



US 20250251401A1

(19) United States

(12) Patent Application Publication (10) Pub. No.: US 2025/0251401 A1

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(43) Pub. Date: Aug. 7, 2025

(54) MARKERS SELECTIVELY DEREGULATED IN TUMOR-INFILTRATING REGULATORY T CELLS

A61K 45/06 (2006.01)*C07K 14/47* (2006.01)*C07K 16/28* (2006.01)*C07K 16/30* (2006.01)*C12N 5/0783* (2010.01)*C12N 15/113* (2010.01)

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(21) Appl. No.: 19/037,818

(22) Filed: Jan. 27, 2025

(52) U.S. Cl.
CPC *G01N 33/57492* (2013.01); *A61K 35/17* (2013.01); *A61K 45/06* (2013.01); *C07K 14/4748* (2013.01); *C07K 16/2866* (2013.01); *C07K 16/30* (2013.01); *C12N 5/0637* (2013.01); *C12N 15/1135* (2013.01); *C12N 15/1138* (2013.01); *C07K 2317/732* (2013.01); *C07K 2317/76* (2013.01); *C12N 2310/11* (2013.01); *C12N 2310/14* (2013.01)**Related U.S. Application Data**

(63) Continuation of application No. 18/295,965, filed on Apr. 5, 2023, now Pat. No. 12,247,982, which is a continuation of application No. 16/301,805, filed on Nov. 15, 2018, now abandoned, filed as application No. PCT/EP2017/061642 on May 15, 2017.

Foreign Application Priority DataMay 16, 2016 (EP) 16169791.7
Nov. 14, 2016 (EP) 16198724.3**Publication Classification**

(51) Int. Cl.

G01N 33/574 (2006.01)
A61K 35/17 (2025.01)

(57)

ABSTRACT

The present invention discloses a number of markers selectively deregulated in tumor-infiltrating regulatory T cells. The invention relates to molecules able to modulate the expression and/or function of at least one such marker for use in the prevention and/or treatment of the tumor. Preferably the molecule specifically binds to the marker and induces antibody-dependent cell-mediated cytotoxicity (ADCC). The invention further relates to a molecule able to modulate the expression and/or function of at least one such marker for use in a method for in vivo depleting tumor-infiltrating regulatory T cell in a subject, or for use in a method to enhance tumor immunity in a subject. Corresponding pharmaceutical compositions are also contemplated.

Specification includes a Sequence Listing.

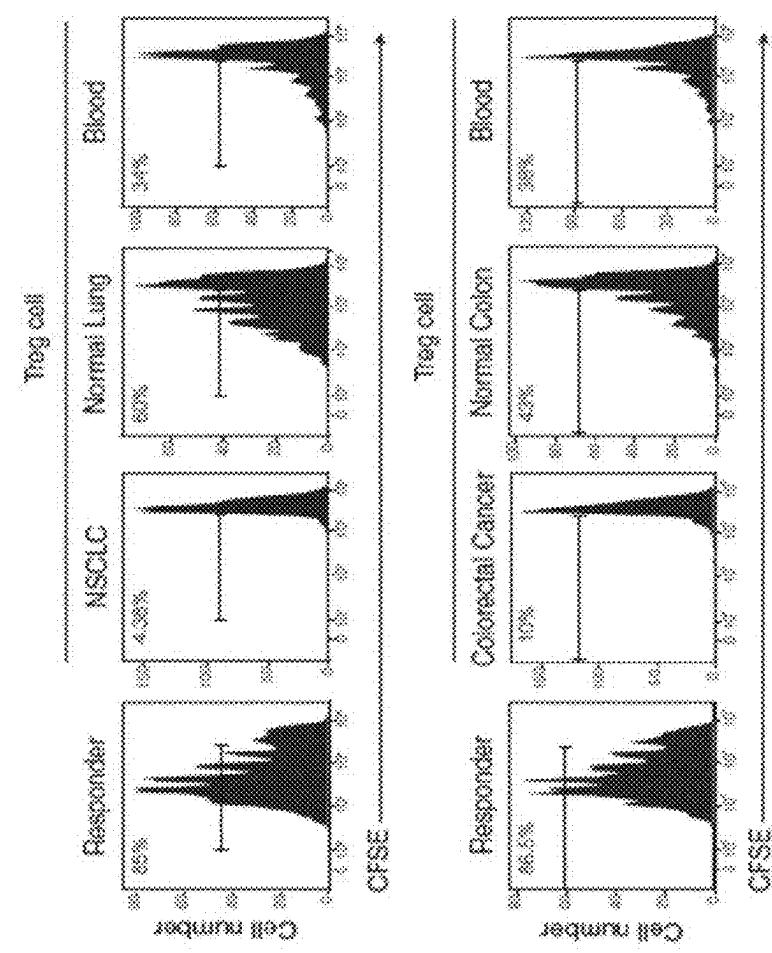
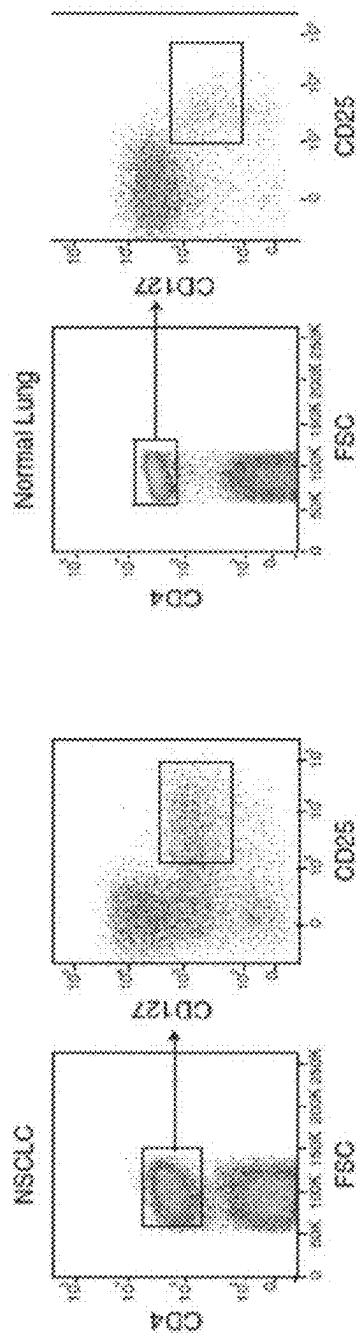
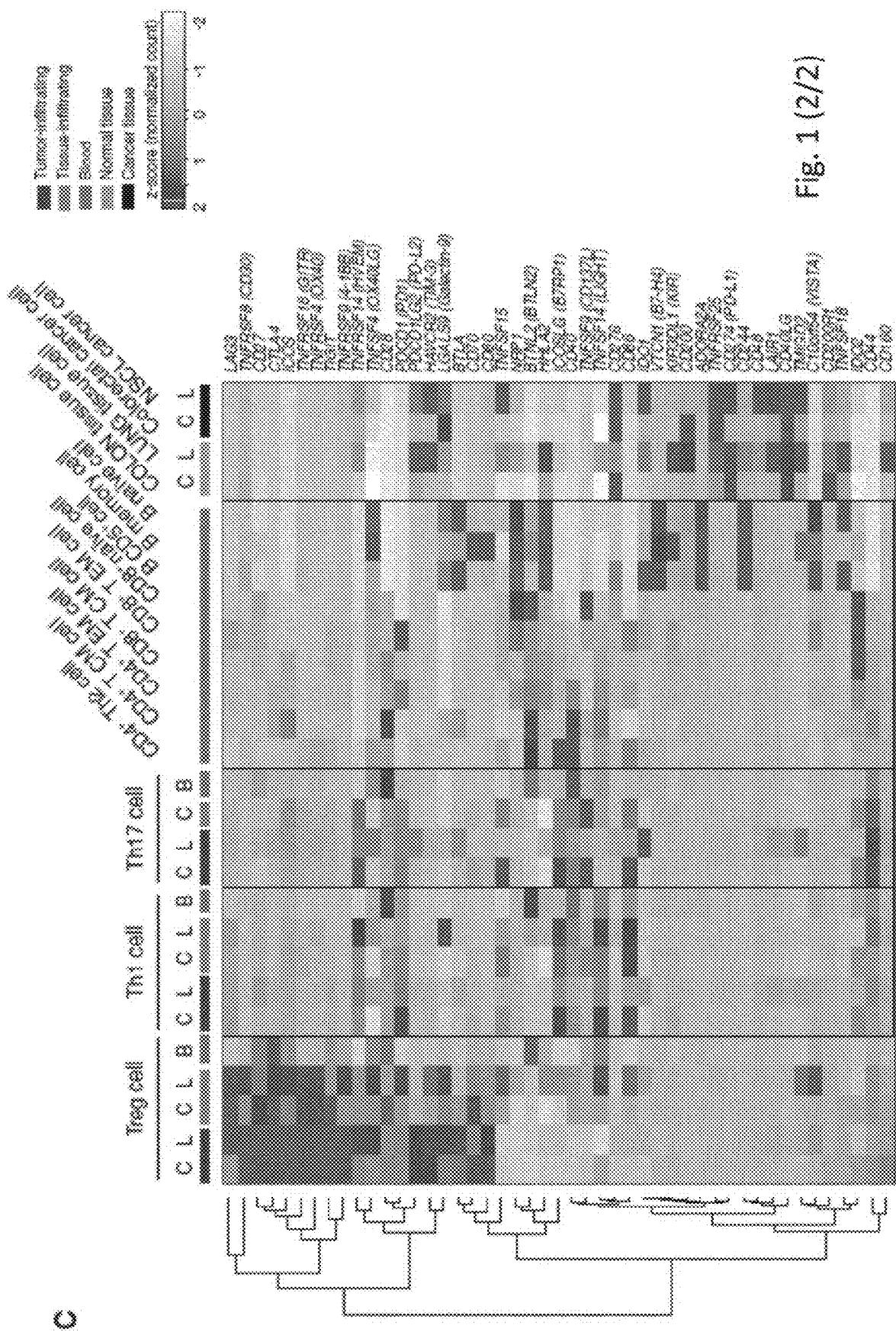
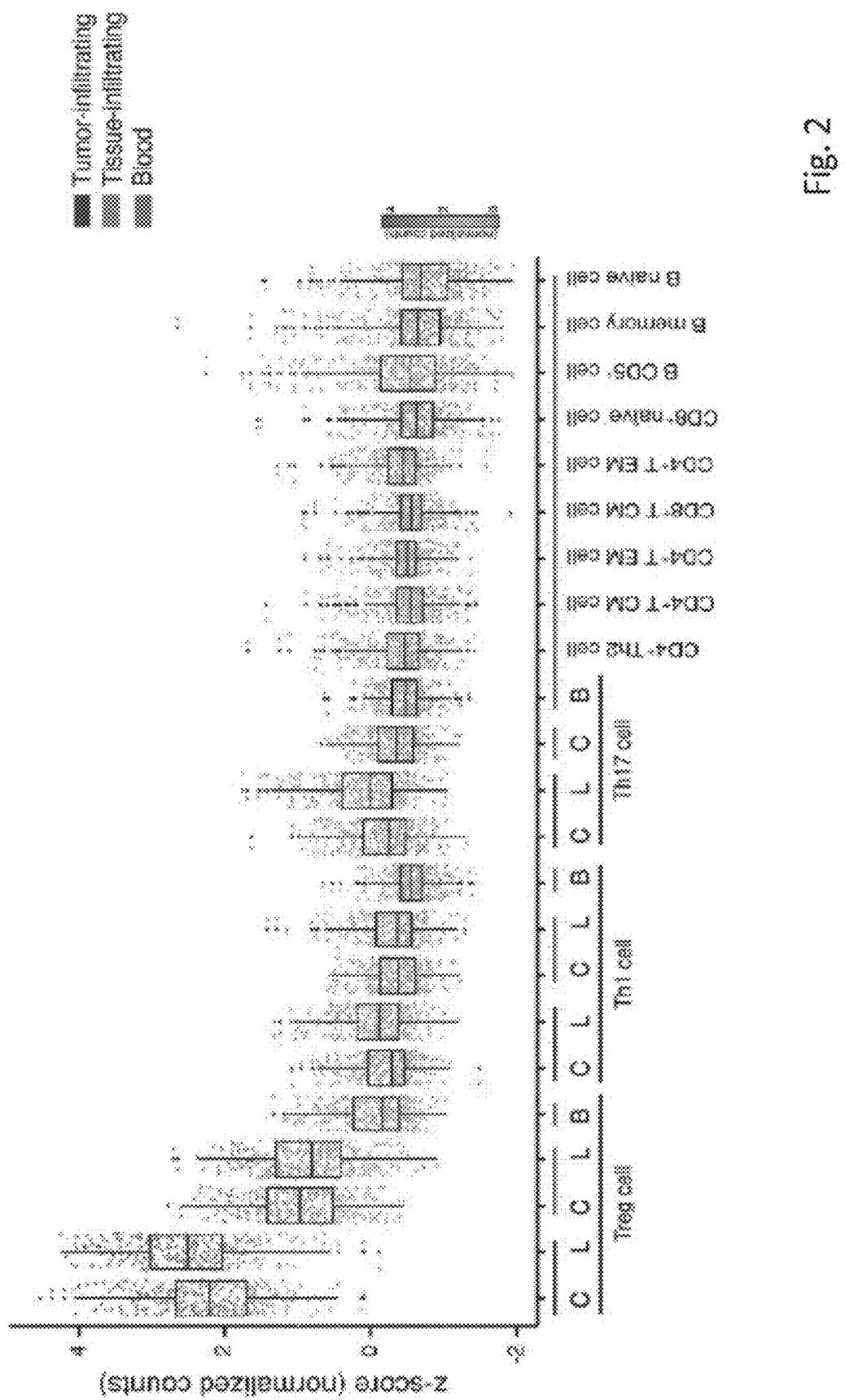


