demonstration for multiplexed EMcapsulin detection across different cells, cell suspensions of HEK293T cells transiently expressing a single class were mixed and pelleted by centrifugation. Following the initial preparation, the material was fixed with 2.5% Glutaraldehyde (Electron Microscopy Sciences) in 0.1 M sodium cacodylate buffer (CB) (pH 6.7-7.0) for 20 min (for *Drosophila* brains, the fixation duration was varying between 20 minutes and 24 hours). After removal of the fixative, the material was postfixed using a 1:1 mixture of 4%0.0 (Electron Microscopy Sciences) with 0.3 M CB, containing 3% potassium hexacyanoferrate (II) (Sigma-Aldrich) for 20 minutes on ice. The post-fixative solution was removed, and the material was washed twice with 0.1 M sodium cacodylate buffer for 2 minutes, followed by 2×5 min ddH_2O washing steps. ddH_2O water was removed, and the material was stained using 1% tannic acid (Sigma-Aldrich) for the duration of 10 min, RT. Then, tannic acid was decanted, and the material was washed 5 times for 5 minutes using ddH_2O water. Subsequently, the material was treated with 1% uranyl acetate (Electron Microscopy Sciences) solution (30 min, RT), with successive ddH_2O 5×5 minutes washing. Afterward, the material was treated with 3% Lead aspartate (Sigma-Aldrich) for 15 min under RT. Again, the material was washed (5×5 min in ddH_2O water) before proceeding to epoxy embedding. The epoxy medium for the embedding process was prepared as follows: 61.5 g 2-Dodecenylsuccinic-acid anhydride (Serva) was mixed with 81.5 g of Methyl nadic anhydride (Serva) as well as with 130.5 g Glycidether 100 (Serva). The resulting mixture was stirred, and 3750 μL of 2,4,6-Tris(dimethylaminomethyl)phenol (Serva) was added to the mixture, stirred, and aliquoted for storage at −20° C. The epoxy embedding process was conducted over 2 days. Immediately after the last washing step, the material was incubated on ice with 75% EtOH for 10 minutes, followed by incubation in 90% EtOH for another 10 minutes. Then, the sample was left in absolute ethanol for 1 hour on ice with the solvent replacement after 30 minutes. The EtOH solution was replaced with pure propylene oxide and incubated for 5 minutes at RT. Next, the solution was discarded, and the material was incubated in 1:1 mixture of Epon and Propylene oxide (Electron Microscopy Sciences) for 30 minutes under RT. Subsequently, the material was incubated at room temperature in 100% Epon for 30 minutes and left in fresh Epon for another 12 hours. Epoxy was removed, and the material was briefly rinsed in fresh 100% epoxy and left in newly-poured 100% epoxy for 72 hours at 60° C. The *Drosophila* brain prior to final epoxy curation was oriented such that optical lobes were parallel to the block's slicing plane. The resulting blocks were subjected to trimming and slicing. For cellular material, the trimming of excess epoxy from the block's surface was done using an EM TRIM milling system (Leica Microsystems, Germany). Using an UltraCut E microtome (Reichert/Leica, Germany) the prepared blocks were prepared with a histo-knife (DIATOME, Switzerland) and then sequentially cut with an ultra-knife (DIATOME, Switzerland) at a slice thickness of 70 nm, verified by the slices' interference pattern. The slices were deposited either on the surface of a 200 mesh copper grid or the polished side of a silicon wafer.

TEM

[0347] TEM images were acquired on a Libra120 TEM (Carl Zeiss GmbH, Germany), equipped with a CCD camera

(TRÖNDLE Restlichtverstärker-Systeme, Germany) using ImageSP software (SYSPROG, Belarus). Before image acquisition, all grid-supported specimens were pre-irradiated at 120 kV beam voltage and 200 μrad illumination angle without apertures. The actual image acquisition took place with the activated BIO-AIS condenser aperture system and a 60 μm objective aperture. The same beam conditions used for pre-irradiation were also applied for imaging, except for an illumination angle of 100 μrad. The magnification for most of the TEM images was chosen such that a pixel size of 1.81 nm was achieved at an exposure time of 1000 milliseconds.

SEM

[0348] SEM images were acquired using a Gemini 360 scanning electron microscope (Carl Zeiss GmbH, Germany), equipped with a sense-BSD detector (Carl Zeiss GmbH, Germany). Silicon wafers, supporting the samples were glued to the stage with silver glue (PLANO GmbH, Germany) and loaded on a sample holder. SEM image acquisition was performed with a beam voltage of 6.5 kV, 2 nm nominal pixel size, a 30 μm objective aperture, and a at a working distance of 3.7 mm. The stage was subjected to a bias voltage of 5 kV.

FIB-SEM

[0349] FIB-SEM images were acquired on an SEM Crossbeam 550 (Carl Zeiss GmbH, Germany), equipped with InLens, BSE, and SESI detectors (Carl Zeiss GmbH, Germany) running ATLAS software. The block with the specimen of interest was firmly attached to the stage using silver glue (PLANO GmbH, Germany). The sample was coated with an electron-transparent carbon layer (approx. 5 nm thickness) using an external carbon evaporator device. The carbon-coated sample was loaded into the FIB-SEM chamber, and a platinum guiding pad was deposited on the identified ROI to aid the localization of the ROI after sputter coating.

[0350] The sample was retrieved and loaded into an external sputter coater, where an electron-opaque iridium layer (~30 nm thickness) was deposited. Back in the FIB-SEM chamber, a 3D platinum pad with a thickness of 2 μm was placed onto the block in proximity to the region of interest. Subsequently, a tracking pattern was milled in the deposited pad to simplify image registration. Finally, the platinum pad and grooves were covered with the carbon layer (2 μm thickness) on top. The following settings were used for image acquisition: SEM beam voltage 1.3 kV, a working distance of 5 mm, 6 μs target dwell time, and 4 nm nominal voxel size using an InLens detector. The FIB Ga beam was accelerated by 30 kV voltage at a current of 700 μA. An image volume of 3696 nm (width)×1956 nm (height)×404 nm (milling length) was acquired in ~70 minutes using ATLAS 3D software (Carl Zeiss GmbH, Germany). The acquired volume was pre-aligned by template matching to the surface landmarks and post-aligned with the Linear Stack Alignment using the SIFT algorithm implemented in ImageJ. Renderings of the acquired FIB-SEM data were computed either in Imaris (Imaris 9.8 Oxford Instruments PLC, Great Britain) or in Dragonfly software (Dragonfly 2021.3, Object Research Systems (ORS) Inc, USA).

End-to-End Multi-Class Semantic Segmentation Network

[0351] We employed a basic U-Net architecture inspired by Falk and colleagues. For our training runs, we used a dropout of 0.1 and mish activation function and otherwise used the defaults of the MONAI implementation (docs.monai.io/en/stable/networks.html #basicunet). This implementation represents a standard U-Net architecture with an encoder and decoder connected by skip connections and has been proven successful in other biomedical segmentation tasks. The network features 1 input and 8 output channels. Besides an output channel for each of the six EMcapsulin classes, we implemented a background channel and a channel for the EMcapsulin patterns consisting of cross-linked 1M-Qt and 1M-Tm (FIG. **22**). A percentile-based normalization is applied for training and inference. Training. We used 250 TEM micrographs (pixel size of 1.81 nm) taken on a Libra120 TEM (Carl Zeiss GmbH, Germany). We trained the model for 3000 epochs with Ranger21 optimizer, an initial learning rate of 1e-2, and a batch size of 2. A batch consisted of 20 random crops sized 512×512 pixels. During training, we employed basic augmentation strategies, namely Gaussian noise, flips, and random affine transformations. An equally weighted sum of soft Dice and Binary Cross Entropy (BCE) inspired by Isensee et al. served as a loss function for our training runs. Inference. To derive segmentations, we combined test time augmentations (TTA), namely flips and Gaussian noise, with a sliding window inference (SWI). For the SWI, we used a batch size of 32 and an overlap of 0.5. We derive multi-class segmentation maps by computing argmax on the six class channels. Further, we provide the possibility to preserve network outputs for all eight channels enabling downstream analysis. Post-Processing. To refine the segmentation maps, we conducted conservative post-processing in a multi-step procedure and provided means to fine-tune each of the steps on an individual basis. Therefore, we first binarize the six-channel segmentation maps. Then we compute a connected component analysis on the binarized segmentation maps using cc3d. We then removed particles with less than 42 pixels because EMcapsulins are at least 20 nm in diameter (~96 pixels area). We chose this threshold value as a compromise to remove 'noise' but maintain partially successful segmentations (e.g., half-rings on the borders of EMcapsulins). Next, we conducted conditional majority voting within each binary connected component. We thus assigned the class represented by the majority of pixels. This step was applied only if the structures were below a maximum of 500 pixels to refrain from modifying the class of touching objects and a circularity larger than 0.2. We also refrained from the majority voting in case of ties (several majority classes with the same number of pixels). Ultimately, we filled up holes in the multi-class segmentation maps for pixels that were completely surrounded by foreground pixels belonging to the same class. Datasets and annotation. An intra-image split into training (70% of the raw image) and validation set (30% of the raw image) was performed by randomly choosing respective 'stripes' in each TEM micrograph. Pixel-accuracy annotations were performed in ImageJ, yielding a total number of 35282 annotated particles in the training data set. Independently acquired TEM micrographs were annotated for the independent test set 1 (57 images, 10 images annotated for the subset "two EMcapsulins classes in adjacent HEK cells") and test 2 (single EMcapsulin class, 26 images, 14 images annotated). Evaluation. Besides qualitative analysis, we relied on quantitative metrics for the comparison of our CNN models. Therefore, we report pixel-wise Dice similarity coefficients (DSC), sensitivity, and precision. Fur-

thermore, we computed instance-level metrics based on an intersection over union (IOU) criterion of 0.5. We further report the three panoptic quality metrics (see Table 1).

[0352] We summed up the respective confusion matrices globally for the computation of both pixel and instance metrics across all microscopy slices.

[0353] We conducted this procedure to treat all EMcapsulins equally, irrespective of their occurrence, in a dense or sparse microscopy image. We approximated instances with a connected component analysis using cc3d since our annotations were not optimized for instance semantic segmentation.

[0354] This heuristic is not perfect, as closely located EMcapsulins touching each other can be merged into one instance. Therefore, factually correct network predictions might be classified as false positives resulting in overly pessimistic instance-level metric computations. Based on the above criteria, we select the checkpoint from epoch 2070, producing the lowest loss and, coincidentally, also the best volumetric DSC for training. We report results on the test set 1 in FIG. **28***d*, inter alia, showing multi-class segmentation maps as an overlay. Hardware. Computations were run on a rack server equipped with an AMD EPYC 7313 16-Core Processor in combination with NVIDIA RTX 8000 and A5000 GPUs using CUDA version 11.4 in conjunction with Pytorch 1.13.0 and MONAI version 1.0.

Sequential Segmentation-Classification Pipeline.

[0355] The model was implemented in PyTorch using the elektronn3 neural network toolkit github.com/ELEKTONN/eletronn3) and trained and tested on NVIDIA A40 GPUs, hosted at the Max Planck Computing facility MPCDF in Garching, Germany. The same 250 TEM micrographs with intra-image splits were also used for training and validation of the segmentation-classification pipeline. The U-Net model for segmentation was enhanced by including an additional batch normalization layer after each convolution layer and trained for 160,000 steps using the AdamW optimizer and a batch size of 8. In order to mitigate the impact of the strong foreground-to-background class imbalance of the training data, the training objective was chosen to be the sum of a weighted dice loss function (and a weighted cross-entropy loss function (foreground pixels were weighted 5 times more than background pixels). The following augmentations were applied during training of the U-net segmentation model: cropping of 384×384 pixel patches from random regions of the source images, random flipping, shifting, scaling and rotation, additive Gaussian noise, random gamma correction, and random brightness and contrast changes.

[0356] The EfficientNetV2-M model for patch-based EMcapsulin classification was trained with random flipping, scaling, and rotation augmentations. It was trained for 120,000 steps using the AdamW optimizer with a batch size of 128. The dataset of patch images was rebalanced by undersampling overrepresented classes. In order to prevent the model from fitting onto potentially informative background information in the vicinity of the EMcapsulins, the background was locally masked from the patches by setting all pixels to 0 values that did not belong to the foreground segmentation mask produced by the U-Net. To filter out falsely merged neighboring EMcapsulin segmentation instances and irregularly shaped segmentation masks, the circularity, defined as $4*\pi*\text{area}/\text{perimeter}^2$, of each connected-component instance was calculated. Segmentation instances below an area of 60 or above 2304 pixels, and instances touching the image borders were not considered for classification. Additionally, objects with a circularity below 0.8 were not classified. To construct the majority-vote-based confusion matrices, we sampled n particles from the test set and assigned them the most frequently occurring class, as determined by the EfficientNetV2-M.

[0357] A napari GUI was developed in Python to enable interactive segmentation, classification, and visualization of TEM images.

SEQUENCES

[0358] The following sequences have been used in the preparation of the invention. It is clear to the skilled person that such sequences are exemplary sequences. Any functional fragment or variant of a sequence is comprised within the scope of the invention. Within the scope of the invention are also sequences having 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% sequence identity with the given sequences.

TABLE 2

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
1	MmMT3 (MT3)	FIG. 1d, FIGS. 9b, 9c, 9d, 9f, 9g, 9h, 9i, 9j, 9k	Metallothionein 3 from *Mus musculus*
2	His-6 MmMT3 (His-6-1xMT3)	FIG. 1 related	Metallothionein 3 from *Mus musculus* with an N-terminal His6 tag for Co/Ni binding
3	His-9 MmMT3	FIG. 1 related	Metallothionein 3 from *Mus musculus* with an N-terminal His9 tag for Co/Ni binding
4	2xMmMT3 (2xMT3)	FIGS. 1a 1b, 1d FIG. 9f	Tandem of Metallothionein 3 from *Mus musculus* connecter via GGGSGGGSGGSA linker.
5	3x chimeric MT (3xMT)	FIGS. 10b, 10d	Chimeric Metallothionein triplet consisting of MmMT3, Metallothionein SmtA from *Synechococcus elongatus*, and the Metallothionein EC1 from *Tricium aestivum* connected via short GS linkers.
6	30xMMKPDM repeats	FIG. 1 e	Methionine-rich repeat protein consisting of 30 MMKPDM repeats. Major protein component of the hinge ligament of the pearl oyster *Pinctada fucata*

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
7	PDB: 2ml7	FIG. 1 f	Cysteine Rich peptide from *Panax ginseng* containing many osmiophilic residues
8	PDB: 4nl8	FIG. 1 f	Cysteine Rich peptide from *Klebsiella pneumoniae* containing many osmiophilic residues
9	PDB: 2jyt	FIG. 1 f	Cysteine Rich peptide from *Homo sapiens* containing many osmiophilic residues
10	PDB: 5lah	FIG. 1 f	Cysteine Rich peptide from *Urticina eques* containing many osmiophilic residues
11	PDB: 3hcu	FIG. 1 f	Cysteine Rich peptide from *Homo sapiens* containing many osmiophilic residues
12	MeLanM (Lanmodulin)	FIGS. 14b, 14d, 14e	Lanthanide-binding protein from Methylobacterium extorquens
13	Lanthanide binding tag 15 (LBT15)	FIG. 2d	Synthethic lanthanide binding tag
14	AssVanabin2 (Vanabin 2	FIGS. 14b, 14d, 14e	Vanadmium-binding protein from *Ascidia sydneiensis samea*
15	EcCusF	FIGS. 14b, 14d, 14e	Silver and Copper-binding protein CusF from *Escherichia coli*
16	QtSig	FIG. 1 e,	Encapsulation signal for the Encapsulin system of *Quasibacillus thermotolerans*
17	PfHRPII-QtSig	FIG. 1 e	Histidine-rich protein II of *Plasmodium falciparum* fused to a QtSig via a GGGGSGGGGS linker.
18	eUnaG-MT3	FIGS. 7a, 7b, 7c, 7d, 7e, 7f	Fusion protein consisting of enhanced UnaG(V2L) from *Anguilla japonica* and MmMT3
19	SNAP-Tag	related to FIG. 7	human O6-alkylguanine-DNA-alkyltransferase variant that forms covalent bonds with benzylguanine derivatives
20	Halo-Tag	related to FIG. 7	modified bacterial dehalogenase that forms covalent bonds with chloroalkane derivatives
21	P2-MT3-QtEnc-FLAG	related to FIG. 7	Fusion of a synthetic coiled-coil (CC) domain (P2), the CGU MmMT3, the QtEnc shell-forming monomer from the Encapsulin system of *Q. thermotolerans* and a FLAG-epitope
22	P1-mEosEM-hPEST	related to FIG. 7	Fusion of synthetic coiled-coil (CC) domain P1 (cognate partner of P2), OsO4 post-fixation stable switchable fluorescent protein mEosEM and a human PEST degradation sequence
23	sGFP_S1-9	FIG. 7g	Strand 1 to 9 of a Tripartite split superfolderGFP
24	QtEnc_sGFP-S1-9	related to FIG. 7	The shell forming monomer of the Ecapsulin system of *Quasibacillus thermotolerans* fused to superfolder GFP strands 1 to 9
25	QtEnc_sGFP-S10	FIG. 7 g	The shell forming monomer of the Ecapsulin system of *Quasibacillus thermotolerans* fused to superfolderGFP strand 10
26	QtEnc_sGFP-S11	FIG. 7 g	The shell forming monomer of the Ecapsulin system of *Quasibacillus thermotolerans* fused to superfolderGFP strand 11
27	QtEnc_eUnaG	FIG. 7-related	The shell forming monomer of the Ecapsulin system of *Quasibacillus thermotolerans* fused to enhanced UnaG(V2L) from *Anguilla japonica* and MmMT3
28	MxEnc_eUnaG	FIG. 7-related	The shell forming monomer of the Ecapsulin system of *Myxococcus xanthus* fused to enhanced UnaG(V2L) from *Anguilla japonica* and MmMT3
29	BM3h (PDB:6H1O)	FIG. 3 d	Heme domain of BM3 a natural fusion protein constructed of cytochrome P450 and NADPH-cytochrome P450 reductase domains from *Priestia megaterium*
30	Liver human FABP	FIG. 3 a	Soluble protein binding fatty acids expressed in human liver
31	Intestinal human FABP	FIG. 3-related	Soluble protein binding fatty acids expressed in human intestine
32	Heart human FABP	FIG. 3-related	Soluble protein binding fatty acids expressed in human heart
33	Adipocyte human FABP	FIG. 3-related	Soluble protein binding fatty acids expressed in human adipocytes
34	Epidermal human FABP	FIG. 3-related	Soluble protein binding fatty acid expressed in human epidermis
35	Ileal human FABP	FIG. 3-related	Soluble protein binding fatty acid expressed in human ileum

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
36	Brain human FABP	FIG. 3 a	Soluble protein binding fatty acid expressed in human brain
37	Myelin human FABP PMP2	FIG. 3-related	Soluble protein binding fatty acid expressed in human peripheral nerves
38	Testis human FABP	FIG. 3-related	Soluble protein binding fatty acid expressed in human testis
39	Retinal human FABP	FIG. 3-related	Soluble protein binding fatty acid expressed in human retina
40	Farn-Signal (Farn)	FIG. 16 a	281-290 of rat H-Ras, C-terminal farnesylation signal
41	SNAP25-derived palmitoylation signal (SNAP25)	FIGS. 1a, 1b, 1c, 1d, also relates to FIG. 3	Amino acids 85-120 of Rattus norvegicus SNAP25
42	Fyn-Kinase derived N-terminal myristoylation signal	relates to FIG. 3	N-terminal myristoylation signal of human Fyn-Kinase, Amino acids 1-15
43	Microtubule-associated proteins 1A/1B light chain 3A (PDB:MLP3A_MOUSE)	relates to FIG. 3	Microtubule-associated proteins 1A/1B light chain 3A (PDB:MLP3A_MOUSE)
44	MSP26	relates to FIG. 3	Engineered apo-lipoprotein A-1 (MSP1) flanked by DnaE split intein fragments C-intein (AA 103-137) on the N-term and N-Intein (AA 1-102) on the C-term (*Homo sapiens*, *Nostoc punctiforme*):
45	MUP2	FIG. 2 a	Designed uranyl binding proteins with 6 binding sites for uranyl ions
46	MUP5	FIG. 2 b	Designed uranyl binding proteins with 6 binding sites for uranyl ions
47	DD-CgPPK2b-QtSig	FIG. 5 a, b, c, d	Degron-tagged polyphosphate kinase 2b of *Corynebacterium glutamicum* C-terminanlly tagged with the encapsulation signal of *Quasibacillus thermotolerans*
48	CgPPK2b	FIGS. 5a, 5b, 5c, 5d	Polyphopsphate kinase 2b of *Corynebacterium glutamicum*
49	AtPCS1-QtSig	FIG. 5 e	Phytochelatin synthase 1 of with a C-terminal encapsulation signal
50	AtPCS2-QtSig	relates to FIG. 5 e	Phytochelatin synthase 2 of *Arabidopsis thaliana* with a C-terminal encapsulation signal
51	BmTyr	FIG. 5 f	*B. megaterium* tyrosinase
52	QtIMEF	FIG. 1 b, FIGS. 6a, 6b, 6c, 6d, FIG. 16 a, FIG. 17 i, FIG. 20 b	Iron-mineraizing ferritin-like cargo protein from the Encapsulin system of *Q. thermotolerans*
53	PP7 phage coat protein (PCP)	FIG. 4-related	The coat protein of the single-stranded RNA bacteriophage *Pseudomonas* phage
54	PP7 phage coat protein tandem dimer (tdPCP)	FIG. 4 a	Tandem dimer of the coat protein of the single-stranded RNA bacteriophage *Pseudomonas* phage binding the PP7 stem loop
55	Spinach Aptamer	FIG. 4 c	Synthetically derived RNA aptamer designed to be an RNA mimic of green fluorescent protein (GFP)
56	PP7 stem loop	FIG. 4 b	Small RNA sequence binding partner of the tandem PCP dimer from *Pseudomonas* phage
57	Dir2s Aptamer	FIG. 4 d	Synthetically derived RNA aptamer designed to be an RNA mimic of red fluorescent protein (RFP)
58	Metal-binding RNA-oligomer	FIG. 4-related	Small synthetic aptamer coordination metal ions in homodimeric form
59	RhoBAST Aptamer	FIG. 4 e	Synthetic aptamer that binds a fluorogenic rhodamine dye with fast association and dissociation kinetics
60	RRM domain	FIG. 4 f	RNA-binding domain that are known to bind single-stranded RNAs.
61	KH2 domain	FIG. 4 f	Protein domain that binds RNA, and can function in RNA recognition
62	Zinc Finger CCHC	FIG. 4 f	Zinc finger domain subspecies know to bind RNA
63	L7Ae	FIG. 4 f related	Multifunctional RNA-binding protein that recognizes the K-turn motif in ribosomal RNA
64	BIV-tat	FIG. 4 f related	BIV-Tat from the Bovine immunodeficiency virus binds to a hairpin structure at the 5'-end of all nascent viral mRNAs
65	QtEnc	FIGS. 1, 2, 3, 5, 6, 7, 8, 9, 15, 16, 17, 18, 19, 20 (in their entirety)	Shell forming monomer of the Encapsulin system of *Q. thermotolerans*

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
66	MxEnc	FIGS. 1, 5, 8, 9, 10 (in their entirety)	Shell forming monomer of the Encapsulin system of *M. xanthus*
67	TmEnc	FIGS. 1, 8, 9, 10 (in their entirety)	Shell forming monomer from the encapsulin system of *T. maritima* (AA 1-264)
68	P1	FIG. 8	Synthetic coiled-coil domain which pairs with P2
69	P2	FIG. 8	Synthetic coiled-coil domain which pairs with P1
70	P3	FIG. 8	Synthetic coiled-coil domain which pairs with P4
71	P4	FIG. 8	Synthetic coiled-coil domain which pairs with P3
72	DHD13a	FIG. 8	Synthetic coiled-coil domain which pairs DHD13b
73	DHD13b	FIG. 8	Synthetic coiled-coil domain which pairs DHD13a
74	RT9s	FIG. 15	DNA sequence promoting ribosomal (translational) read-through after a STOP codon
75	K-turn motif	related to FIG. 4	RNA motif binding to L7Ae
76	RT20s	FIG. 15	DNA sequence promoting ribosomal (translational) read-through after a STOP codon
77	Major vault protein (RnMVP)	FIG. 11	Vault forming protein from *Rattus norvegicus*
78	Major vault protein with SNAP25-derived palmitoylation signal (85-120) (RnMVP-SNAP25)	FIG. 11	Vault forming protein from *Rattus norvegicus* with SNAP25-derived palmitoylation signal (AA 85-120) inserted in helix-loop-helix region
79	RnMVP-APH	FIG. 11	Vault forming protein from *Rattus norvegicus* with antiparallel coiled-coil domain inserted into helix-loop-helix region
80	RnMVP-APH-short	FIG. 11	Vault forming protein from *Rattus norvegicus* with a shortened antiparallel coiled-coil domain inserted into helix-loop-helix region
81	RnMVP-caged-Gp41-1-TEV v1	FIG. 11	TEV protease inducible Vault based on caged Gp41-1 split inteins, Version 1
82	RnMVP-caged-Gp41-1-TEV v2	FIG. 11	TEV protease inducible Vault based on caged Gp41-1 split inteins, Version 2
83	MT3-mINT	FIG. 11	MmMT3 fused to endogenous vault cargo protein mINT
84	RnMVP_HLH-MT3	FIG. 11	MmMT3 inserted into rat Vault Helix-Loop-Helix motif
85	RnMVP_Nterm_BCR HLH-His6_HLH_MT3	FIG. 11	Rat Vault with N-terminal anti-parallel coiled-coil domain stabilizing the holo-vault configuration and MT3 and His6-tag in the HLH domain
86	DeNovoTIM15	FIG. 14 related	Synthetic hyperstable de novo TIM barrel variant
87	Porcine Ribonuclease Inhibitor	FIG. 14 g	Porcine Ribonuclease Inhibitor from Sus scrofa wich exposes modifiable helices
88	Helical Assembly of the Anbu Complex from *Pseudomonas aeruginosa*	FIG. 14 g	Proteasome that forms a dodecameric complex including modifiable helices
89	gp37-gp38 adhesin tip complex. Chain A	FIG. 14 h	Adhesin complex of the bacteriophage S16 long tail fiber. The variable loops can be extended to display binding tags.
90	gp37-gp38 adhesin tip complex. Chain B	FIG. 14 h	Adhesin complex of the bacteriophage S16 long tail fiber. The variable loops can be extended to display binding tags.
91	Adenovirus species 26 knob protein	FIG. 14h	Knob protein from human adenovirus 26. Its loop region can be engineered to display binding tags.
92	emFPv1	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on sfGFP, with ALFA-tags (SRLEEELRRRLT) inserted into loop region and at the termini.
93	emFPv3	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on mGreenLantern, with HA-tags (YPYDVPDYA) inserted into loop region and at the termini.
94	emFPv4	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on mGreenLantern, with Moon-Tags (KNEQELLELDKWASL) inserted into loop region and at the termini.
95	emFPv5	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on mScarlet-I with PepTags (AVERYLKDQQLLGIW) inserted into loop region and at the termini.
96	emFPv6	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on mEosEM, with MoonTags (EELLSKNYHLENEVARLKK) inserted into loop region and at the termini.

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
97	emFPv7	all in FIGS. 14a, 14b, 14c, 14d, 14e	Engineered fluorescent protein based on mScarlet-I, with triple FLAG-tags (DYKDHDGDYKDHDIDYKDDDDK) inserted into loop region and at the termini.
98	24xGCN_v4(SunTag)-emFPv4-24xGCN_v4(SunTag)	FIGS. 14a, 14b, 14c, 14d, 14e-related	Engineered fluorescent protein based on emFPv4 with 24x SunTags on both termini.
99	CCC-Tag(10xP3)-emFPv4-CCC-Tag(10xP3)	FIGS. 14a, 14b, 14c, 14d, 14e-related	Engineered fluorescent protein based on emFPv4 with 10x P3 CCC tags on each terminus.
100	MS2 phage capsid protein	FIG. 14f	Coat protein of the RNA bacteriophage MS2 which binds a specific stem-loop structure in viral RNA to accomplish encapsidation of its genome.
101	MS2 phage Maturation protein A	FIG. 14f	Maturation protein of the RNA bacteriophage MS2 required for the typical attachment of the phage to the side of the bacterial pili. Binds to sequences located toward each end of the genome, hence circularizing it.
102	Qbeta phage capsid protein	FIG. 14f	Coat protein of the Escherichia virus Qbeta which binds a specific stem-loop structure in viral RNA to accomplish encapsidation of its genome.
103	Qbeta phage Maturation protein A2	FIG. 14f	Maturation protein of the Escherichia virus Qbeta required for the typical attachment of the phage to the side of the bacterial pili; Binds to sequences located toward each end of the genome, hence circularizing it.
104	QtEnc-FLAG	FIGS. 9 h, 18 a	Capsid forming monomer from the encapsulin system of *Q. thermotolerans* tagged with C-termina FLAG epitope
105	SasG G51-G52	Related to FIGS. 10 d, 13 a, 17 a, 17 b, 17 c, 17 d, 17 e, 17 f, 17 g, 18 f, 18 g, 18 h, 20 a	G51-E1-G52 domains of *S. aureus* protein SasG (amino acids 419-629) and mCherry
106	QtEnc-antiGFPintrabody ($QtEnc^{aGFPIB}$)	FIGS. 16 d, 18 k, 20 a, 20 b	Capsid forming monomer from the encapsulin system of *Q. thermotolerans* tagged with a C-terminal anti-GFP intrabody
107	MxEnc-FLAG	FIG. 1	Capsid forming monomer from the encapsulin system of *M. xanthus* tagged with C-terminal FLAG epitope
108	TmEnc-BC2Tag	related to FIG. 9	Capsid forming monomer from the encapsulin system of *T. maritima* (amino acids 1-264) tagged with C-termina BC2 epitope
109	P2-TmEnc-antimCherry intrabody (LaM-4)	FIGS. 17 c, 17 d	Capsid forming monomer from the encapsulin system of *T. maritima* (amino acids 1-264) N-terminally fused to a synthetic coiled-coil domain 'P2' (Lebar et al., 2020) and C-terminally fused to an anti-mCherry Intrabody (LaM-4)
110	MT3-DHF119-GFP	FIGS. 12 c, 12 d	Fusion protein consisting of MT3, a de novo designed fibril forming protein(Shen et al. 2018) and GFP
111	His6-SpyCatcher-13-01-MmMT3	FIG. 17 i	Fusion protein consisting of hexa-Histidine Tag, a SpyCatcher domain (Zakeri et al. 2012), a de novo designed, single component icosahedron(Hsia et al. 2016) and an MT3 domain
112	CsgA-SpyTag003	FIGS. 12 a, 12 b	Fusion protein of *E. coli* CsgA where the secretion peptide and N22 were deleted (amino acids 36-144) and SpyTag peptide
113	QtEnc-KinTag	FIG. 16 b	Fusion protein of capsid forming monomer of the Encapsulin system of *Q. thermotolerans* and a synthetic peptide interacting with motor proteins (KinTag(Cross et al. 2021))
114	sfGFP-SasG(G51-G52)-mCherry	FIGS. 17 a, 17 c	Fusion protein consisting of super-folder GFP, the G51-E1-G52 domains of *S. aureus* protein SasG (amino acids 419-629) and mCherry
115	Gp41-1_sfGFP_SasG_G51-G54_SpyCatcher003	FIG. 17 g	Fusion protein consisting of Gp41-1 C-intein, superfolder GFP, SasG (comprising 4 G5 domains yielding GEGEGEG), and engineered SpyCatcher003
116	SnoopTag_mTurquoise_SasG_G51-G54_Gp41-1-N-Int	FIG. 17 g	Fusion protein consisting of a SnoopTag, mTurquoise2, SasG (comprising 4 G5 domains yielding GEGEGEG) and the N-intein split fragment of Gp41-1
117	SpyTag003_mCherry_SasG_G51-G54_SnoopCatcher	FIG. 17 g	Fusion protein consisting of SpyTag003, the red fluorescent protein mCherry, SasG (comprising 4 G5 domains yielding GEGEGEG) and a SnoopCatcher domain
118	sfGFP_SasG_G_Npu DnaE_N-Int_V2	FIG. 18 f, 18 g	Fusion protein consisting of superfolder GFP, the G51 domain of SasG and the Npu DnaE N-intein split part

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
119	NpuDnaE_GEP_C-Int_SasG_EG_mCherry_V2	FIG. 18 h	Fusion protein consisting of Npu DnaE GEP C-Intein split fragment, SasG EG domains, where the proline residue in the G51-E junction was mutated to cysteine to serve as nucleophile in the splicing reaction, and mCherry
120	NpuDnaE_GEP_C-Int_SasG_EG_Npu_DnaE_N-Int_V2	FIGS. 18 g, 18 h	Fusion protein consisting of Npu DnaE GEP C-Intein split fragment, SasG EG domains and the Npu DnaE N-intein split part on its C-terminus. This yields a self-growing fragment which can be capped off with NpuDnaE_GEP_C-Int_SasG_EG_mCherry_V2
121	sfGFP_SasG_G_VidaL-N-Int	FIG. 18 g	Fusion protein consisting of superfolder GFP, the G51 domain of SasG and the VidaL N-Intein split part
122	VidaL-C-Int_SasG_EG_mCherry	FIG. 18 h	Fusion protein consisting of VidaL C-Intein split part, SasG EG domains and mCherry
123	VidaL-C-Int_SasG EG _VidaL-N-Int	FIGS. 17 a, 18 g, 18 h	Fusion protein consisting of VidaL C-Intein split part, SasG EG domains and VidaL N-Intein split part. This building block is a self-growing unit and can be capped off with VidaL-C-Int_SasG_EG_mCherry
124	Tobacco etch virus protease (TEVp)	related to FIGS. 18 b, 18 j	Tobacco etch virus protease
125	plum pox virus protease (PPVp)	related to FIG. 18 (in its entirety)	plum pox virus protease, alternative to TEVp
126	soybean mosaic virus protease (SbMVp)	related to FIG. 18 (in its entirety)	soybean mosaic virus protease, alternative to TEVp
127	sunflower mild mosaic virus protease (SuMMVp)	related to FIG. 18 (in its entirety)	sunflower mild mosaic virus protease, alternative to TEVp
128	3xLBT15-TEVsite-MT3-QtEnc-FLAG	FIG. 18 a	Fusion protein consisting of a triple engineered Lanthanide binding domain (LBT15) (Sculimbrene and Imperiali 2006), a TEV cleavage site, the capsid forming monomer of the Encapsulin system of *Q. thermotolerans* and a FLAG epitope
129	FLAG-N-TEV-1-118-M13	FIG. 18 a	Fusion protein consisting of a FLAG epitope, the N-terminal fragment of the Tobacco etch virus protease (TEV) (amino acids 1-118 and a C-terminal M13 calmodulin-binding peptide
130	Myc-Calmodulin-TEV-119-219	FIG. 18 a	Fusion protein consisting of a Myc epitope, Calmodulin and the C-terminal split fragment of Tobacco etch virus protease (amino acids 119-219, S153N(Sanchez and Ting 2020))
131	MxEnc-RS20	FIG. 19	Fusion of Encapsulin forming monomer of the Encapsulin system *M. xanthus* and the Calmodulin binding peptide RS20
132	QtEnc-RS20	FIG. 19	Fusion of Encapsulin forming monomer of the Encapsulin system *Q. thermotolerans* and the Calmodulin binding peptide RS20
133	TmEnc-RS20	FIG. 19	Fusion of Encapsulin forming monomer of the Encapsulin system *T. maritima* and the Calmodulin binding peptide RS20
134	CaM-HpFtn	FIG. 19 b	Fusion protein of human calmodulin and *H. pylori* ferritin (AA 5-167, N19Q)
135	CaM-MT3	Related to FIG. 19 b	Fusion of human Calmodulin and MmMT3 which will be recruited to the scaffold (Enc) to form a contrast halo around the element when elevated Ca^{2+} levels are present
136	MT3-TnCmin-QtSig	FIG. 19 a	Fusion protein of MT3, an engineered minimal Troponin C domain of *Opsanus tau* and the Encapsulin signal of the Encapsulin system of *Q. thermotolerans*
137	MT3-TnCmin-QtEnc-FLAG	FIG. 19 a	Calcium-responsive contractile linker to MT3.
138	mCherry-dTrim21	FIG. 18 l	Fusion of E3 ubiquitin-protein ligase TRIM21, with inactivating mutations I79R and S80A, and mCherry fluorescence protein
139	sfGFP-dTrim21	FIG. 18 l	Fusion of E3 ubiquitin-protein ligase TRIM21, with inactivating mutations I79R and S80A, and superfolder GFP
140	pcDNA 3.1 (+) Zeocin	FIG. 4 g	mammalian expression vector
141	pIRES	FIG. 4 g	internal ribosome entry site

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
142	QtEnc^{FLAG}	FIG. 1 b	Shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* with a C-terminally appended FLAG epitope connected via a short GSG linker.
143	2xMT3-QtEnc^{FLAG}	FIGS. 1 b, 4 g	A tandem of the *Mus musculus* Metallothionein 3 connected via GGGGSGGGGS linker fused to the shell-forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* with a C-terminally appended FLAG epitope connected via a short GSG linker.
144	MT3-TmEnc$^{BC2\text{-}Tag}$	FIGS. 1 d, 9 b	Fusion of *Mus musculus* Metallothionein 3 fused to the shell forming monomer of the Encapsulin system of *Thermotoga maritima* fused to a C-terminal BC2-Tag
145	LBT15-QtEnc^{FLAG}	FIG. 2 d	Synthetic Lanthanide-bindering tag 15 fused to the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* fused to a C-terminal FLAG tag-
146	Twin-dLBT3-QtEnc^{FLAG}	FIG. 2 d	Engineered tandem Lanthanide-binding tag fused to the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* fused to a C-terminal FLAG tag
147	QtEnc-SpyTag(003)	FIGS. 3 a, 3 e	Capsid forming monomer from the encapsulin system of *Q. thermotolerans* tagged with C-terminal SpyTag003
148	MUP2-QtEnc	FIG. 2 c	Designed Uranyl-binding protein MUP2 fused to the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans*
149	MUP5-QtEnc	Related to FIG. 2 a	Designed Uranyl-binding protein MUP5 fused to the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans*
150	B-FABP-SpyCatcher003	FIG. 3 b	Engineered SpyCatcher 003 domain fused to fatty acid binding protein FABP
151	BM3h-SpyCatcher003	FIG. 3 e	Heme binding domain BM3h fused to engineered SpyCatcher 003 domain
152	MS2 stem loop	FIG. 4 a	RNA motif for MCP
153	2xGGGGS linker	FIG. 5 a	flexible linker
154	DD-N	FIG. 5 a	Engineered FKBP-derived degron
155	eUnaG-MT3-QtEnc^{FLAG}	FIG. 7 b	Fusion of engineered ultrasmall fluorescent protein eUnaG followed by MT3, QtEnc and a FLAG-tag
156	eUnaG-2xMT3-QtEnc^{FLAG}	FIG. 7 c	Fusion of engineered ultrasmall fluorescent protein eUnaG followed by 2xMT3, QtEnc and a FLAG-tag
157	mGreenLantern-MT3-QtEnc^{FLAG}	FIG. 7 d	Fusion of the engineered green fluorescent protein mGreenLantern, MT3, QtEnc and a FLAG epitope
158	CAMPARI2-MT3-QtEnc^{FLAG}	FIG. 7 d	Fusion of the engineered fluorescent Calcium integrator CAMPARI2, MT3, QtEnc and a FLAG tag
159	P2-TmEnc$^{BC2\text{-}Tag}$	FIGS. 5 f, 8 a, 20 c	Synthetic coiled-coil domain P2 (partner of P1) fused to the TmEnc (AA 1-264) with a C-terminal BC2-Tag
160	DHD13a-MxEnc^{StrepTagII}	FIG. 8 a	Synthetic coiled-coil domain DHD13a (partner of DHD13b) fused to MxEnc with a StrepTagII
161	P3-QtEnc^{FLAG}	FIG. 8 a	Synthetic coiled-coil domain P3 (partner of P4) fused to QtEnc with a FLAG-Tag
162	DD-N-mScarlet-I-P1	FIG. 8 a	Fusion of DD-N degron with mScarlet-I and synthetic coiled-coil domain P1 (partner of P2)
163	DD-N-mTaBFP2-DHD13b	FIG. 8 a	Fusion of DD-N degron with mTagBFP2 and synthetic coiled-coil domain DHD13b (partner of DHD13a)
164	DD-N-mGreenLantern-P4	FIG. 8 a	Fusion of DD-N degron with mGreenLantern and synthetic coiled-coil domain P4 (partner of P3)
165	MT3-QtEnc^{FLAG}	FIG. 9 b	Fusion of *Mus musculus* Metallothionein 3, the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* and a C-terminal FLAG-Tag
166	MT3-MxEnc^{FLAG}	FIG. 9 c	Fusion of *Mus musculus* Metallothionein 3, the shell forming monomer of the Encapsulin system of *Myxococcus xanthus* and a C-terminal FLAG-Tag
167	MT3-MxEnc-FLAG-cMyc-NLS	FIGS. 9 h, 9 j	Fusion of *Mus musculus* Metallothionein 3, the shell forming monomer of the Encapsulin system of *Myxococcus xanthus* and a C-terminal FLAG-Tag followed by a cMyc-derived nuclear localization signal (NLS)
168	MT3-QtEnc-FLAG-cMyc-NLS	FIG. 9 i	Fusion of *Mus musculus* Metallothionein 3, the shell forming monomer of the Encapsulin system of *Quasibacillus thermotolerans* and a C-terminal FLAG-Tag followed by a cMyc-derived nuclear localization signal (NLS)

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
169	3xchimericMT (3xMT)-QtEnc^{FLAG}	FIG. 10 a	Fusion of 3xMT with QtEnc and a C-terminal FLAG-Tag.
170	mINT	FIG. 11 a	attachment signal to vault
171	MT3-SpyCatcher003	FIGS. 10 f, 12 b	MT3 fused to SpyCatcher003
172	antiALFATag-intrabody-2xMT3-GB1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiALFATag intrabody with an MT3 tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
173	antiHA-frankenbody-2xMeLanM-GB1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiHA frankenbody with a MeLanM tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
174	antiMoonTag-intrabody-2xAssVanabin2-GB-1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiMoonTag intrabody with a AssVanabin2 tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
175	antiMoonTag-intrabody-2xMeLanM-GB-1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiMoonTag intrabody with a MeLanM tandem, GB1 domain, a FLAG-Tag, and C-terminal RXXG degron.
176	antiMoonTag-intrabody-4x(P3)-GB-1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiMoonTag intrabody with a 4xP3 CCC-Tag, GB1 domain, a FLAG-Tag, and C-terminal RXXG degron.
177	antiMoonTag-intrabody-2xMT3-GB-1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiMoonTag intrabody with an MT3 tandem, GB1 domain, a FLAG-Tag, and C-terminal RXXG degron.
178	antiMoonTag-intrabody-2xEcCusF-GB-1-FLAG-RXXG	FIGS. 14 a, 14 b	Fusion of antiMoonTag intrabody with an EcCusF tandem, GB1 domain, a FLAG-Tag, and C-terminal RXXG degron.
179	LifeAct-emFPv4	FIGS. 14 b, 14 d	Fusion of LifeAct-peptide to emFPv4
180	QtEnc^{FLAG-}(TGA) RT20s-antiGFPintrabody-HiBit	FIG. 15 b	DNA sequence encoding QtEnc-FLAG followed by a TGA stop codon, followed by the read-through promoting sequence "RT20s" followed by an anti-GFPintrabody with a C-terminal HiBit peptide.
181	QtEnc^{FLAG-}(TGA) RT20s-Ssp DnaE (N159A)QtEnc-antiGFPintrabody-HiBit	FIG. 15 b	DNA sequence encoding QtEnc-FLAG followed by a TGA stop codon, followed by a read-through promoting sequence "RT20s", followed by an Ssp DnaE intein mutant (N159A) which exhibits hyperfast N-terminal cleavage, followed by a P2A peptide followed by a second full-length QtEnc with a C-terminal antiGFP-intrabody and a HiBit peptide.
182	P2A peptide	FIG. 15 b	
183	2xMT3-QtEnc-antiGFPintrabody	FIG. 16 c	Tandem MT3 fused to QtEnc which has a C-terminal anti GFP intrabody
184	sfGFP	Related to FIG. 12 c, 12 d , 17 a, 17 b, 17 c, 17 d, 17 e, 17 f, 17 g, 18 g, 18 k	
185	mCherry	FIG. 1 17 a, 17 b, 17 c, 17 d, 17 e, 17 f, 17 g, 18 g, 18 k	
186	antiGFP-intrabody	FIGS. 17 a, 18 l	
187	antimCherry intrabody (LaM-4)	FIG. s17 a, 18 l	
188	sfGFP-SasG-G51-G54-mCherry	FIG. 17 a	SasG capped off with two fluorscent proteins
189	MT3-QtEnc-antiGFPintrabody	FIG. 17 c	MT3 fused to QtEnc with a C-terminal anti GFP intrabody
190	BmTyr-P2	FIG. 20 c	Fusion of BmTyr and synthetic coiled-coil domain P2 (partner of P1)
191	B-FABP-sfGFP	FIG. 10 e	Fusion of Brain FABP and superfolder GFP
192	BM3h-sfGFP	FIG. 10 e	Fusion of BM3h and superfolder GFP
193	cpFABP	FIG. 13 b	Circularly permuted FABP, Nterm and Cterm are both alpha helices
194	Intein C-6xB-FABP-Intein N	FIG. 13 a	Fusion of six B-FABP flanked by DnaE split intein fragments C-intein (AA 103-137) on the N-term and N-Intein (AA 1-102)
195	Intein C-3x(B-ABP-MmMT3)-Intein N	FIG. 13 a	Fusion of three repeats of B-FABP fused to MmMT3 flanked by DnaE split intein fragments C-intein (AA 103-137) on the N-term and N-Intein (AA 1-102)

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
196	Intein C-2xB-FABP-SpyTag003-2xB-FABP-Spycatcher003-2xB-FABP-Intein N	FIG. 13 c	Fusion of three repeats of 2x B-FABP intermixed by SpyTag003 and Spycatcher003 and flanked by DnaE split intein fragments C-intein (AA 103-137) on the N-term and N-Intein (AA 1-102)
197	QtEnc-M13	FIG. 19 a	Fusion of QtEncapsulin and M13 a synthetic peptide binding Calmodulin
198	B-FABP-CaM	FIG. 19 a	Fusion of Brain FABP and Calmodulin
199	AG4	related to FIG. 2	Synthetic Silver mineralizing peptide 4
200	dCas13	related to FIG. 4	Catalytically inactive Cas13b is from Prevotella sp as an RNA-binding protein
201	Pumilio homology domain	related to FIG. 4	RNA-binding protein Uniprot: Q14671
202	eUnaG	Related to FIGs. 7 a, 7 b, 7 c, 7 e, 7 f, 11 e,	Enhanced Ultra small fluorescent protein from eel
203	mGreenLantern	FIG. 7 d	Improved green fluorescent protein based on GFP
204	CAMPARI 2	FIG. 7 d	Engineered fluorescent Calcium integrator
205	mRFP		Monomeric red fluorescent protein
206	FHA2	related to FIG. 19b	phostphopetptide binding Forkhead-associated domain
207	AP205 Phage	FIGS. 10 b, 10d, 14 f	Coat protein
208	mEos4b:APEX2:mINT	FIGS. 11a, 11b	Fusion of mEos4b together with APEX2 to a C-terminal minimal interaction domain (mINT) capable to interact with the interior of the vault complex.
209	MmuGap43-palmi:MVP	FIGS. 11a, 11b	Fusion of mouse Gap43 palmitoylation signal to the N-terminus of the major vault protein (MVP).
210	SNAPtag-QtEnc^{FLAG}	FIG. 8 b	N-terminal fusion of SNAP-tag connected via GS linker to QtEnc with a C-terminal FLAG epitope
211	Halotag-QtEnc^{FLAG}	FIG. 8 b	N-terminal fusion of Halo-tag connected via GS linker to QtEnc with a C-terminal FLAG epitope
212	MT3-PfEnc^{FLAG}	FIG. 9 d	Fusion of MT3 to AA 110-346 of *Pyrococcus furiosus* Encapsulin monomer with a C-terminal FLAG epitope.
213	PfFt	FIG. 19	Ferritin from *Pyrococcus furiosus*
214	mEos4b	Related to FIGS. 11 a, 11 b	~~https://~~www.fpbase.org/protein/meos4b/
215	mEosEM	Related to FIG. 7	~~https://~~www.fpbase.org/protein/meosem/
216	iRFP713		~~https://~~www.fpbase.org/protein/irfp713/
217	TeAPCα		~~https://~~www.fpbase.org/protein/teapc/
218	DMT1	FIG. 6 d	Human divalent metal transporter 1
219	Zip14	FIG. 6 d	Human divalent metal transporter Zip14
220	Cystathionine gamma-lyase-QtSig	FIG. 6 e	Fusion of Cystathionine gamma-lyase with QtSig
221	Secreted alkaline phosphatase-QtSig	FIG. 6 e	Fusion of SEAP, a secreted form of Human embryonic alkaline phosphatase, and QtSig
222	MnxG-QtSig	FIG. 6 e	Fusion of MnxG, component of the *Bacillus* sp. Multimeric multicopper oxidase Mnx, and QtSig
223	MnxE	FIG. 6 e	Component of the *Bacillus* sp. Multimeric multicopper oxidase Mnx
224	MnxF	FIG. 6 e	Component of the *Bacillus* sp. Multimeric multicopper oxidase Mnx
225	SUP	alternative to MUP2 and MUP5 in FIG. 2	Designed uranyl binder with femtomolar affinity
226	P3-MT3-QtEnc	related to FIG. 8	Coiled-coil adapter to recruit an encapsulated cargo, such as the fluorescent protein mEosEM fused to P4 to an encapsulin already harboring an MT3 for dual EM and fluorescence detection.
227	Mt3-QtEnc-eUnaG	alternative option to fluorescent protein complementation shown in FIG. 7	Fusion of the fluorescent protein eUnaG to the outer surface of encapsulin
228	MT3-sfGFP	alternative option to fluorescent protein complementation shown in FIG. 7	CGU for attaching to the outer surface of encapsulin via anti-GFP antibody
229	QtEnc-B-FABP	FIG. 10, particularly 10e, 10f	Fusion of QtEnc and Brain FABP, embodiment of concentric barcodes added to the outer surface of encapsulins