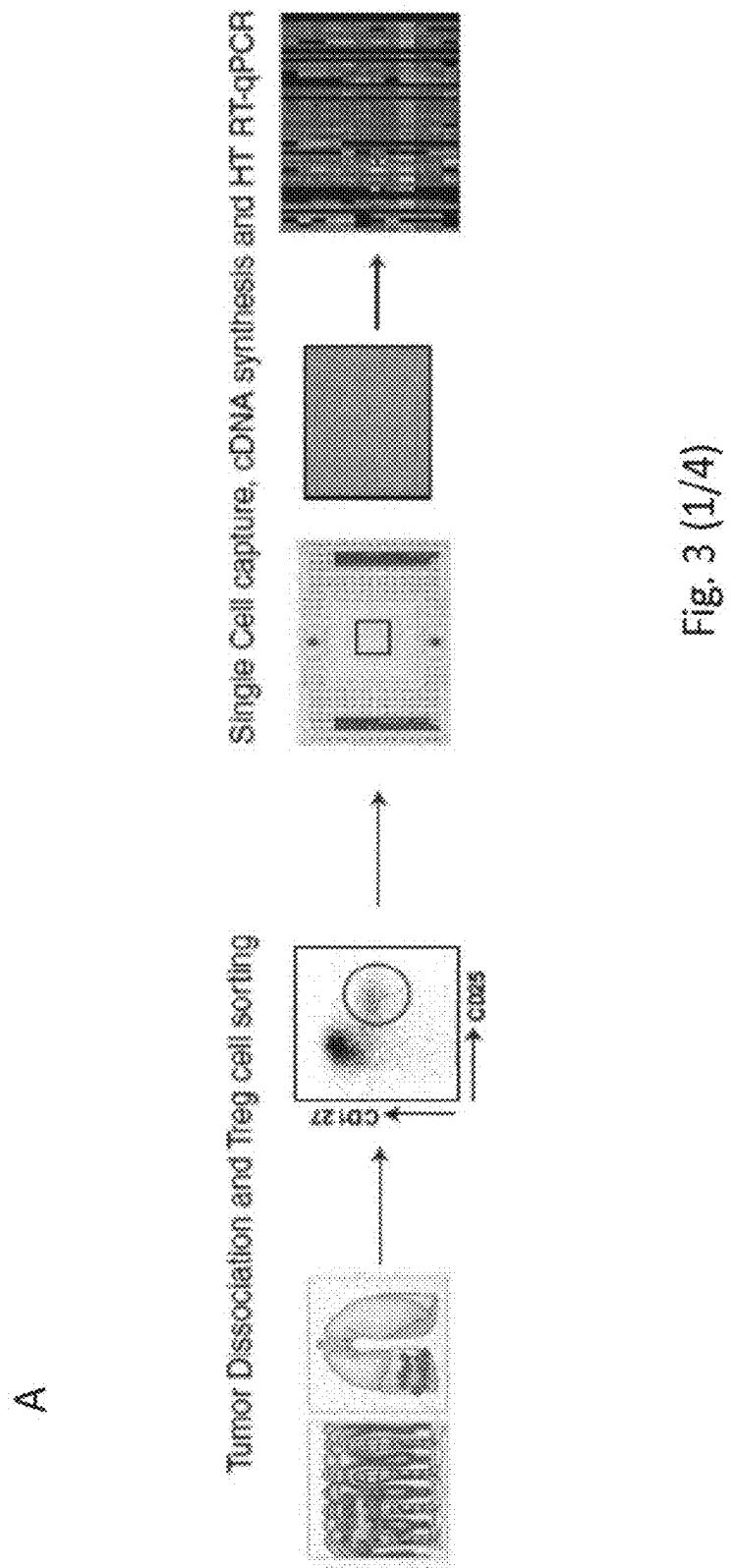
Fig. 1 (1/2)

A

B







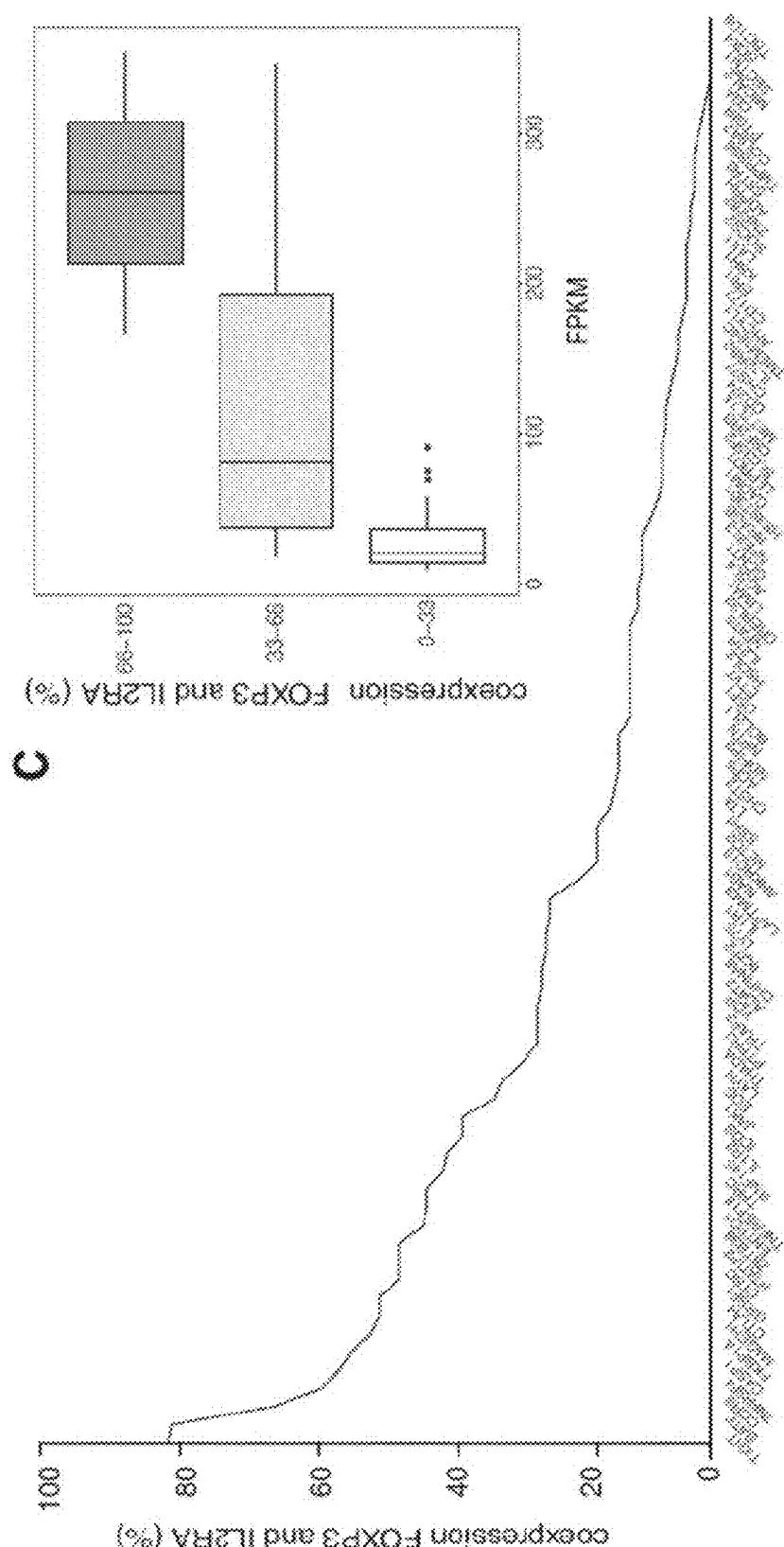
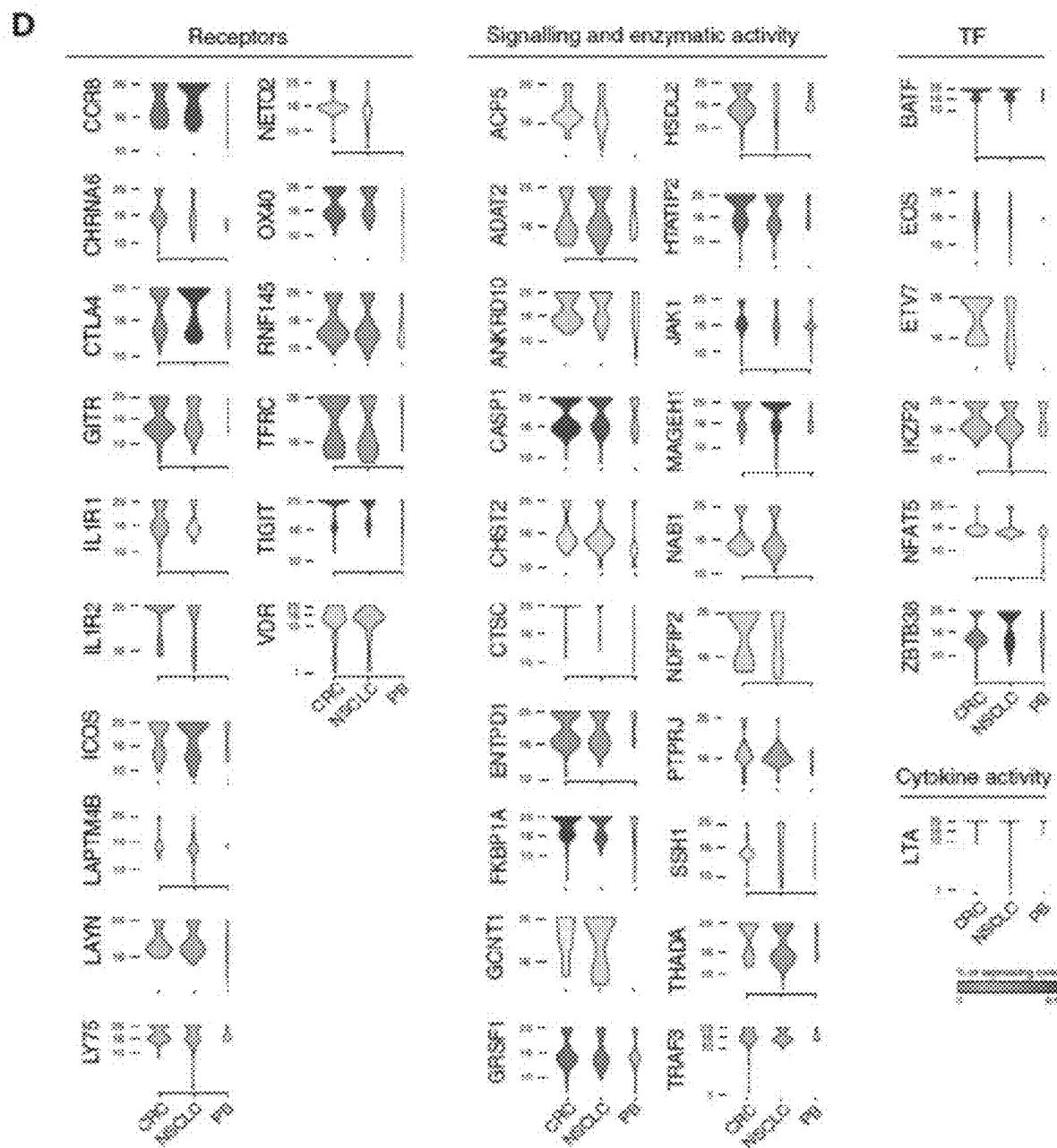


Fig. 3 (2/4)