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
230	QtEnc-Bm3h	FIG. 10, particularly 10e, 10f	Fusion of QtEnc and Bm3h, embodiment of concentric barcodes added to the outer surface of encapsulins
231	QtEnc-MT3	FIG. 10 e	Fusion of QtEnc and MT3, embodiment of concentric barcodes added to the outer surface of encapsulins
232	B-FABP-sfGFP	e.g. FIG. 10e	Fusion of Brain FABP and superfolder GFP, for attachment via anti-GFP intrabody attachment points, e.g. to the outer surface of Encapsulins.
233	Bm3h-sfGFP	e.g. FIG. 10e	Fusion of Bm3h and superfolder GFP, or attachment via anti-GFP intrabody attachment points, e.g. to the outer surface of Encapsulins.
234	MT3-Lam4	related to FIG. 17a	Fusion of MT3 and Lam4, for attachment to mCherry, e.g. on SasG
235	B-FABP-Lam4	related to FIG. 17a	Fusion of Brain FABP and Lam4, for attachment to mCherry, e.g. on SasG
236	Bm3h-Lam4	related to FIG. 17a	Fusion of Bm3h and Lam4, for attachment to mCherry, e.g. on SasG
237	GGSG linker	FIG. 13	General linker used for protein fusions, including direct fusions of CGUs to achieve the nanometer sizes of a structural element
238	Recoverin	FIG. 19c	myristoyl switch motif for calcium-dependent re-localization a structural element such as vaults to the membrane
239	synthide-2-FHA2	related to FIG. 19b	synthide-2 binding for FHA2
240	MT3_QtEnc_MT3_eUnaG_RS20	FIG. 35	Fusion of murine MT3, *Q. thermotolerans* encapsulin forming shell protein, murine MT3, enhanced fluorescent protein eUnaG (*Anguilla japonica*) and the synthetic Calmodulin-binding peptide RS20
241	MT3_QtEnc_eUnaG_RS20	FIG. 35	Fusion of murine MT3, *Q. thermotolerans* encapsulin forming shell protein, enhanced fluorescent protein eUnaG (*Anguilla japonica*) and the synthetic Calmodulin-binding peptide RS20
242	QtEnc_eUnaG_RS20	FIG. 35	Fusion of *Q. thermotolerans* encapsulin forming shell protein, enhanced fluorescent protein eUnaG (*Anguilla japonica*) and the synthetic Calmodulin-binding peptide RS20
243	MT3_QtEnc_eUnaG_RS20_P2A CaM-HpFtn	FIG. 35	Fusion of murine MT3, *Q. thermotolerans* encapsulin forming shell protein, enhanced fluorescent protein eUnaG (*Anguilla japonica*) and the synthetic Calmodulin-binding peptide RS20, followed by a P2A peptide (Tporcine teschovirus-1), followed by CaM-HpFtn (Seq ID 134)
244	MT3_QtEnc_MT3_eUnaG_RS20_P2A_CaM-HpFtn	FIG. 35	Fusion of murine MT3, *Q. thermotolerans* encapsulin forming shell protein, murine MT3, enhanced fluorescent proteine eUnaG (*Anguilla japonica*) and the synthetic Calmodulin-binding peptide RS20, followed by a P2A peptide (porcine teschovirus-1), followed by CaM-HpFtn (Seq ID 134)
245	QtIMEF_P2A_QtEnc_eUnaG_RS20_P2A_CaM-HpFtn_P2A_MmZip14	FIG. 35	*Q. thermotolerans* iron-mineralizing cargo protein IMEF followed by P2A (porcine teschovirus-1), followed by *Q. thermotolerans* shell forming monomer fused to eUnaG, followed by synthetic Calmodulin binding peptide RS20, followed by P2A peptide (porcine teschovirus-1), followed by murine divalent metal uptake pump Zip14
246	1M-PfEnc-miRFP670nano	FIG. 23	Fusion of murine MT3, shell forming portion of the encapsulin system of *Pyrococcus furiosus* and the monomeric far-red fluorescent protein mRFP670nano (Nostoc punctiforme)
247	1M-PfEnc-FLAG-antiGFP	FIG. 23	Fusion of murine MT3, shell forming portion of the encapsulin system of *Pyrococcus furiosus*, a FLAG epitope and an anti-GFP nanobody (intrabody) (Seq ID 186)
248	B-Fabp-ko	FIG. 22	Mutant of Brain FABP inhibiting lipid binding
249	Bm3h-B7	FIG. 22	Mutant of Bm3h binding dopamine
250	QtEnc_B-Fabp-ko	FIG. 22	Fusion of QtEnc and mutant Brain FABP
251	B-Fabp_HpFtn	FIG. 22	Fusion of Brain FABP to *H. pylori* ferritin (AA 5-167, N19Q)
252	B-Fabp-ko_HpFtn	FIG. 22	Fusion of Brain FABP mutant to *H. pylori* ferritin (AA 5-167, N19Q)
253	Bm3h-HpFtn	FIG. 22	Fusion of Bm3h to *H. pylori* ferritin (AA 5-167, N19Q)
254	Bm3h-B7-HpFtn	FIG. 22	Fusion of Bm3h-B7 to *H. pylori* ferritin (AA 5-167, N19Q)

TABLE 2-continued

Sequences used for this invention

EQ ID NO	Name	Used in FIG.	Comment
255	BFabp-FLAG	FIG. 22	Fusion of Brain FABP and the FLAG epitope
256	BFabp-ko-FLAG	FIG. 22	Fusion of the mutant Brain FABP and the FLAG epitope
257	Bm3h-FLAG	FIG. 22	Fusion of Bm3h and the FLAG epitope
258	Bm3h-B7-FLAG	FIG. 22	Fusion of Bm3h-B7 and the FLAG epitope
259	BFabp-αMoon-Tag	FIG. 32	Fusion of B-Fabp to αMoon-Tag for targeting the EmFPs proteins
260	1M_QtEnc_SNAP-Tag	FIGS. 24, 25, 26 (n their entirety)	Fusion to bioconjugation tags for preferred use with fixation stable fluorophores (such as SNAP-cell TMR star) for CLEM
261	1M_QtEnc_Clip-TAG	FIGS. 24, 25, 26 (n their entirety)	Fusion to bioconjugation tags for preferred use with fixation stable fluorophores for CLEM
262	dcAvidin_GpAG83A mCherry	FIGS. 24, 25, 26 (n their entirety)	In addition to SNAP/CLIP tag, also biotinylated ligands could be semi-genetically appended using engineered Avidin variants
263	scdAvidin_GpAG83A_ mCherry	FIGS. 24, 25, 26 (n their entirety)	In addition to SNAP/CLIP tag, also biotinylated ligands could be semi-genetically appended using engineered Avidin variants
264	Mito-mEosEM	FIGS. 24, 25, 26 (n their entirety)	mEosEM as fully-genetic fixation-stable fluorophore
265	QtSig_mEosEM	FIGS. 24, 25, 26 (n their entirety)	fixation-stable fluorophore with cargo targeting sequence for encapsulation into QtSig.
266	SNAP-Tag_1M_QtEnc	FIGS. 24, 25, 26 (n their entirety)	Combination of N-terminal SNATP tag with M for CLEM with fixation-stable fluororphres such as TMR star
267	des_4bhv	FIG. 21	Oligomeric designed uranyl binding protein
268	des_7bau	FIG. 21	Oligomeric designed uranyl binding protein
269	des_2akf_3bs	FIG. 21	Oligomeric designed uranyl binding protein
270	des_2akf_6bs	FIG. 21	Oligomeric designed uranyl binding protein
271	des_5apq_6bs	FIG. 21	Oligomeric designed uranyl binding protein
272	QtEnc_LgBit_M13	FIG. 37	Qt_Encapsulin as scaffold fused to the Large Bit of split nanoluc and the M13 peptide binding Calmodulin (Cam) in the presence of calcium
273	SmBit_B-Fabp_CaM	FIG. 37	Small Bit of split Nanoluciferase fused to B-Fabp (as CGU) and Calmodulin
274	SmBit_CaM_B-Fabp	FIG. 37	Small Bit of split Nanoluciferase fused to Calmodulin and B-Fabp (as CGU)
275	QtEnc_LgBit_CaM	FIG. 37	Fusions of QtEnc to Large Bit of split Nanoluciferase and Calmodulin
276	SpyTag003_CaM_Sas G10_linker_SasG10 B-Fabp_M13	FIG. 37	Spytag003, used for targeting to the structural element, is fused to Calmodulin, Binding the M13 peptide present at the end of the construct only in presence of calcium ions. B-Fabp as a contrasting generating unit is also fused before the M13 Peptide. Separating Calmodulin and B-Fabp_M13 are two rigid protein filaments, SasG G10 linked by a flexible linker permitting rotational freedom.
277	QtEnc_CaM	FIG. 37	QtEnc fusion to calmodulin for correlative calcium indicator imaging
278	M13_B-FABP_TagRFP_ Synzip17	FIG. 36	M13 synthetic peptide binding Cam in the presence of calcium ions is fused to B-Fabp as a CGU for EM contrast, TagRFP a red fluorescent protein as the FRET acceptor and the Synzip17 peptide binding the Synzip18
279	TagGFP2_Synzip18	FIG. 36	TagGFP2 as the FRET donor fused to the antiparallel Synzip18 binding to Synzip 17
280	CaTEV_hLOV_TEVseq_ SpyTag003_B-FABP	FIG. 36	scFLARE system containing Calcium activated protease TEV (CaTEV), the light-dependent hLOVE domain and the cleavable TEV site (TEVseq), fused to Spytag003 and B-FABP as a CGU
281	Skipped sequence		
282	Skipped sequence		
283	Skipped sequence		
284	Nterm-BCR_ RnMVP_HLH$_{outterior}$-His6_HLH$_{interior}$-PCP	FIG. 31	Engineered variant of Major Vault Protein (MVP) with antiparallel coiled coils (Nterm-BCR) for closed Vault conformation, PCP for binding of PP7 aptamers in Vaults interior, His Tag for Vaults purification
285	RnMVP_HLH$_{outterior}$-His6_HLH$_{interior}$-PCP	FIG. 31	Engineered variant of Major Vault Protein (MVP), PCP for binding of PP7 aptamers in Vaults interior, His Tag for Vaults purification
286	RnMVP_HLH$_{outterior}$-SNAP25-palmitoylation-site_HLH$_{interior}$-PCP	FIG. 31	Engineered variant of Major Vault Protein (MVP), PCP for binding of PP7 aptamers in Vaults interior, SNAP Tag for intracellular crystallization
287	MiniSOG_QtEnc-FLAG_NES	FIG. 43	Fluorescent encapsulins with nuclear export signal

TABLE 2-continued

Sequences used for this invention			
EQ ID NO	Name	Used in FIG.	Comment
288	MiniSOG__QtEnc-FLAG__cMycNLS	FIG. 43	Fluorescent encapsulins with nuclear localization signal
289	1xMmMT3__QtEnc__FLAG__NES	FIG. 43	Nuclear export signal to obtain preferentially cytosolic contrast
290	mCherry-RAB11A	FIG. 42	Fluorescent tag on RAB11A for live-microscopy tracking experiments
291	mCherry-PLK1	FIG. 42	Fluorescent tag on RAB11A for live-microscopy tracking experiments
292	mCherry-Myo5b	FIG. 42	Fluorescent tag on RAB11A for live-microscopy tracking experiments
293	pcDNA__Zeo__1M-QtFLAG	No reference to figures is provided-	
294	pcDNA__Zeo__2M-QtFLAG	No reference to figures is provided-	
295	pcDNA__Zeo__3M-QtFLAG	No reference to figures is provided-	
296	pcDNA__Zeo__1M-MxFLAG	No reference to figures is provided-	
297	pcDNA__Zeo__2M-MxFLAG	No reference to figures is provided-	
298	pcDNA__Zeo__1M-TmBC2Tag	No reference to figures is provided-	
299	pcDNA__Zeo__1M-Tm__anti-mCherry	No reference to figures is provided-	
300	pcDNA__Zeo__1M-Qt__anti-GFP	No reference to figures is provided-	
301	pcDNA__sfGFP-2G-mCherry	No reference to figures is provided-	
302	pcDNA__sfGFP-3G-mCherry	No reference to figures is provided-	
303	pcDNA__sfGFP-4G-mCherry	No reference to figures is provided-	
304	pcDNA__sfGFP-5G-mCherry	No reference to figures is provided-	
305	pcDNA__sfGFP-6G-mCherry	No reference to figures is provided-	
306	pcDNA__sfGFP-7G-mCherry	No reference to figures is provided-	
307	pcDNA__sfGFP-8G-mCherry	No reference to figures is provided-	
308	pcDNA__sfGFP-9G-mCherry	No reference to figures is provided-	
309	pcDNA__sfGFP-10G-mCherry	No reference to figures is provided-	
310	pcDNA__1M__QtFLAG__TGA__rt20s__antiGFP	No reference to figures is provided-	
311	EGFP-N1-msfGFP-Cx43, Addgene 69024	No reference to figures is provided-	
312	EGFP-N1-Cx43-msfGFP, Addgene 69007	No reference to figures is provided-	
313	pcDNA__HA-DD-N-mTagBFP2__QtSig	No reference to figures is provided-	
314	pcDNA__HA-DD-N-mScarlet-I__QtSig	No reference to figures is provided-	
315	pcDNA-1M-Qt-eUnaG	No reference to figures is provided-	
316	pcDNA-eUnaG-1M-Qt-anti-mCherry	No reference to figures is provided-	
317	pcDNA-eUnaG-1M-Qt-anti-GFP	No reference to figures is provided-	
318	pcDNA-eUnaG-1M-QtFLAG	No reference to figures is provided-	
319	pcDNA-eUnaG-2M-Qt-anti-mCherry	No reference to figures is provided-	

TABLE 2-continued

Sequences used for this invention			
EQ ID NO	Name	Used in FIG.	Comment
320	pcDNA-eUnaG-2M-Qt-anti-GFP	No reference to figures is provided-	
321	pcDNA-eUnaG-2M-QtFLAG	No reference to figures is provided-	
322	pJFRC7-20XUAS-IVS__1M__QtFLAG-NLS	No reference to figures is provided-	
323	pJFRC7-20XUAS-IVS__1M__MxFLAG-NLS	No reference to figures is provided-	
324	pJFRC19-13XLexAop2-IVS-3M__QtFLAG-NLS	No reference to figures is provided-	
325	pAAV__CaMKIIa__mScarlet-I__P2A__2M__QtFLAG	No reference to figures is provided-	
326	pcDNA__Zeo__QtFLAG	No reference to figures is provided-	
327	pcDNA__Zeo__MxFLAG	No reference to figures is provided-	
328	pcDNA__Zeo__TmBC2Tag	No reference to figures is provided-	
329	pcDNA-mCherryFLAG	No reference to figures is provided-	
330	pcDNA-1M-QtEnc__anti-mCherry	No reference to figures is provided-	
331	pcDNA-1M-QtEnc__StrepTagII	No reference to figures is provided-	
332	pcDNA__sfGFP-OG-mCherry	No reference to figures is provided-	
333	pcDNA__Zeo__DD-N__APEX2__EncTag__GA	No reference to figures is provided-	
334	pcDNA__Zeo__QtEnc__SpyTag	No reference to figures is provided-	
335	pcDNA__Zeo__antiGFP-SpyCatcherFLAG	No reference to figures is provided-	
336	pcDNA__Zeo__QtEnc__P4	No reference to figures is provided-	
337	pCMV__EGFP__CAAX	No reference to figures is provided-	
338	pCMV__P3__EGFP__CAAX	No reference to figures is provided-	
339	pcDNA-QtFLAG__TAG__rt9s__IntP2A__Qt-antiGFP__HiBit	No reference to figures is provided-	
340	pcDNA-QtFLAG__TAG__rt9s__antiGFP__HiBit	No reference to figures is provided-	
341	pcDNA-QtFLAG__TAA__rt9s__antiGFP__HiBit	No reference to figures is provided-	
342	pcDNA-QtFLAG__TGA__rt9s__antiGFP__HiBit	No reference to figures is provided-	
343	pcDNA-QtFLAG__TAG__rt9us__antiGFP__HiBit	No reference to figures is provided-	
344	pcDNA-QtFLAG__TAA__rt9us__antiGFP__HiBit	No reference to figures is provided-	
345	pcDNA-QtFLAG__TGA__rt9us__antiGFP__HiBit	No reference to figures is provided-	
346	mCherry-Rab11a, Addgene 55124	No reference to figures is provided-	
347	mCherry-PLK1, Addgene 55119	No reference to figures is provided-	
348	pcDNA__Zeo__MiniSOG__QtEnc-FLAG__NES	No reference to figures is provided-	
349	pcDNA__Zeo__MiniSOG__QtEnc-FLAG__cMycNLS	No reference to figures is provided-	

TABLE 2-continued

Sequences used for this invention			
EQ ID NO	Name	Used in FIG.	Comment
350	pJFRC7-20XUAS-IVS__1xMmMT3__QtEnc__FLAG__NES	No reference to figures is provided-	
351	pU6__U6 + 27__5'-3'-Tornado__Broccoli-PP7__3'-tevopreQ1__6xT	No reference to figures is provided-	
352	pU6__U6 + 27__5'-3'-Tornado__Broccoli(miniCTE-PP7)__3'-tevopreQ1__6xT	No reference to figures is provided-	
353	pU6__U6 + 27__5'-3'-Tornado__Broccoli(miniCTE(PP7))__3'-tevopreQ1__6xT	No reference to figures is provided-	
354	Nterm-BCR__RnMVP__HLH$_{outterior}$-His6__HLH$_{interior}$-PCP	No reference to figures is provided-	
355	RnMVP__HLH$_{outterior}$-His6__HLH$_{interior}$-PCP	No reference to figures is provided-	
356	RnMVP__HLH$_{outterior}$-SNAP25-palmitoylation-site__HLH$_{interior}$-PCP	No reference to figures is provided-	
357	QtIMEF__P2A__QtEnc__eUnaG__Aff6V18deltaN__P2A__DrBphP__HpFtn	FIG. 35	Encapsulins co-clustering with Ferritin (HpFtn) can also be induced by far-red light (MagRed system). When encapsulins are iron-loaded, this light-triggered clustering can be used to temporally modulate signals in magnetic resonance imaging to improve SNR.
358	QtIMEF__P2A__QtEnc__pMagFast2__P2A__nMagHigh1__HpFtn	FIG. 35	Encapsulins co-clustering with Ferritin (HpFtn) can also be induced by blue-light (pMag/nMag system). When encapsulins are iron-loaded, this light-triggered clustering can be used to temporally modulate signals in magnetic resonance imaging to improve SNR.
359	antiGFPintrabody__TEVsite__FKBP12	Related to 7, 8 , 23, 24, 25, 26, 27, 28, 29, 37	Relate to Encapsulin targeting. These constructs allow for blue-light induced targeting of Encapsulins to GFP-tagged sub-cellular structures.
360	MT3-QtEnc-FRB	Related to 7, 8 , 23, 24, 25, 26, 27, 28, 29, 37	Relate to Encapsulin targeting. These constructs allow for blue-light induced targeting of Encapsulins to GFP-tagged sub-cellular structures.
361	MT3-QtEnc-nMagHigh1	Related to 7, 8 , 23, 24, 25, 26, 27, 28, 29, 37	Relate to Encapsulin targeting. These constructs allow for rapamycin-induced targeting of Encapsulins, in this case to membrane localized EGFP (via CAAX signal)
362	pMagFast2__EGPF__CAAX	Related to 7, 8 , 23, 24, 25, 26, 27, 28, 29, 37	Relate to Encapsulin targeting. These constructs allow for rapamycin-induced targeting of Encapsulins, in this case to membrane localized EGFP (via CAAX signal)
363	pU6__U6 + 27__5'-3'-Tornado__Broccoli-PP7__3'-tevopreQ1__6xT	FIG. 31	Twister-stabliized RNA aptamer (PP7) for CLEM contrast targetable to structural elements containing PCP, tevopreQ1 for 3' RNA stabilization.
364	pU6__U6 + 27__5'-3'-Tornado__Broccoli(miniCTE-PP7)__3'-tevopreQ1__6xT	FIG. 31	Twister-stabilized RNA aptamer (PP7) for CLEM contrast targetable to structural elements containing PCP, miniCTE for nuclear export of RNA components, tevopreQ1 for 3' RNA stabilization.
365	pU6__U6 + 27__5'--3'-Tornado__Broccoli(Spinach-PP7))__3'-tevopreQ1__6xT	FIG. 31	Twister-stabilized RNA aptamer (PP7) for CLEM contrast targetable to structural elements containing PCP,Spinach aptamer for Pb2+ binding, tevopreQ1 for 3' RNA stabilization.
No ID	rt9us (sequence: CTATCC)	FIG. 33	DNA sequence promoting ribosomal (translational) read-through after a STOP codon

SEQUENCE LISTING

```
Sequence total quantity: 365
SEQ ID NO: 1            moltype = AA  length = 68
FEATURE                 Location/Qualifiers
source                  1..68
                        mol_type = protein
```

-continued

```
                        organism = Mus musculus
SEQUENCE: 1
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQ                                                           68

SEQ ID NO: 2            moltype = AA  length = 74
FEATURE                 Location/Qualifiers
source                  1..74
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 2
HHHHHHMDPE TCPCPTGGSC TCSDKCKCKG CKCTNCKKSC CSCCPAGCEK CAKDCVCKGE  60
EGAKAEAEKC SCCQ                                                    74

SEQ ID NO: 3            moltype = AA  length = 77
FEATURE                 Location/Qualifiers
source                  1..77
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 3
HHHHHHHHHM DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG CEKCAKDCVC  60
KGEEGAKAEA EKCSCCQ                                                 77

SEQ ID NO: 4            moltype = AA  length = 147
FEATURE                 Location/Qualifiers
source                  1..147
                        mol_type = protein
                        organism = Mus musculus
SEQUENCE: 4
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGSGGSA DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  120
CEKCAKDCVC KGEEGAKAEA EKCSCCQ                                      147

SEQ ID NO: 5            moltype = AA  length = 214
FEATURE                 Location/Qualifiers
REGION                  1..214
                        note = cimeric metallothionein
source                  1..214
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 5
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG TGGSTSTTLV KCACEPCLCN VDPSKAIDRN GLYYCSEACA DGHTGGSKGC  120
GHTGCNCHGS AGGCDDKCGC AVPCPGGTGC RCTSARSGAA AGEHTTCGCG EHCGCNPCAC  180
GREGTPSGRA NRRANCSCGA ACNCASCGSA TAPG                              214

SEQ ID NO: 6            moltype = AA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = protein
                        organism = Pinctada fucata
SEQUENCE: 6
MKFLAAVAFV AVLSHSTVYS YGPRNRGKMM PMMPPAKKMM NNDMMKMMKP DDAMMKPDKQ  60
NQMKPDDMKQ MMKMMMDKMM MMDKMMMMDM MMKMMKPDMM MKPDMMMKPD MMMKPDMMMK  120
PDMMMKPDMM MKPDMMMKPD MMMKPDMMMK PDMMMKPDMM MKPDMMMKPD MMMKPDMMMK  180
PDMMMKPDMM MKPDMMMKPD MMMKPDMMMK PDMMMKPDMM MKPDMMMKPD MMMKPDMMMK  240
PDMMMKPDMM MKPDMMMKPD MMMKPDMMMK PDMMMKPDMG MMKPDMGMMM HPTPYNLYQG  300

SEQ ID NO: 7            moltype = AA  length = 31
FEATURE                 Location/Qualifiers
source                  1..31
                        mol_type = protein
                        organism = Panax ginseng
SEQUENCE: 7
CKSGGAWCGF DPHGCCGNCG CLVGFCYGTG C                                 31

SEQ ID NO: 8            moltype = AA  length = 28
FEATURE                 Location/Qualifiers
source                  1..28
                        mol_type = protein
                        organism = Klebsiella pneumoniae
SEQUENCE: 8
ECPRCDSYYT LHQAQHHLRC HHCDSQRP                                     28

SEQ ID NO: 9            moltype = AA  length = 26
FEATURE                 Location/Qualifiers
```

-continued

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source                  1..26
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 9
EAVCCSDHQH CCPQGYTCVA EGQCQK                                        26

SEQ ID NO: 10           moltype = AA  length = 45
FEATURE                 Location/Qualifiers
source                  1..45
                        mol_type = protein
                        organism = Utricina eques
SEQUENCE: 10
CYPGQPGCGH CSRPNYCEGA RCESGFHDCG SDHWCDASGD RCCCA                   45

SEQ ID NO: 11           moltype = AA  length = 27
FEATURE                 Location/Qualifiers
source                  1..27
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 11
LMVKCPNEGC LHKMELRHLE DHQAHCE                                       27

SEQ ID NO: 12           moltype = AA  length = 111
FEATURE                 Location/Qualifiers
source                  1..111
                        mol_type = protein
                        organism = Methylobacterium extorquens
SEQUENCE: 12
PTTTTKVDIA AFDPDKDGTI DLKEALAAGS AAFDKLDPDK DGTLDAKELK GRVSEADLKK  60
LDPDNDGTLD KKEYLAAVEA QFKAANPDND GTIDARELAS PAGSALVNLI R           111

SEQ ID NO: 13           moltype = AA  length = 20
FEATURE                 Location/Qualifiers
REGION                  1..20
                        note = Synthethic lanthanide binding tag
source                  1..20
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 13
FIDTNNDGWI EGDELLLEEG                                               20

SEQ ID NO: 14           moltype = AA  length = 119
FEATURE                 Location/Qualifiers
source                  1..119
                        mol_type = protein
                        organism = Ascidia sydneiensis samea
SEQUENCE: 14
SKVIFALVLV VVLVACINAT YVEFEEAYAP VDCKGQCTTP CEPLTACKEK CAESCETSAD  60
KKTCRRNCKK ADCEPQDKVC DACRMKCHKA CRAANCASEC PKHEHKSDTC RACMKTNCK   119

SEQ ID NO: 15           moltype = AA  length = 88
FEATURE                 Location/Qualifiers
source                  1..88
                        mol_type = protein
                        organism = Escherichia coli
SEQUENCE: 15
NEHHHETMSE AQPQVISATG EVKGIDLESK KITIHHDPIA AVNWPEMTMR FTITPQTKMS  60
EIKTGDKVAF NFVQQGNLSL LQDIKVSQ                                      88

SEQ ID NO: 16           moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = Encapsulation signal for the Encapsulin system of
                         Quasibacillus thermotolerans
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 16
KGFTVGSLIQ                                                          10