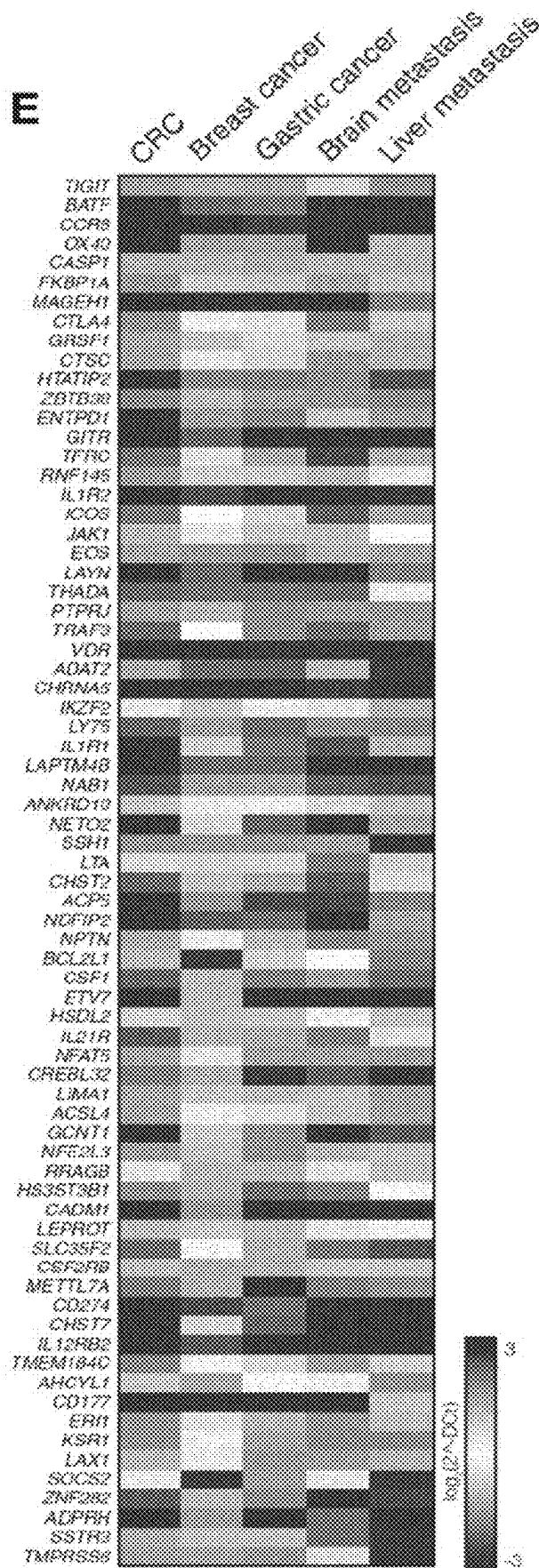


Fig. 3 (4/4)

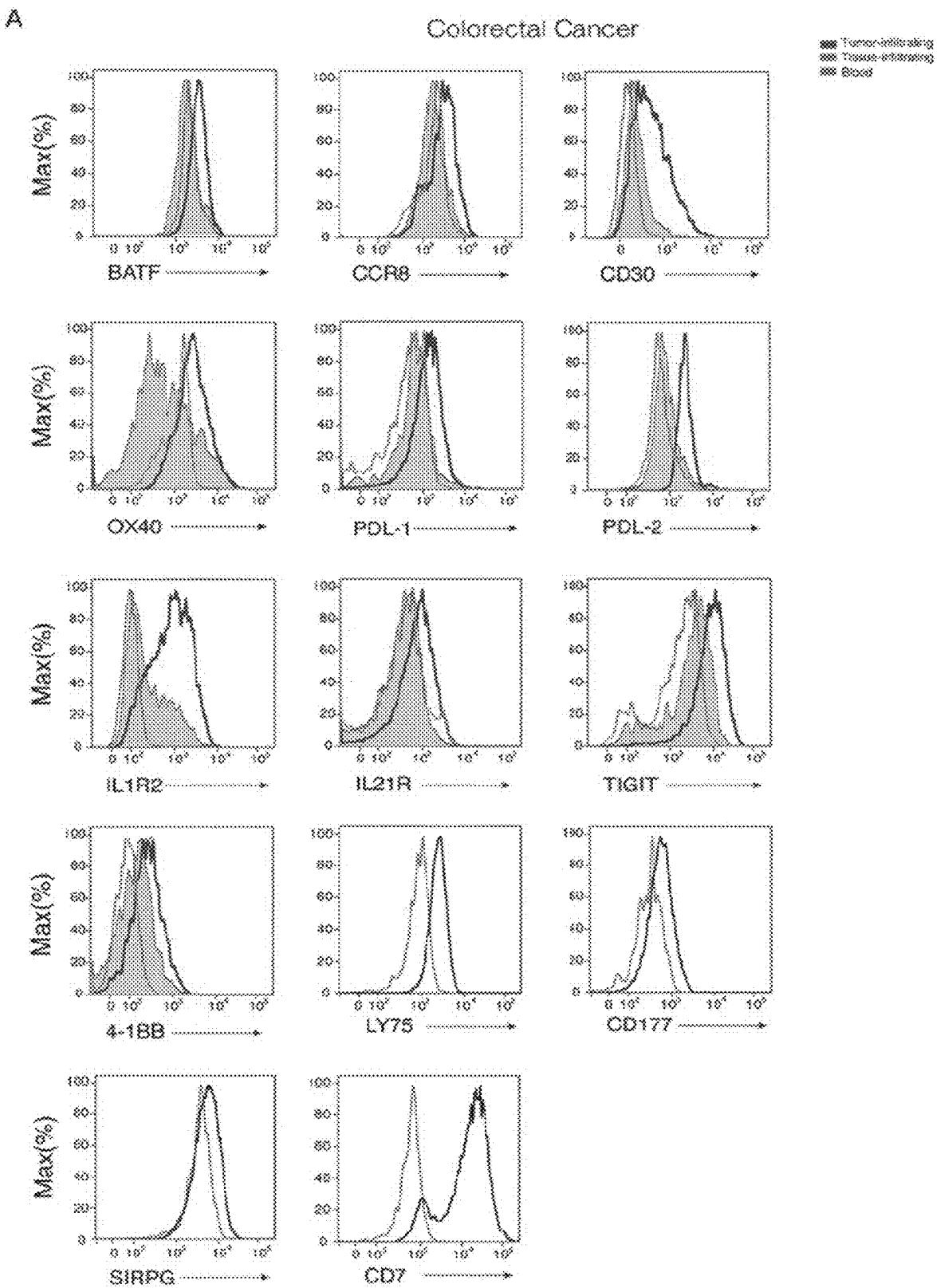


Fig.4 (1/2)