SEQ ID NO: 17           moltype = AA  length = 298
FEATURE                 Location/Qualifiers
source                  1..298
                        mol_type = protein
                        organism = Plasmodium falciparum
SEQUENCE: 17
```

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FNNNLCSKNA KGLNLNKRLL HETQAHVDDA HHAHHVADAH HAHHVADAHH AHHVADAHHA  60
HHAADAHHAH HAADAHHAHH AADAHHAHHA HHAADAHHAH HAADAHHAHH AADAHHAHHA  120
ADAHHAHHAA DAHHAHHASD AHHAHHAAYA HHAHHASDAH HAADAHHAAY AHHAHHAADA  180
HHAADAHHAT DAHHAADAHH AADAHHAADA HHATDAHHAH HAADAHHATD AHHAHHAADA  240
HHAAAHHATD AHHAAAHHAT DAHHAAAHHE AATHCLRHGG GGSGGGGSKG FTVGSLIQ    298

SEQ ID NO: 18          moltype = AA  length = 212
FEATURE                Location/Qualifiers
REGION                 1..212
                       note = Fusion protein consisting of enhanced UnaG(V2L) from
                        Anguilla japonica and MmMT3
source                 1..212
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 18
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQ                                212

SEQ ID NO: 19          moltype = AA  length = 182
FEATURE                Location/Qualifiers
source                 1..182
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 19
MDKDCEMKRT TLDSPLGKLE LSGCEQGLHR IIFLGKGTSA ADAVEVPAPA AVLGGPEPLM  60
QATAWLNAYF HQPEAIEEFP VPALHHPVFQ QESFTRQVLW KLLKVVKFGE VISYSHLAAL  120
AGNPAATAAV KTALSGNPVP ILIPCHRVVQ GDLDVGGYEG GLAVKEWLLA HEGHRLGKPG  180
LG                                                                 182

SEQ ID NO: 20          moltype = AA  length = 297
FEATURE                Location/Qualifiers
REGION                 1..297
                       note = modified bacterial dehalogenase that forms covalent
                        bonds with chloroalkane derivatives
source                 1..297
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 20
MAEIGTGFPF DPHYVEVLGE RMHYVDVGPR DGTPVLFLHG NPTSSYVWRN IIPHVAPTHR  60
CIAPDLIGMG KSDKPDLGYF FDDHVRFMDA FIEALGLEEV VLVIHDWGSA LGFHWAKRNP  120
ERVKGIAFME FIRPIPTWDE WPEFARETFQ AFRTTDVGRK LIIDQNVFIE GTLPMGVVRP  180
LTEVEMDHYR EPFLNPVDRE PLWRFPNELP IAGEPANIVA LVEEYMDWLH QSPVPKLLFW  240
GTPGVLIPPA EAARLAKSLP NCKAVDIGPG LNLLQEDNPD LIGSEIARWL STLEISG     297

SEQ ID NO: 21          moltype = AA  length = 404
FEATURE                Location/Qualifiers
REGION                 1..404
                       note = Fusion of a synthetic coiled-coil domain (P2), the
                        CGU MmMT3, the QtEnc shell-forming monomer from the
                        Encapsulin system of Q.thermotolerans and a FLAG-epitope
source                 1..404
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 21
MSPEDKIAQL KEKNAALKEK NQQLKEKIQA LKYGGGTGGS DPETCPCPTG GSCTCSDKCK  60
CKGCKCTNCK KSCCSCCPAG CEKCAKDCVC KGEEGAKAEA EKCSCCQGSG PGNKSQLYPD  120
SPLTDQDFNQ LDQTVIEAAR RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS  180
FDTEVESSRR VNYTIPMLYK DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF  240
HGSKEFDIPG LMNVKGRLTH LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY  300
SLLHRVHKDT NVLEIEHVRE LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL  360
GEEGMNHPFR VYETVVLRIK RPAAICTLID PEEGSGDYKD DDDK                   404

SEQ ID NO: 22          moltype = AA  length = 333
FEATURE                Location/Qualifiers
REGION                 1..333
                       note = Fusion of synthetic coiled-coil domain P1 (cognate
                        partner of P2), OsO4 post-fixation stable switchable
                        fluorescent protein mEosEM and a human PEST degradation
                        sequence
source                 1..333
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 22
MVSAIKPDMR IKLRMEGNVN GHHFVIDGEG TGKPYEGKQT MDLEVKEGGP LPFAFDILTT  60
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AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSMTFEDGG ICNARNDITM EGDTFYNKVR  120
FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGGAHY RCDFRTTYKA  180
KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARRGGG GSGGGGSGPG  240
TGSPEDEIQA LEEENAQLEQ ENAALEEEIA QLEYGSGSET PGTSESATPE SAISHGFPPE  300
VEEQAAGTLP MSCAQESGMD RHPAACASAR INV                               333

SEQ ID NO: 23          moltype = AA  length = 195
FEATURE                Location/Qualifiers
REGION                 1..195
                       note = Strand 1 to 9 of a Tripartite split superfolderGFP
source                 1..195
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 23
MRGEELFTGV VPILIELDGD VNGHKFFVRG EGEGDATIGK LSLKFICTTG KLPVPWPTLV  60
TTLTYGVQCF SRYPDHMKRH DFFKSAMPEG YVQERTIYFK DDGTYKTRAE VKFEGDTLVN  120
RIELKGIDFK EDGNILGHKL EYNFNSHKVY ITADKQNNGI KANFTIRHNV EDGSVQLADH  180
YQQNTPIGDG PVLLP                                                   195

SEQ ID NO: 24          moltype = AA  length = 487
FEATURE                Location/Qualifiers
REGION                 1..487
                       note = The shell forming monomer of the Ecapsulin system of
                        Quasibacillus thermotolerans fused to superfolder GFP
                        strands 1 to 9
source                 1..487
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 24
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGMRGEELF  300
TGVVPILIEL DGDVNGHKFF VRGEGEGDAT IGKLSLKFIC TTGKLPVPWP TLVTTLTYGV  360
QCFSRYPDHM KRHDFFKSAM PEGYVQERTI YFKDDGTYKT RAEVKFEGDT LVNRIELKGI  420
DFKEDGNILG HKLEYNFNSH KVYITADKQN NGIKANFTIR HNVEDGSVQL ADHYQQNTPI  480
GDGPVLL                                                            487

SEQ ID NO: 25          moltype = AA  length = 313
FEATURE                Location/Qualifiers
REGION                 1..313
                       note = The shell forming monomer of the Ecapsulin system of
                        Quasibacillus thermotolerans fused to superfolderGFP
                        strand 10
source                 1..313
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 25
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGTMDLPDN  300
HYLSTQTILL KDL                                                     313

SEQ ID NO: 26          moltype = AA  length = 315
FEATURE                Location/Qualifiers
REGION                 1..315
                       note = The shell forming monomer of the Ecapsulin system of
                        Quasibacillus thermotolerans fused to superfolderGFP
                        strand 11
source                 1..315
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 26
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGSEKRDHM  300
VLLEYVTAAG ITDAS                                                   315

SEQ ID NO: 27          moltype = AA  length = 432
FEATURE                Location/Qualifiers
REGION                 1..432
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                        note = The shell forming monomer of the Ecapsulin system of
                         Quasibacillus thermotolerans fused to enhanced UnaG(V2L)
                         from Anguilla japonica and MmMT3
source                  1..432
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 27
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGMLEKFVG  300
TWKIADSHNF GEYLKAIGAP KELSDGGDAT TPTLYISQKD GDKMSVKIEN GPPTFLDTQV  360
KFKLGEEFDE FPSDRRKGVK SVVNLVGEKL VYVQKWDGKE TTYVREIKDG KLVVTLTMGD  420
VVAVRSYRRA TE                                                      432

SEQ ID NO: 28           moltype = AA  length = 437
FEATURE                 Location/Qualifiers
REGION                  1..437
                        note = The shell forming monomer of the Ecapsulin system of
                         Myxococcus xanthus fused to enhanced UnaG(V2L) from
                         Anguilla japonica and MmMT3
source                  1..437
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 28
MADFLGHAEN PLREEEWARL NETVIQVARR SLVGRRILDI YGPLGAGVQT VPYDEFQGVS  60
PGAVDIVGEQ ETAMVFTDAR KFKTIPIIYK DFLLHWRDIE AARTHNMPLD VSAAAGAAAL  120
CAQQEDELIF YGDARLGYEG LMTANGRLTV PLGDWTSPGG GFQAIVEATR KLNEQGHFGP  180
YAVVLSPRLY SQLHRIYEKT GVLEIETIRQ LASDGVYQSN RLRGESGVVV STGRENMDLA  240
VSMDMVAAYL GASRMNHPFR VLEALLLRIK HPDAICTLEG AGATERRGGG GSGPGGSGML  300
EKFVGTWKIA DSHNFGEYLK AIGAPKELSD GGDATTPTLY ISQKDGDKMS VKIENGPPTF  360
LDTQVKFKLG EEFDEFPSDR RKGVKSVVNL VGEKLVYVQK WDGKETTYVR EIKDGKLVVT  420
LTMGDVVAVR SYRRATE                                                 437

SEQ ID NO: 29           moltype = AA  length = 456
FEATURE                 Location/Qualifiers
REGION                  1..456
                        note = Heme domain of BM3 a natural fusion protein
                         constructed of cytochrome P450 and NADPH-cytochrome P450
                         reductase domains from Priestia megaterium
source                  1..456
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 29
MTIKEMPQPK TFGELKNLPL LNTDKPVQAL MKIADELGEI FKFEAPGRVT RYLSSQRLIK  60
EACDESRFDK NLSQALKFVR DFAGDGLFTS WTHEKNWKKA HNILLPSFSQ QAMKGYHAMM  120
VDIAVQLVQK WERLNADEHI EVPEDMTRLT LDTIGLCGFN YRFNSFYRDQ PHPFITSMVR  180
ALDEAMNKLQ RANPDDPAYD ENKRQFQEDI KVMNDLVDKI IADRKASGEQ SDDLLTHMLN  240
GKDPETGEPL DDENIRYQII TFLIAGHETT SGLLSFALYF LVKNPHVLQK AAEEAARVLV  300
DPVPSYKQVK QLKYVGMVLN EALRLWPTAP AFSLYAKEDT VLGGEYPLEK GDELMVLIPQ  360
LHRDKTIWGD DVEEFRPERF ENPSAIPQHA FKPFGNGQRA CIGQQFALHE ATLVLGMMLK  420
HFDFEDHTNY ELDIKETLTL KPEGFVVKAK SKKIPL                            456

SEQ ID NO: 30           moltype = AA  length = 127
FEATURE                 Location/Qualifiers
source                  1..127
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 30
MSFSGKYQLQ SQENFEAFMK AIGLPEELIQ KGKDIKGVSE IVQNGKHFKF TITAGSKVIQ  60
NEFTVGEECE LETMTGEKVK TVVQLEGDNK LVTTFKNIKS VTELNGDIIT NTMTLGDIVF  120
KRISKRI                                                            127

SEQ ID NO: 31           moltype = AA  length = 132
FEATURE                 Location/Qualifiers
source                  1..132
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 31
MAFDSTWKVD RSENYDKFME KMGVNIVKRK LAAHDNLKLT ITQEGNKFTV KESSAFRNIE  60
VVFELGVTFN YNLADGTELR GTWSLEGNKL IGKFKRTDNG NELNTVREII GDELVQTYVY  120
EGVEAKRIFK KD                                                      132

SEQ ID NO: 32           moltype = AA  length = 133
FEATURE                 Location/Qualifiers
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source                  1..133
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 32
MVDAFLGTWK LVDSKNFDDY MKSLGVGFAT RQVASMTKPT TIIEKNGDIL TLKTHSTFKN  60
TEISFKLGVE FDETTADDRK VKSIVTLDGG KLVHLQKWDG QETTLVRELI DGKLILTLTH  120
GTAVCTRTYE KEA                                                     133

SEQ ID NO: 33           moltype = AA  length = 132
FEATURE                 Location/Qualifiers
source                  1..132
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 33
MCDAFVGTWK LVSSENFDDY MKEVGVGFAT RKVAGMAKPN MIISVNGDVI TIKSESTFKN  60
TEISFILGQE FDEVTADDRK VKSTITLDGG VLVHVQKWDG KSTTIKRKRE DDKLVVECVM  120
KGVTSTRVYE RA                                                      132

SEQ ID NO: 34           moltype = AA  length = 135
FEATURE                 Location/Qualifiers
source                  1..135
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 34
MATVQQLEGR WRLVDSKGFD EYMKELGVGI ALRKMGAMAK PDCIITCDGK NLTIKTESTL  60
KTTQFSCTLG EKFEETTADG RKTQTVCNFT DGALVQHQEW DGKESTITRK LKDGKLVVEC  120
VMNNVTCTRI YEKVE                                                   135

SEQ ID NO: 35           moltype = AA  length = 128
FEATURE                 Location/Qualifiers
source                  1..128
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 35
MAFTGKFEME SEKNYDEFMK LLGISSDVIE KARNFKIVTE VQQDGQDFTW SQHYSGGHTM  60
TNKFTVGKES NIQTMGGKTF KATVQMEGGK LVVNFPNYHQ TSEIVGDKLV EVSTIGGVTY  120
ERVSKRLA                                                           128

SEQ ID NO: 36           moltype = AA  length = 132
FEATURE                 Location/Qualifiers
source                  1..132
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 36
MVEAFCATWK LTNSQNFDEY MKALGVGFAT RQVGNVTKPT VIISQEGDKV VIRTLSTFKN  60
TEISFQLGEE FDETTADDRN CKSVVSLDGD KLVHIQKWDG KETNFVREIK DGKMVMTLTF  120
GDVVAVRHYE KA                                                      132

SEQ ID NO: 37           moltype = AA  length = 132
FEATURE                 Location/Qualifiers
source                  1..132
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 37
MSNKFLGTWK LVSSENFDDY MKALGVGLAT RKLGNLAKPT VIISKKGDII TIRTESTFKN  60
TEISFKLGQE FEETTADNRK TKSIVTLQRG SLNQVQRWDG KETTIKRKLV NGKMVAECKM  120
KGVVCTRIYE KV                                                      132

SEQ ID NO: 38           moltype = AA  length = 132
FEATURE                 Location/Qualifiers
source                  1..132
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 38
MVEPPLGTWK LVSSENFEDY MKELGVNFAA RNMAGLVKPT VTISVDGKMM TIRTESSFQD  60
TKISFKLGEE FDETTADNRK VKSTITLENG SMIHVQKWLG KETTIKRKIV DEKMVVECKM  120
NNIVSTRIYE KV                                                      132

SEQ ID NO: 39           moltype = AA  length = 140
FEATURE                 Location/Qualifiers
source                  1..140
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 39
MIDQLQGTWK SISCENSEDY MKELGIGRAS RKLGRLAKPT VTISTDGDVI TIKTKSIFKN  60
NEISFKLGEE FEEITPGGHK TKSKVTLDKE SLIQVQDWDG KETTITRKLV DGKMVVESTV  120
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NSVICTRTYE KVSSNSVSNS                                                140

SEQ ID NO: 40          moltype = AA  length = 10
FEATURE                Location/Qualifiers
source                 1..10
                       mol_type = protein
                       organism = Rattus rattus
SEQUENCE: 40
GCMSCKCVLS                                                           10

SEQ ID NO: 41          moltype = AA  length = 36
FEATURE                Location/Qualifiers
source                 1..36
                       mol_type = protein
                       organism = Rattus norvegicus
SEQUENCE: 41
CGLCVCPCNK LKSSDAYKKA WGNNQDGVVA SQPARV                              36

SEQ ID NO: 42          moltype = AA  length = 15
FEATURE                Location/Qualifiers
source                 1..15
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 42
MGCVQCKDKE ATKLT                                                     15

SEQ ID NO: 43          moltype = AA  length = 121
FEATURE                Location/Qualifiers
source                 1..121
                       mol_type = protein
                       organism = Mus musculus
SEQUENCE: 43
MPSDRPFKQR RSFADRCKEV QQIRDQHPSK IPVIIERYKG EKQLPVLDKT KFLVPDHVNM  60
SELVKIIRRR LQLNPTQAFF LLVNQHSMVS VSTPIADIYE QEKDEDGFLY MVYASQETFG  120
F                                                                    121

SEQ ID NO: 44          moltype = AA  length = 338
FEATURE                Location/Qualifiers
REGION                 1..338
                       note = Consisting of engineered apo-lipoprotein A-1 (MSP1)
                        flanked by DnaE split intein fragments C-intein (AA
                        103-137) on the N-term and N-Intein (AA 1-102) on the
                        C-term) (Homo sapiens, Nostoc punctiforme):
source                 1..338
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 44
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNLKLL DNWDSVTSTF SKLREQLGPV  60
TQEFWDNLEK ETEGLRQEMS KDLEEVKAKV QPYLDDFQKK WQEEMELYRQ KVEPLRAELQ  120
EGARQKLHEL QEKLSPLGEE MRDRARAHVD ALRTHLAPYS DELRQRLAAR LEALKENGGA  180
RLAEYHAKAT EHLSTLSEKA KPALEDLRQG LLPVLESFKV SFLSALEEYT KKLNTQCLSY  240
ETEILTVEYG LLPIGKIVEK RIECTVYSVD NNGNIYTQPV AQWHDRGEQE VFEYCLEDGS  300
LIRATKDHKF MTVDGQMLPI DEIFERELDL MRVDNLPN                          338

SEQ ID NO: 45          moltype = AA  length = 139
FEATURE                Location/Qualifiers
REGION                 1..139
                       note = Designed uranyl binding proteins with 6 binding
                        sites for uranyl ions
source                 1..139
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 45
MVSRLEERVR DLEAEVDKLR ERLDRLEETV QAKGGGGSGG GGSGGGGSGG GGSGGVSRLE  60
RVRDLEAEVD KLRERLDRLE ETVQAKGGGG SGGGGSGGGG SGGGGSGGVS RLEERVRDLA  120
EVDKLRERLD RLEETVQAK                                                 139

SEQ ID NO: 46          moltype = AA  length = 220
FEATURE                Location/Qualifiers
REGION                 1..220
                       note = Designed uranyl binding proteins with 6 binding
                        sites for uranyl ions
source                 1..220
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 46
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MQLEDKVEEL LSKVYHLENE VDRLRKLIEN KGGGGSGGGG SQLEDKVEEL ESEVDHLRNE  60
VAKKLVGGGG SGGGGSQLED KVEELLSKVY HLENEVDRLR KLIENKGGGG SGGGGSQLED  120
KVEELESEVD HLRNEVARLK KLVGGGGSGG GGSQLEDKVE ELLSKVYHLE NEVDRLRKLI  180
ENKGGGGSGG GGSQLEDKVE ELESEVDHLR NEVARLKKLV                        220

SEQ ID NO: 47          moltype = AA  length = 435
FEATURE                Location/Qualifiers
REGION                 1..435
                       note = Degron-tagged polyphopsphate kinase 2b of
                        Corynebacterium glutamicum C-terminanlly tagged with the
                        encapsulation signal of Quasibacillus thermotolerans
source                 1..435
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 47
GVQVETISPG DGRTFPKRGQ TCVVHYTGML EDGKKVDSSR DRNKPFKFML GKQEVIRGWE  60
EGVAQMSVGQ RAKLTISPDY AYGATGHPGI IPPHATLVFD VELLKPEGSG VGKLPIMAET  120
NENDLPVIDL AQIEGYVVDD SDEDDPVLLR PDGTPIETWR EDFPYEERVT REDYEKVKRS  180
LQIELLKWQN WTKETGQRHI ILFEGRDAAG KGGTIKRFNE HLNPRGARTV ALEKPSPRES  240
TSWYFQRYIQ HFPAAGEIVF FDRSWYNRSG VERVMGFCTE SQHAEFLREV PMLENMILGS  300
GISLTKFWFS VTRKEQRTRF AIRQVDPVRQ WKLSPMDLAS LDRWDDYTRA KEEQFRYTDT  360
DESPWITIKS NDKKRARINA MRYVLSKFDY TDKDYELVGE PDPKVVLRGR DQIGDGGGGS  420
GGGGSKGFTV GSLIQ                                                   435

SEQ ID NO: 48          moltype = AA  length = 305
FEATURE                Location/Qualifiers
source                 1..305
                       mol_type = protein
                       organism = Corynebacterium glutamicum
SEQUENCE: 48
VGKLPIMAET NENDLPVIDL AQIEGYVVDD SDEDDPVLLR PDGTPIETWR EDFPYEERVT  60
REDYEKVKRS LQIELLKWQN WTKETGQRHI ILFEGRDAAG KGGTIKRFNE HLNPRGARTV  120
ALEKPSPRES TSWYFQRYIQ HFPAAGEIVF FDRSWYNRSG VERVMGFCTE SQHAEFLREV  180
PMLENMILGS GISLTKFWFS VTRKEQRTRF AIRQVDPVRQ WKLSPMDLAS LDRWDDYTRA  240
KEEQFRYTDT DESPWITIKS NDKKRARINA MRYVLSKFDY TDKDYELVGE PDPKVVLRGR  300
DQIGD                                                              305

SEQ ID NO: 49          moltype = AA  length = 469
FEATURE                Location/Qualifiers
REGION                 1..469
                       note = Phytochelatin synthase 1 of Arabidopsis thaliana
                        with a C-terminal encapsulation signal
source                 1..469
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 49
MEGFFRLISY FQTQSEPAYC GLASLSVVLN ALSIDPGRKW KGPWRWFDES MLDCCEPLEV  60
VKEKGISFGK VVCLAHCSGA KVEAFRTSQS TIDDFRKFVV KCTSSENCHM ISTYHRGVFK  120
QTGTGHFSPI GGYNAERDMA LILDVARFKY PPHWVPLKLL WEAMDSIDQS TGKRRGFMLI  180
SRPHREPGLL YTLSCKDESW IEIAKYLKED VPRLVSSQHV DSVEKIISVV FKSLPSNFNQ  240
FIRWVAEIRI TEDSNQNLSA EEKSRLKLKQ LVLKEVHETE LFKHINKFLS TVGYEDSLTY  300
AAAKACCQGA EILSGSPSKE FCCRETCVKC IKGPDDSEGT VVTGVVVRDG NEQKVDLLVP  360
STQTECECGP EATYPAGNDV FTALLLALPP QTWSGIKDQA LMHEMKQLIS MASLPTLLQE  420
EVLHLRRQLQ LLKRCQENKE EDDLAAPAYG GGGSGGGGSK GFTVGSLIQ              469

SEQ ID NO: 50          moltype = AA  length = 472
FEATURE                Location/Qualifiers
REGION                 1..472
                       note = Phytochelatin synthase 2 of Arabidopsis thaliana
                        with a C-terminal encapsulation signal
source                 1..472
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 50
MSMASLYRRS LSPPAIDFAS FEGKQIFNEA LQKGTMEGFF GLISYFQTQS EPAFCGLASL  60
SMVLNSLSID PGRKWKGPWR WFDESMLECC EPLEIVKDKG ISFGKVVCLA HSSGAKVEAF  120
RTNQSTIDDF RKYVVKCSTS DNCHMISTYH RQVLKQTGTG HFSPIGGYNA ERDMALILDV  180
ARFKYPPHWV PLKLLWDAMD SIDQSTGRRR GFMLISRPHR EPGLLYTLSC KDESWISIAK  240
YLKEDVPRLV SSQHVDTIER ILYVVFKSLP ANFNQFIKWM AEIRRTEDVN QNLSSEEKSR  300
LKLKQELLKQ VQETKLFKHV DKFLSSVYED NLPYVAAKVY CDGDEILSGY ESDESCCKET  360
CVKCIKGLGE EKVTVVAYPS GNDVFTALLL ALPPQTWSGI KDQSLLQEMK QLISMVSHPT  420
LLQQEVLHLR RQLEMLKRCQ ENKEDEELSA PAGGGGSGGG GSKGFTVGSL IQ          472

SEQ ID NO: 51          moltype = AA  length = 296
FEATURE                Location/Qualifiers
source                 1..296
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                      mol_type = protein
                      organism = Bacillus megaterium
SEQUENCE: 51
SNKYRVRKNV LHLTDTEKRD FVRTVLILKE KGIYDRYIAW HGAAGKFHTP PGSDRNAAHM  60
SSAFLPWHRE YLLRFERDLQ SINPEVTLPY WEWETDAQMQ DPSQSQIWSA DFMGGNGNPI  120
KDFIVDTGPF AAGRWTTIDE QGNPSGGLKR NFGATKEAPT LPTRDDVLNA LKITQYDTPP  180
WDMTSQNSFR NQLEGFINGP QLHNRVHRWV GGQMGVVPTA PNDPVFFLHH ANVDRIWAVW  240
QIIHRNQNYQ PMKNGPFGQN FRDPMYPWNT TPEDVMNHRK LGYVYDIELR KSKRSS      296

SEQ ID NO: 52          moltype = AA  length = 192
FEATURE                Location/Qualifiers
source                 1..192
                       mol_type = protein
                       organism = Quasibacillus thermotolerans
SEQUENCE: 52
MKEELDAFHQ IFTTTKEAIE RFMAMLTPVI ENAEDDHERL YYHHIYEEEE QRLSRLDVLI  60
PLIEKFQDET DEGLFSPSNN AFNRLLQELN LEKFGLHNFI EHVDLALFSF TDEERQTLLK  120
ELRKDAYEGY QYVKEKLAEI NARFDHDYAD PHAHHDEHRD HLADMPSAGS SHEEVQPVAH  180
KKKGFTVGSL IQ                                                      192

SEQ ID NO: 53          moltype = AA  length = 128
FEATURE                Location/Qualifiers
source                 1..128
                       mol_type = protein
                       organism = Bacteriophage Pseudomonas phage
SEQUENCE: 53
MSKTIVLSVG EATRTLTEIQ STADRQIFEE KVGPLVGRLR LTASLRQNGA KTAYRVNLKL  60
DQADVVDCST SVCGELPKVR YTQVWSHDVT IVANSTEASR KSLYDLTKSL VATSQVEDLV  120
VNLVPLGR                                                           128

SEQ ID NO: 54          moltype = AA  length = 255
FEATURE                Location/Qualifiers
REGION                 1..255
                       note = Tandem dimer of The coat protein of the
                        single-stranded RNA bacteriophage Pseudomonas phage
                        binding the PP7 stem loop
source                 1..255
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 54
MLASKTIVLS VGEATRTLTE IQSTADRQIF EEKVGPLVGR LRLTASLRQN GAKTAYRVNL  60
KLDQADVVDS GLPKVRYTQV WSHDVTIVAN STEASRKSLY DLTKSLVATS QVEDLVVNLV  120
PLGRADPLAS KTIVLSVGEA TRTLTEIQST ADRQIFEEKV GPLVGRLRLT ASLRQNGAKT  180
AYRVNLKLDQ ADVVDSGLPK VRYTQVWSHD VTIVANSTEA SRKSLYDLTK SLVATSQVED  240
LVVNLVPLGR PPVAT                                                   255

SEQ ID NO: 55          moltype = RNA  length = 98
FEATURE                Location/Qualifiers
misc_feature           1..98
                       note = Synthetically derived RNA aptamer designed to be an
                        RNA mimic of green fluorescent protein (GFP)
source                 1..98
                       mol_type = other RNA
                       organism = synthetic construct
SEQUENCE: 55
gacgcaactg aatgaaatgg tgaaggacgg gtccaggtgt ggctgcttcg gcagtgcagc  60
ttgttgagta gagtgtgagc tccgtaacta gtcgcgtc                          98

SEQ ID NO: 56          moltype = RNA  length = 25
FEATURE                Location/Qualifiers
misc_feature           1..25
                       note = Small RNA sequence binding partner of the tandem PCP
                        dimer from Pseudomonas phage
source                 1..25
                       mol_type = other RNA
                       organism = synthetic construct
SEQUENCE: 56
ggagcagacg atatggcgtc gctcc                                        25

SEQ ID NO: 57          moltype = RNA  length = 57
FEATURE                Location/Qualifiers
misc_feature           1..57
                       note = Synthetically derived RNA aptamer designed to be an
                        RNA mimic of red fluorescent protein (RFP)
source                 1..57
                       mol_type = other RNA
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                        organism = synthetic construct
SEQUENCE: 57
ggatgcgcct tgaaaagcct gcttcggcag ctggtgaatg acagctatgg cgcatcc     57

SEQ ID NO: 58           moltype = RNA  length = 19
FEATURE                 Location/Qualifiers
misc_feature            1..19
                        note = Small synthetic aptamer coordination metal ions in
                         homodimeric form
source                  1..19
                        mol_type = other RNA
                        organism = synthetic construct
SEQUENCE: 58
ttgtcgcttc gaaaaagtc                                               19

SEQ ID NO: 59           moltype = RNA  length = 55
FEATURE                 Location/Qualifiers
misc_feature            1..55
                        note = Synthetic aptamer that binds a fluorogenic rhodamine
                         dye with fast association and dissociation kinetics
source                  1..55
                        mol_type = other RNA
                        organism = synthetic construct
SEQUENCE: 59
ccttggactc cgccaattgg aacgcggaga ggaagtggcg aaagcgcctc caagg       55

SEQ ID NO: 60           moltype = AA  length = 85
FEATURE                 Location/Qualifiers
REGION                  1..85
                        note = RNA-binding domain that are known to bind
                         single-stranded RNAs. It was found in many eukaryotic
                         proteins
source                  1..85
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 60
GSMATTKRVL YVGGLAEEVD DKVLHAAFIP FGDITDIQIP LDYETEKHRG FAFVEFELAE  60
DAAAAIDNMN ESELFGRTIR VNLAK                                        85

SEQ ID NO: 61           moltype = AA  length = 78
FEATURE                 Location/Qualifiers
REGION                  1..78
                        note = Protein domain that was first identified in the
                         human binds RNA, and can function in RNA recognition
source                  1..78
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 61
MSPNLPGQTT VQVRVPYRVV GLVVGPKGAT IKRIQQQTHT YIVTPSRDKE PVFEVTGMPE  60
NVDRAREEIE MHIAMRTG                                                78

SEQ ID NO: 62           moltype = AA  length = 87
FEATURE                 Location/Qualifiers
REGION                  1..87
                        note = Zinc finger domain subspecies know to bind RNA
source                  1..87
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 62
MSGGLAPSKS TVYVSNLPFS LTNNDLYRIF SKYGKVVKVT IMKDKDTRKS KGVAFILFLD  60
KDSAQNCTRA INNKQLFGRV IKASIAI                                      87

SEQ ID NO: 63           moltype = AA  length = 127
FEATURE                 Location/Qualifiers
REGION                  1..127
                        note = Multifunctional RNA-binding protein that recognizes
                         the K-turn motif in ribosomal RNA
source                  1..127
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 63
MSKASYVKFE VPQDLADKVL EAVRKAKESG KIKKGTNETT KAVERGQAKL VIIAEDVQPE  60
EIVAHLPLLC DEKKIPYVYV SSKKALGEAC GLQVATASAA ILEPGEAKDL VDEIIKRVNE  120
IKGKTSS                                                            127

SEQ ID NO: 64           moltype = AA  length = 17
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FEATURE                 Location/Qualifiers
REGION                  1..17
                        note = BIV-Tat from the Bovine immunodeficiency virus binds
                         to a hairpin structure at the 5′-end of all nascent viral
                         mRNAs
source                  1..17
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 64
SGPRPRGTRG KGRRIRR                                                  17

SEQ ID NO: 65           moltype = AA  length = 281
FEATURE                 Location/Qualifiers
source                  1..281
                        mol_type = protein
                        organism = Quasibacillus thermotolerans
SEQUENCE: 65
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE E                      281

SEQ ID NO: 66           moltype = AA  length = 287
FEATURE                 Location/Qualifiers
source                  1..287
                        mol_type = protein
                        organism = Myxococcus xanthus
SEQUENCE: 66
MADFLGHAEN PLREEEWARL NETVIQVARR SLVGRRILDI YGPLGAGVQT VPYDEFQGVS  60
PGAVDIVGEQ ETAMVFTDAR KFKTIPIIYK DFLLHWRDIE AARTHNMPLD VSAAAGAAAL  120
CAQQEDELIF YGDARLGYEG LMTANGRLTV PLGDWTSPGG GFQAIVEATR KLNEQGHFGP  180
YAVVLSPRLY SQLHRIYEKT GVLEIETIRQ LASDGVYQSN RLRGESGVVV STGRENMDLA  240
VSMDMVAAYL GASRMNHPFR VLEALLLRIK HPDAICTLEG AGATERR                287

SEQ ID NO: 67           moltype = AA  length = 264
FEATURE                 Location/Qualifiers
source                  1..264
                        mol_type = protein
                        organism = Thermotoga maritima
SEQUENCE: 67
MEFLKRSFAP LTEKQWQEID NRAREIFKTQ LYGRKFVDVE GPYGWEYAAH PLGEVEVLSD  60
ENEVVKWGLR KSLPLIELRA TFTLDLWELD NLERGKPNVD LSSLEETVRK VAEFEDEVIF  120
RGCEKSGVKG LLSFEERKIE CGSTPKDLLE AIVRALSIFS KDGIEGPYTL VINTDRWINF  180
LKEEAGHYPL EKRVEECLRG GKIITTPRIE DALVVSERGG DFKLILGQDL SIGYEDREKD  240
AVRLFITETF TFQVVNPEAL ILLK                                         264

SEQ ID NO: 68           moltype = AA  length = 33
FEATURE                 Location/Qualifiers
REGION                  1..33
                        note = Synthetic coiled-coil domain which pairs with P2
source                  1..33
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 68
SPEDEIQALE EENAQLEQEN AALEEEIAQL EYG                                33

SEQ ID NO: 69           moltype = AA  length = 33
FEATURE                 Location/Qualifiers
REGION                  1..33
                        note = Synthetic coiled-coil domain which pairs with P1
source                  1..33
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 69
SPEDKIAQLK EKNAALKEKN QQLKEKIQAL KYG                                33

SEQ ID NO: 70           moltype = AA  length = 33
FEATURE                 Location/Qualifiers
REGION                  1..33
                        note = Synthetic coiled-coil domain which pairs with P4
source                  1..33
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 70
SPEDEIQQLE EEIAQLEQKN AALKEKNQAL KYG                                33
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SEQ ID NO: 71          moltype = AA  length = 33
FEATURE                Location/Qualifiers
REGION                 1..33
                       note = Synthetic coiled-coil domain which pairs with P3
source                 1..33
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 71
SPEDKIAQLK QKIQALKQEN QQLEEENAAL EYG                                33

SEQ ID NO: 72          moltype = AA  length = 78
FEATURE                Location/Qualifiers
REGION                 1..78
                       note = Synthetic coiled-coil domain which pairs DHD13b
source                 1..78
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 72
MGTKEDILER QRKIIERAQE IHRRQQEILE ELERIIRKPG SSEEAMKRML KLLEESLRLL  60
KELLELSEES AQLLYEQR                                                 78

SEQ ID NO: 73          moltype = AA  length = 83
FEATURE                Location/Qualifiers
REGION                 1..83
                       note = Synthetic coiled-coil domain which pairs DHD13a
source                 1..83
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 73
GTEKRLLEEA ERAHREQKEI IKKAQELHRR LEEIVRQSGS SEEAKKEAKK ILEEIRELSK  60
RSLELLREIL YLSQEQKGSL VPR                                           83

SEQ ID NO: 74          moltype = DNA  length = 16
FEATURE                Location/Qualifiers
misc_feature           1..16
                       note = engineered DNA sequence promoting
                        ribosomal(translational) read-through after a STOP codon
source                 1..16
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 74
ctaggcgctc gaagat                                                   16

SEQ ID NO: 75          moltype = RNA  length = 15
FEATURE                Location/Qualifiers
misc_feature           1..15
                       note = engineered RNA motif binding to L7Ae
source                 1..15
                       mol_type = other RNA
                       organism = synthetic construct
SEQUENCE: 75
cctgattggt gaggg                                                    15

SEQ ID NO: 76          moltype = DNA  length = 24
FEATURE                Location/Qualifiers
misc_feature           1..24
                       note = engineered DNA sequence promoting
                        ribosomal(translational) read-through after a STOP codon
source                 1..24
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 76
caattagctc atccagacat tccg                                          24

SEQ ID NO: 77          moltype = AA  length = 861
FEATURE                Location/Qualifiers
source                 1..861
                       mol_type = protein
                       organism = Rattus norvegicus
SEQUENCE: 77
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
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VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEMSE DTGPDGTLLP KARDQAVFPQ NGLVVSSVDV QSVEPVDQRT RDALQRSVQL  660
AIEITTNSQE AAAKHEAQRL EQEARGRLER QKILDQSEAE KARKELLELE AMSMAVESTG  720
NAKAEAESRA EAARIEGEGS VLQAKLKAQA LAIETEAELE RVKKVREMEL IYARAQLELE  780
VSKAQQLANV EAKKFKEMTE ALGPGTIRDL AVAGPEMQVK LLQSLGLKST LITDGSSPIN  840
LFSTAFGLLG LGSDGQPPAQ K                                            861

SEQ ID NO: 78          moltype = AA  length = 978
FEATURE                Location/Qualifiers
REGION                 1..978
                       note = Vault forming protein from Rattus norvegicus with
                        SNAP25-derived palmitoylation signal (AA 85-120) inserted
                        in helix-loop-helix region
source                 1..978
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 78
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEGSP EDELAANEEE LQQNEQKLAQ IKQKLQAIKY GGGGSGGGGS GGGGCGLCVC  660
PCNKLKSSDA YKKAWGNNQD GVVASQPARV GGGGSGGGGS GGGGSPEDEI QQLEEEIAQL  720
EQKNAALKEK NQALKYGKAR DQAVFPQNGL VVSSVDVQSV EPVDQRTRDA LQRSVQLAIE  780
ITTNSQEAAA KHEAQRLEQE ARGRLERQKI LDQSEAEKAR KELLELEAMS MAVESTGNAK  840
AEAESRAEAA RIEGEGSVLQ AKLKAQALAI ETEAELERVK KVREMELIYA RAQLELEVSK  900
AQQLANVEAK KFKEMTEALG PGTIRDLAVA GPEMQVKLLQ SLGLKSTLIT DGSSPINLFS  960
TAFGLLGLGS DGQPPAQK                                                978

SEQ ID NO: 79          moltype = AA  length = 996
FEATURE                Location/Qualifiers
REGION                 1..996
                       note = Vault forming protein from Rattus norvegicus with
                        aniparallel coiled-coil domain inserted into
                        helix-loop-helix region
source                 1..996
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 79
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEGSP EDELAANEEE LQQNEQKLAQ IKQKLQAIKY GGGGSGGGGS GGGGSGGGGK  660
QLEKELKQLE KELQAIEKQL AQLQWKAQAR KKKLAQLKKK LQAGGGGSGG GGSGGGGSGG  720
GGSPEDEIQQ LEEEIAQLEQ KNAALKEKNQ ALKYGKARDQ AVFPQNGLVV SSVDVQSVEP  780
VDQRTRDALQ RSVQLAIEIT TNSQEAAAKH EAQRLEQEAR GRLERQKILD QSEAEKARKE  840
LLELEAMSMA VESTGNAKAE AESRAEAARI EGEGSVLQAK LKAQALAIET EAELERVKKV  900
REMELIYARA QLELEVSKAQ QLANVEAKKF KEMTEALGPG TIRDLAVAGP EMQVKLLQSL  960
GLKSTLITDG SSPINLFSTA FGLLGLGSDG QPPAQK                            996

SEQ ID NO: 80          moltype = AA  length = 978
FEATURE                Location/Qualifiers
REGION                 1..978
                       note = Vault forming protein from Rattus norvegicus with a
                        shortened aniparallel coiled-coil domain inserted into
                        helix-loop-helix region
source                 1..978
                       mol_type = protein
                       organism = synthetic construct
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SEQUENCE: 80
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEGSP EDELAANEEE LQQNEQKLAQ IKQKLQAIKY GGGGSGGGGS GGGGKELKQL  660
EKELQAIEKQ LAQLQWKAQA RKKKLAQLKK GGGGSGGGGS GGGGSPEDEI QQLEEEIAQL  720
EQKNAALKEK NQALKYGKAR DQAVFPQNGL VVSSVDVQSV EPVDQRTRDA LQRSVQLAIE  780
ITTNSQEAAA KHEAQRLEQE ARGRLERQKI LDQSEAEKAR KELLELEAMS MAVESTGNAK  840
AEAESRAEAA RIEGEGSVLQ AKLKAQALAI ETEAELERVK KVREMELIYA RAQLELEVSK  900
AQQLANVEAK KFKEMTEALG PGTIRDLAVA GPEMQVKLLQ SLGLKSTLIT DGSSPINLFS  960
TAFGLLGLGS DGQPPAQK                                                978

SEQ ID NO: 81          moltype = AA  length = 1255
FEATURE                Location/Qualifiers
REGION                 1..1255
                       note = TEV protease inducible Vault based on caged Gp41-1
                        split inteins, Version 1
source                 1..1255
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 81
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEGSP EDELAANEEE LQQNEQKLAQ IKQKLQAIKY GGGGSGGGGS GGGGCLDLKT  660
QVQTPQGMKE ISNIQVGDLV LSNTGYNEVL NVFPKSKKKS YKITLEDGKE IICSEEHLFP  720
TQTGEMNISG GLKEGMCLYV KEGSGGENLY FQSAMGSHGA AAGSGGMMLK KILKIEELDE  780
RELIDIEVSG NHLFYANDGS GATNFSLLKQ AGDVEENPGP GSSSKKKSYK ITLEDGKEII  840
CSEEHLFPTQ TGEMNISGGL KEGMCLYVKE GSGGENLYFQ SAMGSHGAAA GSGGMMLKKI  900
LKIEELDERE LIDIEVSGNH LFYANDILTH NCGLCVCPCN KLKSSDAYKK AWGNNQDGVV  960
ASQPARVGGG GSGGGGSGGG GSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGKARDQA  1020
VFPQNGLVVS SVDVQSVEPV DQRTRDALQR SVQLAIEITT NSQEAAAKHE AQRLEQEARG  1080
RLERQKILDQ SEAEKARKEL LELEAMSMAV ESTGNAKAEA ESRAEAARIE GEGSVLQAKL  1140
KAQALAIETE AELERVKKVR EMELIYARAQ LELEVSKAQQ LANVEAKKFK EMTEALGPGT  1200
IRDLAVAGPE MQVKLLQSLG LKSTLITDGS SPINLFSTAF GLLGLGSDGQ PPAQK       1255

SEQ ID NO: 82          moltype = AA  length = 1255
FEATURE                Location/Qualifiers
REGION                 1..1255
                       note = TEV protease inducible Vault based on caged Gp41-1
                        split inteins, Version 2
source                 1..1255
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 82
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG HDPLADRGQK GTAKPLQPSA PRNKTRVVSY RVPHNAAVQV YDYRAKRARV  480
VFGPELVTLD PEEQFTVLSL SAGRPKRPHA RRALCLLLGP DFFTDVITIE TADHARLQLQ  540
LAYNWHFELK NRNDPAEAAK LFSVPDFVGD ACKAIASRVR GAVASVTFDD FHKNSARIIR  600
MAVFGFEGSP EDELAANEEE LQQNEQKLAQ IKQKLQAIKY GGGGSGGGGS GGGGCGLCVC  660
PCNKLKCLDL KTQVQTPQGM KEISNIQVGD LVLSNTGYNE VLNVFPKSKK KSYKITLEDG  720
KEIICSEEHL FPTQTGEMNI SGGLKEGMCL YVKEGSGGEN LYFQSAMGSH GAAAGSGGMM  780
LKKILKIEEL DERELIDIEV SGNHLFYAND GSGATNFSLL KQAGDVEENP GPGSSSKKKS  840
YKITLEDGKE IICSEEHLFP TQTGEMNISG GLKEGMCLYV KEGSGGENLY FQSAMGSHGA  900
AAGSGGMMLK KILKIEELDE RELIDIEVSG NHLFYANDIL THNSSDAYKK AWGNNQDGVV  960
ASQPARVGGG GSGGGGSGGG GSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGKARDQA  1020
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VFPQNGLVVS SVDVQSVEPV DQRTRDALQR SVQLAIEITT NSQEAAAKHE AQRLEQEARG  1080
RLERQKILDQ SEAEKARKEL LELEAMSMAV ESTGNAKAEA ESRAEAARIE GEGSVLQAKL  1140
KAQALAIETE AELERVKKVR EMELIYARAQ LELEVSKAQQ LANVEAKKFK EMTEALGPGT  1200
IRDLAVAGPE MQVKLLQSLG LKSTLITDGS SPINLFSTAF GLLGLGSDGQ PPAQK       1255

SEQ ID NO: 83          moltype = AA  length = 241
FEATURE                Location/Qualifiers
REGION                 1..241
                       note = MmMT3 fused to endogenous vault cargo protein mINT
source                 1..241
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 83
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGGSGGG DDEGRQSPVS WTSLFALQTE DGFWKLTPEL GLILKLNVNA  120
LLNSLEEKGI RSLGTKGRER LLDLIATLLV LQFLYTKLEQ EGMAAKSLIK MDDVLISRNI  180
PWAFENIKKA REWARRTEGQ YPSICQRLEL GKDWESATKQ LLGIQHQGNT SLHRILHYSQ  240
G                                                                  241

SEQ ID NO: 84          moltype = AA  length = 996
FEATURE                Location/Qualifiers
REGION                 1..996
                       note = MmMT3 inserted into rat Vault Helix-Loop-Helix motif
source                 1..996
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 84
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG GGGSPEDKLQ AIKYELAQNE EELAQIEEKL AANKEGGSGG GGSGGDPETC  480
PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC  540
CQGGSGGGGS GGPEDENAAL EEKIAQLKQK NAALKEEIQA LEYSAPRNKT RVVSYRVPHN  600
AAVQVYDYRA KRARVVFGPE LVTLDPEEQF TVLSLSAGRP KRPHARRALC LLLGPDFFTD  660
VITIETADHA RLQLQLAYNW HFELKNRNDP AEAAKLFSVP DFVGDACKAI ASRVRGAVAS  720
VTFDDFHKNS ARIIRMAVFG FEMSEDTGPD GTLLPKARDQ AVFPQNGLVV SSVDVQSVEP  780
VDQRTRDALQ RSVQLAIEIT TNSQEAAAKH EAQRLEQEAR GRLERQKILD QSEAEKARKE  840
LLELEAMSMA VESTGNAKAE AESRAEAARI EGEGSVLQAK LKAQALAIET EAELERVKKV  900
REMELIYARA QLELEVSKAQ QLANVEAKKF KEMTEALGPG TIRDLAVAGP EMQVKLLQSL  960
GLKSTLITDG SSPINLFSTA FGLLGLGSDG QPPAQK                            996

SEQ ID NO: 85          moltype = AA  length = 1125
FEATURE                Location/Qualifiers
REGION                 1..1125
                       note = Rat Vault with N-terminal anti-parallel coiled-coil
                        domain stabilizing the holo-vault configuration and MT3
                        and His6-tag in the HLH domain
source                 1..1125
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 85
MADIEQELER LKASIRRLEQ EVNQERARMA ALQTLLAKGG SGGATEEAII RIPPYHYIHV  60
LDQNSNVSRV EVGPKTYIRQ DNERVLFAPV RMVTVPPRHY CIVANPVSRD TQSSVLFDIT  120
GQVRLRHADQ EIRLAQDPFP LYPGEVLEKD ITPLQVVLPN TALHLKALLD FEDKNGDKVM  180
AGDEWLFEGP GTYIPQKEVE VVEIIQATVI KQNQALRLRA RKECFDREGK GRVTGEEWLV  240
RSVGAYLPAV FEEVLDLVDA VILTEKTALH LRALQNFRDL RGVLHRTGEE WLVTVQDTEA  300
HVPDVYEEVL GVVPITTLGP RHYCVILDPM GPDGKNQLGQ KRVVKGEKSF FLQPGERLER  360
GIQDVYVLSE QQGLLLKALQ PLEEGESEEK VSHQAGDCWL IRGPLEYVPS AKVEVVEERQ  420
AIPLDQNEGI YVQDVKTGKV RAVIGSTYML TQDEVLWEKE LPSGVEELLN LGGGGSPEDK  480
LQAIKYELAQ NEEELAQIEE KLAANKEGGS GGGGSGGDPE TCPCPTGGSC TCSDKCKCKG  540
CKCTNCKKSC CSCCPAGCEK CAKDCVCKGE EGAKAEAEKC SCCQGGSGGG GSGGPEDENA  600
ALEEKIAQLK QKNAALKEEI QALEYSAPRN KTRVVSYRVP HNAAVQVYDY RAKRARVVFG  660
PELVTLDPEE QFTVLSLSAG RPKRPHARRA LCLLLGPDFF TDVITIETAD HARLQLQLAY  720
NWHFELKNRN DPAEAAKLFS VPDFVGDACK AIASRVRGAV ASVTFDDFHK NSARIIRMAV  780
FGFEGSPEDE LAANEEELQQ NEQKLAQIKQ KLQAIKYGGG GSGGGGSGGG GHHHHHHGGG  840
GSGGGGSGGG GSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGKARDQA VFPQNGLVVS  900
SVDVQSVEPV DQRTRDALQR SVQLAIEITT NSQEAAAKHE AQRLEQEARG RLERQKILDQ  960
SEAEKARKEL LELEAMSMAV ESTGNAKAEA ESRAEAARIE GEGSVLQAKL KAQALAIETE  1020
AELERVKKVR EMELIYARAQ LELEVSKAQQ LANVEAKKFK EMTEALGPGT IRDLAVAGPE  1080
MQVKLLQSLG LKSTLITDGS SPINLFSTAF GLLGLGSDGQ PPAQK                  1125

SEQ ID NO: 86          moltype = AA  length = 187
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FEATURE                 Location/Qualifiers
REGION                  1..187
                        note = Synthetic Hyperstable de novo TIM barrel varian
source                  1..187
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 86
MDILIVNATD VDEMLKQVEI LRRLGAKQIA VVSDDWRILQ EALKKGGDIL IVNATDVDEM  60
LKQVEILRRL GAKQIAVVSD DWRILQEALK KGGDILIVNA TDVDEMLKQV EILRRLGAKQ  120
IAVVSDDWRI LQEALKKGGD ILIVNATDVD EMLKQVEILR RLGAKQIAVV SDDWRILQEA  180
LKKGGLE                                                            187

SEQ ID NO: 87           moltype = AA  length = 456
FEATURE                 Location/Qualifiers
source                  1..456
                        mol_type = protein
                        organism = Sus scrofa
SEQUENCE: 87
MNLDIHCEQL SDARWTELLP LLQQYEVVRL DDCGLTEEHC KDIGSALRAN PSLTELCLRT  60
NELGDAGVHL VLQGLQSPTC KIQKLSLQNC SLTEAGCGVL PSTLRSLPTL RELHLSDNPL  120
GDAGLRLLCE GLLDPQCHLE KLQLEYCRLT AASCEPLASV LRATRALKEL TVSNNDIGEA  180
GARVLGQGLA DSACQLETLR LENCGLTPAN CKDLCGIVAS QASLRELDLG SNGLGDAGIA  240
ELCPGLLSPA SRLKTLWLWE CDITASGCRD LCRVLQAKET LKELSLAGNK LGDEGARLLC  300
ESLLQPGCQL ESLWVKSCSL TAACCQHVSL MLTQNKHLLE LQLSSNKLGD SGIQELCQAL  360
SQPGTTLRVL CLGDCEVTNS GCSSLASLLL ANRSLRELDL SNNCVGDPGV LQLLGSLEQP  420
GCALEQLVLY DTYWTEEVED RLQALEGSKP GLRVIS                            456

SEQ ID NO: 88           moltype = AA  length = 242
FEATURE                 Location/Qualifiers
source                  1..242
                        mol_type = protein
                        organism = Pseudomonas aeruginosa
SEQUENCE: 88
TYCVAMHLAD GLVFASDSRT NAGIDHIATF RKLFTFGTPG ERLLVVQTAG NLATSQSVIN  60
LLQQRIRRDG ASLLNVPSVY DATALVAETT REVMARDSGN LAGNTDLSCS FMVGGQIAGG  120
PPALYSIYPQ GNFIQATPDT PFLQLGESKY GKPILDRNLT FDTPLEQALR CALVSFDSTI  180
RSNLSVGMPL DLLVYHRDSL ILPEGYRVTE DDAYFSAIRR QWSAGLHDML ERLPSPPSAY  240
NI                                                                 242

SEQ ID NO: 89           moltype = AA  length = 249
FEATURE                 Location/Qualifiers
source                  1..249
                        mol_type = protein
                        organism = Bacteriophage S16
SEQUENCE: 89
MAVQGPWVGS SYVAETGQNW ASLAANELRV TERPFWISSF IGRSKEEIWE WTGENHSFNK  60
DWLIGELRNR GGTPVVINIR AHQVSYTPGA PLFEFPGDLP NAYITLNIYA DIYGRGGTGG  120
VAYLGGNPGG DCIHNWIGNR LRINNQGWIC GGGGGGGGFR VGHTEAGGGG GRPLGAGGVS  180
SLNLNGDNAT LGAPGRGYQL GNDYAGNGGD VGNPGSASSA EMGGGAAGRA VVGTSPQWIN  240
VGNIAGSWL                                                          249

SEQ ID NO: 90           moltype = AA  length = 204
FEATURE                 Location/Qualifiers
source                  1..204
                        mol_type = protein
                        organism = Bacteriophage S16
SEQUENCE: 90
MGSSHHHHHH SQDPENLYFQ GALGSASIAI GDNDTGLRWG GDGIVQIVAN NAIVGGWNST  60
DIFTEAGKHI TSNGNLNQWG GGAIYCRDLN VSSDRRIKKD IKAFENPVDI LSTIGGYTYL  120
IEKGFNEDGS QAYEESAGLI AQEVEAVLPR LVKISNDGTK DVKRLNYNGI TALNTAAINV  180
HTKEINELKK QLKELKDIVK FLTK                                         204

SEQ ID NO: 91           moltype = AA  length = 184
FEATURE                 Location/Qualifiers
source                  1..184
                        mol_type = protein
                        organism = Human adenovirus 26
SEQUENCE: 91
RRTLWTTPDT SPNCKMSTEK DSKLTLTLTK CGSQVLGNVS LLAVTGEYHQ MTATTKKDVK  60