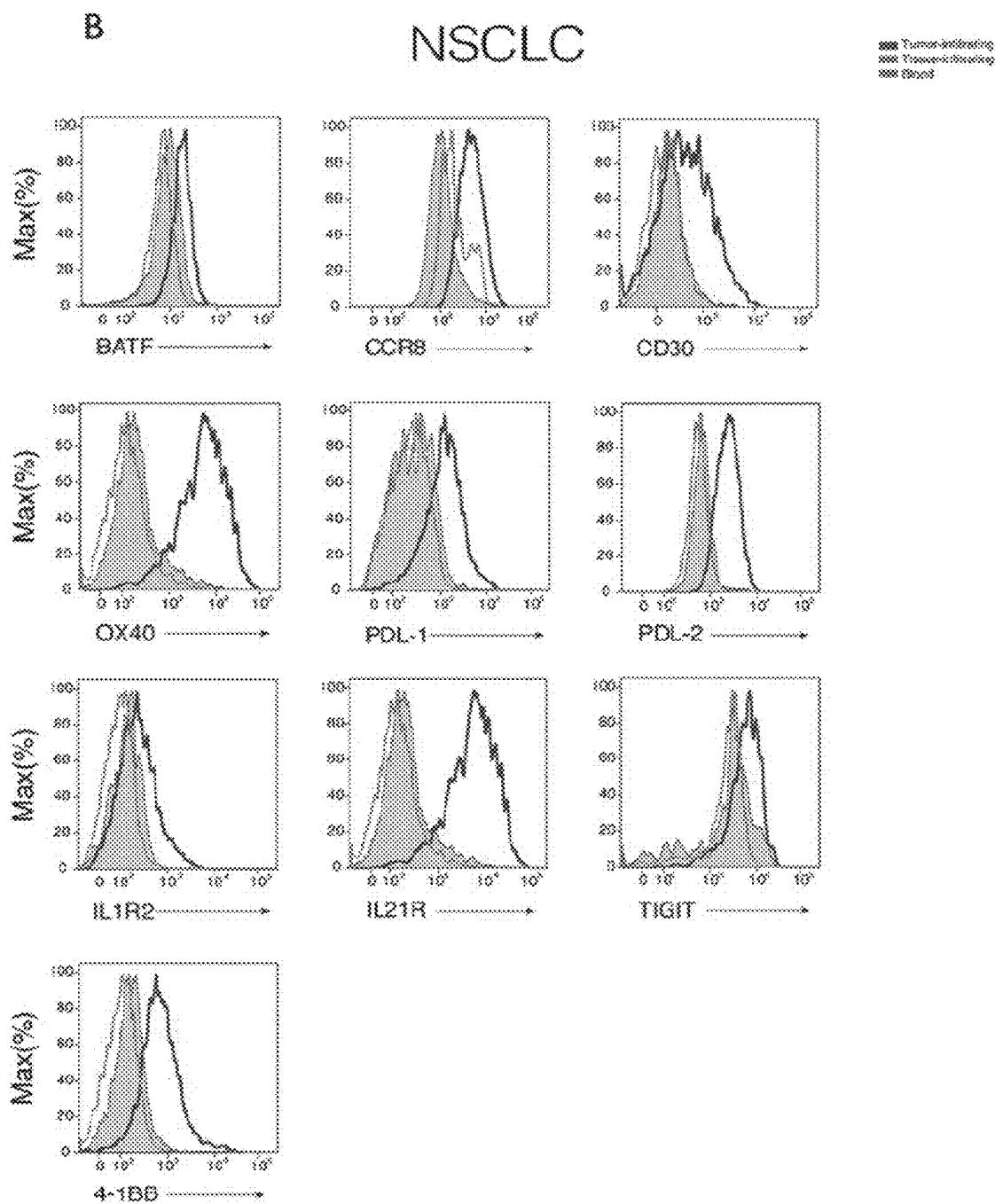


Fig.4 (2/2)

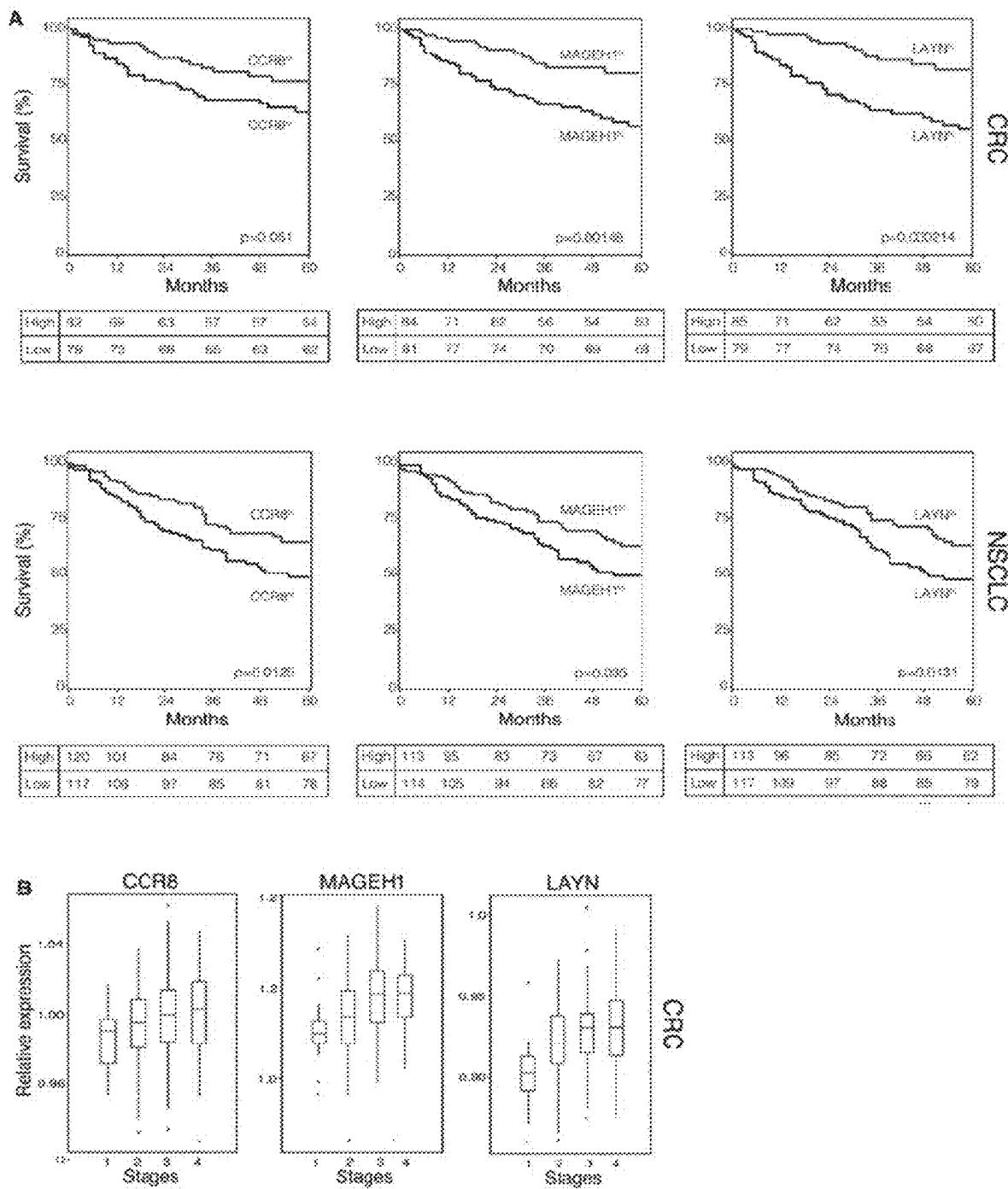


Fig. 5

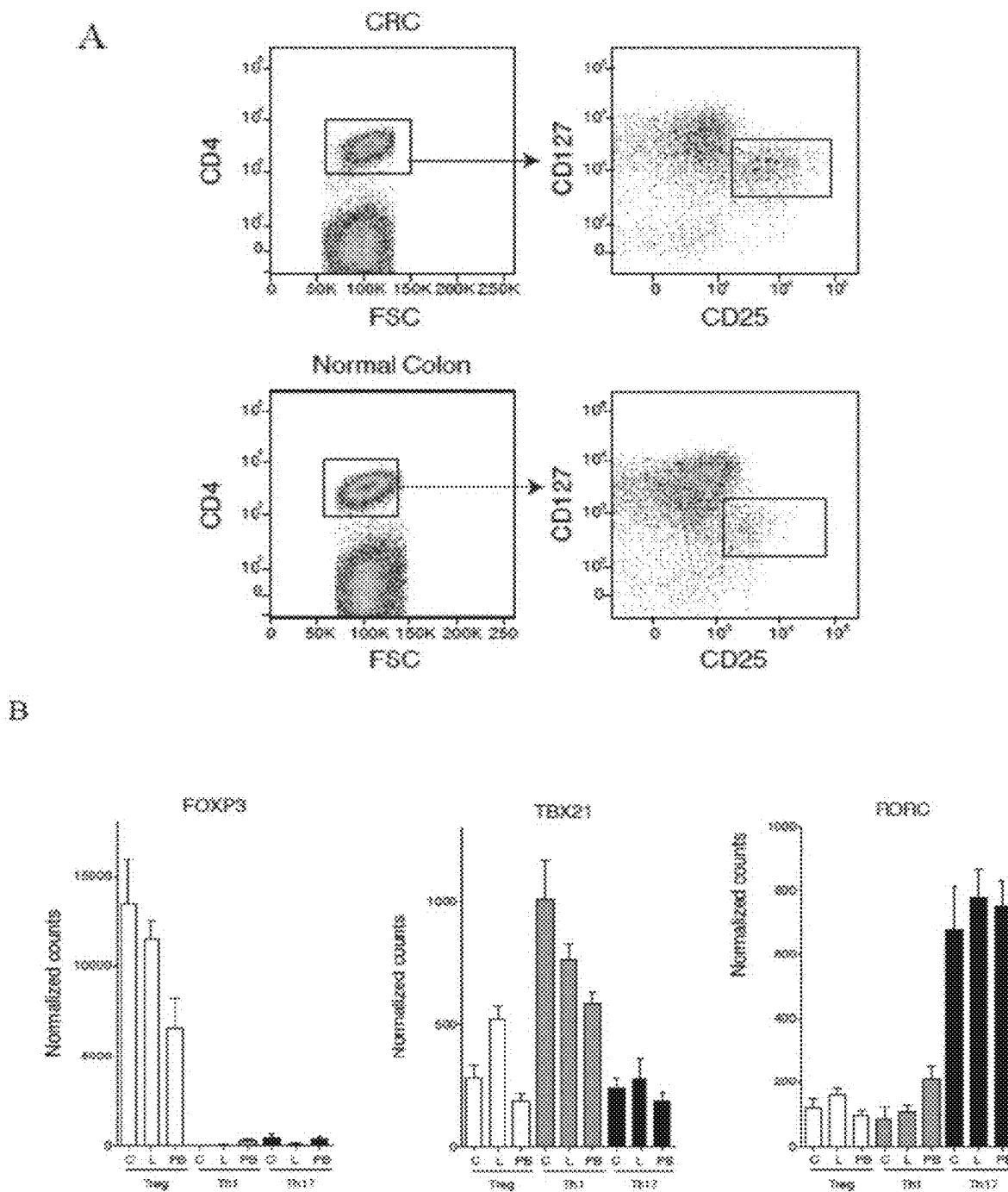


Fig. 6 (1/5)