ISLLFDENGI LLPSSSLSKD YWNYRSDDSI VSQKYNNAVP FMPNLTAYPK PSAQNAKNYS  120
RTKIISNVYL GALTYQPVII TIAFNQETEN GCAYSITFTF TWQKDYSAQQ FDVTSFTFSY  180
LTQE                                                               184

SEQ ID NO: 92           moltype = AA  length = 393
FEATURE                 Location/Qualifiers
REGION                  1..393
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                        note = Engineered fluorescent protein based on sfGFP, with
                         ALFA-tags (SRLEEELRRRLT) inserted into loop region and at
                         the termini
source                  1..393
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 92
MGSRLEEELR RRLTQQQSRL EEELRRRLTQ QQSRLEEELR RRLTGQVSKG EELFTGVVPI  60
LVELDGDVNG HKFSVRGEGE GDATNGKLTL KFICTTGKLP VPWPTLVTTL TYGVQCFSRY  120
PDHMKRHDFF KSAMPEGYVQ ERTISFKDDG TYKTRAEVKF EGDTLVNRIE LKGIDFKEDG  180
NILGHKLEYN FNSHNVYITA DKQKNGIKAN FKIRHNVEGG SRLEEELRRR LTQQQSRLEE  240
ELRRRLTGGQ QGGSRLEEEL RRRLTQQQSR LEEELRRRLT GGDGSVQLAD HYQQNTPIGD  300
GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGQ GSRLEEELRR  360
RLTQQQSRLE EELRRRLTQQ QSRLEEELRR RLT                               393

SEQ ID NO: 93           moltype = AA  length = 350
FEATURE                 Location/Qualifiers
REGION                  1..350
                        note = Engineered fluorescent protein based on
                         mGreenLantern, with HA-tags (YPYDVPDYA) inserted into loop
                         region and at the termini
source                  1..350
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 93
MGYPYDVPDY AGYPYDVPDY AGYPYDVPDY AGGVSKGEEL FTGVVPILVE LDGDVNGHKF  60
SVRGEGEGDA TNGKLTLKFI CTTGKLPVPW PTLVTTLGYG VACFARYPDH MKQHDFFKSA  120
MPEGYVQERT ISFKDDGTYK TRAEVKFEGD TLVNRIVLKG IDFKEDGNIL GHKLEYNFNS  180
HKVYITADKQ KNGIKANFKT RHNVEGGYPY DVPDYAGGYP YDVPDYAGGG GYPYDVPDYA  240
GGYPYDVPDY AGGDGGVQLA DHYQQNTPIG DGPVLLPDNH YLSHQSKLSK DPNEKRDHMV  300
LKERVTAAGI THDMDELYKG GYPYDVPDYA GYPYDVPDYA GYPYDVPDYA             350

SEQ ID NO: 94           moltype = AA  length = 369
FEATURE                 Location/Qualifiers
REGION                  1..369
                        note = Engineered fluorescent protein based on
                         mGreenLantern, with Moon-Tags(KNEQELLELDKWASL) inserted
                         into loop region and at the termini
source                  1..369
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 94
MVSKGEELFT GVVPILVELD GDVNGHKFSV RGEGEGDATN GKLTLKFICT TGKLPVPWPT  60
LVTTLGYGVA CFARYPDHMK QHDFFKSAMP EGYVQERTIS FKDDGTYKTR AEVKFEGDTL  120
VNRIVLKGID FKEDGNILGH KLEYNFNSHK VYITADKQKN GIKANFKTRH NVEGGKNEQE  180
LLELDKWASL QQQKNEQELL ELDKWASLGG QQGGKNEQEL LELDKWASLQ QQKNEQELLE  240
LDKWASLGGD GGVQLADHYQ QNTPIGDGPV LLPDNHYLSH QSKLSKDPNE KRDHMVLKER  300
VTAAGITHDM DELYKGQGKN EQELLELDKW ASLQQQKNEQ ELLELDKWAS LQQQKNEQEL  360
LELDKWASL                                                          369

SEQ ID NO: 95           moltype = AA  length = 422
FEATURE                 Location/Qualifiers
REGION                  1..422
                        note = Engineered fluorescent protein based on
                         mScarlet-I,with PepTags (AVERYLKDQQLLGIW) inserted into
                         loop region and at the termini
source                  1..422
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 95
MGTGSAVERY LKDQQLLGIW QQQAVERYLK DQQLLGIWQQ QAVERYLKDQ QLLGIWGQVS  60
KGEAVIKEFM RFKVHMEGSM NGHEFEIEGE GEGRPYEGTQ TAKLKVTKGG PLPFSWDILS  120
PQFMYGSRAF IKHPADIPDY YKQSFPEGFK WERVMNFEDG GAVTVTQDTS LEDGTLIYKV  180
KLRGTNFPPD GPVMQKKTMG WEASTERLYP EDGVLKGDIK MALRLKGGAV ERYLKDQQLL  240
GIWQQQAVER YLKDQQLLGI WGGQQGGAVE RYLKDQQLLG IWQQQAVERY LKDQQLLGIW  300
GGDGGRYLAD FKTTYKAKKP VQMPGAYNVD RKLDITSHNE DYTVVEQYER SEGRHSTGGM  360
DELYKGQGAV ERYLKDQQLL GIWQQQAVER YLKDQQLLGI WQQQAVERYL KDQQLLGIWG  420
PG                                                                 422

SEQ ID NO: 96           moltype = AA  length = 457
FEATURE                 Location/Qualifiers
REGION                  1..457
                        note = Engineered fluorescent protein based on mEosEM, with
                         MoonTags (EELLSKNYHLENEVARLKK) inserted inserted into loop
                         region and at the termini
source                  1..457
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                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 96
MGTGSEELLS KNYHLENEVA RLKKQQQEEL LSKNYHLENE VARLKKQQQE ELLSKNYHLE  60
NEVARLKKGQ VSAIKPDMRI KLRMEGNVNG HHFVIDGEGT GKPYEGKQTM DLEVKEGGPL  120
PFAFDILTTA FHYGNRVFVK YPDNIQDYFK QSFPKGYSWE RSMTFEDGGI CNARNDITME  180
GDTFYNKVRF YGTNFPANGP VMQKKTLKWE PSTEKMYVRD GVLTGDIEMA LLLEGGEELL  240
SKNYHLENEV ARLKKQQQEE LLSKNYHLEN EVARLKKGGQ QGGEELLSKN YHLENEVARL  300
KKQQQEELLS KNYHLENEVA RLKKGGGGAH YRCDFRTTYK AKEKGVKLPG AHFVDHAIEI  360
LSHDKDYNKV KLYEHAVAHS GLPDNARRGQ GEELLSKNYH LENEVARLKK QQQEELLSKN  420
YHLENEVARL KKQQQEELLS KNYHLENEVA RLKKGPG                           457

SEQ ID NO: 97           moltype = AA  length = 339
FEATURE                 Location/Qualifiers
REGION                  1..339
                        note = Engineered fluorescent protein based on mScarlet-I,
                         with triple FLAG-tags (DYKDHDGDYKDHDIDYKDDDDK) inserted
                         into loop region and at the termini
source                  1..339
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 97
MGTGSDYKDH DGDYKDHDID YKDDDDKGQV SKGEAVIKEF MRFKVHMEGS MNGHEFEIEG  60
EGEGRPYEGT QTAKLKVTKG GPLPFSWDIL SPQFMYGSRA FIKHPADIPD YYKQSFPEGF  120
KWERVMNFED GGAVTVTQDT SLEDGTLIYK VKLRGTNFPP DGPVMQKKTM GWEASTERLY  180
PEDGVLKGDI KMALRLKGGD YKDHDGDYKD HDIDYKDDDD KGGGDYKDHD GDYKDHDIDY  240
KDDDDKGGDG GRYLADFKTT YKAKKPVQMP GAYNVDRKLD ITSHNEDYTV VEQYERSEGR  300
HSTGGMDELY KGQGDYKDHD GDYKDHDIDY KDDDDKGPG                         339

SEQ ID NO: 98           moltype = AA  length = 1511
FEATURE                 Location/Qualifiers
REGION                  1..1511
                        note = Engineered fluorescent protein based on emFPv4 with
                         24x SunTags on both termini
source                  1..1511
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 98
MEELLSKNYH LENEVARLKK GSGSGEELLS KNYHLENEVA RLKKGSGSGE ELLSKNYHLE  60
NEVARLKKGS GSGEELLSKN YHLENEVARL KKGSGSGEEL LSKNYHLENE VARLKKGSGS  120
GEELLSKNYH LENEVARLKK GSGSGEELLS KNYHLENEVA RLKKGSGSGE ELLSKNYHLE  180
NEVARLKKGS GSGEELLSKN YHLENEVARL KKGSGSGEEL LSKNYHLENE VARLKKGSGS  240
GEELLSKNYH LENEVARLKK GSGSGEELLS KNYHLENEVA RLKKGSGSGE ELLSKNYHLE  300
NEVARLKKGS GSGEELLSKN YHLENEVARL KKGSGSGEEL LSKNYHLENE VARLKKGSGS  360
GEELLSKNYH LENEVARLKK GSGSGEELLS KNYHLENEVA RLKKGSGSGE ELLSKNYHLE  420
NEVARLKKGS GSGEELLSKN YHLENEVARL KKGSGSGEEL LSKNYHLENE VARLKKGSGS  480
GEELLSKNYH LENEVARLKK GSGSGEELLS KNYHLENEVA RLKKGSGSGE ELLSKDYHLE  540
NEVARLKKGS GSGEELLSKN YHLENEVARL KKVSKGEELF TGVVPILVEL DGDVNGHKFS  600
VRGEGEGDAT NGKLTLKFIC TTGKLPVPWP TLVTTLGYGV ACFARYPDHM KQHDFFKSAM  660
PEGYVQERTI SFKDDGTYKT RAEVKFEGDT LVNRIVLKGI DFKEDGNILG HKLEYNFNSH  720
KVYITADKQK NGIKANFKTR HNVEGGKNEQ ELLELDKWAS LQQQKNEQEL LELDKWASLG  780
GQQGGKNEQE LLELDKWASL QQQKNEQELL ELDKWASLGG DGGVQLADHY QQNTPIGDGP  840
VLLPDNHYLS HQSKLSKDPN EKRDHMVLKE RVTAAGITHD MDELYKGQGK NEQELLELDK  900
WASLQQQKNE QELLELDKWA SLQQQKNEQE LLELDKWASL EELLSKNYHL ENEVARLKKG  960
SGSGEELLSK NYHLENEVAR LKKGSGSGEE LLSKNYHLEN EVARLKKGSG SGEELLSKNY  1020
HLENEVARLK KGSGSGEELL SKNYHLENEV ARLKKGSGSG EELLSKNYHL ENEVARLKKG  1080
SGSGEELLSK NYHLENEVAR LKKGSGSGEE LLSKNYHLEN EVARLKKGSG SGEELLSKNY  1140
HLENEVARLK KGSGSGEELL SKNYHLENEV ARLKKGSGSG EELLSKNYHL ENEVARLKKG  1200
SGSGEELLSK NYHLENEVAR LKKGSGSGEE LLSKNYHLEN EVARLKKGSG SGEELLSKNY  1260
HLENEVARLK KGSGSGEELL SKNYHLENEV ARLKKGSGSG EELLSKNYHL ENEVARLKKG  1320
SGSGEELLSK NYHLENEVAR LKKGSGSGEE LLSKNYHLEN EVARLKKGSG SGEELLSKNY  1380
HLENEVARLK KGSGSGEELL SKNYHLENEV ARLKKGSGSG EELLSKNYHL ENEVARLKKG  1440
SGSGEELLSK NYHLENEVAR LKKGSGSGEE LLSKDYHLEN EVARLKKGSG SGEELLSKNY  1500
HLENEVARLK K                                                       1511

SEQ ID NO: 99           moltype = AA  length = 1167
FEATURE                 Location/Qualifiers
REGION                  1..1167
                        note = Engineered fluorescent protein based on emFPv4 with
                         10x P3 CCC tags on each terminus
source                  1..1167
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 99
MSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGLKSGPG SGSPEDEIQQ LEEEIAQLEQ  60
KNAALKEKNQ ALKYGTGSGP GSGSPEDEIQ QLEEEIAQLE QKNAALKEKN QALKYGASSG  120
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PGSGSPEDEI QQLEEEIAQL EQKNAALKEK NQALKYGLES GPGSGSPEDE IQQLEEEIAQ  180
LEQKNAALKE KNQALKYGSG PGSGSPEDEI QQLEEEIAQL EQKNAALKEK NQALKYLESG  240
PGSGSPEDEI QQLEEEIAQL EQKNAALKEK NQALKYGASS GPGSGSPEDE IQQLEEEIAQ  300
LEQKNAALKE KNQALKYGTG SGPGSGSPED EIQQLEEEIA QLEQKNAALK EKNQALKYGL  360
KSGPGSGSPE DEIQQLEEEI AQLEQKNAAL KEKNQALKYG VSKGEELFTG VVPILVELDG  420
DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL VTTLGYGVAC FARYPDHMKQ  480
HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV NRIVLKGIDF KEDGNILGHK  540
LEYNFNSHKV YITADKQKNG IKANFKTRHN VEGGKNEQEL LELDKWASLQ QQKNEQELLE  600
LDKWASLGGQ QGGKNEQELL ELDKWASLQQ QKNEQELLEL DKWASLGGDG GVQLADHYQQ  660
NTPIGDGPVL LPDNHYLSHQ SKLSKDPNEK RDHMVLKERV TAAGITHDMD ELYKGQGKNE  720
QELLELDKWA SLQQQKNEQE LLELDKWASL QQQKNEQELL ELDKWASLSP EDEIQQLEEE  780
IAQLEQKNAA LKEKNQALKY GLKSGPGSGS PEDEIQQLEE EIAQLEQKNA ALKEKNQALK  840
YGTGSGPGSG SPEDEIQQLE EEIAQLEQKN AALKEKNQAL KYGASSGPGS GSPEDEIQQL  900
EEEIAQLEQK NAALKEKNQA LKYGLESGPG SGSPEDEIQQ LEEEIAQLEQ KNAALKEKNQ  960
ALKYGSGPGS GSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYLESGPGS GSPEDEIQQL  1020
EEEIAQLEQK NAALKEKNQA LKYGASSGPG SGSPEDEIQQ LEEEIAQLEQ KNAALKEKNQ  1080
ALKYGTGSGP GSGSPEDEIQ QLEEEIAQLE QKNAALKEKN QALKYGLKSG PGSGSPEDEI  1140
QQLEEEIAQL EQKNAALKEK NQALKYG                                      1167

SEQ ID NO: 100          moltype = AA  length = 130
FEATURE                 Location/Qualifiers
source                  1..130
                        mol_type = protein
                        organism = Bacteriophage MS2
SEQUENCE: 100
MASNFTQFVL VDNGGTGDVT VAPSNFANGV AEWISSNSRS QAYKVTCSVR QSSAQNRKYT  60
IKVEVPKVAT QTVGGVELPV AAWRSYLNME LTIPIFATNS DCELIVKAMQ GLLKDGNPIP  120
SAIAANSGIY                                                         130

SEQ ID NO: 101          moltype = AA  length = 393
FEATURE                 Location/Qualifiers
source                  1..393
                        mol_type = protein
                        organism = Bacteriophage MS2
SEQUENCE: 101
MRAFSTLDRE NETFVPSVRV YADGETEDNS FSLKYRSNWT PGRFNSTGAK TKQWHYPSPY  60
SRGALSVTSI DQGAYKRSGS SWGRPYEEKA GFGFSLDARS CYSLFPVSQN LTYIEVPQNV  120
ANRASTEVLQ KVTQGNFNLG VALAEARSTA SQLATQTIAL VKAYTAARRG NWRQALRYLA  180
LNEDRKFRSK HVAGRWLELQ FGWLPLMSDI QGAYEMLTKV HLQEFLPMRA VRQVGTNIKL  240
DGRLSYPAAN FQTTCNISRR IVIWFYINDA RLAWLSSLGI LNPLGIVWEK VPFSFVVDWL  300
LPVGNMLEGL TAPVGCSYMS GTVTDVITGE SIISVDAPYG WTVERQGTAK AQISAMHRGV  360
QSVWPTTGAY VKSPFSMVHT LDALALIRQR LSR                               393

SEQ ID NO: 102          moltype = AA  length = 133
FEATURE                 Location/Qualifiers
source                  1..133
                        mol_type = protein
                        organism = Bacteriophage Q-beta
SEQUENCE: 102
MAKLETVTLG NIGKDGKQTL VLNPRGVNPT NGVASLSQAG AVPALEKRVT VSVSQPSRNR  60
KNYKVQVKIQ NPTACTANGS CDPSVTRQAY ADVTFSFTQY STDEERAFVR TELAALLASP  120
LLIDAIDQLN PAY                                                     133

SEQ ID NO: 103          moltype = AA  length = 420
FEATURE                 Location/Qualifiers
source                  1..420
                        mol_type = protein
                        organism = Bacteriophage Q-beta
SEQUENCE: 103
MPKLPRGLRF GADNEILNDF QELWFPDLFI ESSDTHPWYT LKGRVLNAHL DDRLPNVGGR  60
QVRRTPHRVT VPIASSGLRP VTTVQYDPAA LSFLLNARVD WDFGNGDSAN LVINDFLFRT  120
FAPKEFDFSN SLVPRYTQAF SAFNAKYGTM IGEGLETIKY LGLLLRRLRE GYRAVKRGDL  180
RALRRVIQSY HNGKWKPATA GNLWLEFRYG LMPLFYDIRD VMLDWQNRHD KIQRLLRFSV  240
GHGEDYVVEF DNLYPAVAYF KLKGEITLER RHRHGISYAN REGYAVFDNG SLRPVSDWKE  300
LATAFINPHE VAWELTPYSF VVDWFLNVGD ILAQQGQLYH NIDIVDGFDR RDIRLKSFTI  360
KGERNGRPVN VSASLSAVDL FYSRLHTSNL PFATLDLDTT FSSFKHVLDS IFLLTQRVKR  420

SEQ ID NO: 104          moltype = AA  length = 294
FEATURE                 Location/Qualifiers
REGION                  1..294
                        note = Capsid forming monomer from the encapsulin system of
                         Q.thermotolerans tagged with C-termina FLAG epitope
source                  1..294
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 104
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MMNKSQLYPD SPLTDQDFNQ LDQTVIEAAR RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES  60
HEAKMDFQGS FDTEVESSRR VNYTIPMLYK DFVLYWRDLE QSKALDIPID FSVAANAARD  120
VAFLEDQMIF HGSKEFDIPG LMNVKGRLTH LIGNWYESGN AFQDIVEARN KLLEMNHNGP  180
YALVLSPELY SLLHRVHKDT NVLEIEHVRE LITAGVFQSP VLKGKSGVIV NTGRNNLDLA  240
ISEDFETAYL GEEGMNHPFR VYETVVLRIK RPAAICTLID PEEGSGDYKD DDDK        294

SEQ ID NO: 105         moltype = AA  length = 209
FEATURE                Location/Qualifiers
REGION                 1..209
                       note = Fusion of G51-E1-G52 domains of S.aureus protein
                        SasG (amino acids 419-629) and mCherry
source                 1..209
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 105
APKTITELEK KVEEIPFKKE RKFNPDLAPG TEKVTREGQK GEKTITTPTL KNPLTGVIIS  60
KGEPKEEITK DPINELTEYG PETIAPGHRD EFDPKLPTGE KEEVPGKPGI KNPETGDVVR  120
PPVDSVTKYG PVKGDSIVEK EEIPFEKERK FNPDLAPGTE KVTREGQKGE KTITTPTLKN  180
PLTGEIISKG ESKEEITKDP INELTEYGP                                    209

SEQ ID NO: 106         moltype = AA  length = 407
FEATURE                Location/Qualifiers
REGION                 1..407
                       note = Capsid forming monomer from the encapsulin system of
                        Q.thermotolerans tagged with a C-terminal anti-GFP
                        intrabody
source                 1..407
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 106
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGVQLVESG  300
GALVQPGGSL RLSCAASGFP VNRYSMRWYR QAPGKEREWV AGMSSAGDRS SYEDSVKGRF  360
TISRDDARNT VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG TQVTVSS                407

SEQ ID NO: 107         moltype = AA  length = 298
FEATURE                Location/Qualifiers
REGION                 1..298
                       note = Capsid forming monomer from the encapsulin system of
                        M.xanthus tagged with C-terminal FLAG epitope
source                 1..298
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 107
MPDFLGHAEN PLREEEWARL NETVIQVARR SLVGRRILDI YGPLGAGVQT VPYDEFQGVS  60
PGAVDIVGEQ ETAMVFTDAR KFKTIPIIYK DFLLHWRDIE AARTHNMPLD VSAAAGAAAL  120
CAQQEDELIF YGDARLGYEG LMTANGRLTV PLGDWTSPGG GFQAIVEATR KLNEQGHFGP  180
YAVVLSPRLY SQLHRIYEKT GVLEIETIRQ LASDGVYQSN RLRGESGVVV STGRENMDLA  240
VSMDMVAAYL GASRMNHPFR VLEALLLRIK HPDAICTLEG AGATERRGSG DYKDDDDK    298

SEQ ID NO: 108         moltype = AA  length = 283
FEATURE                Location/Qualifiers
REGION                 1..283
                       note = Capsid forming monomer from the encapsulin system of
                        T.maritima (amino acids 1-264) tagged with C-termina BC2
                        epitope
source                 1..283
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 108
MEFLKRSFAP LTEKQWQEID NRAREIFKTQ LYGRKFVDVE GPYGWEYAAH PLGEVEVLSD  60
ENEVVKWGLR KSLPLIELRA TFTLDLWELD NLERGKPNVD LSSLEETVRK VAEFEDEVIF  120
RGCEKSGVKG LLSFEERKIE CGSTPKDLLE AIVRALSIFS KDGIEGPYTL VINTDRWINF  180
LKEEAGHYPL EKRVEECLRG GKIITTPRIE DALVVSERGG DFKLILGQDL SIGYEDREKD  240
AVRLFITETF TFQVVNPEAL ILLKGGGSGP GPDRKAAVSH WQQ                    283

SEQ ID NO: 109         moltype = AA  length = 439
FEATURE                Location/Qualifiers
REGION                 1..439
                       note = Capsid forming monomer from the encapsulin system of
                        T.maritima (amino acids 1-264) N-terminally fused to a
                        synthetic coiled-coil domain 'P2' and C-terminally fused
                        to an anti-mCherry Intrabody (LaM-4)
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source                  1..439
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 109
MSPEDKIAQL KEKNAALKEK NQQLKEKIQA LKYGGGGGSG PGEFLKRSFA PLTEKQWQEI  60
DNRAREIFKT QLYGRKFVDV EGPYGWEYAA HPLGEVEVLS DENEVVKWGL RKSLPLIELR  120
ATFTLDLWEL DNLERGKPNV DLSSLEETVR KVAEFEDEVI FRGCEKSGVK GLLSFEERKI  180
ECGSTPKDLL EAIVRALSIF SKDGIEGPYT LVINTDRWIN FLKEEAGHYP LEKRVEECLR  240
GGKIITTPRI EDALVVSERG GDFKLILGQD LSIGYEDREK DAVRLFITET FTFQVVNPEA  300
LILLKGSGSG SETTGAQVQL VESGGSLVQP GGSLRLSCAA SGRFAESSSM GWFRQAPGKE  360
REFVAAISWS GGATNYADSA KGRFTLSRDN TKNTVYLQMN SLKPDDTAVY YCAANLGNYI  420
SSNQRLYGYW GQGTQVTVS                                               439

SEQ ID NO: 110          moltype = AA  length = 551
FEATURE                 Location/Qualifiers
REGION                  1..551
                        note = Fusion protein consisting of MT3, a de novo designed
                         fibril forming protein and GFP
source                  1..551
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 110
MDPNCSCATD GSCSCAGSCK CKQCKCTSCK KSCCSCCPVG CAKCSQGCIC KEASDKCSCC  60
AGSGGSGGSG GMGPEDELKR VEKLVKEAEA LLIVAKIKGS KRDLEKALRT AEEAAREAVK  120
VLVQALLEGD PEVALRAVEL VVRVAELLLR IAKESGSREA LLRALIVAEE AAKLAKMVLE  180
LAEKQGDPEV ALRAVELVVR VAELLLRIAK ESGSEEALER ALRVAEEAAR LAKRVLELAE  240
EQGDPLVAKM AVELVKRVAE LLERIARESG SEEAKERAER VREEARELQE RVKELREREG  300
SGSGSGSGSK GEELFTGVVP ILVELDGDVN GHKFSVRGEG EGDATNGKLT LKFICTTGKL  360
PVPWPTLVTT LTYGVQCFAR YPDHMKQHDF FKSAMPEGYV QERTISFKDD GTYKTRAEVK  420
FEGDTLVNRI ELKGIDFKED GNILGHKLEY NFNSHNVYIT ADKQKNGIKA NFKIRHNVED  480
GSVQLADHYQ QNTPIGDGPV LLPDNHYLST QSVLSKDPNE KRDHMVLLEF VTAAGITHGM  540
DELYKGSGSL E                                                       551

SEQ ID NO: 111          moltype = AA  length = 420
FEATURE                 Location/Qualifiers
REGION                  1..420
                        note = Fusion protein consisting of hexa-Histidine Tag, a
                         SpyCatcher domain, a de novo designed, single component
                         icosahedron and an MT3 domain
source                  1..420
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 111
MRGSHHHHHH ENLYFQGAVD TLSGLSSEQG QSGDMTIEED SATHIKFSKR DEDGKELAGA  60
TMELRDSSGK TISTWISDGQ VKDFYLYPGK YTFVETAAPD GYEVATAITF TVNEQGQVTV  120
NGKATKGDAH IGGSGGSGGE KAAKAEEAAR KMEELFKKHK IVAVLRANSV EEAKKKALAV  180
FLGGVHLIEI TFTVPDADTV IKELSFLKEM GAIIGAGTVT SVEQCRKAVE SGAEFIVSPH  240
LDEEISQFCK EKGVFYMPGV MTPTELVKAM KLGHTILKLF PGEVVGPQFV KAMKGPFPNV  300
KFVPTGGVNL DNVCEWFKAG VLAVGVGSAL VKGTPVEVAE KAKAFVEKIR GCTEGSGSGM  360
DPNCSCATDG SCSCAGSCKC KQCKCTSCKK SCCSCCPVGC AKCSQGCICK EASDKCSCCA  420

SEQ ID NO: 112          moltype = AA  length = 129
FEATURE                 Location/Qualifiers
REGION                  1..129
                        note = Fusion protein of E.coli CsgA where the secretion
                         peptide and N22 were deleted (amino acids 36-144) and
                         SpyTag peptide
source                  1..129
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 112
MSELNIYQYG GGNSALALQT DARNSDLTIT QHGGGNGADV GQGSDDSSID LTQRGFGNSA  60
TLDQWNGKNS EMTVKQFGGG NGAAVDQTAS NSSVNVTQVG FGNNATAHQY GSGGSGAHIV  120
MVDAYKPTK                                                          129

SEQ ID NO: 113          moltype = AA  length = 304
FEATURE                 Location/Qualifiers
REGION                  1..304
                        note = Fusion protein of capsid forming monomer of the
                         Encapsulin system of Q.thermotolerans and a synthetic
                         peptide interacting with motor proteins
source                  1..304
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 113
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
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EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGSAGTV FTTEDIYEWD  300
DSAI                                                               304

SEQ ID NO: 114          moltype = AA  length = 697
FEATURE                 Location/Qualifiers
REGION                  1..697
                        note = Fusion protein consisting of super-folder GFP, the
                         G51-E1-G52 domains of S.aureus protein SasG (amino acids
                         419-629) and mCherry
source                  1..697
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 114
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG  300
VIISKGEPKE EITKDPINEL TEYGPETIAP GHRDEFDPKL PTGEKEEVPG KPGIKNPETG  360
DVVRPPVDSV TKYGPVKGDS IVEKEEIPFE KERKFNPDLA PGTEKVTREG QKGEKTITTP  420
TLKNPLTGEI ISKGESKEEI TKDPINELTE YGPETGSGAT GSVSKGEEDN MAIIKEFMRF  480
KVHMEGSVNG HEFEIEGEGE GRPYEGTQTA KLKVTKGGPL PFAWDILSPQ FMYGSKAYVK  540
HPADIPDYLK LSFPEGFKWE RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL RGTNFPSDGP  600
VMQKKTMGWE ASSERMYPED GALKGEIKQR LKLKDGGHYD AEVKTTYKAK KPVQLPGAYN  660
VNIKLDITSH NEDYTIVEQY ERAEGRHSTG GMDELYK                           697

SEQ ID NO: 115          moltype = AA  length = 876
FEATURE                 Location/Qualifiers
REGION                  1..876
                        note = Fusion protein consisting of Gp41-1 C-intein,
                         superfolder GFP, SasG (comprising 4 G5 domains yielding
                         GEGEGEG), and engineered SpyCatcher003
source                  1..876
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 115
MMLKKILKIE ELDERELIDI EVSGNHLFYA NDILTHNSSS GTGSGGSKGE ELFTGVVPIL  60
VELDGDVNGH KFSVRGEGEG DATNGKLTLK FICTTGKLPV PWPTLVTTLT YGVQCFSRYP  120
DHMKRHDFFK SAMPEGYVQE RTISFKDDGT YKTRAEVKFE GDTLVNRIEL KGIDFKEDGN  180
ILGHKLEYNF NSHNVYITAD KQKNGIKANF KIRHNVEDGS VQLADHYQQN TPIGDGPVLL  240
PDNHYLSTQS VLSKDPNEKR DHMVLLEFVT AAGITHGMDE LYKGGTGGSA PKTITELEKK  300
VEEIPFKKER KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGVIISK GEPKEEITKD  360
PINELTEYGP ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP  420
VKGDSIVEKE EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE  480
SKEEITKDPI NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV  540
DSVTKYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  600
GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  660
GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE GQKGEKTITT  720
PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETGSGA TGSVTTLSGL SGEQGPSGDM  780
TTEEDSATHI KFSKRDEDGR ELAGATMELR DSSGKTISTW ISDGHVKDFY LYPGKYTFVE  840
TAAPDGYEVA TPIEFTVNED GQVTVDGEAT EGDAHT                            876

SEQ ID NO: 116          moltype = AA  length = 829
FEATURE                 Location/Qualifiers
REGION                  1..829
                        note = Fusion protein consisting of a SnoopTag,
                         mTurquoise2, SasG (comprising 4 G5 domains yielding
                         GEGEGEG) and the N-intein split fragment of Gp41-1
source                  1..829
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 116
MGKLGDIEFI KVNKSGGGSG VSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG  60
KLTLKFICTT GKLPVPWPTL VTTLSWGVQC FARYPDHMKQ HDFFKSAMPE GYVQERTIFF  120
KDDGNYKTRA EVKFEGDTLV NRIELKGIDF KEDGNILGHK LEYNYFSDNV YITADKQKNG  180
IKANFKIRHN IEDGGVQLAD HYQQNTPIGD GPVLLPDNHY LSTQSKLSKD PNEKRDHMVL  240
LEFVTAAGIT LGMDELYKGG TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR  300
EGQKGEKTIT TPTLKNPLTG VIISKGEPKE EITKDPINEL TEYGPETIAP GHRDEFDPKL  360
PTGEKEEVPG KPGIKNPETG DVVRPPVDSV TKYGPVKGDS IVEKEEIPFE KERKFNPDLA  420
PGTEKVTREG QKGEKTITTP TLKNPLTGEI ISKGESKEEI TKDPINELTE YGPETIAPGH  480
RDEFDPKLPT GEKEEVPGKP GIKNPETGDV VRPPVDSVTK YGPVKGDSIV EKEEIPFEKE  540
RKFNPDLAPG TEKVTREGQK GEKTITTPTL KNPLTGEIIS KGESKEEITK DPINELTEYG  600
PETIAPGHRD EFDPKLPTGE KEEVPGKPGI KNPETGDVVR PPVDSVTKYG PVKGDSIVEK  660
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EEIPFEKERK FNPDLAPGTE KVTREGQKGE KTITTPTLKN PLTGEIISKG ESKEEITKDP  720
INELTEYGPE TGSGATGSSG YCLDLKTQVQ TPQGMKEISN IQVGDLVLSN TGYNEVLNVF  780
PKSKKKSYKI TLEDGKEIIC SEEHLFPTQT GEMNISGGLK EGMCLYVKE              829

SEQ ID NO: 117         moltype = AA  length = 858
FEATURE                Location/Qualifiers
REGION                 1..858
                       note = Fusion protein consisting of SpyTag003, the red
                        fluorescent protein mCherry, SasG (comprising 4 G5 domains
                        yielding GEGEGEG) and a SnoopCatcher domain
source                 1..858
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 117
MGRGVPHIVM VDAYKRYKSG GGSGVSKGEE DNMAIIKEFM RFKVHMEGSV NGHEFEIEGE  60
GEGRPYEGTQ TAKLKVTKGG PLPFAWDILS PQFMYGSKAY VKHPADIPDY LKLSFPEGFK  120
WERVMNFEDG GVVTVTQDSS LQDGEFIYKV KLRGTNFPSD GPVMQKKTMG WEASSERMYP  180
EDGALKGEIK QRLKLKDGGH YDAEVKTTYK AKKPVQLPGA YNVNIKLDIT SHNEDYTIVE  240
QYERAEGRHS TGGMDELYKG GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT  300
REGQKGEKTI TTPTLKNPLT GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK  360
LPTGEKEEVP GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL  420
APGTEKVTRE GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG  480
HRDEFDPKLP TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK  540
ERKFNPDLAP GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY  600
GPETIAPGHR DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE  660
KEEIPFEKER KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD  720
PINELTEYGP ETGSGATGSL EKGSHMKPLR GAVFSLQKQH PDYPDIYGAI DQNGTYQNVR  780
TGEDGKLTFK NLSDGKYRLF ENSEPAGYKP VQNKPIVAFQ IVNGEVRDVT SIVPQDIPAT  840
YEFTNGKHYI TNEPIPPK                                                858

SEQ ID NO: 118         moltype = AA  length = 426
FEATURE                Location/Qualifiers
REGION                 1..426
                       note = Fusion protein consisting of superfolder GFP, the
                        G51 domain of SasG and the Npu DnaE N-intein split part
source                 1..426
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 118
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG  300
VIISKGEPKE EITKDPINEL TEYGCLSYET EILTVEYGLL PIGKIVEKRI ECTVYSVDNN  360
GNIYTQPVAQ WHDRGEQEVF EYCLEDGSLI RATKDHKFMT VDGQMLPIDE IFERELDLMR  420
VDNLPN                                                             426

SEQ ID NO: 119         moltype = AA  length = 409
FEATURE                Location/Qualifiers
REGION                 1..409
                       note = Fusion protein consisting of Npu DnaE GEP C-Intein
                        split fragment, SasG EG domains, where the proline residue
                        in the G51-E junction was mutated to Cysteine to serve as
                        nucleophile in the splicing reaction, and mCherry
source                 1..409
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 119
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNCETI APGHRDEFDP KLPTGEKEEV  60
PGKPGIKNPE TGDVVRPPVD SVTKYGPVKG DSIVEKEEIP FEKERKFNPD LAPGTEKVTR  120
EGQKGEKTIT TPTLKNPLTG EIISKGESKE EITKDPINEL TEYGPETGSG ATGSVSKGEE  180
DNMAIIKEFM RFKVHMEGSV NGHEFEIEGE GEGRPYEGTQ TAKLKVTKGG PLPFAWDILS  240
PQFMYGSKAY VKHPADIPDY LKLSFPEGFK WERVMNFEDG GVVTVTQDSS LQDGEFIYKV  300
KLRGTNFPSD GPVMQKKTMG WEASSERMYP EDGALKGEIK QRLKLKDGGH YDAEVKTTYK  360
AKKPVQLPGA YNVNIKLDIT SHNEDYTIVE QYERAEGRHS TGGMDELYK              409

SEQ ID NO: 120         moltype = AA  length = 266
FEATURE                Location/Qualifiers
REGION                 1..266
                       note = Fusion protein consisting of Npu DnaE GEP C-Intein
                        split fragment, SasG EG domains and the Npu DnaE N-intein
                        split part on its C-terminus. This yields a self-growing
                        fragment which can be capped off with
                        NpuDnaE_GEP_C-Int_SasG_EG_mCherry_V2
source                 1..266
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                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 120
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNCETI APGHRDEFDP KLPTGEKEEV  60
PGKPGIKNPE TGDVVRPPVD SVTKYGPVKG DSIVEKEEIP FEKERKFNPD LAPGTEKVTR  120
EGQKGEKTIT TPTLKNPLTG EIISKGESKE EITKDPINEL TEYGCLSYET EILTVEYGLL  180
PIGKIVEKRI ECTVYSVDNN GNIYTQPVAQ WHDRGEQEVF EYCLEDGSLI RATKDHKFMT  240
VDGQMLPIDE IFERELDLMR VDNLPN                                       266

SEQ ID NO: 121        moltype = AA  length = 340
FEATURE               Location/Qualifiers
REGION                1..340
                      note = Fusion protein consisting of superfolder GFP, the
                       G51 domain of SasG and the VidaL N-Intein split part
source                1..340
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 121
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG  300
VIISKGEPKE EITKDPINEL TEYGCLPKEA VVQIRLTKKG                        340

SEQ ID NO: 122        moltype = AA  length = 496
FEATURE               Location/Qualifiers
REGION                1..496
                      note = Fusion protein consisting of VidaL C-Intein split
                       part, SasG EG domains and mCherry
source                1..496
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 122
MIEEKKVTVQ ELRELYLSGE YTIEIDTPDG YQTIGKWFDK GVLSMVRVAT ATYETVCAFN  60
HMIQLADNTW VQACELDVGV DIQTAAGIQP VMLVEDTSDA ECYDFEVMHP NHRYYGDGIV  120
SHNSETIAPG HRDEFDPKLP TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI  180
VEKEEIPFEK ERKFNPDLAP GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT  240
KDPINELTEY GPETGSGATG SVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG  300
RPYEGTQTAK LKVTKGGPLP FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER  360
VMNFEDGGVV TVTQDSSLQD GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG  420
ALKGEIKQRL KLKDGGHYDA EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE  480
RAEGRHSTGG MDELYK                                                  496

SEQ ID NO: 123        moltype = AA  length = 267
FEATURE               Location/Qualifiers
REGION                1..267
                      note = Fusion protein consisting of VidaL C-Intein split
                       part, SasG EG domains and VidaL N-Intein split part. This
                       building block is a self-growing unit and can be capped
                       off with VidaL-C-Int_SasG_EG_mCherry
source                1..267
                      mol_type = protein
                      organism = synthetic construct
SEQUENCE: 123
MIEEKKVTVQ ELRELYLSGE YTIEIDTPDG YQTIGKWFDK GVLSMVRVAT ATYETVCAFN  60
HMIQLADNTW VQACELDVGV DIQTAAGIQP VMLVEDTSDA ECYDFEVMHP NHRYYGDGIV  120
SHNSETIAPG HRDEFDPKLP TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI  180
VEKEEIPFEK ERKFNPDLAP GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT  240
KDPINELTEY GCLPKEAVVQ IRLTKKG                                      267

SEQ ID NO: 124        moltype = AA  length = 255
FEATURE               Location/Qualifiers
source                1..255
                      mol_type = protein
                      organism = Tobacco etch virus
SEQUENCE: 124
MEQKLISEED LGESLFKGPR DYNPISSTIC HLTNESDGHT TSLYGIGFGP FIITNKHLFR  60
RNNGTLLVQS LHGVFKVKNT TTLQQHLIDG RDMIIIRMPK DFPPFPQKLK FREPQREERI  120
CLVTTNFQTK SMSSMVSDTS CTFPSSDGIF WKHWIQTKDG QCGSPLVSTR DGFIVGIHSA  180
SNFTNTNNYF TSVPKNFMEL LTNQEAQQWV SGWRLNADSV LWGGHKVFMS KPEEPFQPVK  240
EATQLMSELV YSQYP                                                   255

SEQ ID NO: 125        moltype = AA  length = 244
FEATURE               Location/Qualifiers
source                1..244
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                      mol_type = protein
                      organism = Plum pox virus
SEQUENCE: 125
MSKSLFRGLR DYNPIASSIC QLNNSSGARQ SEMFGLGFGG LIVTNQHLFK RNDGELTIRS  60
HHGEFVVKDT KTLKLLPCKG RDIVIIRLPK DFPPFPKRLQ FRTPTTEDRV CLIGSNFQTK  120
SISSTMSETS ATYPVDNSHF WKHWISTKDG HCGLPIVSTR DGSILGLHSL ANSTNTQNFY  180
AAFPDNFETT YLSNQDNDNW IKQWRYNPDE VCWGSLQLKR DIPQSPFTIC KLLTDLDGEF  240
VYTQ                                                               244

SEQ ID NO: 126         moltype = AA  length = 244
FEATURE                Location/Qualifiers
source                 1..244
                       mol_type = protein
                       organism = Soybean mosaic virus
SEQUENCE: 126
MSKSVYKGLR DYSGISTLIC QLTNSSDGHK ETMFGVGYGS FIITNGHLFR RNNGMLTVKT  60
WHGEFVIHNT TQLKIHFIQG RDVILIRMPK DFPPFGKRNL FRQPKREERV CMVGTNFQEK  120
SLRATVSESS MILPEGKGSF WIHWITTQDG FCGLPLVSVN DGHIVGIHGL TSNDSEKNFF  180
VPLTDGFEKE YLENADNLSW DKHWFWEPSK IAWGSLNLVE EQPKEEFKIS KLVSDLFGNT  240
VTVQ                                                               244

SEQ ID NO: 127         moltype = AA  length = 242
FEATURE                Location/Qualifiers
source                 1..242
                       mol_type = protein
                       organism = sunflower mild mosaic virus
SEQUENCE: 127
MGVSLSRGVR DYNAISSMVC RVTNDSGSSS TTMYGIGYGC YIITNKHLFR ENNGRLLITS  60
HHGEYICKNS ASLKLSLVPG RDMLLIRLPK DCPPFPSKLK FREPTSEEKA VLVVTNFQEK  120
HLSSMVSESS CVVQREDSPI WRHWISTKDG HCGAPIVSIR DGYIIGSHCG ENPMTSNFFT  180
SIPKDFQNLL NGKEANEWVS GWKYNIDAVC WGGLSVVNDA PSEPFITAKV VSALDTEGIK  240
VQ                                                                 242

SEQ ID NO: 128         moltype = AA  length = 458
FEATURE                Location/Qualifiers
REGION                 1..458
                       note = Fusion protein consisting of a triple engineered
                        Lanthanide binding domain (LBT15), a TEV cleavage site,
                        the capsid forming monomer of the Encapsulin system of
                        Q.thermotolerans and a FLAG epitope
source                 1..458
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 128
MFIDTNNDGW IEGDELLLEE GGSGGGGSFI DTNNDGWIEG DELLLEEGGS GGGGSFIDTN  60
NDGWIEGDEL LLEEGGSGGG GSENLYFQSG SGPGMDPETC PCPTGGSCTC SDKCKCKGCK  120
CTNCKKSCCS CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGSGGNKSQ LYPDSPLTDQ  180
DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD FQGSFDTEVE  240
SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED QMIFHGSKEF  300
DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS PELYSLLHRV  360
HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE TAYLGEEGMN  420
HPFRVYETVV LRIKRPAAIC TLIDPEEGSG DYKDDDDK                          458

SEQ ID NO: 129         moltype = AA  length = 150
FEATURE                Location/Qualifiers
REGION                 1..150
                       note = Fusion protein consisting of a FLAG epitope, the
                        N-terminal fragment of the Tobacco etch virus protease
                        (TEV) (amino acids 1-118 and a C-terminal M13
                        calmodulin-binding peptide
source                 1..150
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 129
MDYKDDDDKT GGESLFKGPR DYNPISSTIC HLTNESDGHT TSLYGIGFGP FIITNKHLFR  60
RNNGTLVVQS LHGVFKVKNT TTLQQHLIDG RDMIIIRMPK DFPPFPQKLK FREPQREERI  120
CLVTTNFQTS AGRRKWNKGH AVRAIGRLSS                                   150

SEQ ID NO: 130         moltype = AA  length = 266
FEATURE                Location/Qualifiers
REGION                 1..266
                       note = Fusion protein consisting of a Myc epitope,
                        Calmodulin and the C-terminal split fragment of Tobacco
                        etch virus protease (amino acids 119-219, S153N
source                 1..266
                       mol_type = protein
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                        organism = synthetic construct
SEQUENCE: 130
MASMQKLISE EDLTGDQLTE EQIAEFKEAF SLFDKDGDGT ITTKELGTVM RSLGQNPTEA  60
ELQDMINEVD ADGDGTIDFP EFLTMMARKM KDTDSEEEIR EAFRVFDKDG NGYISAAELR  120
HVMTNLGEKL TDEEVDEMIR EADIDGDGQV NYEEFVQMMT AKSAGKSMSS MVSDTSCTFP  180
SGDGIFWKHW IQTKDGQCGN PLVSTRDGFI VGIHSASNFT NTNNYFTSVP KNFMELLTNQ  240
EAQQWVSGWR LNADSVLWGG HKVFMV                                       266

SEQ ID NO: 131         moltype = AA  length = 315
FEATURE                Location/Qualifiers
REGION                 1..315
                       note = Fusion of Encapsulin forming monomer of the
                        Encapsulin system M.xanthus and the Calmodulin binding
                        peptide RS20
source                 1..315
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 131
MADFLGHAEN PLREEEWARL NETVIQVARR SLVGRRILDI YGPLGAGVQT VPYDEFQGVS  60
PGAVDIVGEQ ETAMVFTDAR KFKTIPIIYK DFLLHWRDIE AARTHNMPLD VSAAAGAAAL  120
CAQQEDELIF YGDARLGYEG LMTANGRLTV PLGDWTSPGG GFQAIVEATR KLNEQGHFGP  180
YAVVLSPRLY SQLHRIYEKT GVLEIETIRQ LASDGVYQSN RLRGESGVVV STGRENMDLA  240
VSMDMVAAYL GASRMNHPFR VLEALLLRIK HPDAICTLEG AGATERRGSS EGGSGRRKWQ  300
KTGHAVRAIG RLSSS                                                   315

SEQ ID NO: 132         moltype = AA  length = 305
FEATURE                Location/Qualifiers
REGION                 1..305
                       note = Fusion of Encapsulin forming monomer of the
                        Encapsulin system Q.thermotolerans and the Calmodulin
                        binding peptide RS20
source                 1..305
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 132
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGRRKWQ KTGHAVRAIG  300
RLSSS                                                              305

SEQ ID NO: 133         moltype = AA  length = 287
FEATURE                Location/Qualifiers
REGION                 1..287
                       note = Fusion of Encapsulin forming monomer of the
                        Encapsulin system T.maritima and the Calmodulin binding
                        peptide RS20
source                 1..287
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 133
MEFLKRSFAP LTEKQWQEID NRAREIFKTQ LYGRKFVDVE GPYGWEYAAH PLGEVEVLSD  60
ENEVVKWGLR KSLPLIELRA TFTLDLWELD NLERGKPNVD LSSLEETVRK VAEFEDEVIF  120
RGCEKSGVKG LLSFEERKIE CGSTPKDLLE AIVRALSIFS KDGIEGPYTL VINTDRWINF  180
LKEEAGHYPL EKRVEECLRG GKIITTPRIE DALVVSERGG DFKLILGQDL SIGYEDREKD  240
AVRLFITETF TFQVVNPEAL ILLKGSGRRK WQKTGHAVRA IGRLSSS                287

SEQ ID NO: 134         moltype = AA  length = 315
FEATURE                Location/Qualifiers
REGION                 1..315
                       note = Fusion protein of human calmodulin and H.pylori
                        ferritin (AA 5-167, N19Q)
source                 1..315
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 134
MADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMRSL GQNPTEAELQ DMINEVDADG  60
NGTIDFPEFL TMMARKMKDT DSEEEIREAF RVFDKDGNGY ISAAELRHVM TNLGEKLTDE  120
EVDEMIREAD IDGDGQVNYE EFVQMMTAKS GGDIIKLLNE QVNKEMQSSN LYMSMSSWCY  180
THSLDGAGLF LFDHAAEEYE HAKKLIIFLN ENNVPVQLTS ISAPEHKFEG LTQIFQKAYE  240
HEQHISESIN NIVDHAIKSK DHATFNFLQW YVAEQHEEEV LFKDILDKIE LIGNENHGLY  300
LADQYVKGIA KSRKS                                                   315

SEQ ID NO: 135         moltype = AA  length = 235
FEATURE                Location/Qualifiers
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REGION                  1..235
                        note = Fusion of human Calmodulin and MmMT3 which will be
                         recruited to the scaffold (Enc) to form a contrast halo
                         around the element when elevated Ca2+ levels are present
source                  1..235
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 135
MDIIKLLNEQ VNKEMQSSNL YMSMSSWCYT HSLDGAGLFL FDHAAEEYEH AKKLIIFLNE  60
NNVPVQLTSI SAPEHKFEGL TQIFQKAYEH EQHISESINN IVDHAIKSKD HATFNFLQWY  120
VAEQHEEEVL FKDILDKIEL IGNENHGLYL ADQYVKGIAK SRKSGSGMDP ETCPCPTGGS  180
CTCSDKCKCK GCKCTNCKKS CCSCCPAGCE KCAKDCVCKG EEGAKAEAEK CSCCQ       235

SEQ ID NO: 136          moltype = AA  length = 170
FEATURE                 Location/Qualifiers
REGION                  1..170
                        note = Fusion protein of MT3, an engineered minimal
                         Troponin C domain of Opsanus tau and the Encapsulin signal
                         of the Encapsulin system of Q.thermotolerans
source                  1..170
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 136
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQTG RMQVADASEE ELSECFRIFD FDGNGFIDRE EFGDIIRLTG EQLTDEDVDE  120
IFGDSDTDKN GRIDFDEFLK MVENVQPIYP GGGGSGGGGS KGFTVGSLIQ             170

SEQ ID NO: 137          moltype = AA  length = 443
FEATURE                 Location/Qualifiers
REGION                  1..443
                        note = Fusion protein MT3-TnCmin-QtEnc-FLAG
source                  1..443
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 137
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQTG RMQVADASEE ELSECFRIFD FDGNGFIDRE EFGDIIRLTG EQLTDEDVDE  120
IFGDSDTDKN GRIDFDEFLK MVENVQPIYP GGGGSGGGGS VMNKSQLYPD SPLTDQDFNQ  180
LDQTVIEAAR RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS FDTEVESSRR  240
VNYTIPMLYK DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF HGSKEFDIPG  300
LMNVKGRLTH LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY SLLHRVHKDT  360
NVLEIEHVRE LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL GEEGMNHPFR  420
VYETVVLRIK RPAAICTLID PEE                                          443

SEQ ID NO: 138          moltype = AA  length = 723
FEATURE                 Location/Qualifiers
REGION                  1..723
                        note = Fusion of E3 ubiquitin-protein ligase TRIM21, with
                         inactivating mutations I79R and S80A, and mCherry
                         fluorescence protein
source                  1..723
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 138
TGSGATGSVS KGEEDNMAII KEFMRFKVHM EGSVNGHEFE IEGEGEGRPY EGTQTAKLKV  60
TKGGPLPFAW DILSPQFMYG SKAYVKHPAD IPDYLKLSFP EGFKWERVMN FEDGGVVTVT  120
QDSSLQDGEF IYKVKLRGTN FPSDGPVMQK KTMGWEASSE RMYPEDGALK GEIKQRLKLK  180
DGGHYDAEVK TTYKAKKPVQ LPGAYNVNIK LDITSHNEDY TIVEQYERAE GRHSTGGMDE  240
LYKGGGSGMA SAARLTMMWE EVTCPICLDP FVEPVSIECG HSFCQECISQ VGKGGGSVCP  300
VCRQRFLLKN LRPNRQLANM VNNLKERAQE AREGTQGERC AVHGERLHLF CEKDGKALCW  360
VCAQSRKHRD HAMVPLEEAA QEYQEKLQVA LGELRRKQEL AEKLEVEIAI KRADWKKTVE  420
TQKSRIHAEF VQQKNFLVEE EQRQLQELEK DEREQLRILG EKEAKLAQQS QALQELISEL  480
DRRCHSSALE LLQEVIIVLE RSESWNLKDL DITSPELRSV CHVPGLKKML RTCAVHITLD  540
PDTANPWLIL SEDRRQVRLG DTQQSIPGNE ERFDSYPMVL GAQHFHSGKH YWEVDVTGKE  600
AWDLGVCRDS VRRKGHFLLS SKSGFWTIWL WNKQKYEAGT YPQTPLHLQV PPCQVGIFLD  660
YEAGMVSFYN ITDHGSLIYS FSECAFTGPL RPFFSPGFND GGKNTAPLTL CPLNIGSQGS  720
TDY                                                                723

SEQ ID NO: 139          moltype = AA  length = 806
FEATURE                 Location/Qualifiers
REGION                  1..806
                        note = Fusion of E3 ubiquitin-protein ligase TRIM21, with
                         inactivating mutations I79R and S80A, and superfolder GFP
source                  1..806
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 139
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG  300
VIISKGEPKE EITKDPINEL TEYGPEGGGS GMASAARLTM MWEEVTCPIC LDPFVEPVSI  360
ECGHSFCQEC ISQVGKGGGS VCPVCRQRFL LKNLRPNRQL ANMVNNLKER AQEAREGTQG  420
ERCAVHGERL HLFCEKDGKA LCWVCAQSRK HRDHAMVPLE EAAQEYQEKL QVALGELRRK  480
QELAEKLEVE IAIKRADWKK TVETQKSRIH AEFVQQKNFL VEEEQRQLQE LEKDEREQLR  540
ILGEKEAKLA QQSQALQELI SELDRRCHSS ALELLQEVII VLERSESWNL KDLDITSPEL  600
RSVCHVPGLK KMLRTCAVHI TLDPDTANPW LILSEDRRQV RLGDTQQSIP GNEERFDSYP  660
MVLGAQHFHS GKHYWEVDVT GKEAWDLGVC RDSVRRKGHF LLSSKSGFWT IWLWNKQKYE  720
AGTYPQTPLH LQVPPCQVGI FLDYEAGMVS FYNITDHGSL IYSFSECAFT GPLRPFFSPG  780
FNDGGKNTAP LTLCPLNIGS QGSTDY                                       806

SEQ ID NO: 140          moltype = DNA  length = 4955
FEATURE                 Location/Qualifiers
misc_feature            1..4955
                        note = expression vector pcDNA 3.1 (+) Zeocin containing
                         elements from different organisms
source                  1..4955
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 140
aatggatgag ctgtacaagt gataagcggc cgctcgagtc tagagggccc gtttaaaccc  60
gctgatcagc ctcgactgtg ccttctagtt gccagccatc tgttgtttgc ccctcccccg  120
tgccttcctt gaccctggaa ggtgccactc ccactgtcct ttcctaataa aatgaggaaa  180
ttgcatcgca ttgtctgagt aggtgtcatt ctattctggg gggtggggtg gggcaggaca  240
gcaaggggga ggattgggaa gacaatagca ggcatgctgg ggatgcggtg ggctctatgg  300
cttctgaggc ggaaagaacc agctggggct ctagggggta tccccacgcg ccctgtagcg  360
gcgcattaag cgcggcgggt gtggtggtta cgcgcagcgt gaccgctaca cttgccagcg  420
ccctagcgcc cgctcctttc gctttcttcc cttcctttct cgccacgttc gccggctttc  480
cccgtcaagc tctaaatcgg ggcatccctt tagggttccg atttagtgct ttacggcacc  540
tcgaccccaa aaaacttgat tagggtgatg gttcacgtag tgggccatcg ccctgataga  600
cggtttttcg ccctttgacg ttggagtcca cgttctttaa tagtggactc ttgttccaaa  660
ctggaacaac actcaaccct atctcggtct attcttttga tttataaggg attttgggga  720
tttcggccta ttggttaaaa aatgagctga tttaacaaaa atttaacgcg aattaattct  780
gtggaatgtg tgtcagttag ggtgtggaaa gtccccaggc tccccaggca ggcagaagta  840
tgcaaagcat gcatctcaat tagtcagcaa ccaggtgtgg aaagtcccca ggctccccag  900
caggcagaag tatgcaaagc atgcatctca attagtcagc aaccatagtc ccgcccctaa  960
ctccgcccat cccgccccta actccgccca gttccgccca ttctccgccc catggctgac  1020
taattttttt tatttatgca gaggccgagg ccgcctctgc ctctgagcta ttccagaagt  1080
agtgaggagg cttttttgga ggcctaggct tttgcaaaaa gctcccggga gcttgtatat  1140
ccattttcgg atctgatcag cacgtgttga caattaatca tcggcatagt atatcggcat  1200
agtataatac gacaaggtga ggaactaaac catggccaag ttgaccagtg ccgttccggt  1260
gctcaccgcg cgcgacgtcg ccggagcggt cgagttctgg accgaccggc tcgggttctc  1320
ccgggacttc gtggaggacg acttcgccgg tgtggtccgg gacgacgtga ccctgttcat  1380
cagcgcggtc caggaccagg tggtgccgga caacaccctg gcctgggtgt gggtgcgcgg  1440
cctggacgag ctgtacgccg agtggtcgga ggtcgtgtcc acgaacttcc gggacgcctc  1500
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SEQ ID NO: 141          moltype = DNA  length = 6098
FEATURE                 Location/Qualifiers
misc_feature            1..6098
                        note = pIRES
source                  1..6098
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 141
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gtcattagtt catagcccat atatggagtt ccgcgttaca taacttacgg taaatggccc  240