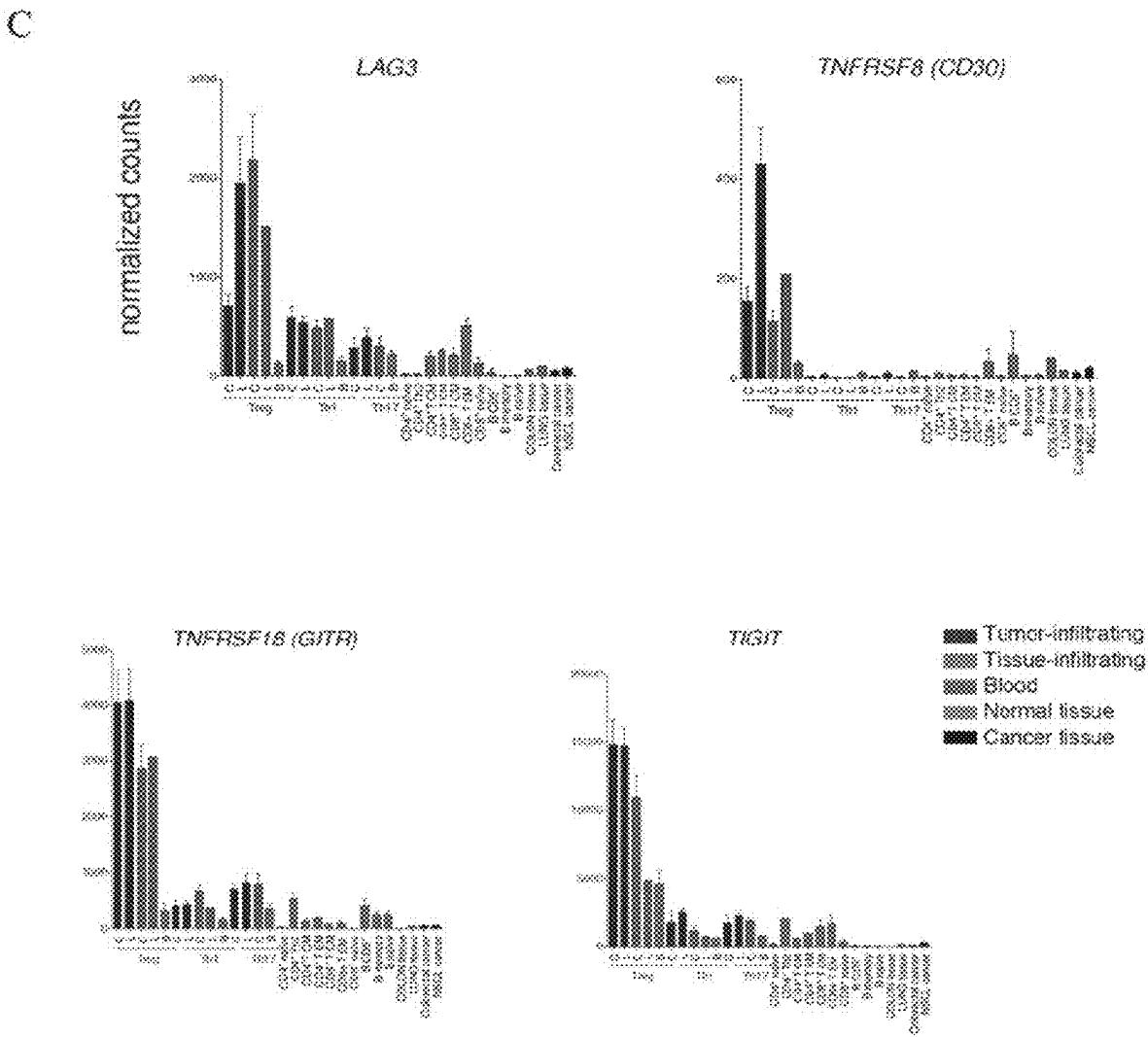


Fig. 6 (2/5)

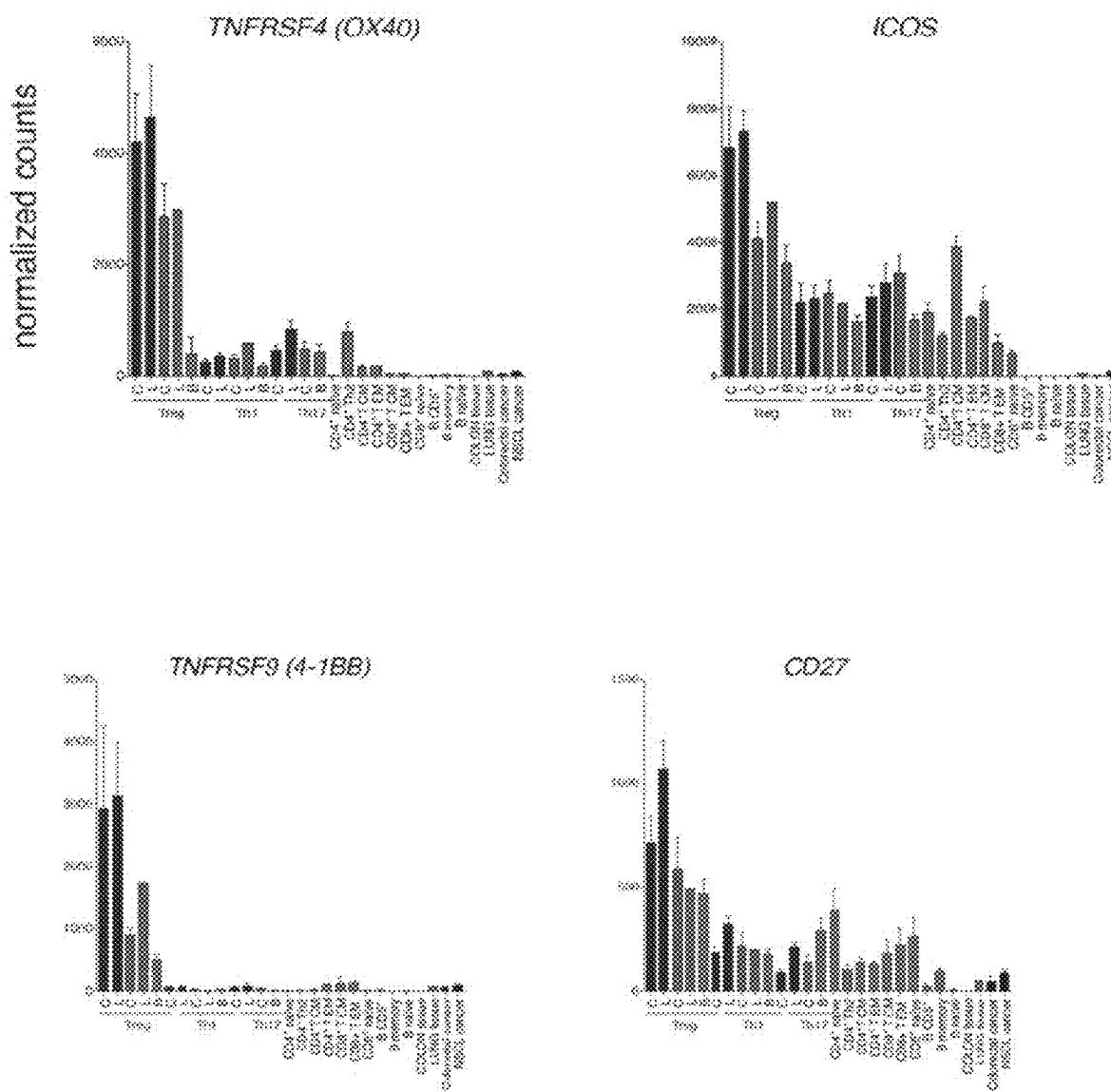


Fig. 6 (3/5)

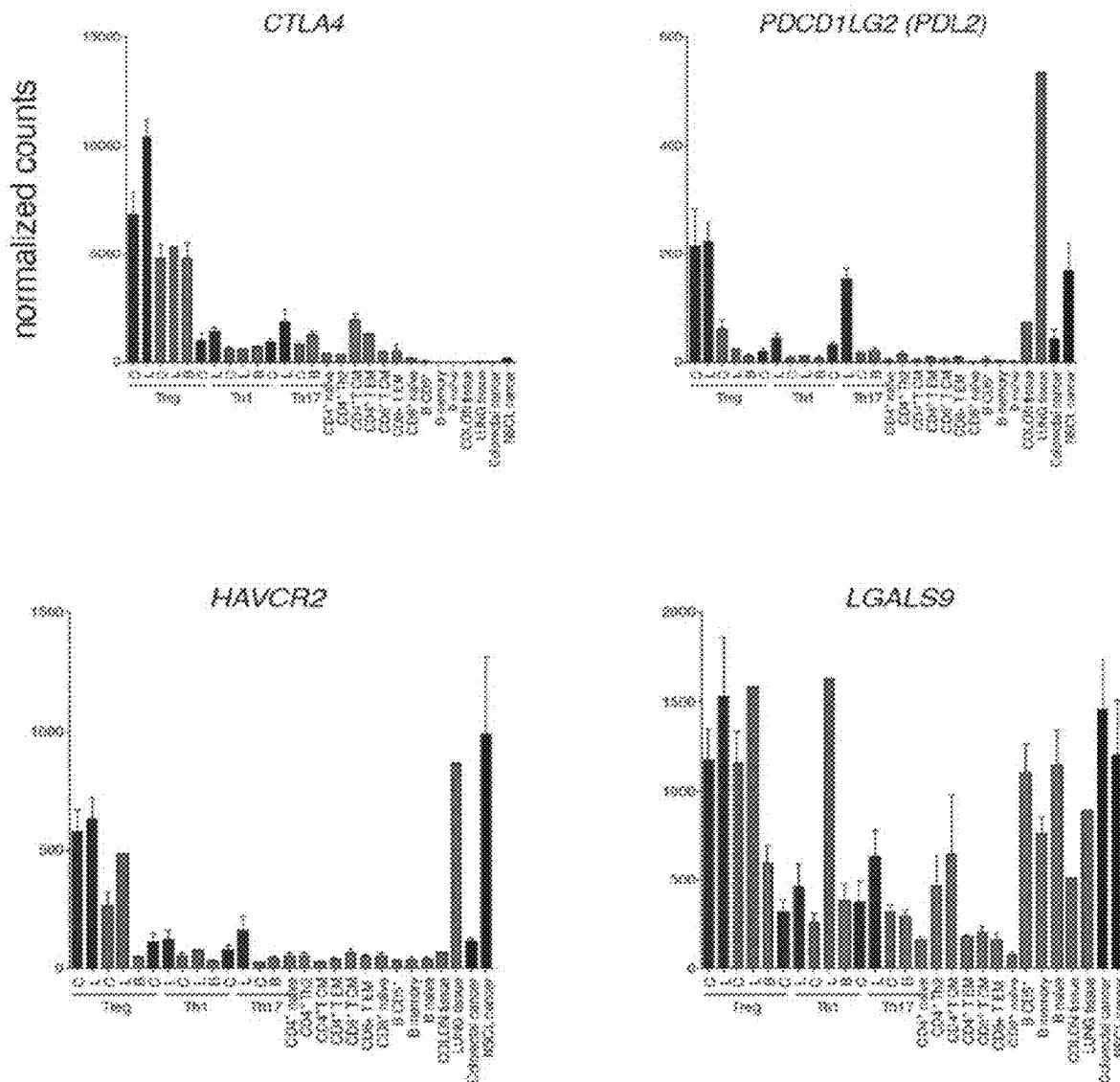


Fig. 6 (4/5)

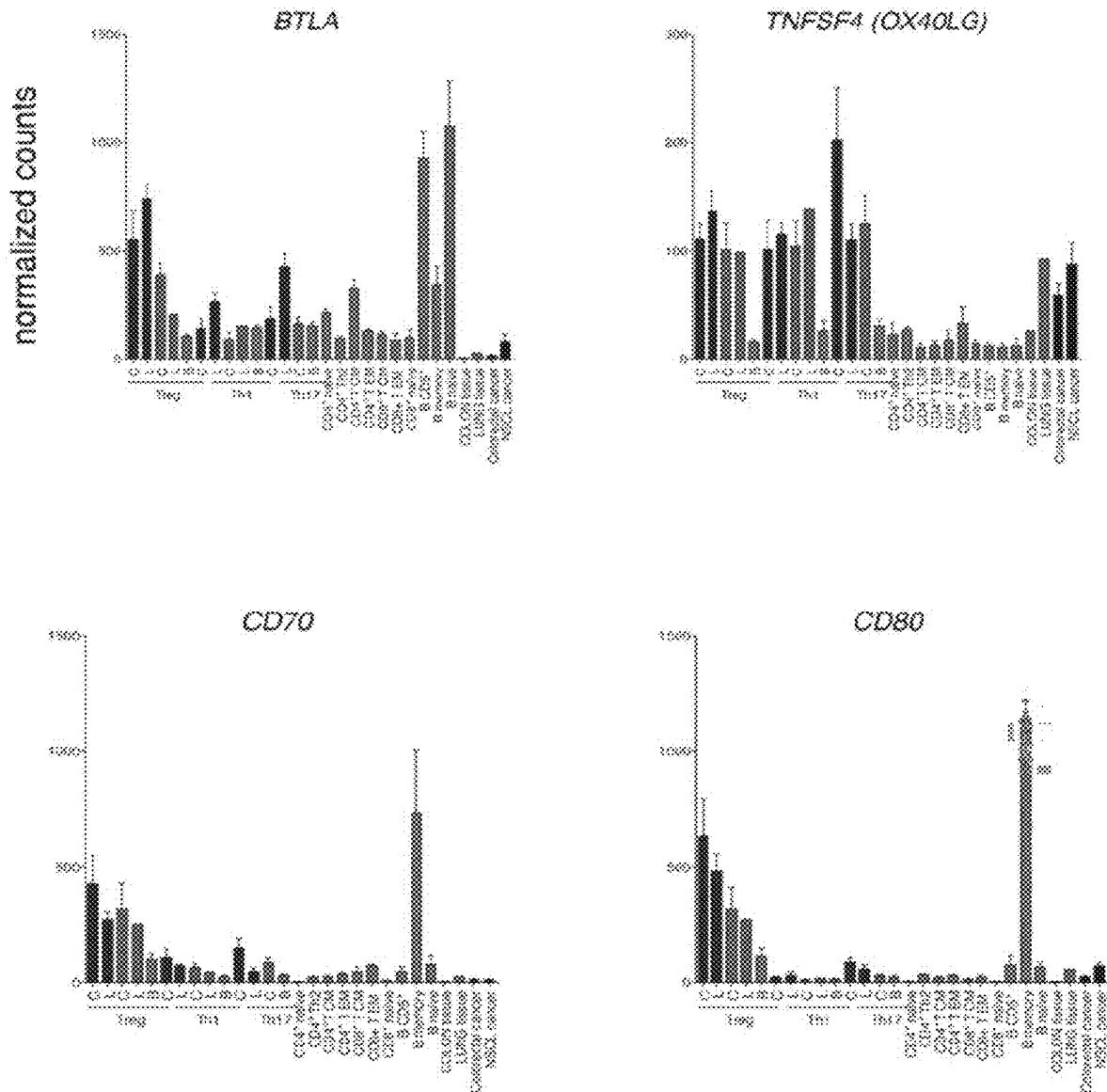
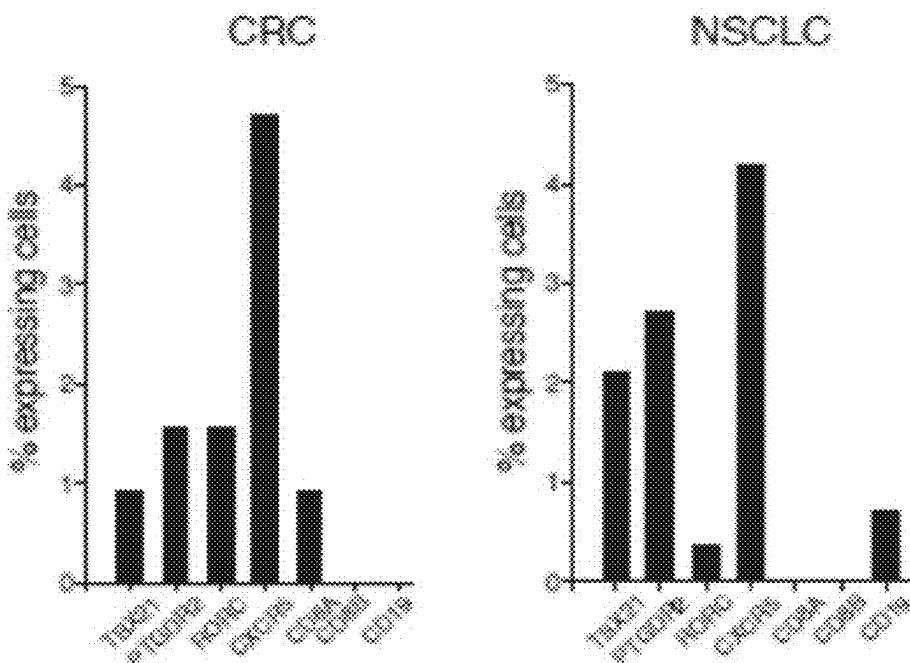