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SEQ ID NO: 142          moltype = AA  length = 293
FEATURE                 Location/Qualifiers
REGION                  1..293
                        note = Shell forming monomer of the Encapsulin system of
                         Quasibacillus thermotolerans with a C-terminally appended
                         FLAG epitope connected via a short GSG linker.
source                  1..293
                        mol_type = protein
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                        organism = synthetic construct
SEQUENCE: 142
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDK         293

SEQ ID NO: 143          moltype = AA  length = 444
FEATURE                 Location/Qualifiers
REGION                  1..444
                        note = A tandem of the Mus musculus Metallothionein 3
                         connected via GGGGSGGGGS linker fused to the shell forming
                         monomer of the Encapsulin system of Quasibacillus
                         thermotolerans with a C-terminally appended FLAG epitope
                         connected via a short GSG
source                  1..444
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 143
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGSGGSA DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  120
CEKCAKDCVC KGEEGAKAEA EKCSCCQGSG PGNKSQLYPD SPLTDQDFNQ LDQTVIEAAR  180
RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS FDTEVESSRR VNYTIPMLYK  240
DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF HGSKEFDIPG LMNVKGRLTH  300
LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY SLLHRVHKDT NVLEIEHVRE  360
LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL GEEGMNHPFR VYETVVLRIK  420
RPAAICTLID PEEGSGDYKD DDDK                                         444

SEQ ID NO: 144          moltype = AA  length = 355
FEATURE                 Location/Qualifiers
REGION                  1..355
                        note = Fusion of Mus musculus Metallothionein 3 fused to
                         the shell forming monomer of the Encapsulin system of
                         Thermotoga maritima fused to a C-terminal BC2-Tag
source                  1..355
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 144
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGEFLKRSF APLTEKQWQE IDNRAREIFK TQLYGRKFVD VEGPYGWEYA  120
AHPLGEVEVL SDENEVVKWG LRKSLPLIEL RATFTLDLWE LDNLERGKPN VDLSSLEETV  180
RKVAEFEDEV IFRGCEKSGV KGLLSFEERK IECGSTPKDL LEAIVRALSI FSKDGIEGPY  240
TLVINTDRWI NFLKEEAGHY PLEKRVEECL RGGKIITTPR IEDALVVSER GGDFKLILGQ  300
DLSIGYEDRE KDAVRLFITE TFTFQVVNPE ALILLKGGGS GPGPDRKAAV SHWQQ       355

SEQ ID NO: 145          moltype = AA  length = 318
FEATURE                 Location/Qualifiers
REGION                  1..318
                        note = Synthetic Lanthanide-bindering tag 15 fused to the
                         shell forming monomer of the Encapsulin system of
                         Quasibacillus thermotolerans fused to a C-terminal FLAG
                         tag-
source                  1..318
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 145
MFIDTNNDGW IEGDELLLEE GGSGPGNKSQ LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR  60
RFIELYGPLG RGMQSVFNDI FMESHEAKMD FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW  120
RDLEQSKALD IPIDFSVAAN AARDVAFLED QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY  180
ESGNAFQDIV EARNKLLEMN HNGPYALVLS PELYSLLHRV HKDTNVLEIE HVRELITAGV  240
FQSPVLKGKS GVIVNTGRNN LDLAISEDFE TAYLGEEGMN HPFRVYETVV LRIKRPAAIC  300
TLIDPEEGSG DYKDDDDK                                                318

SEQ ID NO: 146          moltype = AA  length = 380
FEATURE                 Location/Qualifiers
REGION                  1..380
                        note = Engineered tandem Lanthanide-binding tag fused to
                         the shell forming monomer of the Encapsulin system of
                         Quasibacillus thermotolerans fused to a C-terminal FLAG tag
source                  1..380
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 146
MGPGYIDTNN DGWIEGDELY IDTNNDGWIE GDELLAGGGS GGGSGGSAGP GYIDTNNDGW  60
IEGDELYIDT NNDGWIEGDE LLAGSGPGNK SQLYPDSPLT DQDFNQLDQT VIEAARRQLV  120
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GRRFIELYGP LGRGMQSVFN DIFMESHEAK MDFQGSFDTE VESSRRVNYT IPMLYKDFVL  180
YWRDLEQSKA LDIPIDFSVA ANAARDVAFL EDQMIFHGSK EFDIPGLMNV KGRLTHLIGN  240
WYESGNAFQD IVEARNKLLE MNHNGPYALV LSPELYSLLH RVHKDTNVLE IEHVRELITA  300
GVFQSPVLKG KSGVIVNTGR NNLDLAISED FETAYLGEEG MNHPFRVYET VVLRIKRPAA  360
ICTLIDPEEG SGDYKDDDDK                                              380

SEQ ID NO: 147         moltype = AA  length = 304
FEATURE                Location/Qualifiers
REGION                 1..304
                       note = Capsid forming monomer from the encapsulin system of
                        Q.thermotolerans tagged with C-terminal SpyTag003
source                 1..304
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 147
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGRG VPHIVMVDAY  300
KRYK                                                               304

SEQ ID NO: 148         moltype = AA  length = 434
FEATURE                Location/Qualifiers
REGION                 1..434
                       note = Designed Uranyl-binding protein MUP2 fused to the
                        shell forming monomer of the Encapsulin system of
                        Quasibacillus thermotolerans
source                 1..434
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 148
MVSRLEERVR DLEAEVDKLR ERLDRLEETV QAKGGGGSGG GGSGGGGSGG GGSGGVSRLE  60
ERVRDLEAEV DKLRERLDRL EETVQAKGGG GSGGGGSGGG GSGGGGSGGV SRLEERVRDL  120
EAEVDKLRER LDRLEETVQA KPPPPRPPPP RTGNKSQLYP DSPLTDQDFN QLDQTVIEAA  180
RRQLVGRRFI ELYGPLGRGM QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY  240
KDFVLYWRDL EQSKALDIPI DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT  300
HLIGNWYESG NAFQDIVEAR NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR  360
ELITAGVFQS PVLKGKSGVI VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI  420
KRPAAICTLI DPEE                                                    434

SEQ ID NO: 149         moltype = AA  length = 515
FEATURE                Location/Qualifiers
REGION                 1..515
                       note = Designed Uranyl-binding protein MUP5 fused to the
                        shell forming monomer of the Encapsulin system of
                        Quasibacillus thermotolerans
source                 1..515
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 149
MQLEDKVEEL LSKVYHLENE VDRLRKLIEN KGGGGSGGGG SQLEDKVEEL ESEVDHLRNE  60
VARLKKLVGG GGSGGGGSQL EDKVEELLSK VYHLENEVDR LRKLIENKGG GGSGGGGSQL  120
EDKVEELESE VDHLRNEVAR LKKLVGGGGS GGGGSQLEDK VEELLSKVYH LENEVDRLRK  180
LIENKGGGGS GGGGSQLEDK VEELESEVDH LRNEVARLKK LVPPPPRPPP PRTGNKSQLY  240
PDSPLTDQDF NQLDQTVIEA ARRQLVGRRF IELYGPLGRG MQSVFNDIFM ESHEAKMDFQ  300
GSFDTEVESS RRVNYTIPML YKDFVLYWRD LEQSKALDIP IDFSVAANAA RDVAFLEDQM  360
IFHGSKEFDI PGLMNVKGRL THLIGNWYES GNAFQDIVEA RNKLLEMNHN GPYALVLSPE  420
LYSLLHRVHK DTNVLEIEHV RELITAGVFQ SPVLKGKSGV IVNTGRNNLD LAISEDFETA  480
YLGEEGMNHP FRVYETVVLR IKRPAAICTL IDPEE                             515

SEQ ID NO: 150         moltype = AA  length = 257
FEATURE                Location/Qualifiers
REGION                 1..257
                       note = Engineered SpyCatcher 003 domain fused to fatty acid
                        binding protein FABP
source                 1..257
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 150
MVEAFCATWK LTNSQNFDEY MKALGVGFAT RQVGNVTKPT VIISQEGDKV VIRTLSTFKN  60
TEISFQLGEE FDETTADDRN CKSVVSLDGD KLVHIQKWDG KETNFVREIK DGKMVMTLTF  120
GDVVAVRHYE KAPPPPRTGP PPPRVTTLSG LSGEQGPSGD MTTEEDSATH IKFSKRDEDG  180
RELAGATMEL RDSSGKTIST WISDGHVKDF YLYPGKYTFV ETAAPDGYEV ATPIEFTVNE  240
DGQVTVDGEA TEGDAHT                                                 257
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SEQ ID NO: 151          moltype = AA  length = 581
FEATURE                 Location/Qualifiers
REGION                  1..581
                        note = Heme binding domain BM3h fused to engineered
                         SpyCatcher 003 domain
source                  1..581
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 151
MTIKEMPQPK TFGELKNLPL LNTDKPVQAL MKIADELGEI FKFEAPGRVT RYLSSQRLIK  60
EACDESRFDK NLSQALKFVR DFAGDGLFTS WTHEKNWKKA HNILLPSFSQ QAMKGYHAMM  120
VDIAVQLVQK WERLNADEHI EVPEDMTRLT LDTIGLCGFN YRFNSFYRDQ PHPFITSMVR  180
ALDEAMNKLQ RANPDDPAYD ENKRQFQEDI KVMNDLVDKI IADRKASGEQ SDDLLTHMLN  240
GKDPETGEPL DDENIRYQII TFLIAGHETT SGLLSFALYF LVKNPHVLQK AAEEAARVLV  300
DPVPSYKQVK QLKYVGMVLN EALRLWPTAP AFSLYAKEDT VLGGEYPLEK GDELMVLIPQ  360
LHRDKTIWGD DVEEFRPERF ENPSAIPQHA FKPFGNGQRA CIGQQFALHE ATLVLGMMLK  420
HFDFEDHTNY ELDIKETLTL KPEGFVVKAK SKKIPLPPPP RTGPPPPRVT TLSGLSGEQG  480
PSGDMTTEED SATHIKFSKR DEDGRELAGA TMELRDSSGK TISTWISDGH VKDFYLYPGK  540
YTFVETAAPD GYEVATPIEF TVNEDGQVTV DGEATEGDAH T                      581

SEQ ID NO: 152          moltype = RNA  length = 21
FEATURE                 Location/Qualifiers
source                  1..21
                        mol_type = unassigned RNA
                        organism = Bacteriophage MS2
SEQUENCE: 152
aaacatgagg attacccatg t                                            21

SEQ ID NO: 153          moltype = AA  length = 10
FEATURE                 Location/Qualifiers
REGION                  1..10
                        note = 2xGGGGS linker
source                  1..10
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 153
GGGGSGGGGS                                                         10

SEQ ID NO: 154          moltype = AA  length = 107
FEATURE                 Location/Qualifiers
REGION                  1..107
                        note = Engineered FKBP-derived degron
source                  1..107
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 154
GVQVETISPG DGRTFPKRGQ TCVVHYTGML EDGKKVDSSR DRNKPFKFML GKQEVIRGWE  60
EGVAQMSVGQ RAKLTISPDY AYGATGHPGI IPPHATLVFD VELLKPE                107

SEQ ID NO: 155          moltype = AA  length = 509
FEATURE                 Location/Qualifiers
REGION                  1..509
                        note = Fusion of engineered ultrasmall fluorescent protein
                         eUnaG followed by MT3, QtEnc and a FLAG-tag
source                  1..509
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 155
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGSGPGNKS QLYPDSPLTD QDFNQLDQTV  240
IEAARRQLVG RRFIELYGPL GRGMQSVFND IFMESHEAKM DFQGSFDTEV ESSRRVNYTI  300
PMLYKDFVLY WRDLEQSKAL DIPIDFSVAA NAARDVAFLE DQMIFHGSKE FDIPGLMNVK  360
GRLTHLIGNW YESGNAFQDI VEARNKLLEM NHNGPYALVL SPELYSLLHR VHKDTNVLEI  420
EHVRELITAG VFQSPVLKGK SGVIVNTGRN NLDLAISEDF ETAYLGEEGM NHPFRVYETV  480
VLRIKRPAAI CTLIDPEEGS GDYKDDDDK                                    509

SEQ ID NO: 156          moltype = AA  length = 588
FEATURE                 Location/Qualifiers
REGION                  1..588
                        note = Fusion of engineered ultrasmall fluorescent protein
                         eUnaG followed by 2xMT3, QtEnc and a FLAG-tag
source                  1..588
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 156
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGGGSGGGS GGSADPETCP CPTGGSCTCS  240
DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC QGSGPGNKSQ  300
LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD  360
FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED  420
QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS  480
PELYSLLHRV HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE  540
TAYLGEEGMN HPFRVYETVV LRIKRPAAIC TLIDPEEGSG DYKDDDDK               588

SEQ ID NO: 157         moltype = AA  length = 609
FEATURE                Location/Qualifiers
REGION                 1..609
                       note = Fusion of the engineered green fluorescent protein
                        mGreenLantern, MT3, QtEnc and a FLAG epitope
source                 1..609
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 157
MVSKGEELFT GVVPILVELD GDVNGHKFSV RGEGEGDATN GKLTLKFICT TGKLPVPWPT  60
LVTTLGYGVA CFARYPDHMK QHDFFKSAMP EGYVQERTIS FKDDGTYKTR AEVKFEGDTL  120
VNRIVLKGID FKEDGNILGH KLEYNFNSHK VYITADKQKN GIKANFKTRH NVEDGGVQLA  180
DHYQQNTPIG DGPVLLPDNH YLSHQSKLSK DPNEKRDHMV LKERVTAAGI THDMDELYKG  240
GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS CCPAGCEKCA KDCVCKGEEG  300
AKAEAEKCSC CQGSGPGNKS QLYPDSPLTD QDFNQLDQTV IEAARRQLVG RRFIELYGPL  360
GRGMQSVFND IFMESHEAKM DFQGSFDTEV ESSRRVNYTI PMLYKDFVLY WRDLEQSKAL  420
DIPIDFSVAA NAARDVAFLE DQMIFHGSKE FDIPGLMNVK GRLTHLIGNW YESGNAFQDI  480
VEARNKLLEM NHNGPYALVL SPELYSLLHR VHKDTNVLEI EHVRELITAG VFQSPVLKGK  540
SGVIVNTGRN NLDLAISEDF ETAYLGEEGM NHPFRVYETV VLRIKRPAAI CTLIDPEEGS  600
GDYKDDDDK                                                          609

SEQ ID NO: 158         moltype = AA  length = 778
FEATURE                Location/Qualifiers
REGION                 1..778
                       note = Fusion of the engineered fluorescent Calcium
                        integrator CaMPARI2, MT3, QtEnc and a FLAG tag
source                 1..778
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 158
MGSDQLTEEQ IAEFKEAFSL FDKDGDGTIT TKELGTVMRS LGQNPTEAEL QDMINEVDAD  60
GDGTIDFPEF LTMMARKMKD TDSEEEIREA FRVFDKDGNG YISAAELRHV MTNLGEKLTD  120
EEVDEMIREA DIDGDGQVNY EEFVVMMTAK LECEKIYVRD GVLTGDIHMI LLLEGNAHYR  180
CDFRTTYKAK EKGVKLPGVH YVDHTIEILS HDKDYNKVKI YEYAVAHSGL PDNARRGGTG  240
GSMVSAIKPD MKIKLRMEGN VNGHHFVIDG DGTGKPYEGK QTMDLEVKEG GPLPFAFDIL  300
TTAFHYGNRV FVKYPDNIQD YFKQSFPKGY SWERSMTFED GGICYARSDI TMEGDTFYNK  360
VRFYGTNFPA NGPVMQKKTL KWMPSWTRSS RRKFNKTGHA LRAIGRLSGG TGGSDPETCP  420
CPTGGSCTCS DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC  480
QGSGPGNKSQ LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI  540
FMESHEAKMD FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN  600
AARDVAFLED QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN  660
HNGPYALVLS PELYSLLHRV HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN  720
LDLAISEDFE TAYLGEEGMN HPFRVYETVV LRIKRPAAIC TLIDPEEGSG DYKDDDDK    778

SEQ ID NO: 159         moltype = AA  length = 324
FEATURE                Location/Qualifiers
REGION                 1..324
                       note = Synthetic coiled-coil domain P2 (partner of P1)
                        fused to the TmEnc (AA 1-264) with a C-terminal BC2-Tag
source                 1..324
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 159
MSPEDKIAQL KEKNAALKEK NQQLKEKIQA LKYGGGGGSG PGEFLKRSFA PLTEKQWQEI  60
DNRAREIFKT QLYGRKFVDV EGPYGWEYAA HPLGEVEVLS DENEVVKWGL RKSLPLIELR  120
ATFTLDLWEL DNLERGKPNV DLSSLEETVR KVAEFEDEVI FRGCEKSGVK GLLSFEERKI  180
ECGSTPKDLL EAIVRALSIF SKDGIEGPYT LVINTDRWIN FLKEEAGHYP LEKRVEECLR  240
GGKIITTPRI EDALVVSERG GDFKLILGQD LSIGYEDREK DAVRLFITET FTFQVVNPEA  300
LILLKGGGSG PGPDRKAAVS HWQQ                                         324

SEQ ID NO: 160         moltype = AA  length = 385
FEATURE                Location/Qualifiers
REGION                 1..385
                       note = Synthetic coiled-coil domain DHD13a (partner of
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                        DHD13b) fused to MxEnc with a StrepTagII
source                  1..385
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 160
MGTKEDILER QRKIIERAQE IHRRQQEILE ELERIIRKPG SSEEAMKRML KLLEESLRLL  60
KELLELSEES AQLLYEQRGG GGSGPGPDFL GHAENPLREE EWARLNETVI QVARRSLVGR  120
RILDIYGPLG AGVQTVPYDE FQGVSPGAVD IVGEQETAMV FTDARKFKTI PIIYKDFLLH  180
WRDIEAARTH NMPLDVSAAA GAAALCAQQE DELIFYGDAR LGYEGLMTAN GRLTVPLGDW  240
TSPGGGFQAI VEATRKLNEQ GHFGPYAVVL SPRLYSQLHR IYEKTGVLEI ETIRQLASDG  300
VYQSNRLRGE SGVVVSTGRE NMDLAVSMDM VAAYLGASRM NHPFRVLEAL LLRIKHPDAI  360
CTLEGAGATE RRGSGSAWSH PQFEK                                        385

SEQ ID NO: 161          moltype = AA  length = 334
FEATURE                 Location/Qualifiers
REGION                  1..334
                        note = Synthetic coiled-coil domain P3 (partner of P4)
                         fused to QtEnc with a FLAG-Tag
source                  1..334
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 161
MSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGGGGGSG PGNKSQLYPD SPLTDQDFNQ  60
LDQTVIEAAR RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS FDTEVESSRR  120
VNYTIPMLYK DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF HGSKEFDIPG  180
LMNVKGRLTH LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY SLLHRVHKDT  240
NVLEIEHVRE LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL GEEGMNHPFR  300
VYETVVLRIK RPAAICTLID PEEGSGDYKD DDDK                              334

SEQ ID NO: 162          moltype = AA  length = 389
FEATURE                 Location/Qualifiers
REGION                  1..389
                        note = Fusion of DD-N degron with mScarlet-I and synthetic
                         coiled-coil domain P1 (partner of P2)
source                  1..389
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 162
GVQVETISPG DGRTFPKRGQ TCVVHYTGML EDGKKVDSSR DRNKPFKFML GKQEVIRGWE  60
EGVAQMSVGQ RAKLTISPDY AYGATGHPGI IPPHATLVFD VELLKPEGSG VSKGEAVIKE  120
FMRFKVHMEG SMNGHEFEIE GEGEGRPYEG TQTAKLKVTK GGPLPFSWDI LSPQFMYGSR  180
AFIKHPADIP DYYKQSFPEG FKWERVMNFE DGGAVTVTQD TSLEDGTLIY KVKLRGTNFP  240
PDGPVMQKKT MGWEASTERL YPEDGVLKGD IKMALRLKDG GRYLADFKTT YKAKKPVQMP  300
GAYNVDRKLD ITSHNEDYTV VEQYERSEGR HSTGGMDELY KGGGGSGGGG SGPGTGSPED  360
EIQALEEENA QLEQENAALE EEIAQLEYG                                    389

SEQ ID NO: 163          moltype = AA  length = 444
FEATURE                 Location/Qualifiers
REGION                  1..444
                        note = Fusion of DD-N degron with mTagBFP2 and synthetic
                         coiled-coil domain DHD13b (partner of DHD13a)
source                  1..444
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 163
GVQVETISPG DGRTFPKRGQ TCVVHYTGML EDGKKVDSSR DRNKPFKFML GKQEVIRGWE  60
EGVAQMSVGQ RAKLTISPDY AYGATGHPGI IPPHATLVFD VELLKPEGSG VSKGEELIKE  120
NMHMKLYMEG TVDNHHFKCT SEGEGKPYEG TQTMRIKVVE GGPLPFAFDI LATSFLYGSK  180
TFINHTQGIP DFFKQSFPEG FTWERVTTYE DGGVLTATQD TSLQDGCLIY NVKIRGVNFT  240
SNGPVMQKKT LGWEAFTETL YPADGGLEGR NDMALKLVGG SHLIANAKTT YRSKKPAKNL  300
KMPGVYYVDY RLERIKEANN ETYVEQHEVA VARYCDLPSK LGHKLNGGGG SGGGGSGPGT  360
GGTEKRLLEE AERAHREQKE IIKKAQELHR RLEEIVRQSG SSEEAKKEAK KILEEIRELS  420
KRSLELLREI LYLSQEQKGS LVPR                                         444

SEQ ID NO: 164          moltype = AA  length = 396
FEATURE                 Location/Qualifiers
REGION                  1..396
                        note = Fusion of DD-N degron with mGreenLantern and
                         synthetic coiled-coil domain P4 (partner of P3)
source                  1..396
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 164
GVQVETISPG DGRTFPKRGQ TCVVHYTGML EDGKKVDSSR DRNKPFKFML GKQEVIRGWE  60
EGVAQMSVGQ RAKLTISPDY AYGATGHPGI IPPHATLVFD VELLKPEGSG VSKGEELFTG  120
VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL VTTLGYGVAC  180
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FARYPDHMKQ HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV NRIVLKGIDF  240
KEDGNILGHK LEYNFNSHKV YITADKQKNG IKANFKTRHN VEDGGVQLAD HYQQNTPIGD  300
GPVLLPDNHY LSHQSKLSKD PNEKRDHMVL KERVTAAGIT HDMDELYKGG GGSGGGGSGP  360
GTGSPEDKIA QLKQKIQALK QENQQLEEEN AALEYG                            396

SEQ ID NO: 165          moltype = AA  length = 365
FEATURE                 Location/Qualifiers
REGION                  1..365
                        note = Fusion of Mus musculus Metallothionein 3, the shell
                         forming monomer of the Encapsulin system of Quasibacillus
                         thermotolerans and a C-terminal FLAG-Tag
source                  1..365
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 165
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDK                                                              365

SEQ ID NO: 166          moltype = AA  length = 370
FEATURE                 Location/Qualifiers
REGION                  1..370
                        note = Fusion of Mus musculus Metallothionein 3, the shell
                         forming monomer of the Encapsulin system of Myxococcus
                         xanthus and a C-terminal FLAG-Tag
source                  1..370
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 166
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGPDFLGHA ENPLREEEWA RLNETVIQVA RRSLVGRRIL DIYGPLGAGV  120
QTVPYDEFQG VSPGAVDIVG EQETAMVFTD ARKFKTIPII YKDFLLHWRD IEAARTHNMP  180
LDVSAAAGAA ALCAQQEDEL IFYGDARLGY EGLMTANGRL TVPLGDWTSP GGGFQAIVEA  240
TRKLNEQGHF GPYAVVLSPR LYSQLHRIYE KTGVLEIETI RQLASDGVYQ SNRLRGESGV  300
VVSTGRENMD LAVSMDMVAA YLGASRMNHP FRVLEALLLR IKHPDAICTL EGAGATERRG  360
SGDYKDDDDK                                                         370

SEQ ID NO: 167          moltype = AA  length = 381
FEATURE                 Location/Qualifiers
REGION                  1..381
                        note = Fusion of Mus musculus Metallothionein 3, the shell
                         forming monomer of the Encapsulin system of Myxococcus
                         xanthus and a C-terminal FLAG-Tag followed by a
                         cMyc-derived nuclear localization signal (NLS)
source                  1..381
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 167
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGPDFLGHA ENPLREEEWA RLNETVIQVA RRSLVGRRIL DIYGPLGAGV  120
QTVPYDEFQG VSPGAVDIVG EQETAMVFTD ARKFKTIPII YKDFLLHWRD IEAARTHNMP  180
LDVSAAAGAA ALCAQQEDEL IFYGDARLGY EGLMTANGRL TVPLGDWTSP GGGFQAIVEA  240
TRKLNEQGHF GPYAVVLSPR LYSQLHRIYE KTGVLEIETI RQLASDGVYQ SNRLRGESGV  300
VVSTGRENMD LAVSMDMVAA YLGASRMNHP FRVLEALLLR IKHPDAICTL EGAGATERRG  360
SGDYKDDDDK GGPAAKRVKL D                                            381

SEQ ID NO: 168          moltype = AA  length = 376
FEATURE                 Location/Qualifiers
REGION                  1..376
                        note = Fusion of Mus musculus Metallothionein 3, the shell
                         forming monomer of the Encapsulin system of Quasibacillus
                         thermotolerans and a C-terminal FLAG-Tag followed by a
                         cMyc-derived nuclear localization signal (NLS)
source                  1..376
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 168
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
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VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDKGGPAA KRVKLD                                                  376

SEQ ID NO: 169          moltype = AA  length = 420
FEATURE                 Location/Qualifiers
REGION                  1..420
                        note = Fusion of 3xMT with QtEnc and a C-terminal FLAG-Tag.
source                  1..420
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 169
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG TGGSTSTTLV KCACEPCLCN VDPSKAIDRN GLYYCSEACA DGHTGGSKGC  120
GHTGCNCHGS AGGCDDKCGC AVPCPGGTGC RCTSARSGAA AGEHTTCGCG EHCGCNPCAC  180
GREGTPSGRA NRRANCSCGA ACNCASCGSA TAPGGGGSGG GSGGSANKSQ LYPDSPLTDQ  240
DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD FQGSFDTEVE  300
SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED QMIFHGSKEF  360
DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS PELYSLLHRV  420

SEQ ID NO: 170          moltype = AA  length = 162
FEATURE                 Location/Qualifiers
source                  1..162
                        mol_type = protein
                        organism = Rattus norvegicus
SEQUENCE: 170
GDDEGRQSPV SWTSLFALQT EDGFWKLTPE LGLILKLNVN ALLNSLEEKG IRSLGTKGRE  60
RLLDLIATLL VLQFLYTKLE QEGMAAKSLI KMDDVLISRN IPWAFENIKK AREWARRTEG  120
QYPSICQRLE LGKDWESATK QLLGIQHQGN TSLHRILHYS QG                     162

SEQ ID NO: 171          moltype = AA  length = 193
FEATURE                 Location/Qualifiers
REGION                  1..193
                        note = MT3 fused to SpyCatcher003
source                  1..193
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 171
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQPP PPRTGPPPPR VTTLSGLSGE QGPSGDMTTE EDSATHIKFS KRDEDGRELA  120
GATMELRDSS GKTISTWISD GHVKDFYLYP GKYTFVETAA PDGYEVATPI EFTVNEDGQV  180
TVDGEATEGD AHT                                                     193

SEQ ID NO: 172          moltype = AA  length = 359
FEATURE                 Location/Qualifiers
REGION                  1..359
                        note = Fusion of antiALFATag intrabody with a MT3 tandem,
                         GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..359
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 172
MEVQLQESGG GLVQPGGSLR LSCTASGVTI SALNAMAMGW YRQAPGERRV MVAAVSERGN  60
AMYRESVQGR FTVTRDFTNK MVSLQMDNLK PEDTAVYYCH VLEDRVDSFH DYWGQGTQVT  120
VSSGAPGFSS ISASGGTGGS DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  180
CEKCAKDCVC KGEEGAKAEA EKCSCCQGGG SGGGSGGSAD PETCPCPTGG SCTCSDKCKC  240
KGCKCTNCKK SCCSCCPAGC EKCAKDCVCK GEEGAKAEAE KCSCCQGSGP GYKLILNGKT  300
LKGETTTEAV DAATAEKVFK QYANDNGVDG EWTYDDATKT FTVTEGDYKD DDDKGRRVG   359

SEQ ID NO: 173          moltype = AA  length = 560
FEATURE                 Location/Qualifiers
REGION                  1..560
                        note = Fusion of antiHA frankenbody with a MeLanM tandem,
                         GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..560
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 173
MAEVKLVESG GGLVKPGGSL KLSCAASGFT FSSYGMSWVR QTPEKRLEWV ATISRGGSYT  60
YYPDSVKGRF TISRDNAKNT LYLQMSSLRS EDTAIYYCAR RETYDEKGFA YWGQGTTLTV  120
SSGGGGSGGG GSGGGGSDIV LTQSPASLTV SLGQRATISC KSSQSLLNSG NQKNYLTWYQ  180
QKPGQPPKLL IYWASTRESG IPARFSGSGS GTDFTLNIHP VEEEDAATYY CQNDNSHPLT  240
FGAGTKLEIG GTGGSPTTTT KVDIAAFDPD KDGTIDLKEA LAAGSAAFDK LDPDKDGTLD  300
AKELKGRVSE ADLKKLDPDN DGTLDKKEYL AAVEAQFKAA NPDNDGTIDA RELASPAGSA  360
LVNLIRGGGG SGGGGSPTTT TKVDIAAFDP DKDGTIDLKE ALAAGSAAFD KLDPDKDGTL  420
DAKELKGRVS EADLKKLDPD NDGTLDKKEY LAAVEAQFKA ANPDNDGTID ARELASPAGS  480
ALVNLIRGSG PGYKLILNGK TLKGETTTEA VDAATAEKVF KQYANDNGVD GEWTYDDATK  540
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TFTVTEGDYK DDDDKGRRVG                                                560

SEQ ID NO: 174          moltype = AA  length = 450
FEATURE                 Location/Qualifiers
REGION                  1..450
                        note = Fusion of antiMoonTag intrabody with a AssVanabin2
                         tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..450
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 174
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSS KVIFALVLVV VLVACINATY VEFEEAYAPV DCKGQCTTPC EPLTACKEKC  180
AESCETSADK KTCRRNCKKA DCEPQDKVCD ACRMKCHKAC RAANCASECP KHEHKSDTCR  240
ACMKTNCKGG GGSGGGGSSK VIFALVLVVV LVACINATYV EFEEAYAPVD CKGQCTTPCE  300
PLTACKEKCA ESCETSADKK TCRRNCKKAD CEPQDKVCDA CRMKCHKACR AANCASECPK  360
HEHKSDTCRA CMKTNCKGSG PGYKLILNGK TLKGETTTEA VDAATAEKVF KQYANDNGVD  420
GEWTYDDATK TFTVTEGDYK DDDDKGRRVG                                   450

SEQ ID NO: 175          moltype = AA  length = 434
FEATURE                 Location/Qualifiers
REGION                  1..434
                        note = Fusion of antiMoonTag intrabody with a MeLanM
                         tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..434
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 175
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSP TTTTKVDIAA FDPDKDGTID LKEALAAGSA AFDKLDPDKD GTLDAKELKG  180
RVSEADLKKL DPDNDGTLDK KEYLAAVEAQ FKAANPDNDG TIDARELASP AGSALVNLIR  240
GGGGSGGGGS PTTTTKVDIA AFDPDKDGTI DLKEALAAGS AAFDKLDPDK DGTLDAKELK  300
GRVSEADLKK LDPDNDGTLD KKEYLAAVEA QFKAANPDND GTIDARELAS PAGSALVNLI  360
RGSGPGYKLI LNGKTLKGET TTEAVDAATA EKVFKQYAND NGVDGEWTYD DATKTFTVTE  420
GDYKDDDDKG RRVG                                                    434

SEQ ID NO: 176          moltype = AA  length = 358
FEATURE                 Location/Qualifiers
REGION                  1..358
                        note = Fusion of antiMoonTag intrabody with a 4xP3 CCC-Tag,
                         GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..358
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 176
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSS PEDEIQQLEE EIAQLEQKNA ALKEKNQALK YGLKSGPGSG SPEDEIQQLE  180
EEIAQLEQKN AALKEKNQAL KYGTGSGPGS GSPEDEIQQL EEEIAQLEQK NAALKEKNQA  240
LKYGLKSGPG SGSPEDEIQQ LEEEIAQLEQ KNAALKEKNQ ALKYGGSGPG YKLILNGKTL  300
KGETTTEAVD AATAEKVFKQ YANDNGVDGE WTYDDATKTF TVTEGDYKDD DDKGRRVG    358

SEQ ID NO: 177          moltype = AA  length = 348
FEATURE                 Location/Qualifiers
REGION                  1..348
                        note = Fusion of antiMoonTag intrabody with a MT3 tandem,
                         GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..348
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 177
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSD PETCPCPTGG SCTCSDKCKC KGCKCTNCKK SCCSCCPAGC EKCAKDCVCK  180
GEEGAKAEAE KCSCCQGGGS GGGSGGSADP ETCPCPTGGS CTCSDKCKCK GCKCTNCKKS  240
CCSCCPAGCE KCAKDCVCKG EEGAKAEAEK CSCCQGSGPG YKLILNGKTL KGETTTEAVD  300
AATAEKVFKQ YANDNGVDGE WTYDDATKTF TVTEGDYKDD DDKGRRVG               348

SEQ ID NO: 178          moltype = AA  length = 387
FEATURE                 Location/Qualifiers
REGION                  1..387
                        note = Fusion of antiMoonTag intrabody with a EcCusF
                         tandem, GB1 domain, a FLAG-Tag and C-terminal RXXG degron.
source                  1..387
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                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 178
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSD PETCPCPTGG SCTCSDKCKC KGCKCTNCKK SCCSCCPAGC EKCAKDCVCK  180
GEEGAKAEAE KCSCCQMNEH HHETMSEAQP QVISATGEVK GIDLESKKIT IHHDPIAAVN  240
WPEMTMRFTI TPQTKMSEIK TGDKVAFNFV QQGNLSLLQD IKVSQMNEHH HETMSEAQPQ  300
VISATGEVKG IDLESKKITI HHDPIAAVNW PEMTMRFTIT PQTKMSEIKT GDKVAFNFVQ  360
QGNLSLLQDI KVSQDYKDDD DKGRRVG                                      387

SEQ ID NO: 179          moltype = AA  length = 442
FEATURE                 Location/Qualifiers
REGION                  1..442
                        note = Fusion of LifeAct-peptide to emFPv4
source                  1..442
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 179
MGVADLIKKF ESISKEEGTG SKNEQELLEL DKWASLQQQK NEQELLELDK WASLQQQKNE  60
QELLELDKWA SLGQVSKGEE LFTGVVPILV ELDGDVNGHK FSVRGEGEGD ATNGKLTLKF  120
ICTTGKLPVP WPTLVTTLGY GVACFARYPD HMKQHDFFKS AMPEGYVQER TISFKDDGTY  180
KTRAEVKFEG DTLVNRIVLK GIDFKEDGNI LGHKLEYNFN SHKVYITADK QKNGIKANFK  240
TRHNVEGGKN EQELLELDKW ASLQQQKNEQ ELLELDKWAS LGGQQGGKNE QELLELDKWA  300
SLQQQKNEQE LLELDKWASL GGDGGVQLAD HYQQNTPIGD GPVLLPDNHY LSHQSKLSKD  360
PNEKRDHMVL KERVTAAGIT HDMDELYKGQ GKNEQELLEL DKWASLQQQK NEQELLELDK  420
WASLQQQKNE QELLELDKWA SL                                           442

SEQ ID NO: 180          moltype = DNA  length = 1329
FEATURE                 Location/Qualifiers
misc_feature            1..1329
                        note = DNA sequence encoding QtEnc-FLAG followed by a TGA
                         stop codon, followed by the read-through promoting
                         sequence "RT20s" followed by an anti-GFPintrabody with a
                         C-terminal HiBit peptide.
source                  1..1329
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 180
atgaacaaga gccagctgta ccctgacagc cctctgaccg accaggactt caaccagctg  60
gaccagaccg tgattgaagc cgccagaagg cagctcgtcg gcagaagatt catcgagctg  120
tacggccctc tcggcagagg catgcagagc gtgttcaacg acatcttcat ggaaagccac  180
gaggccaaga tggacttcca gggcagcttc gacaccgagg tggaaagcag cagaagagtg  240
aactacacaa tccccatgct gtacaaggac ttcgtgctgt actggcgcga cctggaacag  300
agcaaggccc tggacatccc catcgatttt tccgtggccg ccaacgccgc tagagatgtg  360
gcctttctgg aagatcagat gatctttcac ggcagcaaag agttcgacat ccccggcctg  420
atgaacgtga agggcagact gacacacctg atcggcaatt ggtacgagag cggcaacgcc  480
ttccaggaca tcgtggaagc ccggaacaag ctgctggaaa tgaaccacaa cggcccctac  540
gctctggtgc tgagccctga gctgtatagc ctgctgcaca gagtgcacaa ggacaccaac  600
gtcctggaaa tcgagcacgt gcgcgagctg attaccgccg gtgtctttca gagccctgtg  660
ctgaagggaa agtccggcgt gatcgtgaac accggcagaa acaacctgga cctggccatc  720
agcgaggact tcgagacagc ctatctgggc gaagagggca tgaatcaccc cttccgggtg  780
tacgagacag tggtgctgcg gattaagagg cctgccgcca tctgcaccct gatcgatcct  840
gaagaaggct ccggcgacta caaggacgac gacgacaaat gacaattagc tcatccagac  900
attccgggcg gaggtggcag cggacctggt ggctccggcg tgcagctggt cgagtccgga  960
ggagctctgg ttcagcccgg cggctctctt cgactcagtt gtgccgcatc tggcttcccc  1020
gtgaaccgat attcaatgag atggtaccgg caggctcccg gaaaggagcg cgaatgggtt  1080
gccggaatgt cctccgccgg cgaccgatca tcttacgaag actctgtcaa aggcagattc  1140
accatcagca gagatgacgc ccggaatacc gtctatctcc agatgaactc tcttaagcct  1200
gaggatacag cagtctacta ctgcaacgtg aacgtgggat tcgagtattg gggacagggg  1260
acccaggtca ctgtgtcctc tggcagcggc ggcgtgagcg gctggcgcct gtttaaaaaa  1320
attagctaa                                                          1329

SEQ ID NO: 181          moltype = DNA  length = 2742
FEATURE                 Location/Qualifiers
misc_feature            1..2742
                        note = DNA sequence encoding QtEnc-FLAG followed by a TGA
                         stop codon, followed by a read-through promoting sequence
                         "RT20s", followed by an Ssp DnaE intein mutant (N159A)
                         which exhibits hyperfast N-terminal cleavage, followed by
                         a P2A peptide followed by a
source                  1..2742
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 181
atgaacaaga gccagctgta ccctgacagc cctctgaccg accaggactt caaccagctg  60
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gaccagaccg tgattgaagc cgccagaagg cagctcgtcg gcagaagatt catcgagctg  120
tacggccctc tcggcagagg catgcagagc gtgttcaacg acatcttcat ggaaagccac  180
gaggccaaga tggacttcca gggcagcttc gacaccgagg tggaaagcag cagaagagtg  240
aactacacaa tccccatgct gtacaaggac ttcgtgctgt actggcgcga cctggaacag  300
agcaaggccc tggacatccc catcgatttt tccgtggccg ccaacgccgc tagagatgtg  360
gcctttctgg aagatcagat gatctttcac ggcagcaaag agttcgacat ccccggcctg  420
atgaacgtga agggcagact gacacacctg atcggcaatt ggtacgagag cggcaacgcc  480
ttccaggaca tcgtggaagc ccggaacaag ctgctggaaa tgaaccacaa cggcccctac  540
gctctggtgc tgagccctga gctgtatagc ctgctgcaca gagtgcacaa ggacaccaac  600
gtcctggaaa tcgagcacgt gcgcgagctg attaccgccg gtgtctttca gagccctgtg  660
ctgaagggaa agtccggcgt gatcgtgaac accggcagaa acaacctgga cctggccatc  720
agcgaggact tcgagacagc ctatctgggc gaagagggca tgaatcaccc cttccgggtg  780
tacgagacag tggtgctgcg gattaagagg cctgccgcca tctgcaccct gatcgatcct  840
gaagaaggct ccggcgacta caaggacgac gacgacaaat agcaattagc tcatccagac  900
attccgtgtc tgtctttcgg caccgagatc ctgaccgtgg aatacggccc tctgcctatc  960
ggcaagatcg tgtccgaaga gatcaactgc agcgtgtaca gcgtggaccc agagggcaga  1020
gtgtacacac aggctatcgc ccagtggcac gacagaggcg aacaagaggt gctggaatac  1080
gagctggaag atggcagcgt gatcagagcc accagcgacc acagatttct gaccaccgac  1140
taccagctgc tggccatcga ggaaatcttc gccagacagc tggacctgct gaccctggaa  1200
aacatcaagc agaccgagga agccctggac aaccacagac tgccctttcc actgctggat  1260
gccggcacca tcaagatggt caaagtgatc ggcagacgca gcctgggcgt gcagagaatc  1320
ttcgatatcg gactgcccca ggaccacaac tttctgctgg ctaacggcgc tatcgccgct  1380
gcctgttctt gtggctctgg atctagaggc ggctctggcg ccacaaactt cagcctgctt  1440
aaacaggccg gcgacgtgga agagaacccc ggacctaaca agagccagct gtaccctgac  1500
agccctctga ccgaccagga cttcaaccag ctggaccaga ccgtgattga agccgccaga  1560
aggcagctcg tcggcagaag attcatcgag ctgtacggcc ctctcggcag aggcatgcag  1620
agcgtgttca acgacatctt catggaaagc cacgaggcca agatggactt ccagggcagc  1680
ttcgacaccg aggtggaaag cagcagaaga gtgaactaca caatccccat gctgtacaag  1740
gacttcgtgc tgtactggcg cgacctggaa cagagcaagg ccctggacat ccccatcgat  1800
ttttccgtgg ccgccaacgc cgctagagat gtggcctttc tggaagatca gatgatcttt  1860
cacggcagca aagagttcga catccccggc ctgatgaacg tgaagggcag actgacacac  1920
ctgatcggca attggtacga gagcggcaac gccttccagg acatcgtgga agcccggaac  1980
aagctgctgg aaatgaacca caacggcccc tacgctctgg tgctgagccc tgagctgtat  2040
agcctgctgc acagagtgca caaggacacc aacgtcctgg aaatcgagca cgtgcgcgag  2100
ctgattaccg ccggtgtctt tcagagccct gtgctgaagg gaaagtccgg cgtgatcgtg  2160
aacaccggca gaaacaacct ggacctggcc atcagcgagg acttcgagac agcctatctg  2220
ggcgaagagg gcatgaatca ccccttccgg gtgtacgaga cagtggtgct gcggattaag  2280
aggcctgccg ccatctgcac cctgatcgat cctgaagaag gcggaggtgg cagcggacct  2340
ggtggctccg gcgtgcagct ggtcgagtcc ggaggagctc tggttcagcc cggcggctct  2400
cttcgactca gttgtgccgc atctggcttc cccgtgaacc gatattcaat gagatggtac  2460
cggcaggctc ccggaaagga gcgcgaatgg gttgccggaa tgtcctccgc cggcgaccga  2520
tcatcttacg aagactctgt caaaggcaga ttcaccatca gcagagatga cgcccggaat  2580
accgtctatc tccagatgaa ctctcttaag cctgaggata cagcagtcta ctactgcaac  2640
gtgaacgtgg gattcgagta ttggggacag gggacccagg tcactgtgtc ctctggcagc  2700
ggcggcgtga gcggctggcg cctgtttaaa aaaattagct aa                     2742

SEQ ID NO: 182          moltype = AA  length = 19
FEATURE                 Location/Qualifiers
source                  1..19
                        mol_type = protein
                        organism = Porcine tescho virus
SEQUENCE: 182
ATNFSLLKQA GDVEENPGP                                               19

SEQ ID NO: 183          moltype = AA  length = 558
FEATURE                 Location/Qualifiers
REGION                  1..558
                        note = Tandem MT3 fused to QtEnc which has a C-terminal
                         anti GFP intrabody
source                  1..558
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 183
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGSGGSA DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  120
CEKCAKDCVC KGEEGAKAEA EKCSCCQGSG PGNKSQLYPD SPLTDQDFNQ LDQTVIEAAR  180
RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS FDTEVESSRR VNYTIPMLYK  240
DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF HGSKEFDIPG LMNVKGRLTH  300
LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY SLLHRVHKDT NVLEIEHVRE  360
LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL GEEGMNHPFR VYETVVLRIK  420
RPAAICTLID PEEGGGGSGP GGSGVQLVES GGALVQPGGS LRLSCAASGF PVNRYSMRWY  480
RQAPGKEREW VAGMSSAGDR SSYEDSVKGR FTISRDDARN TVYLQMNSLK PEDTAVYYCN  540
VNVGFEYWGQ GTQVTVSS                                                558

SEQ ID NO: 184          moltype = AA  length = 238
FEATURE                 Location/Qualifiers
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source                  1..238
                        mol_type = protein
                        organism = Aequorea victoria
SEQUENCE: 184
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYK    238

SEQ ID NO: 185          moltype = AA  length = 235
FEATURE                 Location/Qualifiers
source                  1..235
                        mol_type = protein
                        organism = Anaplasma marginale
SEQUENCE: 185
VSKGEEDNMA IIKEFMRFKV HMEGSVNGHE FEIEGEGEGR PYEGTQTAKL KVTKGGPLPF  60
AWDILSPQFM YGSKAYVKHP ADIPDYLKLS FPEGFKWERV MNFEDGGVVT VTQDSSLQDG  120
EFIYKVKLRG TNFPSDGPVM QKKTMGWEAS SERMYPEDGA LKGEIKQRLK LKDGGHYDAE  180
VKTTYKAKKP VQLPGAYNVN IKLDITSHNE DYTIVEQYER AEGRHSTGGM DELYK       235

SEQ ID NO: 186          moltype = AA  length = 114
FEATURE                 Location/Qualifiers
REGION                  1..114
                        note = antiGFP-intrabody
source                  1..114
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 186
VQLVESGGAL VQPGGSLRLS CAASGFPVNR YSMRWYRQAP GKEREWVAGM SSAGDRSSYE  60
DSVKGRFTIS RDDARNTVYL QMNSLKPEDT AVYYCNVNVG FEYWGQGTQV TVSS        114

SEQ ID NO: 187          moltype = AA  length = 124
FEATURE                 Location/Qualifiers
REGION                  1..124
                        note = antimCherry intrabody (LaM-4)
source                  1..124
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 187
AQVQLVESGG SLVQPGGSLR LSCAASGRFA ESSSMGWFRQ APGKEREFVA AISWSGGATN  60
YADSAKGRFT LSRDNTKNTV YLQMNSLKPD DTAVYYCAAN LGNYISSNQR LYGYWGQGTQ  120
VTVS                                                               124

SEQ ID NO: 188          moltype = AA  length = 953
FEATURE                 Location/Qualifiers
REGION                  1..953
                        note = Fusion of sfGFP-SasG-G51-G54-mCherry
source                  1..953
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 188
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGGSAPKTIT ELEKKVEEIP FKKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG  300
VIISKGEPKE EITKDPINEL TEYGPETIAP GHRDEFDPKL PTGEKEEVPG KPGIKNPETG  360
DVVRPPVDSV TKYGPVKGDS IVEKEEIPFE KERKFNPDLA PGTEKVTREG QKGEKTITTP  420
TLKNPLTGEI ISKGESKEEI TKDPINELTE YGPETIAPGH RDEFDPKLPT GEKEEVPGKP  480
GIKNPETGDV VRPPVDSVTK YGPVKGDSIV EKEEIPFEKE RKFNPDLAPG TEKVTREGQK  540
GEKTITTPTL KNPLTGEIIS KGESKEEITK DPINELTEYG PETIAPGHRD EFDPKLPTGE  600
KEEVPGKPGI KNPETGDVVR PPVDSVTKYG PVKGDSIVEK EEIPFEKERK FNPDLAPGTE  660
KVTREGQKGE KTITTPTLKN PLTGEIISKG ESKEEITKDP INELTEYGPE TGSGATGSVS  720
KGEEDNMAII KEFMRFKVHM EGSVNGHEFE IEGEGEGRPY EGTQTAKLKV TKGGPLPFAW  780
DILSPQFMYG SKAYVKHPAD IPDYLKLSFP EGFKWERVMN FEDGGVVTVT QDSSLQDGEF  840
IYKVKLRGTN FPSDGPVMQK KTMGWEASSE RMYPEDGALK GEIKQRLKLK DGGHYDAEVK  900
TTYKAKKPVQ LPGAYNVNIK LDITSHNEDY TIVEQYERAE GRHSTGGMDE LYK         953

SEQ ID NO: 189          moltype = AA  length = 479
FEATURE                 Location/Qualifiers
REGION                  1..479
                        note = MT3 fused to QtEnc with a C-terminal anti GFP
                         intrabody
source                  1..479
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 189
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGVQLVE SGGALVQPGG SLRLSCAASG FPVNRYSMRW YRQAPGKERE WVAGMSSAGD  420
RSSYEDSVKG RFTISRDDAR NTVYLQMNSL KPEDTAVYYC NVNVGFEYWG QGTQVTVSS   479

SEQ ID NO: 190          moltype = AA  length = 402
FEATURE                 Location/Qualifiers
REGION                  1..402
                        note = Fusion of BmTyr and synthetic coiled-coil domain P2
                         (partner of P1)
source                  1..402
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 190
MGHSNKYRVR KNVLHLTDTE KRDFVRTVLI LKEKGIYDRY IAWHGAAGKF HTPPGSDRNA  60
AHMSSAFLPW HREYLLRFER DLQSINPEVT LPYWEWETDA QMQDPSQSQI WSADFMGGNG  120
NPIKDFIVDT GPFAAGRWTT IDEQGNPSGG LKRNFGATKE APTLPTRDDV LNALKITQYD  180
TPPWDMTSQN SFRNQLEGFI NGPQLHNRVH RWVGGQMGVV PTAPNDPVFF LHHANVDRIW  240
AVWQIIHRNQ NYQPMKNGPF GQNFRDPMYP WNTTPEDVMN HRKLGYVYDI ELRKSKRSSG  300
GGGSGGGGST GSPEDEIQAL EEENAQLEQE NAALEEEIAQ LEYGSGSETP GTSESATPES  360
AISHGFPPEV EEQAAGTLPM SCAQESGMDR HPAACASARI NV                     402

SEQ ID NO: 191          moltype = AA  length = 375
FEATURE                 Location/Qualifiers
REGION                  1..375
                        note = Fusion of Brain FABP and superfolder GFP
source                  1..375
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 191
VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
DVVAVRHYEK APPPPRTGSK GEELFTGVVP ILVELDGDVN GHKFSVRGEG EGDATNGKLT  180
LKFICTTGKL PVPWPTLVTT LTYGVQCFSR YPDHMKRHDF FKSAMPEGYV QERTISFKDD  240
GTYKTRAEVK FEGDTLVNRI ELKGIDFKED GNILGHKLEY NFNSHNVYIT ADKQKNGIKA  300
NFKIRHNVED GSVQLADHYQ QNTPIGDGPV LLPDNHYLST QSVLSKDPNE KRDHMVLLEF  360
VTAAGITHGM DELYK                                                   375

SEQ ID NO: 192          moltype = AA  length = 699
FEATURE                 Location/Qualifiers
REGION                  1..699
                        note = Fusion of BM3h and superfolder GFP
source                  1..699
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 192
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQALKFVRD FAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLQR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLIAGHETTS GLLSFALYFL VKNPHVLQKA AEEAARVLVD  300
PVPSYKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTIWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLPPPPR TGSKGEELFT GVVPILVELD  480
GDVNGHKFSV RGEGEGDATN GKLTLKFICT TGKLPVPWPT LVTTLTYGVQ CFSRYPDHMK  540
RHDFFKSAMP EGYVQERTIS FKDDGTYKTR AEVKFEGDTL VNRIELKGID FKEDGNILGH  600
KLEYNFNSHN VYITADKQKN GIKANFKIRH NVEDGSVQLA DHYQQNTPIG DGPVLLPDNH  660
YLSTQSVLSK DPNEKRDHMV LLEFVTAAGI THGMDELYK                         699

SEQ ID NO: 193          moltype = AA  length = 135
FEATURE                 Location/Qualifiers
source                  1..135
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 193
FATRQVGNVT KPTVIISQEG DKVVIRTLST FKNTEISFQL GEEFDETTAD DRNCKSVVSL  60
DGDKLVHIQK WDGKETNFVR EIKDGKMVMT LTFGDVVAVR HYEKAGGGSG MVEAFCATWK  120
LTNSQNFDEY MKALG                                                   135

SEQ ID NO: 194          moltype = AA  length = 955
FEATURE                 Location/Qualifiers
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REGION                  1..955
                        note = Fusion of six B-FABP flanked by DnaE split intein
                         fragments C-intein (AA 103-137) on the N-term and N-Intein
                         (AA 1-102)
source                  1..955
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 194
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNGGGV EAFCATWKLT NSQNFDEYMK  60
ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE ISFQLGEEFD ETTADDRNCK  120
SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD VVAVRHYEKA GGGSGVEAFC  180
ATWKLTNSQN FDEYMKALGV GFATRQVGNV TKPTVIISQE GDKVVIRTLS TFKNTEISFQ  240
LGEEFDETTA DDRNCKSVVS LDGDKLVHIQ KWDGKETNFV REIKDGKMVM TLTFGDVVAV  300
RHYEKAGGGS GVEAFCATWK LTNSQNFDEY MKALGVGFAT RQVGNVTKPT VIISQEGDKV  360
VIRTLSTFKN TEISFQLGEE FDETTADDRN CKSVVSLDGD KLVHIQKWDG KETNFVREIK  420
DGKMVMTLTF GDVVAVRHYE KAGGGSGVEA FCATWKLTNS QNFDEYMKAL GVGFATRQVG  480
NVTKPTVIIS QEGDKVVIRT LSTFKNTEIS FQLGEEFDET TADDRNCKSV VSLDGDKLVH  540
IQKWDGKETN FVREIKDGKM VMTLTFGDVV AVRHYEKAGG GSGVEAFCAT WKLTNSQNFD  600
EYMKALGVGF ATRQVGNVTK PTVIISQEGD KVVIRTLSTF KNTEISFQLG EEFDETTADD  660
RNCKSVVSLD GDKLVHIQKW DGKETNFVRE IKDGKMVMTL TFGDVVAVRH YEKAGGGSGV  720
EAFCATWKLT NSQNFDEYMK ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE  780
ISFQLGEEFD ETTADDRNCK SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD  840
VVAVRHYEKA GGGCLSYETE ILTVEYGLLP IGKIVEKRIE CTVYSVDNNG NIYTQPVAQW  900
HDRGEQEVFE YCLEDGSLIR ATKDHKFMTV DGQMLPIDEI FERELDLMRV DNLPN       955

SEQ ID NO: 195          moltype = AA  length = 651
FEATURE                 Location/Qualifiers
REGION                  1..651
                        note = Fusion of three repeats of B-FABP fused to MmMT3
                         flanked by DnaE split intein fragments C-intein (AA
                         103-137) on the N-term and N-Intein (AA 1-102)
source                  1..651
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 195
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNGGGV EAFCATWKLT NSQNFDEYMK  60
ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE ISFQLGEEFD ETTADDRNCK  120
SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD VVAVRHYEKA GGGMDPETCP  180
CPTGGSCTCS DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC  240
QGGGVEAFCA TWKLTNSQNF DEYMKALGVG FATRQVGNVT KPTVIISQEG DKVVIRTLST  300
FKNTEISFQL GEEFDETTAD DRNCKSVVSL DGDKLVHIQK WDGKETNFVR EIKDGKMVMT  360
LTFGDVVAVR HYEKAGGGMD PETCPCPTGG SCTCSDKCKC KGCKCTNCKK SCCSCCPAGC  420
EKCAKDCVCK GEEGAKAEAE KCSCCQVEAF CATWKLTNSQ NFDEYMKALG VGFATRQVGN  480
VTKPTVIISQ EGDKVVIRTL STFKNTEISF QLGEEFDETT ADDRNCKSVV SLDGDKLVHI  540
QKWDGKETNF VREIKDGKMV MTLTFGDVVA VRHYEKAGGG MDPETCPCPT GGSCTCSDKC  600
KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE AEKCSCCQGG G           651

SEQ ID NO: 196          moltype = AA  length = 1094
FEATURE                 Location/Qualifiers
REGION                  1..1094
                        note = Fusion of three repeats of 2x B-FABP intermixed by
                         SpyTag003 and Spycatcher003 and flanked by DnaE split
                         intein fragments C-intein (AA 103-137) on the N-term and
                         N-Intein (AA 1-102)
source                  1..1094
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 196
MIKIATRKYL GKQNVYDIGV GEPHNFALKN GFIASNGGGV EAFCATWKLT NSQNFDEYMK  60
ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE ISFQLGEEFD ETTADDRNCK  120
SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD VVAVRHYEKA GGGSGVEAFC  180
ATWKLTNSQN FDEYMKALGV GFATRQVGNV TKPTVIISQE GDKVVIRTLS TFKNTEISFQ  240
LGEEFDETTA DDRNCKSVVS LDGDKLVHIQ KWDGKETNFV REIKDGKMVM TLTFGDVVAV  300
RHYEKAGGGS GRGVPHIVMV DAYKRYKGGG SGVEAFCATW KLTNSQNFDE YMKALGVGFA  360
TRQVGNVTKP TVIISQEGDK VVIRTLSTFK NTEISFQLGE EFDETTADDR NCKSVVSLDG  420
DKLVHIQKWD GKETNFVREI KDGKMVMTLT FGDVVAVRHY EKAGGGSGVE AFCATWKLTN  480
SQNFDEYMKA LGVGFATRQV GNVTKPTVII SQEGDKVVIR TLSTFKNTEI SFQLGEEFDE  540
TTADDRNCKS VVSLDGDKLV HIQKWDGKET NFVREIKDGK MVMTLTFGDV VAVRHYEKAG  600
GGSGVTTLSG LSGEQGPSGD MTTEEDSATH IKFSKRDEDG RELAGATMEL RDSSGKTIST  660
WISDGHVKDF YLYPGKYTFV ETAAPDGYEV ATPIEFTVNE DGQVTVDGEA TEGDAHTGGG  720
SGVEAFCATW KLTNSQNFDE YMKALGVGFA TRQVGNVTKP TVIISQEGDK VVIRTLSTFK  780
NTEISFQLGE EFDETTADDR NCKSVVSLDG DKLVHIQKWD GKETNFVREI KDGKMVMTLT  840
FGDVVAVRHY EKAGGGSGVE AFCATWKLTN SQNFDEYMKA LGVGFATRQV GNVTKPTVII  900
SQEGDKVVIR TLSTFKNTEI SFQLGEEFDE TTADDRNCKS VVSLDGDKLV HIQKWDGKET  960
NFVREIKDGK MVMTLTFGDV VAVRHYEKAG GGCLSYETEI LTVEYGLLPI GKIVEKRIEC  1020
TVYSVDNNGN IYTQPVAQWH DRGEQEVFEY CLEDGSLIRA TKDHKFMTVD GQMLPIDEIF  1080
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ERELDLMRVD NLPN                                                    1094

SEQ ID NO: 197          moltype = AA  length = 317
FEATURE                 Location/Qualifiers
REGION                  1..317
                        note = Fusion of QtEncapsulin and M13 a synthetic peptide
                         binding Calmodulin
source                  1..317
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 197
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EPPPPRPPPP RKRRWKKNFI  300
AVSAANRFKK ISSSGAL                                                 317

SEQ ID NO: 198          moltype = AA  length = 283
FEATURE                 Location/Qualifiers
source                  1..283
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 198
VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
DVVAVRHYEK PPPPRADQLT DEQIAEFKEA FSLFDKDGDG TITTKELGTV MRSLGQNPTE  180
AELQDMINEV DADGNGTIDF PEFLNLMARK MKDTDSEEKL KEAFRVFDKD GNGFISAAEL  240
RHVMTNLGEK LTDEEVDEMI READVDGDGQ VNYEEFVQVM MAK                    283

SEQ ID NO: 199          moltype = AA  length = 13
FEATURE                 Location/Qualifiers
REGION                  1..13
                        note = Synthetic Silver mineralizing peptide 4
source                  1..13
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 199
MNPSSLFRYL PSD                                                     13

SEQ ID NO: 200          moltype = AA  length = 1020
FEATURE                 Location/Qualifiers
source                  1..1020
                        mol_type = protein
                        organism = Prevotella sp.
SEQUENCE: 200
MKRTADGSEF ESPKKKRKVN IPALVENQKK YFGTYSVMAM LNAQTVLDHI QKVADIEGEQ  60
NENNENLWFH PVMSHLYNAK NGYDKQPEKT MFIIERLQSY FPFLKIMAEN QREYSNGKYK  120
QNRVEVNSND IFEVLKRAFG VLKMYRDLTN AYKTYEEKLN DGCEFLTSTE QPLSGMINNY  180
YTVALRNMNE RYGYKTEDLA FIQDKRFKFV KDAYGKKKSQ VNTGFFLSLQ DYNGDTQKKL  240
HLSGVGIALL ICLFLDKQYI NIFLSRLPIF SSYNAQSEER RIIIRSFGIN SIKLPKDRIH  300
SEKSNKSVAM DMLNEVKRCP DELFTTLSAE KQSRFRIISD DHNEVLMKRS SDRFVPLLLQ  360
YIDYGKLFDH IRFHVNMGKL RYLLKADKTC IDGQTRVRVI EQPLNGFGRL EEAETMRKQE  420
NGTFGNSGIR IRDFENMKRD DANPANYPYI VDTYTHYILE NNKVEMFIND KEDSAPLLPV  480
IEDDRYVVKT IPSCRMSTLE IPAMAFHMFL FGSKKTEKLI VDVHNRYKRL FQAMQKEEVT  540
AENIASFGIA ESDLPQKILD LISGNAHGKD VDAFIRLTVD DMLTDTERRI KRFKDDRKSI  600
RSADNKMGKR GFKQISTGKL ADFLAKDIVL FQPSVNDGEN KITGLNYRIM QSAIAVYDSG  660
DDYEAKQQFK LMFEKARLIG KGTTEPHPFL YKVFARSIPA NAVEFYERYL IERKFYLTGL  720
SNEIKKGNRV DVPFIRRDQN KWKTPAMKTL GRIYSEDLPV ELPRQMFDNE IKSHLKSLPQ  780
MEGIDFNNAN VTYLIAEYMK RVLDDDFQTF YQWNRNYRYM DMLKGEYDRK GSLQHCFTSV  840
EEREGLWKER ASRTERYRKQ ASNKIRSNRQ MRNASSEEIE TILDKRLSNS RNEYQKSEKV  900
IRRYRVQDAL LFLLAKKTLT ELADFDGERF KLKEIMPDAE KGILSEIMPM SFTFEKGGKK  960
YTITSEGMKL KNYGDFFVLA SDKRIGNLLE LVGSDIVSKE DGSKRTADGS EFEPKKKRKV  1020

SEQ ID NO: 201          moltype = AA  length = 1186
FEATURE                 Location/Qualifiers
source                  1..1186
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 201
MSVACVLKRK AVLWQDSFSP HLKHHPQEPA NPNMPVVLTS GTGSQAQPQP AANQALAAGT  60
HSSPVPGSIG VAGRSQDDAM VDYFFQRQHG EQLGGGGSGG GGYNNSKHRW PTGDNIHAEH  120
QVRSMDELNH DFQALALEGR AMGEQLLPGK KFWETDESSK DGPKGIFLGD QWRDSAWGTS  180
DHSVSQPIMV QRRPGQSFHV NSEVNSVLSP RSESGGLGVS MVEYVLSSSP GDSCLRKGGF  240
GPRDADSDEN DKGEKKNKGT FDGDKLGDLK EEGDVMDKTN GLPVQNGIDA DVKDFSRTPG  300
NCQNSANEVD LLGPNQNGSE GLAQLTSTNG AKPVEDFSNM ESQSVPLDPM EHVGMEPLQF  360
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DYSGTQVPVD SAAATVGLFD YNSQQQLFQR PNALAVQQLT AAQQQQYALA AAHQPHIGLA  420
PAAFVPNPYI ISAAPPGTDP YTAGLAAAAT LGPAVVPHQY YGVTPWGVYP ASLFQQQAAA  480
AAAATNSANQ QTTPQAQQGQ QQVLRGGASQ RPLTPNQNQQ GQQTDPLVAA AAVNSALAFG  540
QGLAAGMPGY PVLAPAAYYD QTGALVVNAG ARNGLGAPVR LVAPAPVIIS SSAAQAAVAA  600
AAASANGAAG GLAGTTNGPF RPLGTQQPQP QPQQQPNNNL ASSSFYGNNS LNSNSQSSSL  660
FSQGSAQPAN TSLGFGSSSS LGATLGSALG GFGTAVANSN TGSGSRRDSL TGSSDLYKRT  720
SSSLTPIGHS FYNGLSFSSS PGPVGMPLPS QGPGHSQTPP PSLSSHGSSS SLNLGGLTNG  780
SGRYISAAPG AEAKYRSASS ASSLFSPSST LFSSSRLRYG MSDVMPSGRS RLLEDFRNNR  840
YPNLQLREIA GHIMEFSQDQ HGSRFIQLKL ERATPAERQL VFNEILQAAY QLMVDVFGNY  900
VIQKFFEFGS LEQKLALAER IRGHVLSLAL QMYGCRVIQK ALEFIPSDQQ NEMVRELDGH  960
VLKCVKDQNG NHVVQKCIEC VQPQSLQFII DAFKGQVFAL STHPYGCRVI QRILEHCLPD  1020
QTLPILEELH QHTEQLVQDQ YGNYVIQHVL EHGRPEDKSK IVAEIRGNVL VLSQHKFASN  1080
VVEKCVTHAS RTERAVLIDE VCTMNDGPHS ALYTMMKDQY ANYVVQKMID VAEPGQRKIV  1140
MHKIRPHIAT LRKYTYGKHI LAKLEKYYMK NGVDLGPICG PPNGII                 1186

SEQ ID NO: 202         moltype = AA  length = 139
FEATURE                Location/Qualifiers
source                 1..139
                       mol_type = protein
                       organism = Anguilla anguilla
SEQUENCE: 202
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATE                                               139

SEQ ID NO: 203         moltype = AA  length = 239
FEATURE                Location/Qualifiers
source                 1..239
                       mol_type = protein
                       organism = Aequorea victoria
SEQUENCE: 203
MVSKGEELFT GVVPILVELD GDVNGHKFSV RGEGEGDATN GKLTLKFICT TGKLPVPWPT  60
LVTTLGYGVA CFARYPDHMK QHDFFKSAMP EGYVQERTIS FKDDGTYKTR AEVKFEGDTL  120
VNRIVLKGID FKEDGNILGH KLEYNFNSHK VYITADKQKN GIKANFKTRH NVEDGGVQLA  180
DHYQQNTPIG DGPVLLPDNH YLSHQSKLSK DPNEKRDHMV LKERVTAAGI THDMDELYK   239

SEQ ID NO: 204         moltype = AA  length = 408
FEATURE                Location/Qualifiers
REGION                 1..408
                       note = Engineered fluorescent Calcium integrator
source                 1..408
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 204
MGSDQLTEEQ IAEFKEAFSL FDKDGDGTIT TKELGTVMRS LGQNPTEAEL QDMINEVDAD  60
GDGTIDFPEF LTMMARKMKD TDSEEEIREA FRVFDKDGNG YISAAELRHV MTNLGEKLTD  120
EEVDEMIREA DIDGDGQVNY EEFVVMMTAK LECEKIYVRD GVLTGDIHMI LLLEGNAHYR  180
CDFRTTYKAK EKGVKLPGVH YVDHTIEILS HDKDYNKVKI YEYAVAHSGL PDNARRGGTG  240
GSMVSAIKPD MKIKLRMEGN VNGHHFVIDG DGTGKPYEGK QTMDLEVKEG GPLPFAFDIL  300
TTAFHYGNRV FVKYPDNIQD YFKQSFPKGY SWERSMTFED GGICYARSDI TMEGDTFYNK  360
VRFYGTNFPA NGPVMQKKTL KWMPSWTRSS RRKFNKTGHA LRAIGRLS               408

SEQ ID NO: 205         moltype = AA  length = 225
FEATURE                Location/Qualifiers
source                 1..225
                       mol_type = protein
                       organism = Discosoma sp.
SEQUENCE: 205
MASSEDVIKE FMRFKVRMEG SVNGHEFEIE GEGEGRPYEG TQTAKLKVTK GGPLPFAWDI  60
LSPQFQYGSK AYVKHPADIP DYLKLSFPEG FKWERVMNFE DGGVVTVTQD SSLQDGEFIY  120
KVKLRGTNFP SDGPVMQKKT MGWEASTERM YPEDGALKGE IKMRLKLKDG GHYDAEVKTT  180
YMAKKPVQLP GAYKTDIKLD ITSHNEDYTI VEQYERAEGR HSTGA                  225

SEQ ID NO: 206         moltype = AA  length = 121
FEATURE                Location/Qualifiers
REGION                 1..121
                       note = phostphopetptide binding Forkhead-associated domain
source                 1..121
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 206
FLTLKPLPDS IIQESLEIQQ GVNPFFIGRS EDCNCKIEDN RLSRVHCFIF KKRHAVGKSM  60
YESPAQGLDD IWYCHTGTNV SYLNNNRMIQ GTKFLLQDGD EIKIIWDKNN KFVIGFKVEI  120
N                                                                  121

SEQ ID NO: 207         moltype = AA  length = 131
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FEATURE                 Location/Qualifiers
REGION                  1..131
                        note = Coat protein
source                  1..131
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 207
MANKPMQPIT STANKIVWSD PTRLSTTFSA SLLRQRVKVG IAELNNVSGQ YVSVYKRPAP  60
KPEGCADACV IMPNENQSIR TVISGSAENL ATLKAEWETH KRNVDTLFAS GNAGLGFLDP  120
TAAIVSSDTT A                                                       131

SEQ ID NO: 208          moltype = AA  length = 678
FEATURE                 Location/Qualifiers
REGION                  1..678
                        note = Fusion of mEos4b together with APEX2 to a C-terminal
                         minimal interaction domain (mINT)
source                  1..678
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 208
MVSAIKPDMR IKLRMEGNVN GHHFVIDGDG TGKPYEGKQT MDLEVKEGGP LPFAFDILTT  60
AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSLTFEDGG ICNARNDITM EGDTFYNKVR  120
FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGNAHY RCDFRTTYKA  180
KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARRGGG GSGGGGDYKD  240
DDDKGKSYPT VSADYQDAVE KAKKKLRGFI AEKRCAPLML RLAFHSAGTF DKGTKTGGPF  300
GTIKHPAELA HSANNGLDIA VRLLEPLKAE FPILSYADFY QLAGVVAVEV TGGPKVPFHP  360
GREDKPEPPP EGRLPDPTKG SDHLRDVFGK AMGLTDQDIV ALSGGHTIGA AHKERSGFEG  420
PWTSNPLIFD NSYFTELLSG EKEGLLQLPS DKALLSDPVF RPLVDKYAAD EDAFFADYAE  480
AHQKLSELGF ADALQLPPLE RLTLDGGGSG GGGSGGGDDE GRQSPVSWTS LPALQTEDGF  540
WKLTPELGLI LKLNVNALLN SLEEKGIRSL GTKGRERLLD LIATLLVLQF LYTKLEQEGM  600
AAKSLIKMDD VLISRNIPWA FENIKKAREW ARRTEGQYPS ICQRLELGKD WESATKQLLG  660
IQHQGNTSLH RILHYSQG                                                678

SEQ ID NO: 209          moltype = AA  length = 880
FEATURE                 Location/Qualifiers
REGION                  1..880
                        note = Fusion of mouse Gap43 palmitoylation signal to the
                         N-terminus of the major vault protein (MVP).
source                  1..880
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 209
MLCCMRRTKQ VEKNDEDQKI ATEEAIIRIP PYHYIHVLDQ NSNVSRVEVG PKTYIRQDNE  60
RVLFAPVRMV TVPPRHYCIV ANPVSRDTQS SVLFDITGQV RLRHADQEIR LAQDPFPLYP  120
GEVLEKDITP LQVVLPNTAL HLKALLDFED KNGDKVMAGD EWLFEGPGTY IPQKEVEVVE  180
IIQATVIKQN QALRLRARKE CFDREGKGRV TGEEWLVRSV GAYLPAVFEE VLDLVDAVIL  240
TEKTALHLRA LQNFRDLRGV LHRTGEEWLV TVQDTEAHVP DVYEEVLGVV PITTLGPRHY  300
CVILDPMGPD GKNQLGQKRV VKGEKSFFLQ PGERLERGIQ DVYVLSEQQG LLLKALQPLE  360
EGESEEKVSH QAGDCWLIRG PLEYVPSAKV EVVEERQAIP LDQNEGIYVQ DVKTGKVRAV  420
IGSTYMLTQD EVLWEKELPS GVEELLNLGH DPLADRGQKG TAKPLQPSAP RNKTRVVSYR  480
VPHNAAVQVY DYRAKRARVV FGPELVTLDP EEQFTVLSLS AGRPKRPHAR RALCLLLGPD  540
FFTDVITIET ADHARLQLQL AYNWHFELKN RNDPAEAAKL FSVPDFVGDA CKAIASRVRG  600
AVASVTFDDF HKNSARIIRM AVFGFEMSED TGPDGTLLPK ARDQAVFPQN GLVVSSVDVQ  660
SVEPVDQRTR DALQRSVQLA IEITTNSQEA AAKHEAQRLE QEARGRLERQ KILDQSEAEK  720
ARKELLELEA MSMAVESTGN AKAEAESRAE AARIEGEGSV LQAKLKAQAL AIETEAELER  780
VKKVREMELI YARAQLELEV SKAQQLANVE AKKFKEMTEA LGPGTIRDLA VAGPEMQVKL  840
LQSLGLKSTL ITDGSSPINL FSTAFGLLGL GSDGQPPAQK                        880

SEQ ID NO: 210          moltype = AA  length = 485
FEATURE                 Location/Qualifiers
REGION                  1..485
                        note = N-terminal fusion of SNAP-tag connected via GS
                         linker to QtEnc with a C-terminal FLAG epitope
source                  1..485
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 210
MDKDCEMKRT TLDSPLGKLE LSGCEQGLHR IIFLGKGTSA ADAVEVPAPA AVLGGPEPLM  60
QATAWLNAYF HQPEAIEEFP VPALHHPVFQ QESFTRQVLW KLLKVVKFGE VISYSHLAAL  120
AGNPAATAAV KTALSGNPVP ILIPCHRVVQ GDLDVGGYEG GLAVKEWLLA HEGHRLGKPG  180
LGGGTGGSGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  240
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  300
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  360
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  420
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  480
DDDDK                                                              485
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SEQ ID NO: 211          moltype = AA  length = 600
FEATURE                 Location/Qualifiers
REGION                  1..600
                        note = N-terminal fusion of Halo-tag connected via GS
                         linker to QtEnc with a C-terminal FLAG epitope
source                  1..600
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 211
MAEIGTGFPF DPHYVEVLGE RMHYVDVGPR DGTPVLFLHG NPTSSYVWRN IIPHVAPTHR  60
CIAPDLIGMG KSDKPDLGYF FDDHVRFMDA FIEALGLEEV VLVIHDWGSA LGFHWAKRNP  120
ERVKGIAFME FIRPIPTWDE WPEFARETFQ AFRTTDVGRK LIIDQNVFIE GTLPMGVVRP  180
LTEVEMDHYR EPFLNPVDRE PLWRFPNELP IAGEPANIVA LVEEYMDWLH QSPVPKLLFW  240
GTPGVLIPPA EAARLAKSLP NCKAVDIGPG LNLLQEDNPD LIGSEIARWL STLEISGGGT  300
GGSGSGPGNK SQLYPDSPLT DQDFNQLDQT VIEAARRQLV GRRFIELYGP LGRGMQSVFN  360
DIFMESHEAK MDFQGSFDTE VESSRRVNYT IPMLYKDFVL YWRDLEQSKA LDIPIDFSVA  420
ANAARDVAFL EDQMIFHGSK EFDIPGLMNV KGRLTHLIGN WYESGNAFQD IVEARNKLLE  480
MNHNGPYALV LSPELYSLLH RVHKDTNVLE IEHVRELITA GVFQSPVLKG KSGVIVNTGR  540
NNLDLAISED FETAYLGEEG MNHPFRVYET VVLRIKRPAA ICTLIDPEEG SGDYKDDDDK  600

SEQ ID NO: 212          moltype = AA  length = 320
FEATURE                 Location/Qualifiers
REGION                  1..320
                        note = Fusion of MT3 to AA 110-346 of Pyrococcus furiosus
                         Encapsulin monomer with a C-terminal FLAG epitope.
source                  1..320
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 212
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGVEYFEKL RSALLDGVNK GRSLLKHLPV TRIEGQSFRV DIIKFEDGVR  120
VVKQEYKPIP LLKKKFYVGI RELNDGTYDV SIATKAGELL VKDEESLVIR EILSTEGIKK  180
MKLSSWDNPE EALNDLMNAL QEASNASAGP FGLIINPKRY AKLLKIYEKS GKMLVEVLKE  240
IFRGGIIVTL NIDENKVIIF ANTPAVLDVV VGQDVTLQEL GPEGDDVAFL VSEAIGIRIK  300
NPEAIVVLEG SGDYKDDDDK                                              320

SEQ ID NO: 213          moltype = AA  length = 320
FEATURE                 Location/Qualifiers
source                  1..320
                        mol_type = protein
                        organism = Pyrococcus furiosus
SEQUENCE: 213
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGVEYFEKL RSALLDGVNK GRSLLKHLPV TRIEGQSFRV DIIKFEDGVR  120
VVKQEYKPIP LLKKKFYVGI RELNDGTYDV SIATKAGELL VKDEESLVIR EILSTEGIKK  180
MKLSSWDNPE EALNDLMNAL QEASNASAGP FGLIINPKRY AKLLKIYEKS GKMLVEVLKE  240
IFRGGIIVTL NIDENKVIIF ANTPAVLDVV VGQDVTLQEL GPEGDDVAFL VSEAIGIRIK  300
NPEAIVVLEG SGDYKDDDDK                                              320

SEQ ID NO: 214          moltype = AA  length = 227
FEATURE                 Location/Qualifiers
REGION                  1..227
                        note = mEos4b
source                  1..227
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 214
MVSAIKPDMR IKLRMEGNVN GHHFVIDGDG TGKPYEGKQT MDLEVKEGGP LPFAFDILTT  60
AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSLTFEDGG ICNARNDITM EGDTFYNKVR  120
FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGNAHY RCDFRTTYKA  180
KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARR                227

SEQ ID NO: 215          moltype = AA  length = 227
FEATURE                 Location/Qualifiers
REGION                  1..227
                        note = mEosEM
source                  1..227
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 215
MVSAIKPDMR IKLRMEGNVN GHHFVIDGEG TGKPYEGKQT MDLEVKEGGP LPFAFDILTT  60
AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSMTFEDGG ICNARNDITM EGDTFYNKVR  120
FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGGAHY RCDFRTTYKA  180
KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARR                227
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SEQ ID NO: 216          moltype = AA  length = 316
FEATURE                 Location/Qualifiers
REGION                  1..316
                        note = iRFP713
source                  1..316
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 216
MAEGSVARQP DLLTCDDEPI HIPGAIQPHG LLLALAADMT IVAGSDNLPE LTGLAIGALI  60
GRSAADVFDS ETHNRLTIAL AEPGAAVGAP ITVGFTMRKD AGFIGSWHRH DQLIFLELEP  120
PQRDVAEPQA FFRRTNSAIR RLQAAETLES ACAAAAQEVR KITGFDRVMI YRFASDFSGE  180
VIAEDRCAEV ESKLGLHYPA STVPAQARRL YTINPVRIIP DINYRPVPVT PDLNPVTGRP  240
IDLSFAILRS VSPVHLEFMR NIGMHGTMSI SILRGERLWG LIVCHHRTPY YVDLDGRQAC  300
ELVAQVLAWQ IGVMEE                                                  316

SEQ ID NO: 217          moltype = AA  length = 132
FEATURE                 Location/Qualifiers
REGION                  1..132
                        note = TeAPCalpha
source                  1..132
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 217
MKTGEQRVKI ATLLSENEKK IVDKASQDLW RRRPDFIAPG GNAFGQRERA LCLRDYGWYL  60
RLITYGLLAG DKDPIESIGL IGVREMYNSL GVPVPGMVES IRCLKEASLS LLDEEDAKET  120
APYFDYIIQA MS                                                      132

SEQ ID NO: 218          moltype = AA  length = 494
FEATURE                 Location/Qualifiers
source                  1..494
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 218
DLSLSDINST VEVPEGHSFW KTLLAYSGPG ALVAVGYMDP GNWSTSITGG QNFQYLLLSI  60
IVISSLLAML LQNMAAKLGI VCQLDLAQAI RARTSRRLGF IFWILTELAI MATDIAEVIG  120
AAIALYLLFK IPIFLAVVIT VLDVFLLLLL NRIGFRKIEA LVVCLIFVIL FVFLYQIILS  180
QPAWHQVAKG LIPSWASVQT SPKIGGQTPL SASLGIIGAT IMPHNLFLHS AISQSRKIDR  240
TDSSKVAEAV RFSNWDSNIQ LSLAMVVNAL LLIMGVAVFK SGAVQDPSFF GLYQALSNPD  300
MVSNPVLAEA ARSGVLSTLF AVALLASGQN STITGTITGQ VIMEGFIHLR LPLWLRRLVT  360
RLIAIIPVVV CVAITSHQGS LDEHQALNNL MNNSQVFLAL ALPFSIVPLL MLTDSAAQMG  420
NQFKNTRWVK VMGWLTVIIL TLLNLISISS QIAGFFGDNP SSQDLLLSQV ISIGIILAMI  480
GLLIWTIIDI RRFT                                                    494

SEQ ID NO: 219          moltype = AA  length = 492
FEATURE                 Location/Qualifiers
source                  1..492
                        mol_type = protein
                        organism = Homo sapiens
SEQUENCE: 219
MKLLLLHPAF QSCLLLTLLG LWRTTPEAHA SSLGAPAISA ASFLQDLIHR YGEGDSLTLQ  60
QLKALLNHLD VGVGRGNVTQ HVQGHRNLST CFSSGDLFTA HNFSEQSRIG SSELQEFCPT  120
ILQQLDSRAC TSENQENEEN EQTEEGRPSA VEVWGYGLLC VTVISLCSLL GASVVPFMKK  180
TFYKRLLLYF IALAIGTLYS NALFQLIPEA FGFNPLEDYY VSKSAVVFGG FYLFFFTEKI  240
LKILLKQKNE HHHGHSHYAS ESLPSKKDQE EGVMEKLQNG DLDHMIPQHC SSELDGKAPM  300
VDEKVIVGSL SVQDLQASQS ACYWLKGVRY SDIGTLAWMI TLSDGLHNFI DGLAIGASFT  360
VSVFQGISTS VAILCEEFPH ELGDFVILLN AGMSIQQALF FNFLSACCCY LGLAFGILAG  420
SHFSANWIFA LAGGMFLYIS LADMFPEMNE VCQEDERKGS ILIPFIIQNL GLLTGFTIMV  480
VLTMYSGQIQ IG                                                      492

SEQ ID NO: 220          moltype = AA  length = 425
FEATURE                 Location/Qualifiers
REGION                  1..425
                        note = Fusion of Cystathionine gamma-lyase with QtSig
source                  1..425
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 220
MQEKDASSQG FLPHFQHFAT QAIHVGQDPE QWTSRAVVPP ISLSTTFKQG APGQHSGFEY  60
SRSGNPTRNC LEKAVAALDG AKYCLAFASG LAATVTITHL LKAGDQIICM DDVYGGTNRY  120
FRQVASEFGL KISFVDCSKI KLLEAAITPE TKLVWIETPT NPTQKVIDIE GCAHIVHKHG  180
DIILVVDNTF MSPYFQRPLA LGADISMYSA TKYMNGHSDV VMGLVSVNCE SLHNRLRFLQ  240
NSLGAVPSPI DCYLCNRGLK TLHVRMEKHF KNGMAVAQFL ESNPWVEKVI YPGLPSHPQH  300
ELVKRQCTGC TGMVTFYIKG TLQHAEIFLK NLKLFTLAES LGGFESLAEL PAIMTHASVL  360
KNDRDVLGIS DTLIRLSVGL EDEEDLLEDL DQALKAAHPP SGSHSGGGGS GGGGSKGFTV  420
GSLIQ                                                              425
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SEQ ID NO: 221          moltype = AA  length = 1070
FEATURE                 Location/Qualifiers
REGION                  1..1070
                        note = Fusion of Seap, a secreted form of Human embryonic
                         alkaline phosphatase, and QtSig
source                  1..1070
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 221
MLGPCMLLLL LLLGLRLQLS LGIIPVEEEN PDFWNREAAE ALGAAKKLQP AQTAAKNLII  60
FLGDGMGVST VTAARILKGQ KKDKLGPEIP LAMDRFPYVA LSKTYNVDKH VPDSGATATA  120
YLCGVKGNFQ TIGLSAAARF NQCNTTRGNE VISVMNRAKK AGKSVGVVTT TRVQHASPAG  180
TYAHTVNRNW YSDADVPASA RQEGCQDIAT QLISNMDIDV ILGGGRKYMF RMGTPDPEYP  240
DDYSQGGTRL DGKNLVQEWL AKRQGARYVW NRTELMQASL DPSVTHLMGL FEPGDMKYEI  300
HRDSTLDPSL MEMTEAALRL LSRNPRGFFL FVEGGRIDHG HHESRAYRAL TETIMFDDAI  360
ERAGQLTSEE DTLSLVTADH SHVFSFGGYP LRGSSIFGLA PGKARDRKAY TVLLYGNGPG  420
YVLKDGARPD VTESESGSPE YRQQSAVPLD EETHAGEDVA VFARGPQAHL VHGVQEQTFI  480
AHVMAFAACL EPYTACDLAP PAGTTDAAHP GRSVVPALLP LLAGTLLLLE TATAPMLGPC  540
MLLLLLLLGL RLQLSLGIIP VEEENPDFWN REAAEALGAA KKLQPAQTAA KNLIIFLGDG  600
MGVSTVTAAR ILKGQKKDKL GPEIPLAMDR FPYVALSKTY NVDKHVPDSG ATATAYLCGV  660
KGNFQTIGLS AAARFNQCNT TRGNEVISVM NRAKKAGKSV GVVTTTRVQH ASPAGTYAHT  720
VNRNWYSDAD VPASARQEGC QDIATQLISN MDIDVILGGG RKYMFRMGTP DPEYPDDYSQ  780
GGTRLDGKNL VQEWLAKRQG ARYVWNRTEL MQASLDPSVT HLMGLFEPGD MKYEIHRDST  840
LDPSLMEMTE AALRLLSRNP RGFFLFVEGG RIDHGHHESR AYRALTETIM FDDAIERAGQ  900
LTSEEDTLSL VTADHSHVFS FGGYPLRGSS IFGLAPGKAR DRKAYTVLLY GNGPGYVLKD  960
GARPDVTESE SGSPEYRQQS AVPLDEETHA GEDVAVFARG PQAHLVHGVQ EQTFIAHVMA  1020
FAACLEPYTA CDLAPPAGTT DAAHPGRSVV PALLPLLAGT LLLLETATAP             1070

SEQ ID NO: 222          moltype = AA  length = 1237
FEATURE                 Location/Qualifiers
REGION                  1..1237
                        note = Fusion of MnxG, component of the Bacillus sp.
                         Multimeric multicopper oxidase Mnx, and QtSig
source                  1..1237
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 222
MKRCFHVVAI PIRIVVNNFG DYNPNGMMYV LKENEHKVKR LVKKNPFSVV DLVQPLIIRA  60
NEGDEVEVLF ENQLPFNTSM HFQEAEYDVL TSDGANVGFN PDTTVAPGCK ILYRLRLPKE  120
GAYIFSDLGN PSSSEQGSNS NGLFGALFVE RRFSWWTDPV TGGPLNSGLY ADVHHPILPS  180
FREYAWLFSD EMEINDLTGN NPIDPVTGEP TESFHGVNYR YEPLHRRKQL IDEGVVCPDC  240
DGEEVHHDSW VFGDPATPIF RGYVGDPAKI RLIHAGVKET HVFHYHVHQW FNDPDNLESE  300
IFDSQAASPQ SHYDIEPLYG LGSLQRAIGD AIIHCHLYPH FGIGMWGMNR VFDTLQDGSQ  360
SYPNGVKIDA LQPLPDRPAP PRPTKEKPGF PNFIPGKPGF KAPRPPLGIV GGRGLTELEK  420
NAAVPKARPG AVFADPCIEN ANVIEYNISL IELPLVYNKQ GWHDPKGRIY ILDEDIDDVC  480
SGRKEPEPLI IHQPANTCIR INYTNRLPHI LDGDAFQLVT RSYEAGMHIH FVKFDVLVND  540
GANVGWNYDS SILPGETMRY EYYADVELKA WFFHDHLFAV QHQQHGVFGS GVVHPRFTKF  600
IDSNGGGEVG AGAQVTAVNP LIPDYRDFSL MVQDFSLLFD KKGNPIQPPE FPGSQDDPGL  660
FGVNYKNEPL QFRLGPDCDP AYTFSSFVHG DPCTPILRAY EGDPIRIRLL QGAQEESHSF  720
NVHGLRWSKE RSDLDSMFRE QQHIGISESF TFESYIPRAG DYLWAFETEE DLWNGLWGLI  780
RAYDEVVPDL IPLTDRPRPL KRSRLLPYRT GKPPRKGDCF KDDLIIPHKR CVKEFDIVAF  840
QVPIIYNEFG DVDQNGIVFS LREDMDDILS GLKNPEPLII RANVGDEVRV KLTSLLEFDK  900
FPFKDGIYPY PTVKEQAFYP PSLRISLHPQ LIQYDVKTSS GETVGYNYDQ TVGPGESITY  960
KWYVDFPVGA CGMWDMADIR NHKSQGAFGA FIAEPRGTEY LDPHTLKPVK TGASVVLRNN  1020
LLPDKREFVI IMHDGVRLHD KDGILITDPI DGILLGPDNP FEGDLVDTYD NGSRGFNYRS  1080
ERLINRYRKH PVLHDLFSSK LFGDPSTPLF ESYAGDPVTL RLIAPAERRR SHTFHLHGHY  1140
WRKDISDINS VTASFEGFNL AGSKQDFELF GGAGGFNQFP GDYMYRSGNI QWDIEQGMWG  1200
IMRVHGKRQP HLPPLEKGGG GSGGGGSKGF TVGSLIQ                           1237

SEQ ID NO: 223          moltype = AA  length = 1237
FEATURE                 Location/Qualifiers
source                  1..1237
                        mol_type = protein
                        organism = Bacillus sp.
SEQUENCE: 223
MKRCFHVVAI PIRIVVNNFG DYNPNGMMYV LKENEHKVKR LVKKNPFSVV DLVQPLIIRA  60
NEGDEVEVLF ENQLPFNTSM HFQEAEYDVL TSDGANVGFN PDTTVAPGCK ILYRLRLPKE  120
GAYIFSDLGN PSSSEQGSNS NGLFGALFVE RRFSWWTDPV TGGPLNSGLY ADVHHPILPS  180
FREYAWLFSD EMEINDLTGN NPIDPVTGEP TESFHGVNYR YEPLHRRKQL IDEGVVCPDC  240
DGEEVHHDSW VFGDPATPIF RGYVGDPAKI RLIHAGVKET HVFHYHVHQW FNDPDNLESE  300
IFDSQAASPQ SHYDIEPLYG LGSLQRAIGD AIIHCHLYPH FGIGMWGMNR VFDTLQDGSQ  360
SYPNGVKIDA LQPLPDRPAP PRPTKEKPGF PNFIPGKPGF KAPRPPLGIV GGRGLTELEK  420
NAAVPKARPG AVFADPCIEN ANVIEYNISL IELPLVYNKQ GWHDPKGRIY ILDEDIDDVC  480
SGRKEPEPLI IHQPANTCIR INYTNRLPHI LDGDAFQLVT RSYEAGMHIH FVKFDVLVND  540
GANVGWNYDS SILPGETMRY EYYADVELKA WFFHDHLFAV QHQQHGVFGS GVVHPRFTKF  600
IDSNGGGEVG AGAQVTAVNP LIPDYRDFSL MVQDFSLLFD KKGNPIQPPE FPGSQDDPGL  660
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FGVNYKNEPL QFRLGPDCDP AYTFSSFVHG DPCTPILRAY EGDPIRIRLL QGAQEESHSF  720
NVHGLRWSKE RSDLDSMFRE QQHIGISESF TFESYIPRAG DYLWAFETEE DLWNGLWGLI  780
RAYDEVVPDL IPLTDRPRPL KRSRLLPYRT GKPPRKGDCF KDDLIIPHKR CVKEFDIVAF  840
QVPIIYNEFG DVDQNGIVFS LREDMDDILS GLKNPEPLII RANVGDEVRV KLTSLLEFDK  900
FPFKDGIYPY PTVKEQAFYP PSLRISLHPQ LIQYDVKTSS GETVGYNYDQ TVGPGESITY  960
KWYVDFPVGA CGMWDMADIR NHKSQGAFGA FIAEPRGTEY LDPHTLKPVK TGASVVLRNN  1020
LLPDKREFVI IMHDGVRLHD KDGILITDPI DGILLGPDNP FEGDLVDTYD NGSRGFNYRS  1080
ERLINRYRKH PVLHDLFSSK LFGDPSTPLF ESYAGDPVTL RLIAPAERRR SHTFHLHGHY  1140
WRKDISDINS VTASFEGFNL AGSKQDFELF GGAGGFNQFP GDYMYRSGNI QWDIEQGMWG  1200
IMRVHGKRQP HLPPLEKGGG GSGGGGSKGF TVGSLIQ                           1237

SEQ ID NO: 224         moltype = AA  length = 103
FEATURE                Location/Qualifiers
source                 1..103
                       mol_type = protein
                       organism = Bacillus sp.
SEQUENCE: 224
MEALFPMSTD YSKMTDVNEI HDSAILEHFR NGIGHKTLVI SPSYPYMFVG IIKELIGDTV  60
MIDVETTHFA QLENREWYIH IHNIEVFYIE RPGAPKIPKL EDY                    103

SEQ ID NO: 225         moltype = AA  length = 82
FEATURE                Location/Qualifiers
REGION                 1..82
                       note = Designed uranyl binder with femtomolar affinity
source                 1..82
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 225
SNALDCRERI EKDLEDLEKE LMEMKSIKLS DDEEAVVERA LNYRDDSVYY LEKGDHITSF  60
GCITYAEGLT DSLRMLHRII EG                                           82

SEQ ID NO: 226         moltype = AA  length = 388
FEATURE                Location/Qualifiers
REGION                 1..388
                       note = Coiled-coil adapter to recruit an encapsulated
                        cargo, such as the fluorescent protein mEosEM fused to P4
                        to an encapsulin already harboring an MT3 for dual EM and
                        fluorescence detection.
source                 1..388
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 226
SPEDEIQQLE EEIAQLEQKN AALKEKNQAL KYGSGMDPET CPCPTGGSCT CSDKCKCKGC  60
KCTNCKKSCC SCCPAGCEKC AKDCVCKGEE GAKAEAEKCS CCQGSGGNKS QLYPDSPLTD  120
QDFNQLDQTV IEAARRQLVG RRFIELYGPL GRGMQSVFND IFMESHEAKM DFQGSFDTEV  180
ESSRRVNYTI PMLYKDFVLY WRDLEQSKAL DIPIDFSVAA NAARDVAFLE DQMIFHGSKE  240
FDIPGLMNVK GRLTHLIGNW YESGNAFQDI VEARNKLLEM NHNGPYALVL SPELYSLLHR  300
VHKDTNVLEI EHVRELITAG VFQSPVLKGK SGVIVNTGRN NLDLAISEDF ETAYLGEEGM  360
NHPFRVYETV VLRIKRPAAI CTLIDPEE                                     388

SEQ ID NO: 227         moltype = AA  length = 497
FEATURE                Location/Qualifiers
REGION                 1..497
                       note = Fusion of the fluorescent protein eUnaG to the outer
                        surface of encapsulin
source                 1..497
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 227
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GGNKSQLYPD SPLTDQDFNQ LDQTVIEAAR RQLVGRRFIE LYGPLGRGMQ  120
SVFNDIFMES HEAKMDFQGS FDTEVESSRR VNYTIPMLYK DFVLYWRDLE QSKALDIPID  180
FSVAANAARD VAFLEDQMIF HGSKEFDIPG LMNVKGRLTH LIGNWYESGN AFQDIVEARN  240
KLLEMNHNGP YALVLSPELY SLLHRVHKDT NVLEIEHVRE LITAGVFQSP VLKGKSGVIV  300
NTGRNNLDLA ISEDFETAYL GEEGMNHPFR VYETVVLRIK RPAAICTLID PEEGGGSGML  360
EKFVGTWKIA DSHNFGEYLK AIGAPKELSD GGDATTPTLY ISQKDGDKMS VKIENGPPTF  420
LDTQVKFKLG EEFDEFPSDR RKGVKSVVNL VGEKLVYVQK WDGKETTYVR EIKDGKLVVT  480
LTMGDVVAVR SYRRATE                                                 497

SEQ ID NO: 228         moltype = AA  length = 312
FEATURE                Location/Qualifiers
REGION                 1..312
                       note = CGU for attaching to the outer surface of encapsulin
                        via anti-GFP antibody
source                 1..312
                       mol_type = protein
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                        organism = synthetic construct
SEQUENCE: 228
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQPP PPRTGSKGEE LFTGVVPILV ELDGDVNGHK FSVRGEGEGD ATNGKLTLKF  120
ICTTGKLPVP WPTLVTTLTY GVQCFSRYPD HMKRHDFFKS AMPEGYVQER TISFKDDGTY  180
KTRAEVKFEG DTLVNRIELK GIDFKEDGNI LGHKLEYNFN SHNVYITADK QKNGIKANFK  240
IRHNVEDGSV QLADHYQQNT PIGDGPVLLP DNHYLSTQSV LSKDPNEKRD HMVLLEFVTA  300
AGITHGMDEL YK                                                      312

SEQ ID NO: 229         moltype = AA  length = 418
FEATURE                Location/Qualifiers
REGION                 1..418
                       note = Fusion of QtEnc and Brain FABP, embodiment of
                        concentric barcodes added to the outer surface of
                        encapsulins
source                 1..418
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 229
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EGGGGSGVEA FCATWKLTNS  300
QNFDEYMKAL GVGFATRQVG NVTKPTVIIS QEGDKVVIRT LSTFKNTEIS FQLGEEFDET  360
TADDRNCKSV VSLDGDKLVH IQKWDGKETN FVREIKDGKM VMTLTFGDVV AVRHYEKA    418

SEQ ID NO: 230         moltype = AA  length = 742
FEATURE                Location/Qualifiers
REGION                 1..742
                       note = Fusion of QtEnc and Bm3h, embodiment of concentric
                        barcodes added to the outer surface of encapsulins
source                 1..742
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 230
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EGGGGSGTIK EMPQPKTFGE  300
LKNLPLLNTD KPVQALMKIA DELGEIFKFE APGRVTRYLS SQRLIKEACD ESRFDKNLSQ  360
ALKFVRDFAG DGLFTSWTHE KNWKKAHNIL LPSFSQQAMK GYHAMMVDIA VQLVQKWERL  420
NADEHIEVPE DMTRLTLDTI GLCGFNYRFN SFYRDQPHPF ITSMVRALDE AMNKLQRANP  480
DDPAYDENKR QFQEDIKVMN DLVDKIIADR KASGEQSDDL LTHMLNGKDP ETGEPLDDEN  540
IRYQIITFLI AGHETTSGLL SFALYFLVKN PHVLQKAAEE AARVLVDPVP SYKQVKQLKY  600
VGMVLNEALR LWPTAPAFSL YAKEDTVLGG EYPLEKGDEL MVLIPQLHRD KTIWGDDVEE  660
FRPERFENPS AIPQHAFKPF GNGQRACIGQ QFALHEATLV LGMMLKHFDF EDHTNYELDI  720
KETLTLKPEG FVVKAKSKKI PL                                           742

SEQ ID NO: 231         moltype = AA  length = 355
FEATURE                Location/Qualifiers
REGION                 1..355
                       note = Fusion of QtEnc and MT3, embodiment of concentric
                        barcodes added to the outer surface of encapsulins
source                 1..355
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 231
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EGGGGSGMDP ETCPCPTGGS  300
CTCSDKCKCK GCKCTNCKKS CCSCCPAGCE KCAKDCVCKG EEGAKAEAEK CSCCQ       355

SEQ ID NO: 232         moltype = AA  length = 380
FEATURE                Location/Qualifiers
REGION                 1..380
                       note = Fusion of Brain FABP and superfolder GFP, for
                        attachment via anti-GFP intrabody attachment points, e.g.
                        to the outer surface of Encapsulins.
source                 1..380
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 232
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VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
DVVAVRHYEK APPPPRTGPP PPRSKGEELF TGVVPILVEL DGDVNGHKFS VRGEGEGDAT  180
NGKLTLKFIC TTGKLPVPWP TLVTTLTYGV QCFSRYPDHM KRHDFFKSAM PEGYVQERTI  240
SFKDDGTYKT RAEVKFEGDT LVNRIELKGI DFKEDGNILG HKLEYNFNSH NVYITADKQK  300
NGIKANFKIR HNVEDGSVQL ADHYQQNTPI GDGPVLLPDN HYLSTQSVLS KDPNEKRDHM  360
VLLEFVTAAG ITHGMDELYK                                              380

SEQ ID NO: 233         moltype = AA  length = 704
FEATURE                Location/Qualifiers
REGION                 1..704
                       note = Fusion of Bm3h and superfolder GFP, or attachment
                        via anti-GFP intrabody attachment points, e.g. to the
                        outer surface of Encapsulins.
source                 1..704
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 233
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQALKFVRD FAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLQR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLIAGHETTS GLLSFALYFL VKNPHVLQKA AEEAARVLVD  300
PVPSYKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTIWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLPPPPR TGPPPPRSKG EELFTGVVPI  480
LVELDGDVNG HKFSVRGEGE GDATNGKLTL KFICTTGKLP VPWPTLVTTL TYGVQCFSRY  540
PDHMKRHDFF KSAMPEGYVQ ERTISFKDDG TYKTRAEVKF EGDTLVNRIE LKGIDFKEDG  600
NILGHKLEYN FNSHNVYITA DKQKNGIKAN FKIRHNVEDG SVQLADHYQQ NTPIGDGPVL  660
LPDNHYLSTQ SVLSKDPNEK RDHMVLLEFV TAAGITHGMD ELYK                   704

SEQ ID NO: 234         moltype = AA  length = 204
FEATURE                Location/Qualifiers
REGION                 1..204
                       note = Fusion of MT3 and Lam4, for attachment to mCherry,
                        e.g. on SasG
source                 1..204
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 234
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQPP PPRTGPPPPR AQVQLVESGG SLVQPGGSLR LSCAASGRFA ESSSMGWFRQ  120
APGKEREFVA AISWSGGATN YADSAKGRFT LSRDNTKNTV YLQMNSLKPD DTAVYYCAAN  180
LGNYISSNQR LYGYWGQGTQ VTVS                                         204

SEQ ID NO: 235         moltype = AA  length = 267
FEATURE                Location/Qualifiers
REGION                 1..267
                       note = Fusion of Brain FABP and Lam4, , for attachment to
                        mCherry, e.g. on SasG
source                 1..267
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 235
VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
DVVAVRHYEK APPPPRTGPP PPRAQVQLVE SGGSLVQPGG SLRLSCAASG RFAESSSMGW  180
FRQAPGKERE FVAAISWSGG ATNYADSAKG RFTLSRDNTK NTVYLQMNSL KPDDTAVYYC  240
AANLGNYISS NQRLYGYWGQ GTQVTVS                                      267

SEQ ID NO: 236         moltype = AA  length = 591
FEATURE                Location/Qualifiers
REGION                 1..591
                       note = Fusion of Bm3h and Lam4, , for attachment to
                        mCherry, e.g. on SasG
source                 1..591
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 236
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQALKFVRD FAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLQR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLIAGHETTS GLLSFALYFL VKNPHVLQKA AEEAARVLVD  300
PVPSYKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTIWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
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FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLPPPPR TGPPPPRAQV QLVESGGSLV  480
QPGGSLRLSC AASGRFAESS SMGWFRQAPG KEREFVAAIS WSGGATNYAD SAKGRFTLSR  540
DNTKNTVYLQ MNSLKPDDTA VYYCAANLGN YISSNQRLYG YWGQGTQVTV S          591

SEQ ID NO: 237         moltype = AA  length = 4
FEATURE                Location/Qualifiers
REGION                 1..4
                       note = General linker used for protein fusions, including
                        direct fusions of CGUs to achieve the nanometer sizes of a
                        structural element
source                 1..4
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 237
GGSG                                                               4

SEQ ID NO: 238         moltype = AA  length = 201
FEATURE                Location/Qualifiers
REGION                 1..201
                       note = myristoyl switch motif for calicum-rependent
                        relocalization a structural element such as vaults to the
                        membrane
source                 1..201
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 238
GNSKSGALSK EILEELQLNT KFTEEELSSW YQSFLKECPS GRITRQEFQT IYSKFFPEAD  60
PKAYAQHVFR SFDANSDGTL DFKEYVIALH MTSAGKTNQK LEWAFSLYDV DGNGTISKNE  120
VLEIVTAIFK MISPEDTKHL PEDENTPEKR AEKIWGFFGK KDDDKLTEKE FIEGTLANKE  180
ILRLIQFEPQ KVKEKLKEKK L                                            201

SEQ ID NO: 239         moltype = AA  length = 15
FEATURE                Location/Qualifiers
REGION                 1..15
                       note = synthide-2 binding for FHA2
source                 1..15
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 239
PLARALTVAG LPGKK                                                   15

SEQ ID NO: 240         moltype = AA  length = 599
FEATURE                Location/Qualifiers
source                 1..599
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 240
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS CCPAGCEKCA KDCVCKGEEG  420
AKAEAEKCSC CQGSGLEKFV GTWKIADSHN FGEYLKAIGA PKELSDGGDA TTPTLYISQK  480
DGDKMSVKIE NGPPTFLDTQ VKFKLGEEFD EFPSDRRKGV KSVVNLVGEK LVYVQKWDGK  540
ETTYVREIKD GKLVVTLTMG DVVAVRSYRR ATEGSSEGGR RKWQKTGHAV RAIGRLSSS   599

SEQ ID NO: 241         moltype = AA  length = 521
FEATURE                Location/Qualifiers
source                 1..521
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 241
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGLEK  360
FVGTWKIADS HNFGEYLKAI GAPKELSDGG DATTPTLYIS QKDGDKMSVK IENGPPTFLD  420
TQVKFKLGEE FDEFPSDRRK GVKSVVNLVG EKLVYVQKWD GKETTYVREI KDGKLVVTLT  480
MGDVVAVRSY RRATEGSSEG GRRKWQKTGH AVRAIGRLSS S                      521

SEQ ID NO: 242         moltype = AA  length = 448
FEATURE                Location/Qualifiers
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source                  1..448
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 242
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EGSGLEKFVG TWKIADSHNF  300
GEYLKAIGAP KELSDGGDAT TPTLYISQKD GDKMSVKIEN GPPTFLDTQV KFKLGEEFDE  360
FPSDRRKGVK SVVNLVGEKL VYVQKWDGKE TTYVREIKDG KLVVTLTMGD VVAVRSYRRA  420
TEGSSEGGRR KWQKTGHAVR AIGRLSSS                                     448

SEQ ID NO: 243          moltype = AA  length = 857
FEATURE                 Location/Qualifiers
source                  1..857
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 243
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGLEK  360
FVGTWKIADS HNFGEYLKAI GAPKELSDGG DATTPTLYIS QKDGDKMSVK IENGPPTFLD  420
TQVKFKLGEE FDEFPSDRRK GVKSVVNLVG EKLVYVQKWD GKETTYVREI KDGKLVVTLT  480
MGDVVAVRSY RRATEGSSEG GRRKWQKTGH AVRAIGRLSS SGSGATNFSL LKQAGDVEEN  540
PGPADQLTEE QIAEFKEAFS LFDKDGDGTI TTKELGTVMR SLGQNPTEAE LQDMINEVDA  600
DGNGTIDFPE FLTMMARKMK DTDSEEEIRE AFRVFDKDGN GYISAAELRH VMTNLGEKLT  660
DEEVDEMIRE ADIDGDGQVN YEEFVQMMTA KSGGDIIKLL NEQVNKEMQS SNLYMSMSSW  720
CYTHSLDGAG LFLFDHAAEE YEHAKKLIIF LNENNVPVQL TSISAPEHKF EGLTQIFQKA  780
YEHEQHISES INNIVDHAIK SKDHATFNFL QWYVAEQHEE EVLFKDILDK IELIGNENHG  840
LYLADQYVKG IAKSRKS                                                 857

SEQ ID NO: 244          moltype = AA  length = 935
FEATURE                 Location/Qualifiers
source                  1..935
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 244
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS CCPAGCEKCA KDCVCKGEEG  420
AKAEAEKCSC CQGSGLEKFV GTWKIADSHN FGEYLKAIGA PKELSDGGDA TTPTLYISQK  480
DGDKMSVKIE NGPPTFLDTQ VKFKLGEEFD EFPSDRRKGV KSVVNLVGEK LVYVQKWDGK  540
ETTYVREIKD GKLVVTLTMG DVVAVRSYRR ATEGSSEGGR RKWQKTGHAV RAIGRLSSSG  600
SGATNFSLLK QAGDVEENPG PADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMRSL  660
GQNPTEAELQ DMINEVDADG NGTIDFPEFL TMMARKMKDT DSEEEIREAF RVFDKDGNGY  720
ISAAELRHVM TNLGEKLTDE EVDEMIREAD IDGDGQVNYE EFVQMMTAKS GGDIIKLLNE  780
QVNKEMQSSN LYMSMSSWCY THSLDGAGLF LFDHAAEEYE HAKKLIIFLN ENNVPVQLTS  840
ISAPEHKFEG LTQIFQKAYE HEQHISESIN NIVDHAIKSK DHATFNFLQW YVAEQHEEEV  900
LFKDILDKIE LIGNENHGLY LADQYVKGIA KSRKS                             935

SEQ ID NO: 245          moltype = AA  length = 1539
FEATURE                 Location/Qualifiers
source                  1..1539
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 245
MKEELDAPHQ IFTTTKEAIE RFMAMLTPVI ENAEDDHERL YYHHIYEEEE QRLSRLDVLI  60
PLIEKFQDET DEGLFSPSNN AFNRLLQELN LEKFGLHNFI EHVDLALFSF TDEERQTLLK  120
ELRKDAYEGY QYVKEKLAEI NARFDHDYAD PHAHHDEHRD HLADMPSAGS SHEEVQPVAH  180
KKKGFTVGSL IQGSGATNFS LLKQAGDVEE NPGPMNKSQL YPDSPLTDQD FNQLDQTVIE  240
AARRQLVGRR FIELYGPLGR GMQSVFNDIF MESHEAKMDF QGSFDTEVES SRRVNYTIPM  300
LYKDFVLYWR DLEQSKALDI PIDFSVAANA ARDVAFLEDQ MIFHGSKEFD IPGLMNVKGR  360
LTHLIGNWYE SGNAFQDIVE ARNKLLEMNH NGPYALVLSP ELYSLLHRVH KDTNVLEIEH  420
VRELITAGVF QSPVLKGKSG VIVNTGRNNL DLAISEDFET AYLGEEGMNH PFRVYETVVL  480
RIKRPAAICT LIDPEEGSGG GGGSGPGGSG LEKFVGTWKI ADSHNFGEYL KAIGAPKELS  540
DGGDATTPTL YISQKDGDKM SVKIENGPPT FLDTQVKFKL GEEFDEFPSD RRKGVKSVVN  600
LVGEKLVYVQ KWDGKETTYV REIKDGKLVV TLTMGDVVAV RSYRRATEGS SEGGRRKWQK  660
TGHAVRAIGR LSSSGSGATN FSLLKQAGDV EENPGPMADQ LTEEQIAEFK EAFSLFDKDG  720
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DGTITTKELG TVMRSLGQNP TEAELQDMIN EVDADGNGTI DFPEFLTMMA RKMKDTDSEE  780
EIREAFRVFD KDGNGYISAA ELRHVMTNLG EKLTDEEVDE MIREADIDGD GQVNYEEFVQ  840
MMTAKSGGDI IKLLNEQVNK EMQSSNLYMS MSSWCYTHSL DGAGLFLFDH AAEEYEHAKK  900
LIIFLNENNV PVQLTSISAP EHKFEGLTQI FQKAYEHEQH ISESINNIVD HAIKSKDHAT  960
FNFLQWYVAE QHEEEVLFKD ILDKIELIGN ENHGLYLADQ YVKGIAKSRK SGSGATNFSL  1020
LKQAGDVEEN PGPMKRLHPA LPSCLLLVLF GIWRTAPQTH ASSAGLPPLS ATSFLEDLMD  1080
RYGKNDSLTT QLKSLLDHLH VGVGRDNVSQ PKEGPRNLST CFSSGDLFAA HNLSERSQIG  1140
ASEFQEFCPT ILQQLDSQAC TSENQKSEEN EQTEEGKPSA IEVWGFGFLS VSLINLASLL  1200
GVLVLPCTEK AFFSRVLTYF IALSIGTLLS NALFQLIPEA FGFNPQDNYV SKSAVVFGGF  1260
YLFFFTEKIL KMLLKQKNEH HHGHNHFTSE TLPSKKDQEE GVTEKLQNGD LDHMIPQHCN  1320
SELDGKAPGT DEKVIVNSMS VQDLQASQSA CYWLKGVRYS DIGTLAWMIT LSDGLHNFID  1380
GLAIGASFTV SVFQGISTSV AILCEEFPHE LGDFVILLNA GMSIQQALFF NFLSACCCYL  1440
GLAFGILAGS HFSANWIFAL AGGMFLYIAL ADMFPEMNEV CQEDEKNDSF LVPFVIQNLG  1500
LLTGFSIMLV LTMYSGQIQI GGGGGSGGGG SDYKDDDDK                         1539

SEQ ID NO: 246          moltype = AA  length = 477
FEATURE                 Location/Qualifiers
source                  1..477
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 246
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGVEYFEKL RSALLDGVNK GRSLLKHLPV TRIEGQSFRV DIIKFEDGVR  120
VVKQEYKPIP LLKKKFYVGI RELNDGTYDV SIATKAGELL VKDEESLVIR EILSTEGIKK  180
MKLSSWDNPE EALNDLMNAL QEASNASAGP FGLIINPKRY AKLLKIYEKS GKMLVEVLKE  240
IFRGGIIVTL NIDENKVIIF ANTPAVLDVV VGQDVTLQEL GPEGDDVAFL VSEAIGIRIK  300
NPEAIVVLEG SGDYKDDDDK GGGGSGPGGS GANLDKMLNT TVTEVRQFLQ VDRVCVFQFE  360
EDYSGVVVVE AVDDRWISIL KTQVRDRYFM ETRGEEYSHG RYQAIADIYT ANLTECYRDL  420
LTQFQVRAIL AVPILQGKKL WGLLVAHQLA APRQWQTWEI DFLKQQAVVV GIAIQQS     477

SEQ ID NO: 247          moltype = AA  length = 445
FEATURE                 Location/Qualifiers
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 247
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGVEYFEKL RSALLDGVNK GRSLLKHLPV TRIEGQSFRV DIIKFEDGVR  120
VVKQEYKPIP LLKKKFYVGI RELNDGTYDV SIATKAGELL VKDEESLVIR EILSTEGIKK  180
MKLSSWDNPE EALNDLMNAL QEASNASAGP FGLIINPKRY AKLLKIYEKS GKMLVEVLKE  240
IFRGGIIVTL NIDENKVIIF ANTPAVLDVV VGQDVTLQEL GPEGDDVAFL VSEAIGIRIK  300
NPEAIVVLEG SGDYKDDDDK GGGGSGPGGS GVQLVESGGA LVQPGGSLRL SCAASGFPVN  360
RYSMRWYRQA PGKEREWVAG MSSAGDRSSY EDSVKGRFTI SRDDARNTVY LQMNSLKPED  420
TAVYYCNVNV GFEYWGQGTQ VTVSS                                        445

SEQ ID NO: 248          moltype = AA  length = 131
FEATURE                 Location/Qualifiers
source                  1..131
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 248
VEAFCATWKL TNSQNWDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRRLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNMVMEIKD GKMVMTLTFG  120
DVVAVSHWEK A                                                       131

SEQ ID NO: 249          moltype = AA  length = 464
FEATURE                 Location/Qualifiers
source                  1..464
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 249
MTIKEMPQPK TFGELKNLPL LNTDKPVQAL MKIADELGEI FKFEAPGRVT RYLSSQRLIK  60
EACDESRFDK NLSQAPKFVR DLAGDGLFTS WTHEKNWKKA HNILLPSFSQ QAMKGYHAMM  120
VDIAVQLVQK WERLNADEHI EVPEDMTRLT LDTIGLCGFN YRFNSFYRDQ PHPFITSMVR  180
ALDEAMNKLR RANPDDPAYD ENKRQFQEDI KVMNDLVDKI IADRKASGEQ SDDLLTHMLN  240
GKDPETGEPL DDENIRYQII TFLAAGHEAT SGLLSFALYF LVKNPHELQK AAEEAARVLV  300
DPVPSHKQVK QLKYVGMVLN EALRLWPTAP AFSLYAKEDT VLGGEYPLEK GDELMVLIPQ  360
LHRDKTVWGD DVEEFRPERF ENPSAIPQHA FKPFGNGQRA CIGQQFALHE ATLVLGMMLK  420
HFDFEDHTNY ELDIKETLTL KPEGFVVKAK SKKIPLGGIP SPST                   464

SEQ ID NO: 250          moltype = AA  length = 415
FEATURE                 Location/Qualifiers
source                  1..415
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 250
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MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGVEAFCA TWKLTNSQNW  300
DEYMKALGVG FATRQVGNVT KPTVIISQEG DKVVIRRLST FKNTEISFQL GEEFDETTAD  360
DRNCKSVVSL DGDKLVHIQK WDGKETNMVM EIKDGKMVMT LTFGDVVAVS HWEKA       415

SEQ ID NO: 251         moltype = AA  length = 297
FEATURE                Location/Qualifiers
source                 1..297
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 251
VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
DVVAVRHYEK ASGGDIIKLL NEQVNKEMQS SNLYMSMSSW CYTHSLDGAG LFLFDHAAEE  180
YEHAKKLIIF LNENNVPVQL TSISAPEHKF EGLTQIFQKA YEHEQHISES INNIVDHAIK  240
SKDHATFNFL QWYVAEQHEE EVLFKDILDK IELIGNENHG LYLADQYVKG IAKSRKS     297

SEQ ID NO: 252         moltype = AA  length = 298
FEATURE                Location/Qualifiers
source                 1..298
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 252
MVEAFCATWK LTNSQNWDEY MKALGVGFAT RQVGNVTKPT VIISQEGDKV VIRRLSTFKN  60
TEISFQLGEE FDETTADDRN CKSVVSLDGD KLVHIQKWDG KETNMVMEIK DGKMVMTLTF  120
GDVVAVSHWE KASGGDIIKL LNEQVNKEMQ SSNLYMSMSS WCYTHSLDGA GLFLFDHAAE  180
EYEHAKKLII FLNENNVPVQ LTSISAPEHK FEGLTQIFQK AYEHEQHISE SINNIVDHAI  240
KSKDHATFNF LQWYVAEQHE EEVLFKDILD KIELIGNENH GLYLADQYVK GIAKSRKS    298

SEQ ID NO: 253         moltype = AA  length = 621
FEATURE                Location/Qualifiers
source                 1..621
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 253
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQALKFVRD FAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLQR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLIAGHETTS GLLSFALYFL VKNPHVLQKA AEEAARVLVD  300
PVPSYKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTIWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLSGGDI IKLLNEQVNK EMQSSNLYMS  480
MSSWCYTHSL DGAGLFLFDH AAEEYEHAKK LIIFLNENNV PVQLTSISAP EHKFEGLTQI  540
FQKAYEHEQH ISESINNIVD HAIKSKDHAT FNFLQWYVAE QHEEEVLFKD ILDKIELIGN  600
ENHGLYLADQ YVKGIAKSRK S                                            621

SEQ ID NO: 254         moltype = AA  length = 629
FEATURE                Location/Qualifiers
source                 1..629
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 254
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQAPKFVRD LAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLRR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLAAGHEATS GLLSFALYFL VKNPHELQKA AEEAARVLVD  300
PVPSHKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTVWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLGGIPS PSTSGGDIIK LLNEQVNKEM  480
QSSNLYMSMS SWCYTHSLDG AGLFLFDHAA EEYEHAKKLI IFLNENNVPV QLTSISAPEH  540
KFEGLTQIFQ KAYEHEQHIS ESINNIVDHA IKSKDHATFN FLQWYVAEQH EEEVLFKDIL  600
DKIELIGNEN HGLYLADQYV KGIAKSRKS                                    629

SEQ ID NO: 255         moltype = AA  length = 142
FEATURE                Location/Qualifiers
source                 1..142
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 255
VEAFCATWKL TNSQNFDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRTLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNFVREIKD GKMVMTLTFG  120
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DVVAVRHYEK AGSGDYKDDD DK                                            142

SEQ ID NO: 256          moltype = AA  length = 142
FEATURE                 Location/Qualifiers
source                  1..142
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 256
VEAFCATWKL TNSQNWDEYM KALGVGFATR QVGNVTKPTV IISQEGDKVV IRRLSTFKNT  60
EISFQLGEEF DETTADDRNC KSVVSLDGDK LVHIQKWDGK ETNMVMEIKD GKMVMTLTFG  120
DVVAVSHWEK AGSGDYKDDD DK                                            142

SEQ ID NO: 257          moltype = AA  length = 466
FEATURE                 Location/Qualifiers
source                  1..466
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 257
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQALKFVRD FAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLQR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLIAGHETTS GLLSFALYFL VKNPHVLQKA AEEAARVLVD  300
PVPSYKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTIWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLGSGDY KDDDDK                 466

SEQ ID NO: 258          moltype = AA  length = 474
FEATURE                 Location/Qualifiers
source                  1..474
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 258
TIKEMPQPKT FGELKNLPLL NTDKPVQALM KIADELGEIF KFEAPGRVTR YLSSQRLIKE  60
ACDESRFDKN LSQAPKFVRD LAGDGLFTSW THEKNWKKAH NILLPSFSQQ AMKGYHAMMV  120
DIAVQLVQKW ERLNADEHIE VPEDMTRLTL DTIGLCGFNY RFNSFYRDQP HPFITSMVRA  180
LDEAMNKLRR ANPDDPAYDE NKRQFQEDIK VMNDLVDKII ADRKASGEQS DDLLTHMLNG  240
KDPETGEPLD DENIRYQIIT FLAAGHEATS GLLSFALYFL VKNPHELQKA AEEAARVLVD  300
PVPSHKQVKQ LKYVGMVLNE ALRLWPTAPA FSLYAKEDTV LGGEYPLEKG DELMVLIPQL  360
HRDKTVWGDD VEEFRPERFE NPSAIPQHAF KPFGNGQRAC IGQQFALHEA TLVLGMMLKH  420
FDFEDHTNYE LDIKETLTLK PEGFVVKAKS KKIPLGGIPS PSTGSGDYKD DDDK        474

SEQ ID NO: 259          moltype = AA  length = 260
FEATURE                 Location/Qualifiers
source                  1..260
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 259
MEVQLVESGG GLVQPGGSLR LSCAASGSIS SVDVMSWYRQ APGKQRELVA FITDRGRTNY  60
KVSVKGRFTI SRDNSKNMVY LQMNSLKPED TADYLCRAES RTSWSSPSPL DVWGRGTQVT  120
VSSGGTGGSV EAFCATWKLT NSQNFDEYMK ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI  180
RTLSTFKNTE ISFQLGEEFD ETTADDRNCK SVVSLDGDKL VHIQKWDGKE TNFVREIKDG  240
KMVMTLTFGD VVAVRHYEKA                                               260

SEQ ID NO: 260          moltype = AA  length = 541
FEATURE                 Location/Qualifiers
source                  1..541
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 260
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGTGGS  360
DKDCEMKRTT LDSPLGKLEL SGCEQGLHRI IFLGKGTSAA DAVEVPAPAA VLGGPEPLMQ  420
ATAWLNAYFH QPEAIEEFPV PALHHPVFQQ ESFTRQVLWK LLKVVKFGEV ISYSHLAALA  480
GNPAATAAVK TALSGNPVPI LIPCHRVVQG DLDVGGYEGG LAVKEWLLAH EGHRLGKPGL  540
G                                                                   541

SEQ ID NO: 261          moltype = AA  length = 541
FEATURE                 Location/Qualifiers
source                  1..541
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 261
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGTGGS  360
DKDCEMKRTT LDSPLGKLEL SGCEQGLHEI IFLGKGTSAA DAVEVPAPAA VLGGPEPLIQ  420
ATAWLNAYFH QPEAIEEFPV PALHHPVFQQ ESFTRQVLWK LLKVVKFGEV ISESHLAALV  480
GNPAATAAVN TALDGNPVPI LIPCHRVVQG DSDVGPYLGG LAVKEWLLAH EGHRLGKPGL  540
G                                                                  541

SEQ ID NO: 262          moltype = AA  length = 620
FEATURE                 Location/Qualifiers
source                  1..620
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 262
MGVKVLFALI CIAVAEAKRG TQPTFGFTVN WKFSESTTVF TGQCFIDRNG KEVLKTMWLL  60
RSSVNDIGDD WKATRVGINI FTRLRTQKEG GSGGSARKCS LTGKWTNDLG SNMTIGAVNS  120
RGEFTGTYIT AVTATSNEIK ESPLHGTQNT INKSGGSTTV FTGQCFIDRN GKEVLKTMWL  180
LRSSVNDIGD DWKATRVGIN IFTRLRTQKE GGSGGSARKC SLTGKWTNDL GSNMTIGAVN  240
SRGEFTGTYI TAVTATSNEI KESPLHGTQN TINKRTQPTF GFTVNWKFSE GGGGSGGGGS  300
GENLYFQSGG GGSGGGGSGG GGSAHHFSEP EITLIIFGVM AGVIGTILLI SYGIRRLIKK  360
SPSGGGGSGG GGSGGGGSGG GGSTGVSKGE EDNMAIIKEF MRFKVHMEGS VNGHEFEIEG  420
EGEGRPYEGT QTAKLKVTKG GPLPFAWDIL SPQFMYGSKA YVKHPADIPD YLKLSFPEGF  480
KWERVMNFED GGVVTVTQDS SLQDGEFIYK VKLRGTNFPS DGPVMQKKTM GWEASSERMY  540
PEDGALKGEI KQRLKLKDGG HYDAEVKTTY KAKKPVQLPG AYNVNIKLDI TSHNEDYTIV  600
EQYERAEGRH STGGMDELYK                                              620

SEQ ID NO: 263          moltype = AA  length = 872
FEATURE                 Location/Qualifiers
source                  1..872
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 263
MGVKVLFALI CIAVAEAKRG TQPTFGFTVN WKFSESTTVF TGQCFIDRNG KEVLKTMWLL  60
RSSVNDIGDD WKATRVGINI FTRLRTQKEG GSGGSARKCS LTGKWTNDLG SNMTIGAVNS  120
RGEFTGTYIT AVTATSNEIK ESPLHGTQNT INKSGGSTTV FTGQCFIDRN GKEVLKTMWL  180
LRSSVNDIGD DWKATRVGIN IFTRLRTQKE GGSGGSARKC SLTGKWTNDL GSNMTIGAVN  240
SRGEFTGTYI TAVTATSNEI KESPLHGTQN TINKRTQPTF GFTVNWKFSE GGSGSGSGSG  300
SGRTQPTFGF TVNWKFSEST TVFTGQCFID RNGKEVLKTM WLLRSSVNDI GDDWKATRVG  360
INIFTRLRTQ KEGGSGGSAR KCSLTGKWTN DLGSNMTIGA VNSRGEFTGT YITAVTATSN  420
EIKESPLHGT QNTINKSGGS TTVFTGQCFI DRNGKEVLKT MWLLRSSVND IGDDWKATRV  480
GINIFTRLRT QKEGGSGGSA RKCSLTGKWT NDLGSNMTIG AVNSRGEFTG TYITAVTATS  540
NEIKESPLHG TQNTINKRTQ PTFGFTVNWK FSEGGGGSGG GGSGGGGSGG GGSAHHFSEP  600
EITLIIFGVM ALVIGTILLI SYGIRRLIKK SPSGGGGSTG SELIKENMHM KLYMEGTVDN  660
HHFKCTSEGE GKPYEGTQTM RIKVVEGGPL PFAFDILATS FLYGSKTFIN HTQGIPDFFK  720
QSFPEGFTWE RVTTYEDGGV LTATQDTSLQ DGCLIYNVKI RGVNFTSNGP VMQKKTLGWE  780
AFTETLYPAD GGLEGRNDMA LKLVGGSHLI ANAKTTYRSK KPAKNLKMPG VYYVDYRLER  840
IKEANNETYV EQHEVAVARY CDLPSKLGHK LN                                872

SEQ ID NO: 264          moltype = AA  length = 227
FEATURE                 Location/Qualifiers
source                  1..227
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 264
MVSAIKPDMR IKLRMEGNVN GHHFVIDGEG TGKPYEGKQT MDLEVKEGGP LPFAFDILTT  60
AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSMTFEDGG ICNARNDITM EGDTFYNKVR  120
FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGGAHY RCDFRTTYKA  180
KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARR                227

SEQ ID NO: 265          moltype = AA  length = 187
FEATURE                 Location/Qualifiers
source                  1..187
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 265
LPFAFDILTT AFHYGNRVFV KYPDNIQDYF KQSFPKGYSW ERSMTFEDGG ICNARNDITM  60
EGDTFYNKVR FYGTNFPANG PVMQKKTLKW EPSTEKMYVR DGVLTGDIEM ALLLEGGAHY  120
RCDFRTTYKA KEKGVKLPGA HFVDHAIEIL SHDKDYNKVK LYEHAVAHSG LPDNARRKGF  180
TVGSLIQ                                                            187

SEQ ID NO: 266          moltype = AA  length = 57
FEATURE                 Location/Qualifiers
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source                  1..57
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 266
GDHYDDELES EVDDIRTALA KIHEDNQKII SKLESLLLLK GEVESIKKQI NRQNISI     57

SEQ ID NO: 267          moltype = AA  length = 552
FEATURE                 Location/Qualifiers
source                  1..552
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 267
MDKDCEMKRT TLDSPLGKLE LSGCEQGLHR IIFLGKGTSA ADAVEVPAPA AVLGGPEPLM  60
QATAWLNAYF HQPEAIEEFP VPALHHPVFQ QESFTRQVLW KLLKVVKFGE VISYSHLAAL  120
AGNPAATAAV KTALSGNPVP ILIPCHRVVQ GDLDVGGYEG GLAVKEWLLA HEGHRLGKPG  180
LGGGTGGSDP ETCPCPTGGS CTCSDKCKCK GCKCTNCKKS CCSCCPAGCE KCAKDCVCKG  240
EEGAKAEAEK CSCCQGSGPG NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY  300
GPLGRGMQSV FNDIFMESHE AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS  360
KALDIPIDFS VAANAARDVA FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF  420
QDIVEARNKL LEMNHNGPYA LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL  480
KGKSGVIVNT GRNNLDLAIS EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE  540
EGSGDYKDDD DK                                                      552

SEQ ID NO: 268          moltype = AA  length = 30
FEATURE                 Location/Qualifiers
source                  1..30
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 268
GEIAQTIEEI ADTIREIAYT IKEIAQTIKG                                   30

SEQ ID NO: 269          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 269
VSRLEEDVRN LEAEVDKLRE RLDRLEETVQ AK                                32

SEQ ID NO: 270          moltype = AA  length = 32
FEATURE                 Location/Qualifiers
source                  1..32
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 270
VSRLEERVRD LEAEVDKLRE RLDRLEETVQ AK                                32

SEQ ID NO: 271          moltype = AA  length = 61
FEATURE                 Location/Qualifiers
source                  1..61
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 271
QLEDKVEELL SKVYHLENEV DRLRKLIENK ADMKQLEDKV EELESEVDHL RNEVARLKKL  60
V                                                                  61

SEQ ID NO: 272          moltype = AA  length = 485
FEATURE                 Location/Qualifiers
source                  1..485
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 272
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EPPPPRPPPP RVFTLEDFVG  300
DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV IIPYEGLSAD  360
QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA VFDGKKITVT  420
GTLWNGNKII DERLITPDGS MLFRVTINSP PPPRPPPPRK RRWKKNFIAV SAANRFKKIS  480
SSGAL                                                              485

SEQ ID NO: 273          moltype = AA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = protein
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                        organism = synthetic construct
SEQUENCE: 273
VTGYRLFEEI LPPPPRVEAF CATWKLTNSQ NFDEYMKALG VGFATRQVGN VTKPTVIISQ  60
EGDKVVIRTL STFKNTEISF QLGEEFDETT ADDRNCKSVV SLDGDKLVHI QKWDGKETNF  120
VREIKDGKMV MTLTFGDVVA VRHYEKAPPP PRADQLTDEQ IAEFKEAFSL FDKDGDGTIT  180
TKELGTVMRS LGQNPTEAEL QDMINEVDAD GNGTIDFPEF LNLMARKMKD TDSEEKLKEA  240
FRVFDKDGNG FISAAELRHV MTNLGEKLTD EEVDEMIREA DVDGDGQVNY EEFVQVMMAK  300

SEQ ID NO: 274          moltype = AA  length = 300
FEATURE                 Location/Qualifiers
source                  1..300
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 274
VTGYRLFEEI LPPPPRADQL TDEQIAEFKE AFSLFDKDGD GTITTKELGT VMRSLGQNPT  60
EAELQDMINE VDADGNGTID FPEFLNLMAR KMKDTDSEEK LKEAFRVFDK DGNGFISAAE  120
LRHVMTNLGE KLTDEEVDEM IREADVDGDG QVNYEEFVQV MMAKPPPPRV EAFCATWKLT  180
NSQNFDEYMK ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE ISFQLGEEFD  240
ETTADDRNCK SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD VVAVRHYEKA  300

SEQ ID NO: 275          moltype = AA  length = 602
FEATURE                 Location/Qualifiers
source                  1..602
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 275
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EPPPPRPPPP RVFTLEDFVG  300
DWEQTAAYNL DQVLEQGGVS SLLQNLAVSV TPIQRIVRSG ENALKIDIHV IIPYEGLSAD  360
QMAQIEEVFK VVYPVDDHHF KVILPYGTLV IDGVTPNMLN YFGRPYEGIA VFDGKKITVT  420
GTLWNGNKII DERLITPDGS MLFRVTINSP PPPRADQLTD EQIAEFKEAF SLFDKDGDGT  480
ITTKELGTVM RSLGQNPTEA ELQDMINEVD ADGNGTIDFP EFLNLMARKM KDTDSEEKLK  540
EAFRVFDKDG NGFISAAELR HVMTNLGEKL TDEEVDEMIR EADVDGDGQV NYEEFVQVMM  600
AK                                                                 602

SEQ ID NO: 276          moltype = AA  length = 2841
FEATURE                 Location/Qualifiers
source                  1..2841
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 276
RGVPHIVMVD AYKRYKGGSG GGSGADQLTD EQIAEFKEAF SLFDKDGDGT ITTKELGTVM  60
RSLGQNPTEA ELQDMINEVD ADGNGTIDFP EFLNLMARKM KDTDSEEKLK EAFRVFDKDG  120
NGFISAAELR HVMTNLGEKL TDEEVDEMIR EADVDGDGQV NYEEFVQVMM AKGGSGGGSG  180
APKTITELEK KVEEIPFKKE RKFNPDLAPG TEKVTREGQK GEKTITTPTL KNPLTGVIIS  240
KGEPKEEITK DPINELTEYG PETIAPGHRD EFDPKLPTGE KEEVPGKPGI KNPETGDVVR  300
PPVDSVTKYG YGPVKGDSIV EKEEIPFEKE RKFNPDLAPG TEKVTREGQK GEKTITTPTL  360
KNPLTGEIIS KGESKEEITK DPINELTEYG PETIAPGHRD EFDPKLPTGE KEEVPGKPGI  420
KNPETGDVVR PPVDSVTKYG PVKGDSIVEK EEIPFEKERK FNPDLAPGTE KVTREGQKGE  480
KTITTPTLKN PLTGEIISKG ESKEEITKDP INELTEYGPE TIAPGHRDEF DPKLPTGEKE  540
EVPGKPGIKN PETGDVVRPP VDSVTKYGPV KGDSIVEKEE IPFEKERKFN PDLAPGTEKV  600
TREGQKGEKT ITTPTLKNPL TGEIISKGES KEEITKDPIN ELTEYGPETI APGHRDEFDP  660
KLPTGEKEEV PGKPGIKNPE TGDVVRPPVD SVTKYGPVKG DSIVEKEEIP FEKERKFNPD  720
LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG EIISKGESKE EITKDPINEL TEYGPETIAP  780
GHRDEFDPKL PTGEKEEVPG KPGIKNPETG DVVRPPVDSV TKYGPVKGDS IVEKEEIPFE  840
KERKFNPDLA PGTEKVTREG QKGEKTITTP TLKNPLTGEI ISKGESKEEI TKDPINELTE  900
YGPETIAPGH RDEFDPKLPT GEKEEVPGKP GIKNPETGDV VRPPVDSVTK YGPVKGDSIV  960
EKEEIPFEKE RKFNPDLAGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD  1020
PINELTEYGP ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP  1080
VKGDSIVEKE EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE  1140
SKEEITKDPI NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV  1200
DSVTKYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  1260
GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  1320
GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE GQKGEKTITT  1380
PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPEGGGSG GGSSGGGGSG GSSGGGSGPK  1440
TITELEKKVE EIPFKKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGVIISKGE  1500
PKEEITKDPI NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV  1560
DSVTKYGYGP VKGDSIVEKE EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP  1620
LTGEIISKGE SKEEITKDPI NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP  1680
ETGDVVRPPV DSVTKYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  1740
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  1800
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  1860
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  1920
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TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  1980
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  2040
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  2100
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  2160
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  2220
EIPFEKERKF NPDLAGTEKV TREGQKGEKT ITTPTLKNPL TGEIISKGES KEEITKDPIN  2280
ELTEYGPETI APGHRDEFDP KLPTGEKEEV PGKPGIKNPE TGDVVRPPVD SVTKYGPVKG  2340
DSIVEKEEIP FEKERKFNPD LAPGTEKVTR EGQKGEKTIT TPTLKNPLTG EIISKGESKE  2400
EITKDPINEL TEYGPETIAP GHRDEFDPKL PTGEKEEVPG KPGIKNPETG DVVRPPVDSV  2460
TKYGPVKGDS IVEKEEIPFE KERKFNPDLA PGTEKVTREG QKGEKTITTP TLKNPLTGEI  2520
ISKGESKEEI TKDPINELTE YGPETIAPGH RDEFDPKLPT GEKEEVPGKP GIKNPETGDV  2580
VRPPVDSVTK YGPVKGDSIV EKEEIPFEKE RKFNPDLAPG TEKVTREGQK GEKTITTPTL  2640
KNPLTGEIIS KGESKEEITK DPINELTEYG PEGGSGVEAF CATWKLTNSQ NFDEYMKALG  2700
VGFATRQVGN VTKPTVIISQ EGDKVVIRTL STFKNTEISF QLGEEFDETT ADDRNCKSVV  2760
SLDGDKLVHI QKWDGKETNF VREIKDGKMV MTLTFGDVVA VRHYEKAGGS GGSSGKRRWK  2820
KNFIAVSAAN RFKKISSSGA L                                            2841

SEQ ID NO: 277          moltype = AA  length = 434
FEATURE                 Location/Qualifiers
source                  1..434
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 277
NKSQLYPDSP LTDQDFNQLD QTVIEAARRQ LVGRRFIELY GPLGRGMQSV FNDIFMESHE  60
AKMDFQGSFD TEVESSRRVN YTIPMLYKDF VLYWRDLEQS KALDIPIDFS VAANAARDVA  120
FLEDQMIFHG SKEFDIPGLM NVKGRLTHLI GNWYESGNAF QDIVEARNKL LEMNHNGPYA  180
LVLSPELYSL LHRVHKDTNV LEIEHVRELI TAGVFQSPVL KGKSGVIVNT GRNNLDLAIS  240
EDFETAYLGE EGMNHPFRVY ETVVLRIKRP AAICTLIDPE EGGGSGADQL TDEQIAEFKE  300
AFSLFDKDGD GTITTKELGT VMRSLGQNPT EAELQDMINE VDADGNGTID FPEFLNLMAR  360
KMKDTDSEEK LKEAFRVFDK DGNGFISAAE LRHVMTNLGE KLTDEEVDEM IREADVDGDG  420
QVNYEEFVQV MMAK                                                    434

SEQ ID NO: 278          moltype = AA  length = 445
FEATURE                 Location/Qualifiers
source                  1..445
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 278
KRRWKKNFIA VSAANRFKKI SSSGALGGGS GVEAFCATWK LTNSQNFDEY MKALGVGFAT  60
RQVGNVTKPT VIISQEGDKV VIRTLSTFKN TEISFQLGEE FDETTADDRN CKSVVSLDGD  120
KLVHIQKWDG KETNFVREIK DGKMVMTLTF GDVVAVRHYE KAGGGSGSEL IKENMHMKLY  180
MEGTVNNHHF KCTSEGEGKP YEGTQTMRIK VVEGGPLPFA FDILATSFMY GSRTFINHTQ  240
GIPDFFKQSF PEGFTWERVT TYEDGGVLTA TQDTSLQDGC LIYNVKIRGV NFPSNGPVMQ  300
KKTLGWEANT EMLYPADGGL EGRSDMALKL VGGGHLICNF KTTYRSKKPA KNLKMPGVYY  360
VDHRLERIKE ADKETYVEQH EVAVARYCDL PSKLGHKSRG GSGNEKEELK SKKAELRNRI  420
EQLKQKREQL KQKIANLRKE IEAYK                                        445

SEQ ID NO: 279          moltype = AA  length = 284
FEATURE                 Location/Qualifiers
source                  1..284
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 279
MSGGEELFAG IVPVLIELDG DVHGHKFSVR GEGEGDADYG KLEIKFICTT GKLPVPWPTL  60
VTTLCYGIQC FARYPEHMKM NDFFKSAMPE GYIQERTIQF QDDGKYKTRG EVKFEGDTLV  120
NRIELKGKDF KEDGNILGHK LEYSFNSHNV YIRPDKANNG LEANFKTRHN IEGGGVQLAD  180
HYQTNVPLGD GPVLIPINHY LSTQTKISKD RNEARDHMVL LESFSACCHT HGMDELYRGG  240
GSGFYAEERE LKALDRELNA IDKELRANEN ELRALDNELT AAIS                   284

SEQ ID NO: 280          moltype = AA  length = 720
FEATURE                 Location/Qualifiers
source                  1..720
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 280
ESLFKGPRDY NPISSTICHL TNESDGHTTS LYGIGFGPFI ITNKHLFRRN NGTLLVQSLH  60
LEDQLTEEQI AEFKELFSLF DKDGDGTITT KELGTVMRSL GQNPTEAELQ DMINEVDADG  120
DGTIDFPEFL TMMARKMKDT GGVKLIPSWT TVILVKSMLR KRSFGNPFGG DSEEEIREAF  180
GVFDKDGNGY ISAAELRHVM TNLGEKLTDE EVDEMIREAD IDGDGQVNYE EFVQMMTAKA  240
AAGVFKVKNT TTLQQHLIDG RDMIIIRMPK DFPPFPQKLK FREPQREERI CLVTTNFQTK  300
SMSSMVSDTS CTFPSSDGIF WKHWIQTKDG QCGNPLVSTR DGFIVGIHSA SNFTNTNNYF  360
TSVPKNFMEL LTNQEAQQWV SGWRLNADSV LWGGHKVFMV ELAEKLAGLD INGGASEFRA  420
TTLERIEKSF VITDPRLPDN PIIFVSDSFL QLTEYSREEI LGRNCRFLQG PETDRATVRK  480
IRDAIDNQTE VTVQLINYTK SGKKFWNVFH LQPMRDYKGD VQYFIGVQLD GTERLHGAAE  540
REAVCLVKKT AFQIAENLYF QMGGGSGGRG VPHIVMVDAY KRYKGGGSGV EAFCATWKLT  600
NSQNFDEYMK ALGVGFATRQ VGNVTKPTVI ISQEGDKVVI RTLSTFKNTE ISFQLGEEFD  660
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ETTADDRNCK SVVSLDGDKL VHIQKWDGKE TNFVREIKDG KMVMTLTFGD VVAVRHYEKA  720

SEQ ID NO: 281          moltype =   length =
SEQUENCE: 281
000

SEQ ID NO: 282          moltype =   length =
SEQUENCE: 282
000

SEQ ID NO: 283          moltype =   length =
SEQUENCE: 283
000

SEQ ID NO: 284          moltype = AA  length = 1179
FEATURE                 Location/Qualifiers
source                  1..1179
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 284
MADIEQELER LKASIRRLEQ EVNQERARMA ALQTLLAKGG SGGATEEAII RIPPYHYIHV  60
LDQNSNVSRV EVGPKTYIRQ DNERVLFAPV RMVTVPPRHY CIVANPVSRD TQSSVLFDIT  120
GQVRLRHADQ EIRLAQDPFP LYPGEVLEKD ITPLQVVLPN TALHLKALLD FEDKNGDKVM  180
AGDEWLFEGP GTYIPQKEVE VVEIIQATVI KQNQALRLRA RKECFDREGK GRVTGEEWLV  240
RSVGAYLPAV FEEVLDLVDA VILTEKTALH LRALQNFRDL RGVLHRTGEE WLVTVQDTEA  300
HVPDVYEEVL GVVPITTLGP RHYCVILDPM GPDGKNQLGQ KRVVKGEKSF FLQPGERLER  360
GIQDVYVLSE QQGLLLKALQ PLEEGESEEK VSHQAGDCWL IRGPLEYVPS AKVEVVEERQ  420
AIPLDQNEGI YVQDVKTGKV RAVIGSTYML TQDEVLWEKE LPSGVEELLN LGGGGSPEDK  480
LQAIKYELAQ NEEELAQIEE KLAANKEGGS GGGGSGSKTI VLSVGEATRT LTEIQSTADR  540
QIFEEKVGPL VGRLRLTASL RQNGAKTAYR VNLKLDQADV VDSGLPKVRY TQVWSHDVTI  600
VANSTEASRK SLYDLTKSLV ATSQVEDLVV NLVPLGRGPG SGGGGSGGPE DENAALEEKI  660
AQLKQKNAAL KEEIQALEYS APRNKTRVVS YRVPHNAAVQ VYDYRAKRAR VVFGPELVTL  720
DPEEQFTVLS LSAGRPKRPH ARRALCLLLG PDFFTDVITI ETADHARLQL QLAYNWHFEL  780
KNRNDPAEAA KLFSVPDFVG DACKAIASRV RGAVASVTFD DFHKNSARII RMAVFGFEGS  840
PEDELAANEE ELQQNEQKLA QIKQKLQAIK YGGGGSGGGG SGGGGHHHHH HGGGGSGGGG  900
SGGGGSPEDE IQQLEEEIAQ LEQKNAALKE KNQALKYGKA RDQAVFPQNG LVVSSVDVQS  960
VEPVDQRTRD ALQRSVQLAI EITTNSQEAA AKHEAQRLEQ EARGRLERQK ILDQSEAEKA  1020
RKELLELEAM SMAVESTGNA KAEAESRAEA ARIEGEGSVL QAKLKAQALA IETEAELERV  1080
KKVREMELIY ARAQLELEVS KAQQLANVEA KKFKEMTEAL GPGTIRDLAV AGPEMQVKLL  1140
QSLGLKSTLI TDGSSPINLF STAFGLLGLG SDGQPPAQK                         1179

SEQ ID NO: 285          moltype = AA  length = 1137
FEATURE                 Location/Qualifiers
source                  1..1137
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 285
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG GGGSPEDKLQ AIKYELAQNE EELAQIEEKL AANKEGGSGG GGSGSKTIVL  480
SVGEATRTLT EIQSTADRQI FEEKVGPLVG RLRLTASLRQ NGAKTAYRVN LKLDQADVVD  540
SGLPKVRYTQ VWSHDVTIVA NSTEASRKSL YDLTKSLVAT SQVEDLVVNL VPLGRGPGSG  600
GGGSGGPEDE NAALEEKIAQ LKQKNAALKE EIQALEYSAP RNKTRVVSYR VPHNAAVQVY  660
DYRAKRARVV FGPELVTLDP EEQFTVLSLS AGRPKRPHAR RALCLLLGPD FFTDVITIET  720
ADHARLQLQL AYNWHFELKN RNDPAEAAKL FSVPDFVGDA CKAIASRVRG AVASVTFDDF  780
HKNSARIIRM AVFGFEGSPE DELAANEEEL QQNEQKLAQI KQKLQAIKYG GGGSGGGGSG  840
GGGHHHHHHG GGGSGGGGSG GGGSPEDEIQ QLEEEIAQLE QKNAALKEKN QALKYGKARD  900
QAVFPQNGLV VSSVDVQSVE PVDQRTRDAL QRSVQLAIEI TTNSQEAAAK HEAQRLEQEA  960
RGRLERQKIL DQSEAEKARK ELLELEAMSM AVESTGNAKA EAESRAEAAR IEGEGSVLQA  1020
KLKAQALAIE TEAELERVKK VREMELIYAR AQLELEVSKA QQLANVEAKK FKEMTEALGP  1080
GTIRDLAVAG PEMQVKLLQS LGLKSTLITD GSSPINLFST AFGLLGLGSD GQPPAQK     1137

SEQ ID NO: 286          moltype = AA  length = 1167
FEATURE                 Location/Qualifiers
source                  1..1167
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 286
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
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ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG GGGSPEDKLQ AIKYELAQNE EELAQIEEKL AANKEGGSGG GGSGSKTIVL  480
SVGEATRTLT EIQSTADRQI FEEKVGPLVG RLRLTASLRQ NGAKTAYRVN LKLDQADVVD  540
SGLPKVRYTQ VWSHDVTIVA NSTEASRKSL YDLTKSLVAT SQVEDLVVNL VPLGRGPGSG  600
GGGSGGPEDE NAALEEKIAQ LKQKNAALKE EIQALEYSAP RNKTRVVSYR VPHNAAVQVY  660
DYRAKRARVV FGPELVTLDP EEQFTVLSLS AGRPKRPHAR RALCLLLGPD FFTDVITIET  720
ADHARLQLQL AYNWHFELKN RNDPAEAAKL FSVPDFVGDA CKAIASRVRG AVASVTFDDF  780
HKNSARIIRM AVFGFEGSPE DELAANEEEL QQNEQKLAQI KQKLQAIKYG GGGSGGGGSG  840
GGGCGLCVCP CNKLKSSDAY KKAWGNNQDG VVASQPARVG GGGSGGGGSG GGGSPEDEIQ  900
QLEEEIAQLE QKNAALKEKN QALKYGKARD QAVFPQNGLV VSSVDVQSVE PVDQRTRDAL  960
QRSVQLAIEI TTNSQEAAAK HEAQRLEQEA RGRLERQKIL DQSEAEKARK ELLELEAMSM  1020
AVESTGNAKA EAESRAEAAR IEGEGSVLQA KLKAQALAIE TEAELERVKK VREMELIYAR  1080
AQLELEVSKA QQLANVEAKK FKEMTEALGP GTIRDLAVAG PEMQVKLLQS LGLKSTLITD  1140
GSSPINLFST AFGLLGLGSD GQPPAQK                                      1167

SEQ ID NO: 287          moltype = AA  length = 423
FEATURE                 Location/Qualifiers
source                  1..423
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 287
MEKSFVITDP RLPDNPIIFA SDGFLELTEY SREEILGRNG RFLQGPETDQ ATVQKIRDAI  60
RDQREITVQL INYTKSGKKF WNLLHLQPMR DQKGELQYFI GVQLDGGGGG SGGGGSGSGP  120
GNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  180
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  240
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  300
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  360
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKGLPPLER  420
LTL                                                                423

SEQ ID NO: 288          moltype = AA  length = 424
FEATURE                 Location/Qualifiers
source                  1..424
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 288
MEKSFVITDP RLPDNPIIFA SDGFLELTEY SREEILGRNG RFLQGPETDQ ATVQKIRDAI  60
RDQREITVQL INYTKSGKKF WNLLHLQPMR DQKGELQYFI GVQLDGGGGG SGGGGSGSGP  120
GNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  180
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  240
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  300
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  360
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKGGPAAKR  420
VKLD                                                               424

SEQ ID NO: 289          moltype = AA  length = 375
FEATURE                 Location/Qualifiers
source                  1..375
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 289
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDKGLPPL ERLTL                                                   375

SEQ ID NO: 290          moltype = AA  length = 457
FEATURE                 Location/Qualifiers
source                  1..457
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 290
MVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  60
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  120
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  180
EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYKYSDL  240
EMGTRDDEYD YLFKVVLIGD SGVGKSNLLS RFTRNEFNLE SKSTIGVEFA TRSIQVDGKT  300
IKAQIWDTAG QERYRAITSA YYRGAVGALL VYDIAKHLTY ENVERWLKEL RDHADSNIVI  360
MLVGNKSDLR HLRAVPTDEA RAFAEKNGLS FIETSALDST NVEAAFQTIL TEIYRIVSQK  420
QMSDRRENDM SPSNNVVPIH VPPTTENKPK VQCCQNI                           457
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SEQ ID NO: 291          moltype = AA  length = 850
FEATURE                 Location/Qualifiers
source                  1..850
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 291
MVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  60
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  120
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  180
EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYKYSDL  240
ELKLRILMSA AVTAGKLARA PADPGKAGVP GVAAPGAPAA APPAKEIPEV LVDPRSRRRY  300
VRGRFLGKGG FAKCFEISDA DTKEVFAGKI VPKSLLLKPH QREKMSMEIS IHRSLAHQHV  360
VGFHGFFEDN DFVFVVLELC RRRSLLELHK RRKALTEPEA RYYLRQIVLG CQYLHRNRVI  420
HRDLKLGNLF LNEDLEVKIG DFGLATKVEY DGERKKTLCG TPNYIAPEVL SKKGHSFEVD  480
VWSIGCIMYT LLVGKPPFET SCLKETYLRI KKNEYSIPKH INPVAASLIQ KMLQTDPTAR  540
PTINELLNDE FFTSGYIPAR LPITCLTIPP RFSIAPSSLD PSNRKPLTVL NKGLENPLPE  600
RPREKEEPVV RETGEVVDCH LSDMLQQLHS VNASKPSERG LVRQEEAEDP ACIPIFWVSK  660
WVDYSDKYGL GYQLCDNSVG VLFNDSTRLI LYNDGDSLQY IERDGTESYL TVSSHPNSLM  720
KKITLLKYFR NYMSEHLLKA GANITPREGD ELARLPYLRT WFRTRSAIIL HLSNGSVQIN  780
FFQDHTKLIL CPLMAAVTYI DEKRDFRTYR LSLLEEYGCC KELASRLRYA RTMVDKLLSS  840
RSASNRLKAS                                                        850

SEQ ID NO: 292          moltype = AA  length = 2090
FEATURE                 Location/Qualifiers
source                  1..2090
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 292
MVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  60
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  120
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  180
EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYKSGLR  240
SSSSMTYSEL YSRYTRVWIP DPDEVWRSAE LTKDYKDGDE SLQLRLEDDT ILDYPIDVQN  300
NQVPFLRNPD ILVGENDLTA LSHLHEPAVL HNLKVRFLES NHIYTYCGIV LVAINPYEQL  360
PIYGQDVIYA YSGQNMGDMD PHIFAVAEEA YKQMARDEKN QSIIVSGESG AGKTVSAKYA  420
MRYFATVGGS ASDTNIEEKV LASSPIMEAI GNAKTTRNDN SSRFGKYIEI GFDKKYHIIG  480
ANMRTYLLEK SRVVFQADDE RNYHIFYQLC AAASLPEFKE LALTCAEDFF YTAHGGNTTI  540
EGVDDAEDFE KTRQALTLLG VRESHQISIF KIIASILHLG SVEIQAERDG DSCSISPQDE  600
HLSNFCRLLG IEHSQMEHWL CHRKLVTTSE TYVKTMSLQQ VVNARNALAK HIYAQLFSWI  660
VEHINKALQT SLKQHSFIGV LDIYGFETFE INSFEQFCIN YANEKLQQQF NSHVFKLEQE  720
EYMKEQIPWT LIDFYDNQPC IDLIEAKLGI LDLLDEECKV PKGTDQNWAQ KLYERHSNSQ  780
HFQKPRMSNT AFIVIHFADK VEYLSDGFLE KNRDTVYEEQ INILKASKFP LVADLFRDDE  840
DSVPATNTAK SRSSSKINVR SSRPLMKAPN KEHKKSVGYQ FRTSLNLLME TLNATTPHYV  900
RCIKPNDEKL PFHFDPKRAV QQLRACGVLE TIRISAAGYP SRWTYHDFFN RYRVLMKKRE  960
LANTTDKKNI CKSVLESLIK DPDKFQFGRT KIFFRAGQVA YLEKLRADKF REATIMIQKT  1020
VRGWLQRVKY RRLRAATLTL QRFCRGYLAR RLTEHLRRTR AAIVFQKQYR MLKARRAYCR  1080
VRRAAVIIQS YTRGHVCTQK LPPVLTEHKA TIIQKYARGW MARRHFQRQR DAAIVIQCAF  1140
RRLKARQALK ALKIEARSAE HLKRLNVGME NKVVQLQRKI DDQNKEFKTL SEQLSAVTST  1200
HAMEVEKLKK ELARYQQNQE ADPSLQLQEE VQSLRTELQK AHSERRVLED AHNRENGELR  1260
KRVADLEHEN ALLKDEKEHL NHQILRQSKA ESSQSSVEEN LLIKKELEEE RSRYQNLVKE  1320
YSQLEQRYEN LRDEQQTPGH RKNPSNQSSL ESDSNYPSIS TSEIGDTEDA LQQVEEIGIE  1380
KAAMDMTVFL KLQKRVRELE QERKKLQVQL EKEQQDSKKV QVEQQNNGLD VDQDADIAYN  1440
SLKRQELESE NKKLKNDLNE RWKAVADQAM QDNSTHSSPD SYSLLLNQLK LANEELEVRK  1500
EEVLILRTQI MNADQRRLSG KNMEPNINAR TSWPNSEKHV DQEDAIEAYH GVCQTNSQTE  1560
DWGYLNEDGE LGLAYQGLKQ VARLLEAQLQ AQNLKHEEEV EHLKAQVEAM KEEMDKQQQT  1620
FCQTLLLSPE AQVEFGVQQE ISRLTNENLD FKELVEKLEK NEKKLKKQLK IYMKKVQDLE  1680
AAQALAQSDR RHHELTRQVT VQRKEKDFQG MLEYHKEDEA LLIRNLVTDL KPQMLSGTVP  1740
CLPAYILYMC IRHADYTNDD LKVHSLLSST INGIKKVLKK HNEDFEMTSF WLSNTCRLLH  1800
CLKQYSGDEG FMTQNTAKQN EHCLKNFDLT EYRQVLSDLS IQIYQQLIKI AEGLLQPMIV  1860
SAMLENESIQ GLSGVRPTGY RKRSSSMVDG ENSYCLEAII RQMNFFHTVL CDQGLDPEII  1920
LQVFKQLFYM INAVTLNNLL LRKDACSWST GMQLRYNISQ LEEWLRGKNL QQSGAVQTME  1980
PLIQAAQLLQ LKKKTQEDAE AICSLCTSLS TQQIVKILNL YTPLNGFEER VTVSFIRTIQ  2040
AQLQERSDPQ QLLLDSKHMF PVLFPFNPSA LTMDSIHIPA CLNLEFLNEV             2090

SEQ ID NO: 293          moltype = AA  length = 365
FEATURE                 Location/Qualifiers
source                  1..365
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 293
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
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VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDK                                                              365

SEQ ID NO: 294          moltype = AA  length = 444
FEATURE                 Location/Qualifiers
source                  1..444
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 294
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGSGGSA DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  120
CEKCAKDCVC KGEEGAKAEA EKCSCCQGSG PGNKSQLYPD SPLTDQDFNQ LDQTVIEAAR  180
RQLVGRRFIE LYGPLGRGMQ SVFNDIFMES HEAKMDFQGS FDTEVESSRR VNYTIPMLYK  240
DFVLYWRDLE QSKALDIPID FSVAANAARD VAFLEDQMIF HGSKEFDIPG LMNVKGRLTH  300
LIGNWYESGN AFQDIVEARN KLLEMNHNGP YALVLSPELY SLLHRVHKDT NVLEIEHVRE  360
LITAGVFQSP VLKGKSGVIV NTGRNNLDLA ISEDFETAYL GEEGMNHPFR VYETVVLRIK  420
RPAAICTLID PEEGSGDYKD DDDK                                         444

SEQ ID NO: 295          moltype = AA  length = 511
FEATURE                 Location/Qualifiers
source                  1..511
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 295
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG TGGSTSTTLV KCACEPCLCN VDPSKAIDRN GLYYCSEACA DGHTGGSKGC  120
GHTGCNCHGS AGGCDDKCGC AVPCPGGTGC RCTSARSGAA AGEHTTCGCG EHCGCNPCAC  180
GREGTPSGRA NRRANCSCGA ACNCASCGSA TAPGGSGPGN KSQLYPDSPL TDQDFNQLDQ  240
TVIEAARRQL VGRRFIELYG PLGRGMQSVF NDIFMESHEA KMDFQGSFDT EVESSRRVNY  300
TIPMLYKDFV LYWRDLEQSK ALDIPIDFSV AANAARDVAF LEDQMIFHGS KEFDIPGLMN  360
VKGRLTHLIG NWYESGNAFQ DIVEARNKLL EMNHNGPYAL VLSPELYSLL HRVHKDTNVL  420
EIEHVRELIT AGVFQSPVLK GKSGVIVNTG RNNLDLAISE DFETAYLGEE GMNHPFRVYE  480
TVVLRIKRPA AICTLIDPEE GSGDYKDDDD K                                 511

SEQ ID NO: 296          moltype = AA  length = 370
FEATURE                 Location/Qualifiers
source                  1..370
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 296
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGPDFLGHA ENPLREEEWA RLNETVIQVA RRSLVGRRIL DIYGPLGAGV  120
QTVPYDEFQG VSPGAVDIVG EQETAMVFTD ARKFKTIPII YKDFLLHWRD IEAARTHNMP  180
LDVSAAAGAA ALCAQQEDEL IFYGDARLGY EGLMTANGRL TVPLGDWTSP GGGFQAIVEA  240
TRKLNEQGHF GPYAVVLSPR LYSQLHRIYE KTGVLEIETI RQLASDGVYQ SNRLRGESGV  300
VVSTGRENMD LAVSMDMVAA YLGASRMNHP FRVLEALLLR IKHPDAICTL EGAGATERRG  360
SGDYKDDDDK                                                         370

SEQ ID NO: 297          moltype = AA  length = 449
FEATURE                 Location/Qualifiers
source                  1..449
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 297
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG GSGGGSGGSA DPETCPCPTG GSCTCSDKCK CKGCKCTNCK KSCCSCCPAG  120
CEKCAKDCVC KGEEGAKAEA EKCSCCQGSG PGPDFLGHAE NPLREEEWAR LNETVIQVAR  180
RSLVGRRILD IYGPLGAGVQ TVPYDEFQGV SPGAVDIVGE QETAMVFTDA RKFKTIPIIY  240
KDFLLHWRDI EAARTHNMPL DVSAAAGAAA LCAQQEDELI FYGDARLGYE GLMTANGRLT  300
VPLGDWTSPG GGFQAIVEAT RKLNEQGHFG PYAVVLSPRL YSQLHRIYEK TGVLEIETIR  360
QLASDGVYQS NRLRGESGVV VSTGRENMDL AVSMDMVAAY LGASRMNHPF RVLEALLLRI  420
KHPDAICTLE GAGATERRGS GDYKDDDDK                                    449

SEQ ID NO: 298          moltype = AA  length = 353
FEATURE                 Location/Qualifiers
source                  1..353
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 298
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGEFLKRSF APLTEKQWQE IDNRAREIFK TQLYGRKFVD VEGPYGWEYA  120
AHPLGEVEVL SDENEVVKWG LRKSLPLIEL RATFTLDLWE LDNLERGKPN VDLSSLEETV  180
RKVAEFEDEV IFRGCEKSGV KGLLSFEERK IECGSTPKDL LEAIVRALSI FSKDGIEGPY  240
TLVINTDRWI NFLKEEAGHY PLEKRVEECL RGGKIITTPR IEDALVVSER GGDFKLILGQ  300
DLSIGYEDRE KDAVRLFITE TFTFQVVNPE ALILLKGGGS GPDRKAAVSH WQQ         353
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SEQ ID NO: 299          moltype = AA  length = 470
FEATURE                 Location/Qualifiers
source                  1..470
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 299
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGEFLKRSF APLTEKQWQE IDNRAREIFK TQLYGRKFVD VEGPYGWEYA  120
AHPLGEVEVL SDENEVVKWG LRKSLPLIEL RATFTLDLWE LDNLERGKPN VDLSSLEETV  180
RKVAEFEDEV IFRGCEKSGV KGLLSFEERK IECGSTPKDL LEAIVRALSI FSKDGIEGPY  240
TLVINTDRWI NFLKEEAGHY PLEKRVEECL RGGKIITTPR IEDALVVSER GGDFKLILGQ  300
DLSIGYEDRE KDAVRLFITE TFTFQVVNPE ALILLKGSGS GSETTGAQVQ LVESGGSLVQ  360
PGGSLRLSCA ASGRFAESSS MGWFRQAPGK EREFVAAISW SGGATNYADS AKGRFTLSRD  420
NTKNTVYLQM NSLKPDDTAV YYCAANLGNY ISSNQRLYGY WGQGTQVTVS             470

SEQ ID NO: 300          moltype = AA  length = 479
FEATURE                 Location/Qualifiers
source                  1..479
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 300
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGVQLVE SGGALVQPGG SLRLSCAASG FPVNRYSMRW YRQAPGKERE WVAGMSSAGD  420
RSSYEDSVKG RFTISRDDAR NTVYLQMNSL KPEDTAVYYC NVNVGFEYWG QGTQVTVSS   479

SEQ ID NO: 301          moltype = AA  length = 700
FEATURE                 Location/Qualifiers
source                  1..700
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 301
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETGS GATGSVSKGE EDNMAIIKEF  480
MRFKVHMEGS VNGHEFEIEG EGEGRPYEGT QTAKLKVTKG GPLPFAWDIL SPQFMYGSKA  540
YVKHPADIPD YLKLSFPEGF KWERVMNFED GGVVTVTQDS SLQDGEFIYK VKLRGTNFPS  600
DGPVMQKKTM GWEASSERMY PEDGALKGEI KQRLKLKDGG HYDAEVKTTY KAKKPVQLPG  660
AYNVNIKLDI TSHNEDYTIV EQYERAEGRH STGGMDELYK                        700

SEQ ID NO: 302          moltype = AA  length = 827
FEATURE                 Location/Qualifiers
source                  1..827
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 302
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPTGSGAT GSVSKGEEDN  600
MAIIKEFMRF KVHMEGSVNG HEFEIEGEGE GRPYEGTQTA KLKVTKGGPL PFAWDILSPQ  660
FMYGSKAYVK HPADIPDYLK LSFPEGFKWE RVMNFEDGGV VTVTQDSSLQ DGEFIYKVKL  720
RGTNFPSDGP VMQKKTMGWE ASSERMYPED GALKGEIKQR LKLKDGGHYD AEVKTTYKAK  780
KPVQLPGAYN VNIKLDITSH NEDYTIVEQY ERAEGRHSTG GMDELYK                827

SEQ ID NO: 303          moltype = AA  length = 956
FEATURE                 Location/Qualifiers
source                  1..956
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 303
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MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETGSGATG  720
SVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  780
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  840
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  900
EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYK      956

SEQ ID NO: 304          moltype = AA  length = 1084
FEATURE                 Location/Qualifiers
source                  1..1084
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 304
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETGSGATGSV SKGEEDNMAI IKEFMRFKVH MEGSVNGHEF EIEGEGEGRP YEGTQTAKLK  900
VTKGGPLPFA WDILSPQFMY GSKAYVKHPA DIPDYLKLSF PEGFKWERVM NFEDGGVVTV  960
TQDSSLQDGE FIYKVKLRGT NFPSDGPVMQ KKTMGWEASS ERMYPEDGAL KGEIKQRLKL  1020
KDGGHYDAEV KTTYKAKKPV QLPGAYNVNI KLDITSHNED YTIVEQYERA EGRHSTGGMD  1080
ELYK                                                               1084

SEQ ID NO: 305          moltype = AA  length = 1212
FEATURE                 Location/Qualifiers
source                  1..1212
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 305
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  900
EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE SKEEITKDPI  960
NELTEYGPET GSGATGSVSK GEEDNMAIIK EFMRFKVHME GSVNGHEFEI EGEGEGRPYE  1020
GTQTAKLKVT KGGPLPFAWD ILSPQFMYGS KAYVKHPADI PDYLKLSFPE GFKWERVMNF  1080
EDGGVVTVTQ DSSLQDGEFI YKVKLRGTNF PSDGPVMQKK TMGWEASSER MYPEDGALKG  1140
EIKQRLKLKD GGHYDAEVKT TYKAKKPVQL PGAYNVNIKL DITSHNEDYT IVEQYERAEG  1200
RHSTGGMDEL YK                                                      1212

SEQ ID NO: 306          moltype = AA  length = 1340
FEATURE                 Location/Qualifiers
source                  1..1340
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 306
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  900
EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE SKEEITKDPI  960
NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV DSVTKYGPVK  1020
GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT GEIISKGESK  1080
EEITKDPINE LTEYGPETGS GATGSVSKGE EDNMAIIKEF MRFKVHMEGS VNGHEFEIEG  1140
EGEGRPYEGT QTAKLKVTKG GPLPFAWDIL SPQFMYGSKA YVKHPADIPD YLKLSFPEGF  1200
KWERVMNFED GGVVTVTQDS SLQDGEFIYK VKLRGTNFPS DGPVMQKKTM GWEASSERMY  1260
PEDGALKGEI KQRLKLKDGG HYDAEVKTTY KAKKPVQLPG AYNVNIKLDI TSHNEDYTIV  1320
EQYERAEGRH STGGMDELYK                                              1340

SEQ ID NO: 307          moltype = AA  length = 1468
FEATURE                 Location/Qualifiers
source                  1..1468
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 307
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  900
EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE SKEEITKDPI  960
NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV DSVTKYGPVK  1020
GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT GEIISKGESK  1080
EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET GDVVRPPVDS  1140
VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE GQKGEKTITT PTLKNPLTGE  1200
IISKGESKEE ITKDPINELT EYGPETGSGA TGSVSKGEED NMAIIKEFMR FKVHMEGSVN  1260
GHEFEIEGEG EGRPYEGTQT AKLKVTKGGP LPFAWDILSP QFMYGSKAYV KHPADIPDYL  1320
KLSFPEGFKW ERVMNFEDGG VVTVTQDSSL QDGEFIYKVK LRGTNFPSDG PVMQKKTMGW  1380
EASSERMYPE DGALKGEIKQ RLKLKDGGHY DAEVKTTYKA KKPVQLPGAY NVNIKLDITS  1440
HNEDYTIVEQ YERAEGRHST GGMDELYK                                     1468

SEQ ID NO: 308          moltype = AA  length = 1596
FEATURE                 Location/Qualifiers
source                  1..1596
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 308
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
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KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  900
EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE SKEEITKDPI  960
NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV DSVTKYGPVK  1020
GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT GEIISKGESK  1080
EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET GDVVRPPVDS  1140
VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE GQKGEKTITT PTLKNPLTGE  1200
IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP TGEKEEVPGK PGIKNPETGD  1260
VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP GTEKVTREGQ KGEKTITTPT  1320
LKNPLTGEII SKGESKEEIT KDPINELTEY GPETGSGATG SVSKGEEDNM AIIKEFMRFK  1380
VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP FAWDILSPQF MYGSKAYVKH  1440
PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD GEFIYKVKLR GTNFPSDGPV  1500
MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA EVKTTYKAKK PVQLPGAYNV  1560
NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYK                            1596

SEQ ID NO: 309          moltype = AA  length = 1724
FEATURE                 Location/Qualifiers
source                  1..1724
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 309
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
GTGGSAPKTI TELEKKVEEI PFKKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT  300
GVIISKGEPK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET  360
GDVVRPPVDS VTKYGYGPVK GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI  420
TTPTLKNPLT GEIISKGESK EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP  480
GKPGIKNPET GDVVRPPVDS VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE  540
GQKGEKTITT PTLKNPLTGE IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP  600
TGEKEEVPGK PGIKNPETGD VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP  660
GTEKVTREGQ KGEKTITTPT LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR  720
DEFDPKLPTG EKEEVPGKPG IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER  780
KFNPDLAPGT EKVTREGQKG EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP  840
ETIAPGHRDE FDPKLPTGEK EEVPGKPGIK NPETGDVVRP PVDSVTKYGP VKGDSIVEKE  900
EIPFEKERKF NPDLAPGTEK VTREGQKGEK TITTPTLKNP LTGEIISKGE SKEEITKDPI  960
NELTEYGPET IAPGHRDEFD PKLPTGEKEE VPGKPGIKNP ETGDVVRPPV DSVTKYGPVK  1020
GDSIVEKEEI PFEKERKFNP DLAPGTEKVT REGQKGEKTI TTPTLKNPLT GEIISKGESK  1080
EEITKDPINE LTEYGPETIA PGHRDEFDPK LPTGEKEEVP GKPGIKNPET GDVVRPPVDS  1140
VTKYGPVKGD SIVEKEEIPF EKERKFNPDL APGTEKVTRE GQKGEKTITT PTLKNPLTGE  1200
IISKGESKEE ITKDPINELT EYGPETIAPG HRDEFDPKLP TGEKEEVPGK PGIKNPETGD  1260
VVRPPVDSVT KYGPVKGDSI VEKEEIPFEK ERKFNPDLAP GTEKVTREGQ KGEKTITTPT  1320
LKNPLTGEII SKGESKEEIT KDPINELTEY GPETIAPGHR DEFDPKLPTG EKEEVPGKPG  1380
IKNPETGDVV RPPVDSVTKY GPVKGDSIVE KEEIPFEKER KFNPDLAPGT EKVTREGQKG  1440
EKTITTPTLK NPLTGEIISK GESKEEITKD PINELTEYGP ETGSGATGSV SKGEEDNMAI  1500
IKEFMRFKVH MEGSVNGHEF EIEGEGEGRP YEGTQTAKLK VTKGGPLPFA WDILSPQFMY  1560
GSKAYVKHPA DIPDYLKLSF PEGFKWERVM NFEDGGVVTV TQDSSLQDGE FIYKVKLRGT  1620
NFPSDGPVMQ KKTMGWEASS ERMYPEDGAL KGEIKQRLKL KDGGHYDAEV KTTYKAKKPV  1680
QLPGAYNVNI KLDITSHNED YTIVEQYERA EGRHSTGGMD ELYK                   1724

SEQ ID NO: 310          moltype = AA  length = 532
FEATURE                 Location/Qualifiers
source                  1..532
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 310
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDKTGACA ATTAGCTCAT CCAGACATTC CGGGGGSGPG GSGVQLVESG GALVQPGGSL  420
RLSCAASGFP VNRYSMRWYR QAPGKEREWV AGMSSAGDRS SYEDSVKGRF TISRDDARNT  480
VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG TQVTVSSGSG GVSGWRLFKK IS          532

SEQ ID NO: 311          moltype = AA  length = 629
FEATURE                 Location/Qualifiers
source                  1..629
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 311
MVSKGEELFT GVVPILVELD GDVNGHKFSV RGEGEGDATN GKLTLKFICT TGKLPVPWPT  60
LVTTLTYGVQ CFSRYPDHMK RHDFFKSAMP EGYVQERTIS FKDDGTYKTR AEVKFEGDTL  120
VNRIELKGID FKEDGNILGH KLEYNFNSHN VYITADKQKN GIKANFKIRH NVEDGSVQLA  180
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DHYQQNTPIG DGPVLLPDNH YLSTQSKLSK DPNEKRDHMV LLEFVTAAGI THGMDELYKS  240
GLRSRAQMGD WSALGKLLDK VQAYSTAGGK VWLSVLFIFR ILLLGTAVES AWGDEQSAFR  300
CNTQQPGCEN VCYDKSFPIS HVRFWVLQII FVSVPTLLYL AHVFYVMRKE EKLNKKEEEL  360
KVAQTDGVNV EMHLKQIEIK KFKYGIEEHG KVKMRGGLLR TYIISILFKS VFEVAFLLIQ  420
WYIYGFSLSA VYTCKRDPCP HQVDCFLSRP TEKTIFIIFM LVVSLVSLAL NIIELFYVFF  480
KGVKDRVKGR SDPYHATTGP LSPSKDCGSP KYAYFNGCSS PTAPLSPMSP PGYKLVTGDR  540
NNSSCRNYNK QASEQNWANY SAEQNRMGQA GSTISNSHAQ PFDFPDDNQN AKKVAAGHEL  600
QPLAIVDQRP SSRASSRASS RPRPDDLEI                                    629

SEQ ID NO: 312          moltype = AA  length = 630
FEATURE                 Location/Qualifiers
source                  1..630
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 312
MGDWSALGKL LDKVQAYSTA GGKVWLSVLF IFRILLLGTA VESAWGDEQS AFRCNTQQPG  60
CENVCYDKSF PISHVRFWVL QIIFVSVPTL LYLAHVFYVM RKEEKLNKKE EELKVAQTDG  120
VNVEMHLKQI EIKKFKYGIE EHGKVKMRGG LLRTYIISIL FKSVFEVAFL LIQWYIYGFS  180
LSAVYTCKRD PCPHQVDCFL SRPTEKTIFI IFMLVVSLVS LALNIIELFY VFFKGVKDRV  240
KGRSDPYHAT TGPLSPSKDC GSPKYAYFNG CSSPTAPLSP MSPPGYKLVT GDRNNSSCRN  300
YNKQASEQNW ANYSAEQNRM GQAGSTISNS HAQPFDFPDD NQNAKKVAAG HELQPLAIVD  360
QRPSSRASSR ASSRPRPDDL EISARDPPVA TMVSKGEELF TGVVPILVEL DGDVNGHKFS  420
VRGEGEGDAT NGKLTLKFIC TTGKLPVPWP TLVTTLTYGV QCFSRYPDHM KRHDFFKSAM  480
PEGYVQERTI SFKDDGTYKT RAEVKFEGDT LVNRIELKGI DFKEDGNILG HKLEYNFNSH  540
NVYITADKQK NGIKANFKIR HNVEDGSVQL ADHYQQNTPI GDGPVLLPDN HYLSTQSKLS  600
KDPNEKRDHM VLLEFVTAAG ITHGMDELYK                                   630

SEQ ID NO: 313          moltype = AA  length = 379
FEATURE                 Location/Qualifiers
source                  1..379
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 313
MYPYDVPDYA GTGVQVETIS PGDGRTFPKR GQTCVVHYTG MLEDGKKVDS SRDRNKPFKF  60
MLGKQEVIRG WEEGVAQMSV GQRAKLTISP DYAYGATGHP GIIPPHATLV FDVELLKPEG  120
SGMVSKGEEL IKENMHMKLY MEGTVDNHHF KCTSEGEGKP YEGTQTMRIK VVEGGPLPFA  180
FDILATSFLY GSKTFINHTQ GIPDFFKQSF PEGFTWERVT TYEDGGVLTA TQDTSLQDGC  240
LIYNVKIRGV NFTSNGPVMQ KKTLGWEAFT ETLYPADGGL EGRNDMALKL VGGSHLIANA  300
KTTYRSKKPA KNLKMPGVYY VDYRLERIKE ANNETYVEQH EVAVARYCDL PSKLGHKLNG  360
GGGSGGGGSK GFTVGSLIQ                                               379

SEQ ID NO: 314          moltype = AA  length = 373
FEATURE                 Location/Qualifiers
source                  1..373
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 314
MYPYDVPDYA GTGVQVETIS PGDGRTFPKR GQTCVVHYTG MLEDGKKVDS SRDRNKPFKF  60
MLGKQEVIRG WEEGVAQMSV GQRAKLTISP DYAYGATGHP GIIPPHATLV FDVELLKPEG  120
SGVSKGEAVI KEFMRFKVHM EGSMNGHEFE IEGEGEGRPY EGTQTAKLKV TKGGPLPFSW  180
DILSPQFMYG SRAFIKHPAD IPDYYKQSFP EGFKWERVMN FEDGGAVTVT QDTSLEDGTL  240
IYKVKLRGTN FPPDGPVMQK KTMGWEASTE RLYPEDGVLK GDIKMALRLK DGGRYLADFK  300
TTYKAKKPVQ MPGAYNVDRK LDITSHNEDY TVVEQYERSE GRHSTGGMDE LYKGGGGSGG  360
GGSKGFTVGS LIQ                                                     373

SEQ ID NO: 315          moltype = AA  length = 503
FEATURE                 Location/Qualifiers
source                  1..503
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 315
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGLEKFV GTWKIADSHN FGEYLKAIGA PKELSDGGDA TTPTLYISQK DGDKMSVKIE  420
NGPPTFLDTQ VKFKLGEEFD EFPSDRRKGV KSVVNLVGEK LVYVQKWDGK ETTYVREIKD  480
GKLVVTLTMG DVVAVRSYRR ATE                                          503

SEQ ID NO: 316          moltype = AA  length = 632
FEATURE                 Location/Qualifiers
source                  1..632
                        mol_type = protein
                        organism = synthetic construct
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SEQUENCE: 316
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGSGPGNKS QLYPDSPLTD QDFNQLDQTV  240
IEAARRQLVG RRFIELYGPL GRGMQSVFND IFMESHEAKM DFQGSFDTEV ESSRRVNYTI  300
PMLYKDFVLY WRDLEQSKAL DIPIDFSVAA NAARDVAFLE DQMIFHGSKE FDIPGLMNVK  360
GRLTHLIGNW YESGNAFQDI VEARNKLLEM NHNGPYALVL SPELYSLLHR VHKDTNVLEI  420
EHVRELITAG VFQSPVLKGK SGVIVNTGRN NLDLAISEDF ETAYLGEEGM NHPFRVYETV  480
VLRIKRPAAI CTLIDPEEGS GSGSETTGAQ VQLVESGGSL VQPGGSLRLS CAASGRFAES  540
SSMGWFRQAP GKEREFVAAI SWSGGATNYA DSAKGRFTLS RDNTKNTVYL QMNSLKPDDT  600
AVYYCAANLG NYISSNQRLY GYWGQGTQVT VS                                632

SEQ ID NO: 317          moltype = AA  length = 622
FEATURE                 Location/Qualifiers
source                  1..622
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 317
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGSGPGNKS QLYPDSPLTD QDFNQLDQTV  240
IEAARRQLVG RRFIELYGPL GRGMQSVFND IFMESHEAKM DFQGSFDTEV ESSRRVNYTI  300
PMLYKDFVLY WRDLEQSKAL DIPIDFSVAA NAARDVAFLE DQMIFHGSKE FDIPGLMNVK  360
GRLTHLIGNW YESGNAFQDI VEARNKLLEM NHNGPYALVL SPELYSLLHR VHKDTNVLEI  420
EHVRELITAG VFQSPVLKGK SGVIVNTGRN NLDLAISEDF ETAYLGEEGM NHPFRVYETV  480
VLRIKRPAAI CTLIDPEEGS GSGSETTGVQ LVESGGALVQ PGGSLRLSCA ASGFPVNRYS  540
MRWYRQAPGK EREWVAGMSS AGDRSSYEDS VKGRFTISRD DARNTVYLQM NSLKPEDTAV  600
YYCNVNVGFE YWGQGTQVTV SS                                           622

SEQ ID NO: 318          moltype = AA  length = 516
FEATURE                 Location/Qualifiers
source                  1..516
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 318
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGSGPGNKS QLYPDSPLTD QDFNQLDQTV  240
IEAARRQLVG RRFIELYGPL GRGMQSVFND IFMESHEAKM DFQGSFDTEV ESSRRVNYTI  300
PMLYKDFVLY WRDLEQSKAL DIPIDFSVAA NAARDVAFLE DQMIFHGSKE FDIPGLMNVK  360
GRLTHLIGNW YESGNAFQDI VEARNKLLEM NHNGPYALVL SPELYSLLHR VHKDTNVLEI  420
EHVRELITAG VFQSPVLKGK SGVIVNTGRN NLDLAISEDF ETAYLGEEGM NHPFRVYETV  480
VLRIKRPAAI CTLIDPEEGS GSGSETTGDY KDDDDK                            516

SEQ ID NO: 319          moltype = AA  length = 711
FEATURE                 Location/Qualifiers
source                  1..711
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 319
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGGGSGGGS GGSADPETCP CPTGGSCTCS  240
DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC QGSGPGNKSQ  300
LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD  360
FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED  420
QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS  480
PELYSLLHRV HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE  540
TAYLGEEGMN HPFRVYETVV LRIKRPAAIC TLIDPEEGSG SGSETTGAQV QLVESGGSLV  600
QPGGSLRLSC AASGRFAESS SMGWFRQAPG KEREFVAAIS WSGGATNYAD SAKGRFTLSR  660
DNTKNTVYLQ MNSLKPDDTA VYYCAANLGN YISSNQRLYG YWGQGTQVTV S           711

SEQ ID NO: 320          moltype = AA  length = 701
FEATURE                 Location/Qualifiers
source                  1..701
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 320
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGGGSGGGS GGSADPETCP CPTGGSCTCS  240
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DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC QGSGPGNKSQ  300
LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD  360
FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED  420
QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS  480
PELYSLLHRV HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE  540
TAYLGEEGMN HPFRVYETVV LRIKRPAAIC TLIDPEEGSG SGSETTGVQL VESGGALVQP  600
GGSLRLSCAA SGFPVNRYSM RWYRQAPGKE REWVAGMSSA GDRSSYEDSV KGRFTISRDD  660
ARNTVYLQMN SLKPEDTAVY YCNVNVGFEY WGQGTQVTVS S                      701

SEQ ID NO: 321          moltype = AA  length = 595
FEATURE                 Location/Qualifiers
source                  1..595
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 321
MLEKFVGTWK IADSHNFGEY LKAIGAPKEL SDGGDATTPT LYISQKDGDK MSVKIENGPP  60
TFLDTQVKFK LGEEFDEFPS DRRKGVKSVV NLVGEKLVYV QKWDGKETTY VREIKDGKLV  120
VTLTMGDVVA VRSYRRATEG GTGGSDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS  180
CCPAGCEKCA KDCVCKGEEG AKAEAEKCSC CQGGGSGGGS GGSADPETCP CPTGGSCTCS  240
DKCKCKGCKC TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC QGSGPGNKSQ  300
LYPDSPLTDQ DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD  360
FQGSFDTEVE SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED  420
QMIFHGSKEF DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS  480
PELYSLLHRV HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE  540
TAYLGEEGMN HPFRVYETVV LRIKRPAAIC TLIDPEEGSG SGSETTGDYK DDDDK       595

SEQ ID NO: 322          moltype = AA  length = 376
FEATURE                 Location/Qualifiers
source                  1..376
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 322
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDKGGPAA KRVKLD                                                  376

SEQ ID NO: 323          moltype = AA  length = 381
FEATURE                 Location/Qualifiers
source                  1..381
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 323
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGPDFLGHA ENPLREEEWA RLNETVIQVA RRSLVGRRIL DIYGPLGAGV  120
QTVPYDEFQG VSPGAVDIVG EQETAMVFTD ARKFKTIPII YKDFLLHWRD IEAARTHNMP  180
LDVSAAAGAA ALCAQQEDEL IFYGDARLGY EGLMTANGRL TVPLGDWTSP GGGFQAIVEA  240
TRKLNEQGHF GPYAVVLSPR LYSQLHRIYE KTGVLEIETI RQLASDGVYQ SNRLRGESGV  300
VVSTGRENMD LAVSMDMVAA YLGASRMNHP FRVLEALLLR IKHPDAICTL EGAGATERRG  360
SGDYKDDDDK GGPAAKRVKL D                                            381

SEQ ID NO: 324          moltype = AA  length = 529
FEATURE                 Location/Qualifiers
source                  1..529
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 324
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGG TGGSTSTTLV KCACEPCLCN VDPSKAIDRN GLYYCSEACA DGHTGGSKGC  120
GHTGCNCHGS AGGCDDKCGC AVPCPGGTGC RCTSARSGAA AGEHTTCGCG EHCGCNPCAC  180
GREGTPSGRA NRRANCSCGA ACNCASCGSA TAPGGGGSGG GSGGSANKSQ LYPDSPLTDQ  240
DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD FQGSFDTEVE  300
SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED QMIFHGSKEF  360
DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS PELYSLLHRV  420
HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE TAYLGEEGMN  480
HPFRVYETVV LRIKRPAAIC TLIDPEEGSG DYKDDDDKGG PAAKRVKLD              529

SEQ ID NO: 325          moltype = AA  length = 698
FEATURE                 Location/Qualifiers
source                  1..698
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 325
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MVSKGEAVIK EFMRFKVHME GSMNGHEFEI EGEGEGRPYE GTQTAKLKVT KGGPLPFSWD  60
ILSPQFMYGS RAFIKHPADI PDYYKQSFPE GFKWERVMNF EDGGAVTVTQ DTSLEDGTLI  120
YKVKLRGTNF PPDGPVMQKK TMGWEASTER LYPEDGVLKG DIKMALRLKD GGRYLADFKT  180
TYKAKKPVQM PGAYNVDRKL DITSHNEDYT VVEQYERSEG RHSTGGMDEL YKGSGATNFS  240
LLKQAGDVEE NPGPMDPETC PCPTGGSCTC SDKCKCKGCK CTNCKKSCCS CCPAGCEKCA  300
KDCVCKGEEG AKAEAEKCSC CQGGGSGGGS GGSADPETCP CPTGGSCTCS DKCKCKGCKC  360
TNCKKSCCSC CPAGCEKCAK DCVCKGEEGA KAEAEKCSCC QGSGPGNKSQ LYPDSPLTDQ  420
DFNQLDQTVI EAARRQLVGR RFIELYGPLG RGMQSVFNDI FMESHEAKMD FQGSFDTEVE  480
SSRRVNYTIP MLYKDFVLYW RDLEQSKALD IPIDFSVAAN AARDVAFLED QMIFHGSKEF  540
DIPGLMNVKG RLTHLIGNWY ESGNAFQDIV EARNKLLEMN HNGPYALVLS PELYSLLHRV  600
HKDTNVLEIE HVRELITAGV FQSPVLKGKS GVIVNTGRNN LDLAISEDFE TAYLGEEGMN  660
HPFRVYETVV LRIKRPAAIC TLIDPEEGSG DYKDDDDK                          698

SEQ ID NO: 326          moltype = AA  length = 293
FEATURE                 Location/Qualifiers
source                  1..293
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 326
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDK         293

SEQ ID NO: 327          moltype = AA  length = 297
FEATURE                 Location/Qualifiers
source                  1..297
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 327
PDFLGHAENP LREEEWARLN ETVIQVARRS LVGRRILDIY GPLGAGVQTV PYDEFQGVSP  60
GAVDIVGEQE TAMVFTDARK FKTIPIIYKD FLLHWRDIEA ARTHNMPLDV SAAAGAAALC  120
AQQEDELIFY GDARLGYEGL MTANGRLTVP LGDWTSPGGG FQAIVEATRK LNEQGHFGPY  180
AVVLSPRLYS QLHRIYEKTG VLEIETIRQL ASDGVYQSNR LRGESGVVVS TGRENMDLAV  240
SMDMVAAYLG ASRMNHPFRV LEALLLRIKH PDAICTLEGA GATERRGSGD YKDDDDK     297

SEQ ID NO: 328          moltype = AA  length = 282
FEATURE                 Location/Qualifiers
source                  1..282
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 328
EFLKRSFAPL TEKQWQEIDN RAREIFKTQL YGRKFVDVEG PYGWEYAAHP LGEVEVLSDE  60
NEVVKWGLRK SLPLIELRAT FTLDLWELDN LERGKPNVDL SSLEETVRKV AEFEDEVIFR  120
GCEKSGVKGL LSFEERKIEC GSTPKDLLEA IVRALSIFSK DGIEGPYTLV INTDRWINFL  180
KEEAGHYPLE KRVEECLRGG KIITTPRIED ALVVSERGGD FKLILGQDLS IGYEDREKDA  240
VRLFITETFT FQVVNPEALI LLKGGGSGPG PDRKAAVSHW QQ                     282

SEQ ID NO: 329          moltype = AA  length = 247
FEATURE                 Location/Qualifiers
source                  1..247
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 329
MVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  60
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  120
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  180
EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYKGSGD  240
YKDDDDK                                                            247

SEQ ID NO: 330          moltype = AA  length = 488
FEATURE                 Location/Qualifiers
source                  1..488
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 330
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGSGS  360
ETTGAQVQLV ESGGSLVQPG GSLRLSCAAS GRFAESSSMG WFRQAPGKER EFVAAISWSG  420
GATNYADSAK GRFTLSRDNT KNTVYLQMNS LKPDDTAVYY CAANLGNYIS SNQRLYGYWG  480
QGTQVTVS                                                           488
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SEQ ID NO: 331          moltype = AA  length = 365
FEATURE                 Location/Qualifiers
source                  1..365
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 331
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGWSH  360
PQFEK                                                              365

SEQ ID NO: 332          moltype = AA  length = 481
FEATURE                 Location/Qualifiers
source                  1..481
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 332
MSKGEELFTG VVPILVELDG DVNGHKFSVR GEGEGDATNG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKR HDFFKSAMPE GYVQERTISF KDDGTYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNFNSHNV YITADKQKNG IKANFKIRHN VEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSVLSKD PNEKRDHMVL LEFVTAAGIT HGMDELYKGG  240
TGATGSVSKG EEDNMAIIKE FMRFKVHMEG SVNGHEFEIE GEGEGRPYEG TQTAKLKVTK  300
GGPLPFAWDI LSPQFMYGSK AYVKHPADIP DYLKLSFPEG FKWERVMNFE DGGVVTVTQD  360
SSLQDGEFIY KVKLRGTNFP SDGPVMQKKT MGWEASSERM YPEDGALKGE IKQRLKLKDG  420
GHYDAEVKTT YKAKKPVQLP GAYNVNIKLD ITSHNEDYTI VEQYERAEGR HSTGGMDELY  480
K                                                                  481

SEQ ID NO: 333          moltype = AA  length = 390
FEATURE                 Location/Qualifiers
source                  1..390
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 333
MGVQVETISP GDGRTFPKRG QTCVVHYTGM LEDGKKVDSS RDRNKPFKFM LGKQEVIRGW  60
EEGVAQMSVG QRAKLTISPD YAYGATGHPG IIPPHATLVF DVELLKPEGS GGKSYPTVSA  120
DYQDAVEKAK KKLRGFIAEK RCAPLMLRLA FHSAGTFDKG TKTGGPFGTI KHPAELAHSA  180
NNGLDIAVRL LEPLKAEFPI LSYADFYQLA GVVAVEVTGG PKVPFHPGRE DKPEPPPEGR  240
LPDPTKGSDH LRDVFGKAMG LTDQDIVALS GGHTIGAAHK ERSGFEGPWT SNPLIFDNSY  300
FTELLSGEKE GLLQLPSDKA LLSDPVFRPL VDKYAADEDA FFADYAEAHQ KLSELGFADA  360
LQLPPLERLT LDGGGGSGGG GSLTVGSLRR                                   390

SEQ ID NO: 334          moltype = AA  length = 298
FEATURE                 Location/Qualifiers
source                  1..298
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 334
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGAHIVM VDAYKPTK    298

SEQ ID NO: 335          moltype = AA  length = 231
FEATURE                 Location/Qualifiers
source                  1..231
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 335
MVQLVESGGA LVQPGGSLRL SCAASGFPVN RYSMRWYRQA PGKEREWVAG MSSAGDRSSY  60
EDSVKGRFTI SRDDARNTVY LQMNSLKPED TAVYYCNVNV GFEYWGQGTQ VTVSSGGGGS  120
GGGGSGDYDS ATHIKFSKRD EDGKELAGAT MELRDSSGKT ISTWISDGQV KDFYLYPGKY  180
TFVETAAPDG YEVATAITFT VNEQGQVTVN GKATKGDAHI GSGDYKDDDD K           231

SEQ ID NO: 336          moltype = AA  length = 326
FEATURE                 Location/Qualifiers
source                  1..326
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 336
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
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AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGGGGSGPG GSGSPEDKIA  300
QLKQKIQALK QENQQLEEEN AALEYG                                       326

SEQ ID NO: 337          moltype = AA  length = 260
FEATURE                 Location/Qualifiers
source                  1..260
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 337
VSKGEELFTG VVPILVELDG DVNGHKFSVS GEGEGDATYG KLTLKFICTT GKLPVPWPTL  60
VTTLTYGVQC FSRYPDHMKQ HDFFKSAMPE GYVQERTIFF KDDGNYKTRA EVKFEGDTLV  120
NRIELKGIDF KEDGNILGHK LEYNYNSHNV YIMADKQKNG IKVNFKIRHN IEDGSVQLAD  180
HYQQNTPIGD GPVLLPDNHY LSTQSALSKD PNEKRDHMVL LEFVTAAGIT LGMDELYKSG  240
LRSRAQASNS GCMSCKCVLS                                              260

SEQ ID NO: 338          moltype = AA  length = 302
FEATURE                 Location/Qualifiers
source                  1..302
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 338
MSPEDEIQQL EEEIAQLEQK NAALKEKNQA LKYGGGGGSG PGVSKGEELF TGVVPILVEL  60
DGDVNGHKFS VSGEGEGDAT YGKLTLKFIC TTGKLPVPWP TLVTTLTYGV QCFSRYPDHM  120
KQHDFFKSAM PEGYVQERTI FFKDDGNYKT RAEVKFEGDT LVNRIELKGI DFKEDGNILG  180
HKLEYNYNSH NVYIMADKQK NGIKVNFKIR HNIEDGSVQL ADHYQQNTPI GDGPVLLPDN  240
HYLSTQSALS KDPNEKRDHM VLLEFVTAAG ITLGMDELYK SGLRSRAQAS NSGCMSCKCV  300
LS                                                                 302

SEQ ID NO: 339          moltype = AA  length = 922
FEATURE                 Location/Qualifiers
source                  1..922
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 339
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTAGCTAG  300
GCGCTCGAAG ACLSFGTEIL TVEYGPLPIG KIVSEEINCS VYSVDPEGRV YTQAIAQWHD  360
RGEQEVLEYE LEDGSVIRAT SDHRFLTTDY QLLAIEEIFA RQLDLLTLEN IKQTEEALDN  420
HRLPFPLLDA GTIKMVKVIG RRSLGVQRIF DIGLPQDHNF LLANGAIAAA CSCGSGSRGG  480
SGATNFSLLK QAGDVEENPG PNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL  540
YGPLGRGMQS VFNDIFMESH EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ  600
SKALDIPIDF SVAANAARDV AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA  660
FQDIVEARNK LLEMNHNGPY ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV  720
LKGKSGVIVN TGRNNLDLAI SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP  780
EEGGGGSGPG GSGVQLVESG GALVQPGGSL RLSCAASGFP VNRYSMRWYR QAPGKEREWV  840
AGMSSAGDRS SYEDSVKGRF TISRDDARNT VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG  900
TQVTVSSGSG GVSGWRLFKK IS                                           922

SEQ ID NO: 340          moltype = AA  length = 451
FEATURE                 Location/Qualifiers
source                  1..451
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 340
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTAGCTAG  300
GCGCTCGAAG AGGGGSGPGG SGVQLVESGG ALVQPGGSLR LSCAASGFPV NRYSMRWYRQ  360
APGKEREWVA GMSSAGDRSS YEDSVKGRFT ISRDDARNTV YLQMNSLKPE DTAVYYCNVN  420
VGFEYWGQGT QVTVSSGSGG VSGWRLFKKI S                                 451

SEQ ID NO: 341          moltype = AA  length = 451
FEATURE                 Location/Qualifiers
source                  1..451
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 341
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
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AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTAACTAG  300
GCGCTCGAAG AGGGGSGPGG SGVQLVESGG ALVQPGGSLR LSCAASGFPV NRYSMRWYRQ  360
APGKEREWVA GMSSAGDRSS YEDSVKGRFT ISRDDARNTV YLQMNSLKPE DTAVYYCNVN  420
VGFEYWGQGT QVTVSSGSGG VSGWRLFKKI S                                 451

SEQ ID NO: 342         moltype = AA  length = 451
FEATURE                Location/Qualifiers
source                 1..451
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 342
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTGACTAG  300
GCGCTCGAAG AGGGGSGPGG SGVQLVESGG ALVQPGGSLR LSCAASGFPV NRYSMRWYRQ  360
APGKEREWVA GMSSAGDRSS YEDSVKGRFT ISRDDARNTV YLQMNSLKPE DTAVYYCNVN  420
VGFEYWGQGT QVTVSSGSGG VSGWRLFKKI S                                 451

SEQ ID NO: 343         moltype = AA  length = 442
FEATURE                Location/Qualifiers
source                 1..442
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 343
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTAGCTAT  300
CCGGGGSGPG GSGVQLVESG GALVQPGGSL RLSCAASGFP VNRYSMRWYR QAPGKEREWV  360
AGMSSAGDRS SYEDSVKGRF TISRDDARNT VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG  420
TQVTVSSGSG GVSGWRLFKK IS                                           442

SEQ ID NO: 344         moltype = AA  length = 442
FEATURE                Location/Qualifiers
source                 1..442
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 344
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTAACTAT  300
CCGGGGSGPG GSGVQLVESG GALVQPGGSL RLSCAASGFP VNRYSMRWYR QAPGKEREWV  360
AGMSSAGDRS SYEDSVKGRF TISRDDARNT VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG  420
TQVTVSSGSG GVSGWRLFKK IS                                           442

SEQ ID NO: 345         moltype = AA  length = 442
FEATURE                Location/Qualifiers
source                 1..442
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 345
MNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  60
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  120
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  180
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  240
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKTGACTAT  300
CCGGGGSGPG GSGVQLVESG GALVQPGGSL RLSCAASGFP VNRYSMRWYR QAPGKEREWV  360
AGMSSAGDRS SYEDSVKGRF TISRDDARNT VYLQMNSLKP EDTAVYYCNV NVGFEYWGQG  420
TQVTVSSGSG GVSGWRLFKK IS                                           442

SEQ ID NO: 346         moltype = AA  length = 459
FEATURE                Location/Qualifiers
source                 1..459
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 346
MVSKGEEDNM AIIKEFMRFK VHMEGSVNGH EFEIEGEGEG RPYEGTQTAK LKVTKGGPLP  60
FAWDILSPQF MYGSKAYVKH PADIPDYLKL SFPEGFKWER VMNFEDGGVV TVTQDSSLQD  120
GEFIYKVKLR GTNFPSDGPV MQKKTMGWEA SSERMYPEDG ALKGEIKQRL KLKDGGHYDA  180
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EVKTTYKAKK PVQLPGAYNV NIKLDITSHN EDYTIVEQYE RAEGRHSTGG MDELYKSGLR  240
SRAMGTRDDE YDYLFKVVLI GDSGVGKSNL LSRFTRNEFN LESKSTIGVE FATRSIQVDG  300
KTIKAQIWDT AGQERYRAIT SAYYRGAVGA LLVYDIAKHL TYENVERWLK ELRDHADSNI  360
VIMLVGNKSD LRHLRAVPTD EARAFAEKNG LSFIETSALD STNVEAAFQT ILTEIYRIVS  420
QKQMSDRREN DMSPSNNVVP IHVPPTTENK PKVQCCQNI                         459

SEQ ID NO: 347         moltype = AA  length = 855
FEATURE                Location/Qualifiers
source                 1..855
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 347
MSAAVTAGKL ARAPADPGKA GVPGVAAPGA PAAAPPAKEI PEVLVDPRSR RRYVRGRFLG  60
KGGFAKCFEI SDADTKEVFA GKIVPKSLLL KPHQREKMSM EISIHRSLAH QHVVGFHGFF  120
EDNDFVFVVL ELCRRRSLLE LHKRRKALTE PEARYYLRQI VLGCQYLHRN RVIHRDLKLG  180
NLFLNEDLEV KIGDFGLATK VEYDGERKKT LCGTPNYIAP EVLSKKGHSF EVDVWSIGCI  240
MYTLLVGKPP FETSCLKETY LRIKKNEYSI PKHINPVAAS LIQKMLQTDP TARPTINELL  300
NDEFFTSGYI PARLPITCLT IPPRFSIAPS SLDPSNRKPL TVLNKGLENP LPERPREKEE  360
PVVRETGEVV DCHLSDMLQQ LHSVNASKPS ERGLVRQEEA EDPACIPIFW VSKWVDYSDK  420
YGLGYQLCDN SVGVLFNDST RLILYNDGDS LQYIERDGTE SYLTVSSHPN SLMKKITLLK  480
YFRNYMSEHL LKAGANITPR EGDELARLPY LRTWFRTRSA IILHLSNGSV QINFFQDHTK  540
LILCPLMAAV TYIDEKRDFR TYRLSLLEEY GCCKELASRL RYARTMVDKL LSSRSASNRL  600
KASGSGSASG GSGSGPVATM VSKGEEDNMA IIKEFMRFKV HMEGSVNGHE FEIEGEGEGR  660
PYEGTQTAKL KVTKGGPLPF AWDILSPQFM YGSKAYVKHP ADIPDYLKLS FPEGFKWERV  720
MNFEDGGVVT VTQDSSLQDG EFIYKVKLRG TNFPSDGPVM QKKTMGWEAS SERMYPEDGA  780
LKGEIKQRLK LKDGGHYDAE VKTTYKAKKP VQLPGAYNVN IKLDITSHNE DYTIVEQYER  840
AEGRHSTGGM DELYK                                                   855

SEQ ID NO: 348         moltype = AA  length = 423
FEATURE                Location/Qualifiers
source                 1..423
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 348
MEKSFVITDP RLPDNPIIFA SDGFLELTEY SREEILGRNG RFLQGPETDQ ATVQKIRDAI  60
RDQREITVQL INYTKSGKKF WNLLHLQPMR DQKGELQYFI GVQLDGGGGG SGGGGSGSGP  120
GNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  180
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  240
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  300
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  360
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKGLPPLER  420
LTL                                                                423

SEQ ID NO: 349         moltype = AA  length = 424
FEATURE                Location/Qualifiers
source                 1..424
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 349
MEKSFVITDP RLPDNPIIFA SDGFLELTEY SREEILGRNG RFLQGPETDQ ATVQKIRDAI  60
RDQREITVQL INYTKSGKKF WNLLHLQPMR DQKGELQYFI GVQLDGGGGG SGGGGSGSGP  120
GNKSQLYPDS PLTDQDFNQL DQTVIEAARR QLVGRRFIEL YGPLGRGMQS VFNDIFMESH  180
EAKMDFQGSF DTEVESSRRV NYTIPMLYKD FVLYWRDLEQ SKALDIPIDF SVAANAARDV  240
AFLEDQMIFH GSKEFDIPGL MNVKGRLTHL IGNWYESGNA FQDIVEARNK LLEMNHNGPY  300
ALVLSPELYS LLHRVHKDTN VLEIEHVREL ITAGVFQSPV LKGKSGVIVN TGRNNLDLAI  360
SEDFETAYLG EEGMNHPFRV YETVVLRIKR PAAICTLIDP EEGSGDYKDD DDKGGPAAKR  420
VKLD                                                               424

SEQ ID NO: 350         moltype = AA  length = 375
FEATURE                Location/Qualifiers
source                 1..375
                       mol_type = protein
                       organism = synthetic construct
SEQUENCE: 350
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGSGDYK  360
DDDDKGLPPL ERLTL                                                   375

SEQ ID NO: 351         moltype = DNA  length = 596
FEATURE                Location/Qualifiers
source                 1..596
                       mol_type = other DNA
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                        organism = synthetic construct
SEQUENCE: 351
ccccttcacc gagggcctat ttcccatgat tccttcatat ttgcatatac gatacaaggc  60
tgttagagag ataattggaa ttaatttgac tgtaaacaca aagatattag tacaaaatac  120
gtgacgtaga aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat  180
ggactatcat atgcttaccg taacttgaaa gtatttcgat ttcttggctt tatatatctt  240
gtggaaagga cgaaacaccg tgctcgcttc ggcagcacat atactagtcg acgggccgca  300
ctcgccggtc ccaagcccgg ataaaatggg agggggcggg aaaccgccta accatgccga  360
gtgcggccgc gagacggtcg ggtccagata gaattccgac cagaagatat ggcttcggtt  420
gggttctatc tgtcgagtag agtgtgggct cgtggccgcg gtcggcgtgg actgtagaac  480
actgccaatg ccggtcccaa gcccggataa aagtggaggg tacagtccac gctctagagc  540
ggacttcggt ccgcgcggtt ctatctagtt acgcgttaaa ccaactagaa tttttt      596

SEQ ID NO: 352          moltype = DNA  length = 660
FEATURE                 Location/Qualifiers
source                  1..660
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 352
ccccttcacc gagggcctat ttcccatgat tccttcatat ttgcatatac gatacaaggc  60
tgttagagag ataattggaa ttaatttgac tgtaaacaca aagatattag tacaaaatac  120
gtgacgtaga aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat  180
ggactatcat atgcttaccg taacttgaaa gtatttcgat ttcttggctt tatatatctt  240
gtggaaagga cgaaacaccg tgctcgcttc ggcagcacat atactagtcg acgggccgca  300
ctcgccggtc ccaagcccgg ataaaatggg agggggcggg aaaccgccta accatgccga  360
gtgcggccgc gagacggtcg ggtccagata ggcactaacc taagacagga gggccgggaa  420
acctgcctaa tccaatgacg ggtaatagtg tcgaattccg accagaagat atggcttcgg  480
ttgggttcgt tatctgtcga gtagagtgtg ggctcgtggc cgcggtcggc gtggactgta  540
gaacactgcc aatgccggtc ccaagcccgg ataaaagtgg agggtacagt ccacgctcta  600
gagcggactt cggtccgcgc ggttctatct agttacgcgt taaaccaact agaatttttt  660

SEQ ID NO: 353          moltype = DNA  length = 658
FEATURE                 Location/Qualifiers
source                  1..658
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 353
ccccttcacc gagggcctat ttcccatgat tccttcatat ttgcatatac gatacaaggc  60
tgttagagag ataattggaa ttaatttgac tgtaaacaca aagatattag tacaaaatac  120
gtgacgtaga aagtaataat ttcttgggta gtttgcagtt ttaaaattat gttttaaaat  180
ggactatcat atgcttaccg taacttgaaa gtatttcgat ttcttggctt tatatatctt  240
gtggaaagga cgaaacaccg tgctcgcttc ggcagcacat atactagtcg acgggccgca  300
ctcgccggtc ccaagcccgg ataaaatggg agggggcggg aaaccgccta accatgccga  360
gtgcggccgc gagacggtcg ggtccagata ggcactaacc taagacagga gggccgggag  420
aattccgacc agaagatatg gcttcggttg ggttcaacct gcctaatcca atgacgggta  480
atagtgtcta tctgtcgagt agagtgtggg ctcgtggccg cggtcggcgt ggactgtaga  540
acactgccaa tgccggtccc aagcccggat aaaagtggag ggtacagtcc acgctctaga  600
gcggacttcg gtccgcgcgg ttctatctag ttacgcgtta aaccaactag aatttttt    658

SEQ ID NO: 354          moltype = AA  length = 1179
FEATURE                 Location/Qualifiers
source                  1..1179
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 354
MADIEQELER LKASIRRLEQ EVNQERARMA ALQTLLAKGG SGGATEEAII RIPPYHYIHV  60
LDQNSNVSRV EVGPKTYIRQ DNERVLFAPV RMVTVPPRHY CIVANPVSRD TQSSVLFDIT  120
GQVRLRHADQ EIRLAQDPFP LYPGEVLEKD ITPLQVVLPN TALHLKALLD FEDKNGDKVM  180
AGDEWLFEGP GTYIPQKEVE VVEIIQATVI KQNQALRLRA RKECFDREGK GRVTGEEWLV  240
RSVGAYLPAV FEEVLDLVDA VILTEKTALH LRALQNFRDL RGVLHRTGEE WLVTVQDTEA  300
HVPDVYEEVL GVVPITTLGP RHYCVILDPM GPDGKNQLGQ KRVVKGEKSF FLQPGERLER  360
GIQDVYVLSE QQGLLLKALQ PLEEGESEEK VSHQAGDCWL IRGPLEYVPS AKVEVVEERQ  420
AIPLDQNEGI YVQDVKTGKV RAVIGSTYML TQDEVLWEKE LPSGVEELLN LGGGGSPEDK  480
LQAIKYELAQ NEEELAQIEE KLAANKEGGS GGGGSGSKTI VLSVGEATRT LTEIQSTADR  540
QIFEEKVGPL VGRLRLTASL RQNGAKTAYR VNLKLDQADV VDSGLPKVRY TQVWSHDVTI  600
VANSTEASRK SLYDLTKSLV ATSQVEDLVV NLVPLGRGPG SGGGGSGGPE DENAALEEKI  660
AQLKQKNAAL KEEIQALEYS APRNKTRVVS YRVPHNAAVQ VYDYRAKRAR VVFGPELVTL  720
DPEEQFTVLS LSAGRPKRPH ARRALCLLLG PDFFTDVITI ETADHARLQL QLAYNWHFEL  780
KNRNDPAEAA KLFSVPDFVG DACKAIASRV RGAVASVTFD DFHKNSARII RMAVFGFEGS  840
PEDELAANEE ELQQNEQKLA QIKQKLQAIK YGGGGSGGGG SGGGGHHHHH HGGGGSGGGG  900
SGGGGSPEDE IQQLEEEIAQ LEQKNAALKE KNQALKYGKA RDQAVFPQNG LVVSSVDVQS  960
VEPVDQRTRD ALQRSVQLAI EITTNSQEAA AKHEAQRLEQ EARGRLERQK ILDQSEAEKA  1020
RKELLELEAM SMAVESTGNA KAEAESRAEA ARIEGEGSVL QAKLKAQALA IETEAELERV  1080
KKVREMELIY ARAQLELEVS KAQQLANVEA KKFKEMTEAL GPGTIRDLAV AGPEMQVKLL  1140
QSLGLKSTLI TDGSSPINLF STAFGLLGLG SDGQPPAQK                         1179
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SEQ ID NO: 355          moltype = AA  length = 1137
FEATURE                 Location/Qualifiers
source                  1..1137
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 355
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG GGGSPEDKLQ AIKYELAQNE EELAQIEEKL AANKEGGSGG GGSGSKTIVL  480
SVGEATRTLT EIQSTADRQI FEEKVGPLVG RLRLTASLRQ NGAKTAYRVN LKLDQADVVD  540
SGLPKVRYTQ VWSHDVTIVA NSTEASRKSL YDLTKSLVAT SQVEDLVVNL VPLGRGPGSG  600
GGGSGGPEDE NAALEEKIAQ LKQKNAALKE EIQALEYSAP RNKTRVVSYR VPHNAAVQVY  660
DYRAKRARVV FGPELVTLDP EEQFTVLSLS AGRPKRPHAR RALCLLLGPD FFTDVITIET  720
ADHARLQLQL AYNWHFELKN RNDPAEAAKL FSVPDFVGDA CKAIASRVRG AVASVTFDDF  780
HKNSARIIRM AVFGFEGSPE DELAANEEEL QQNEQKLAQI KQKLQAIKYG GGGSGGGGSG  840
GGGHHHHHHG GGGSGGGGSG GGGSPEDEIQ QLEEEIAQLE QKNAALKEKN QALKYGKARD  900
QAVFPQNGLV VSSVDVQSVE PVDQRTRDAL QRSVQLAIEI TTNSQEAAAK HEAQRLEQEA  960
RGRLERQKIL DQSEAEKARK ELLELEAMSM AVESTGNAKA EAESRAEAAR IEGEGSVLQA  1020
KLKAQALAIE TEAELERVKK VREMELIYAR AQLELEVSKA QQLANVEAKK FKEMTEALGP  1080
GTIRDLAVAG PEMQVKLLQS LGLKSTLITD GSSPINLFST AFGLLGLGSD GQPPAQK     1137

SEQ ID NO: 356          moltype = AA  length = 1167
FEATURE                 Location/Qualifiers
source                  1..1167
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 356
MATEEAIIRI PPYHYIHVLD QNSNVSRVEV GPKTYIRQDN ERVLFAPVRM VTVPPRHYCI  60
VANPVSRDTQ SSVLFDITGQ VRLRHADQEI RLAQDPFPLY PGEVLEKDIT PLQVVLPNTA  120
LHLKALLDFE DKNGDKVMAG DEWLFEGPGT YIPQKEVEVV EIIQATVIKQ NQALRLRARK  180
ECFDREGKGR VTGEEWLVRS VGAYLPAVFE EVLDLVDAVI LTEKTALHLR ALQNFRDLRG  240
VLHRTGEEWL VTVQDTEAHV PDVYEEVLGV VPITTLGPRH YCVILDPMGP DGKNQLGQKR  300
VVKGEKSFFL QPGERLERGI QDVYVLSEQQ GLLLKALQPL EEGESEEKVS HQAGDCWLIR  360
GPLEYVPSAK VEVVEERQAI PLDQNEGIYV QDVKTGKVRA VIGSTYMLTQ DEVLWEKELP  420
SGVEELLNLG GGGSPEDKLQ AIKYELAQNE EELAQIEEKL AANKEGGSGG GGSGSKTIVL  480
SVGEATRTLT EIQSTADRQI FEEKVGPLVG RLRLTASLRQ NGAKTAYRVN LKLDQADVVD  540
SGLPKVRYTQ VWSHDVTIVA NSTEASRKSL YDLTKSLVAT SQVEDLVVNL VPLGRGPGSG  600
GGGSGGPEDE NAALEEKIAQ LKQKNAALKE EIQALEYSAP RNKTRVVSYR VPHNAAVQVY  660
DYRAKRARVV FGPELVTLDP EEQFTVLSLS AGRPKRPHAR RALCLLLGPD FFTDVITIET  720
ADHARLQLQL AYNWHFELKN RNDPAEAAKL FSVPDFVGDA CKAIASRVRG AVASVTFDDF  780
HKNSARIIRM AVFGFEGSPE DELAANEEEL QQNEQKLAQI KQKLQAIKYG GGGSGGGGSG  840
GGGCGLCVCP CNKLKSSDAY KKAWGNNQDG VVASQPARVG GGGSGGGGSG GGGSPEDEIQ  900
QLEEEIAQLE QKNAALKEKN QALKYGKARD QAVFPQNGLV VSSVDVQSVE PVDQRTRDAL  960
QRSVQLAIEI TTNSQEAAAK HEAQRLEQEA RGRLERQKIL DQSEAEKARK ELLELEAMSM  1020
AVESTGNAKA EAESRAEAAR IEGEGSVLQA KLKAQALAIE TEAELERVKK VREMELIYAR  1080
AQLELEVSKA QQLANVEAKK FKEMTEALGP GTIRDLAVAG PEMQVKLLQS LGLKSTLITD  1140
GSSPINLFST AFGLLGLGSD GQPPAQK                                      1167

SEQ ID NO: 357          moltype = AA  length = 1257
FEATURE                 Location/Qualifiers
source                  1..1257
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 357
MKEELDAPHQ IFTTTKEAIE RFMAMLTPVI ENAEDDHERL YYHHIYEEEE QRLSRLDVLI  60
PLIEKFQDET DEGLFSPSNN AFNRLLQELN LEKFGLHNFI EHVLALFSFT DEERQTLLKE  120
LRKDAYEGYQ YVKEKLAEIN ARFDHDYADP HAHHDEHRDH LADMPSAGSS HEEVQPVAHK  180
KKGFTVGSLI QGSGATNFSL LKQAGDVEEN PGPMNKSQLY PDSPLTDQDF NQLDQTVIEA  240
ARRQLVGRRF IELYGPLGRG MQSVFNDIFM ESHEAKMDFQ GSFDTEVESS RRVNYTIPML  300
YKDFVLYWRD LEQSKALDIP IDFSVAANAA RDVAFLEDQM IFHGSKEFDI PGLMNVKGRL  360
THLIGNWYES GNAFQDIVEA RNKLLEMNHN GPYALVLSPE LYSLLHRVHK DTNVLEIEHV  420
RELITAGVFQ SPVLKGKSGV IVNTGRNNLD LAISEDFETA YLGEEGMNHP FRVYETVVLR  480
IKRPAAICTL IDPEEGSGGG GGSGPGGSGM KFNKEKWQAI KEIAFLPNLN QPQHLAFIVS  540
LLDDPSQSAN LLAEAKKLND AQAPKGSGAT NFSLLKQAGD VEENPGPMSR DPLPFFPPLY  600
LGGPEITTEN CEREPIHIPG SIQPHGALLT ADGHSGEVLQ MSLNAATFLG QEPTVLRGQT  660
LAALLPEQWP ALQAALPPGC PDALQYRATL DWPAAGHLSL TVHRVGELLI LEFEPTEAWD  720
STGPHALRNA MFALESAPNL RALAEVATQT VRELTGFDRV MLYKFAPDAT GEVIAEARRE  780
GLHAFLGHRF PASDIPAQAR ALYTRHLLRL TADTRAAAVP LDPVLNPQTN APTPLGGAVL  840
RATSPMHMQY LRNMGVGSSL SVSVVVGGQL WGLIACHHQT PYVLPPDLRT TLEYLGRLLS  900
LQVQVKEAAD VAAFRQSLRE HHARVALAAA HSLSPHDTLS DPALDLLGLM RAGGLILRFE  960
GRWQTLGEVP PAPAVDALLA WLETQPGALV QTDALGQLWP AGADLAPSAA GLLAISVGEG  1020
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WSECLVWLRP ELRLEVAWGG ATPDQAKDDL GPRHSFDTYL EEKRGYAEPW HPGEIEEAQD  1080
LRDTLTGALL ESGGDIIKLL NEQVNKEMQS SNLYMSMSSW CYTHSLDGAG LFLFDHAAEE  1140
YEHAKKLIIF LNENNVPVQL TSISAPEHKF EGLTQIFQKA YEHEQHISES INNIVDHAIK  1200
SKDHATFNFL QWYVAEQHEE EVLFKDILDK IELIGNENHG LYLADQYVKG IAKSRKS     1257

SEQ ID NO: 358          moltype = AA  length = 1019
FEATURE                 Location/Qualifiers
source                  1..1019
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 358
MKEELDAFHQ IFTTTKEAIE RFMAMLTPVI ENAEDDHERL YYHHIYEEEE QRLSRLDVLI  60
PLIEKFQDET DEGLFSPSNN AFNRLLQELN LEKFGLHNFI EHVDLALFSF TDEERQTLLK  120
ELRKDAYEGY QYVKEKLAEI NARFDHDYAD PHAHHDEHRD HLADMPSAGS SHEEVQPVAH  180
KKKGFTVGSL IQGSGATNFS LLKQAGDVEE NPGPMNKSQL YPDSPLTDQD FNQLDQTVIE  240
AARRQLVGRR FIELYGPLGR GMQSVFNDIF MESHEAKMDF QGSFDTEVES SRRVNYTIPM  300
LYKDFVLYWR DLEQSKALDI PIDFSVAANA ARDVAFLEDQ MIFHGSKEFD IPGLMNVKGR  360
LTHLIGNWYE SGNAFQDIVE ARNKLLEMNH NGPYALVLSP ELYSLLHRVH KDTNVLEIEH  420
VRELITAGVF QSPVLKGKSG VIVNTGRNNL DLAISEDFET AYLGEEGMNH PFRVYETVVL  480
RIKRPAAICT LIDPEEGSGG SGGSGGSGGT GGSGGSGGSG MHTLYAPGGY DIMGYLRQIR  540
NRPNPQVELG PVDTSCALVL CDLKQKDTPV VYASEAFLYM TGYSNAEVLG RNCRFLQSPD  600
GMVKPKSTRK YVDSNTINTM RKAIDRNAEV QVEVVNFKKN GQRFVNFLTM IPVRDETGEY  660
RYSMGFQCET EGSGATNFSL LKQAGDVEEN PGPMGHTLYA PGGYDIMGYL DQIGNRPNPQ  720
VELGPVDTSC ALILCDLKQK DTPIVYASEA FLYMTGYSNA EVLGRNCRFL QSPDGMVKPK  780
STRKYVDSNT INTIRKAIDR NAEVQVEVVN FKKNGQRFVN FLTIIPVRDE TGEYRYSMGF  840
QCETEGGGGS GGGGSGDIIK LLNEQVNKEM QSSNLYMSMS SWCYTHSLDG AGLFLFDHAA  900
EEYEHAKKLI IFLNENNVPV QLTSISAPEH KFEGLTQIFQ KAYEHEQHIS ESINNIVDHA  960
IKSKDHATFN FLQWYVAEQH EEEVLFKDIL DKIELIGNEN HGLYLADQYV KGIAKSRKS   1019

SEQ ID NO: 359          moltype = AA  length = 255
FEATURE                 Location/Qualifiers
source                  1..255
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 359
MVQLVESGGA LVQPGGSLRL SCAASGFPVN RYSMRWYRQA PGKEREWVAG MSSAGDRSSY  60
EDSVKGRFTI SRDDARNTVY LQMNSLKPED TAVYYCNVNV GFEYWGQGTQ VTVSSGGGGS  120
GGGGSGENLY FQSGGGGSGG GGSGGGGSGV QVETISPGDG RTFPKRGQTC VVHYTGMLED  180
GKKFDSSRDR NKPFKFMLGK QEVIRGWEEG VAQMSVGQRA KLTISPDYAY GATGHPGIIP  240
PHATLVFDVE LLKLE                                                   255

SEQ ID NO: 360          moltype = AA  length = 459
FEATURE                 Location/Qualifiers
source                  1..459
                        mol_type = protein
                        organism = synthetic construct
SEQUENCE: 360
MDPETCPCPT GGSCTCSDKC KCKGCKCTNC KKSCCSCCPA GCEKCAKDCV CKGEEGAKAE  60
AEKCSCCQGS GPGNKSQLYP DSPLTDQDFN QLDQTVIEAA RRQLVGRRFI ELYGPLGRGM  120
QSVFNDIFME SHEAKMDFQG SFDTEVESSR RVNYTIPMLY KDFVLYWRDL EQSKALDIPI  180
DFSVAANAAR DVAFLEDQMI FHGSKEFDIP GLMNVKGRLT HLIGNWYESG NAFQDIVEAR  240
NKLLEMNHNG PYALVLSPEL YSLLHRVHKD TNVLEIEHVR ELITAGVFQS PVLKGKSGVI  300
VNTGRNNLDL AISEDFETAY LGEEGMNHPF RVYETVVLRI KRPAAICTLI DPEEGGGGSG  360
PGGSGMILWH EMWHEGLEEA SRLYFGERNV KGMFEVLEPL HAMMERGPQT LKETSFNQAY  420
GRDLMEAQEW CRKYMKSGNV KDLTQAWDLY YHVFRRISK                         459

SEQ ID NO: 361          moltype = AA  length = 517
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source                  1..517
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```

1. A genetically controlled nanoscopy contrast-generating unit for providing enhanced resolution of a molecular target comprising a metal interactor,

wherein the metal interactor is compatible with nanoscopy fixation protocols, nanoscopy post-fixation protocols, and nanoscopy metal staining protocols,

wherein the metal interactor is a molecule to which a metal ion binds to or reacts with, and

wherein the metal interactor is not a ferroxidase or an enzymatic product from an exogenous substrate.

2. The genetically controlled nanoscopy contrast-generating unit according to claim **1**, wherein the metal interactor comprises one or more of the following elements:

a metal-interacting peptide/protein,

a metal-binding peptide/protein,

a lipid-binding protein,

an RNA-binding protein,

a DNA or RNA molecule,

a polymerizing or synthesizing enzyme,

a biomineralizing enzyme,

a bioconjugation tag,

or a combination thereof.

3. The genetically controlled nanoscopy contrast-generating unit according to claim **1**, wherein the metal interactor comprises one or more of the following elements:

a metallothionein,

osmiophilic amino acids,

a lead binder,

a lanthanide binder,

a uranyl-binder,

a vanadium binder,

a copper and silver-binder,

a cobalt or nickel binder,

a fatty-acid-binding protein,

a lipid-binding domain of a cytochrome P450,

an RNA aptamer-binder:RNA aptamer pair,

a programmable RNA binding protein,

a polymerizing kinase,

a phytochelatin synthase, or

a tyrosinase.

4. The genetically controlled nanoscopy contrast-generating unit according to claim **1**,

wherein the genetically controlled nanoscopy contrast-generating unit further comprises a fluorophore or a chromophore, wherein

(i) the fluorophore is a fluorescent, a co-factor in a fluorescent protein, or an exogenous fluorophore, or

(ii) the chromophore is a chromoprotein, a co-factor in a chromoprotein, or an exogenous chromophore, and

wherein the exogenous fluorophore or the exogenous chromophore binds directly to the metal interactor.

5. The genetically controlled nanoscopy contrast-generating unit according to claim **1**, wherein the metal interactor comprises

(i) at least one metallothionein, at least one fatty-acid binding protein, at least one lipid-binding domain, or at least one RNA molecule, and

ii) a fluorophore, wherein the fluorophore is a fluorescent protein.

6. (canceled)

7. A genetically controlled structural element for nanoscopic detection,

wherein the genetically controlled structural element spatially organizes the genetically controlled nanoscopy contrast-generating unit according to claim **1**,

wherein the genetically controlled structural element has a pre-determined shape and a pre-determined nanoscale size, and

wherein the genetically controlled structural element generates a shape that can be differentiated at nanoscale resolution.

8. The genetically controlled structural element according to claim **7** further comprising a binder or at least one attachment point for labeling a subcellular target of interest selected from a member of the encapsulin family, a vault, an MS2 phage, a Qbeta phage, an AP205 phage, an engineered mono-to-polyvalent hub, a filament, a linker, or combinations thereof.

9. The genetically controlled structural element according to claim **8**,

wherein said at least one attachment point is selected from the group consisting of nanobodies, frankenbodies, coiled-coil domains, isopeptide-forming partners, bioconjugation-tags, split-inteins, calmodulin-binding peptides, phosphorylatable peptides, conformation-changing peptides including troponins, and combinations thereof, and

wherein the genetically controlled nanoscopy contrast-generating unit interacts with or binds to the at least one attachment point.

10. The genetically controlled structural element according to claim **7**,

wherein the genetically controlled structural element is an encapsulin,

wherein the genetically controlled contrast-generating unit is selected from the group of one or more metallothionein MT3, one or more different metallothionein species, one or more fatty acid-binding proteins (FABPs), and one or more of the lipid-binding domain of the cytochrome P450, or combinations thereof,

wherein one to three copies of the MT3 or one to three different metallothionein species are bound to the N-terminus of the encapsulin,

wherein one or more MT3s, FABPs, or BM3hs are bound to the surface of the encapsulin, and

wherein the spatial organization is configured to generate the distinct shape of a barcode, wherein the barcode is a concentric barcode differentiable at nanoscale resolution.

11. A genetically controlled scaffold for organizing structural elements for nanoscopic detection,

wherein the genetically controlled scaffold comprises and spatially organizes the genetically controlled structural elements according to claim **7**, and

wherein the spatial organization generates distinct geometric patterns that are differentiated at nanoscale resolution.

12. The genetically controlled scaffold according to claim **11**, wherein the genetically controlled scaffold is selected from the group consisting of an endogenous cellular scaffold, a designed scaffold, a CsgA element, a SasG element, an RNA or DNA structure, and combinations thereof.

13. The genetically controlled scaffold according to claim **11**, comprising

a SasG of variable length,

at least one encapsulin structural element, and

at least one contrast generating unit MT3, or a series of different metallothionein species,

wherein the at least one encapsulin is connected and spatially organized via SasG, and

wherein the at least one encapsulin comprises the at least one contrast generating unit MT3, or a series of different metallothionein species contrast generating units.

14. A nanoscopy method for nanoscopic detection comprising:

(a) providing the genetically controlled nanoscopy contrast-generating unit according to claim **1**, and/or

(b) providing the genetically controlled structural element according to claim **7**, and/or

(c) the genetically controlled scaffold according to claim **11**,

wherein the nanoscopy detection comprises molecular mapping and/or geometric sensing.

15. The method according to claim **14**,

wherein the nanoscopy detection is molecular mapping, and

wherein the molecular mapping provides information on the subcellular distribution of a molecule of interest within a cell or tissue via the binding of the genetically controlled structural element and/or genetically controlled scaffold to the molecule, which thus determines the subcellular localization of the genetically controlled structural element and/or the genetically controlled scaffold.

16. The method according to claim **14**,

wherein the nanoscopy detection is geometric sensing, and

wherein the geometric sensing provides information on a specific cellular state, a cellular process, or the presence or absence of an analyte or environmental parameter of interest within a cell or tissue, or the response to an external stimulus, and

wherein the shape generated by the genetically controlled structural element and/or the geometric pattern generated by the genetically controlled scaffold changes in response to a pre-defined cellular state, a pre-defined cellular process, at least one analyte, at least one environmental parameter, or an external stimulus.

17. The method according to claim **14**,

wherein the nanoscopy detection comprising mapping and/or the geometrical sensing further comprises geometric actuation,

wherein the geometric actuation alters a cellular state or process by a biomechanical, and/or biochemical effect or via an external stimulus, or the deposition of external energy, electromagnetic radiation, mechanical energy, or magnetic gradients.

18. The method according to claim **14**,

wherein the contrast generating unit, structural element and/or scaffold is compatible with intact cell systems, preferably with mammalian cells and organoids or biomedical model organisms.

19-133. (canceled)

134. The genetically controlled structural element according to claim **7**, wherein the generated shape is a barcode encoding information for a cellular state using geometric sensing.

135. The genetically controlled structural element according to claim **10**, wherein the one or more metallothioneins, the lipid binder, the RNA aptamer, and the one or more fluorescent proteins of the genetically controlled nanoscopy contrast-generating unit are bound to the surface of the encapsulin genetically controlled structural element.

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