Fig. 6 (5/5)



CELL TYPE	MARKERS
CD4+ Th1	TBX21
CD4+ Th2	PTGDR2
CD4+ Th17	RORC
CD4+ Tfh	CXCR6
CD8+ cells	CD8A, CD8B
B cells	CD19

Fig. 7

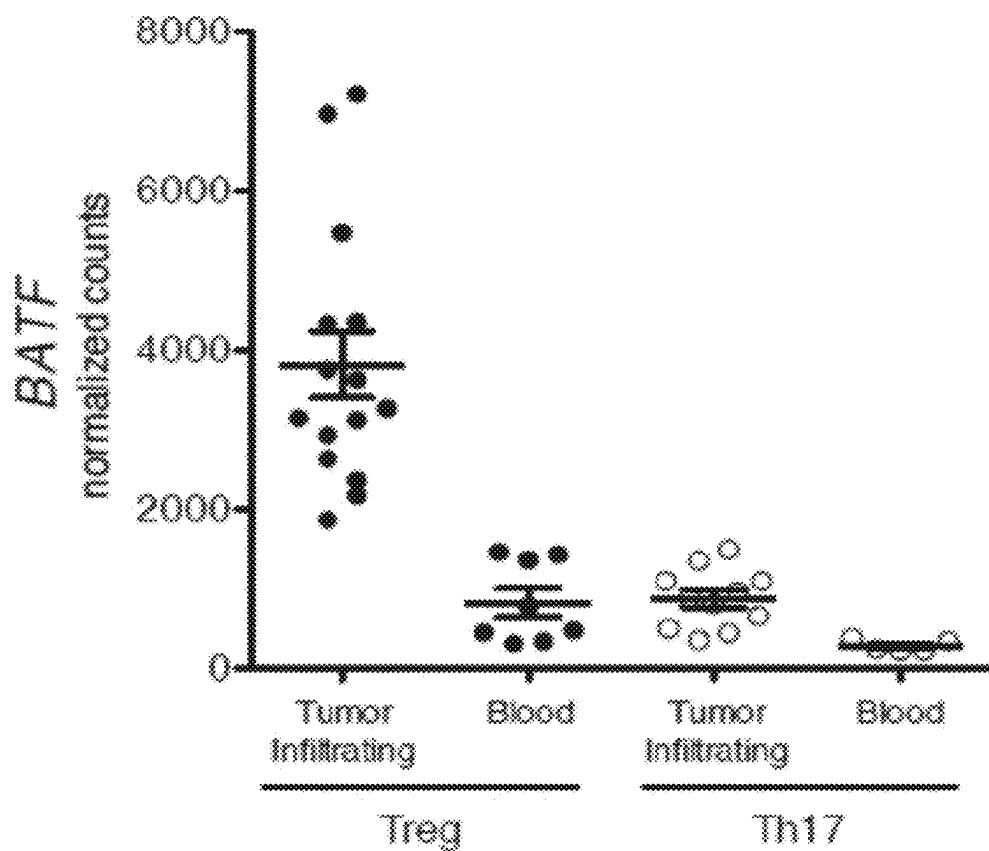
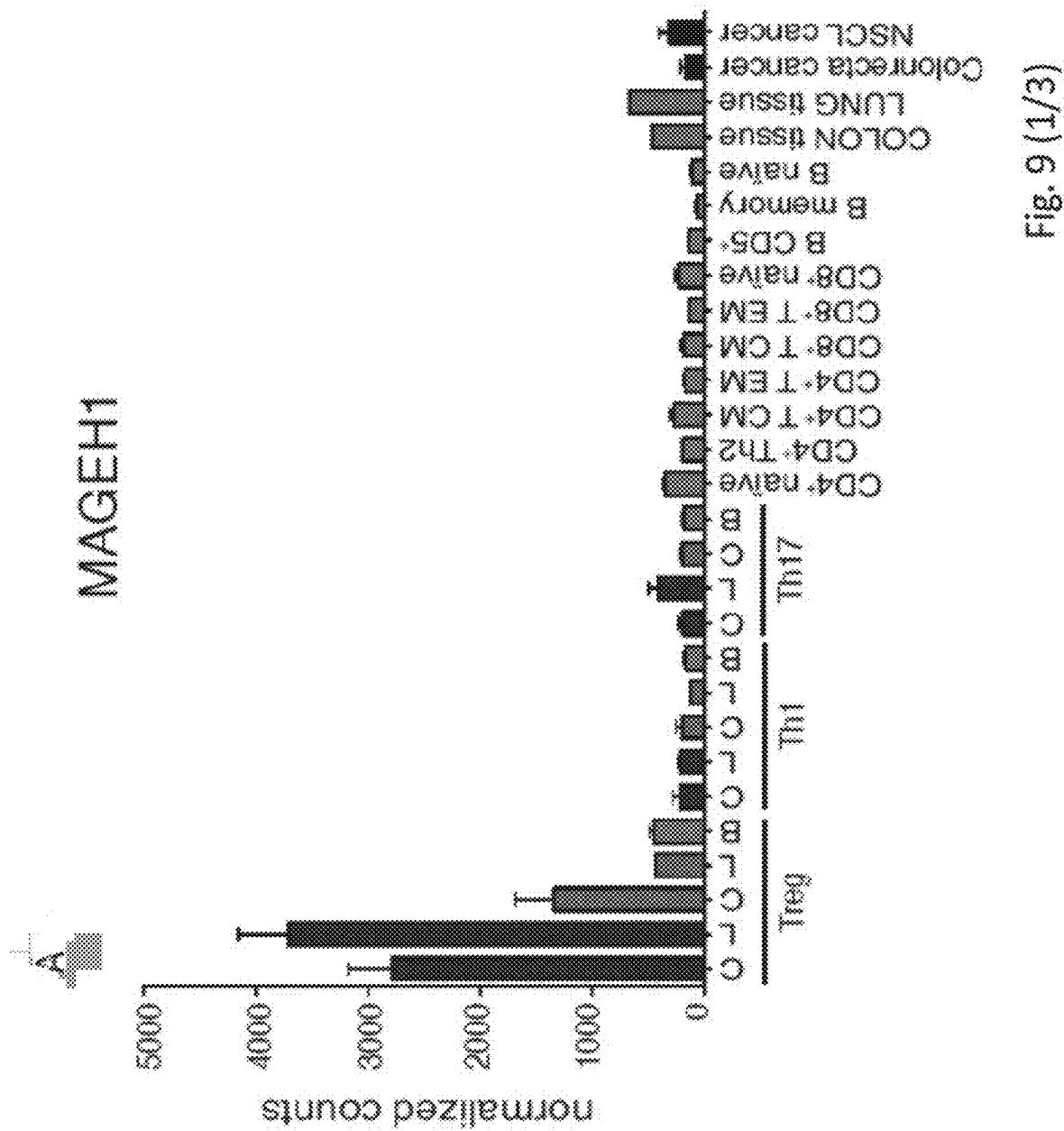
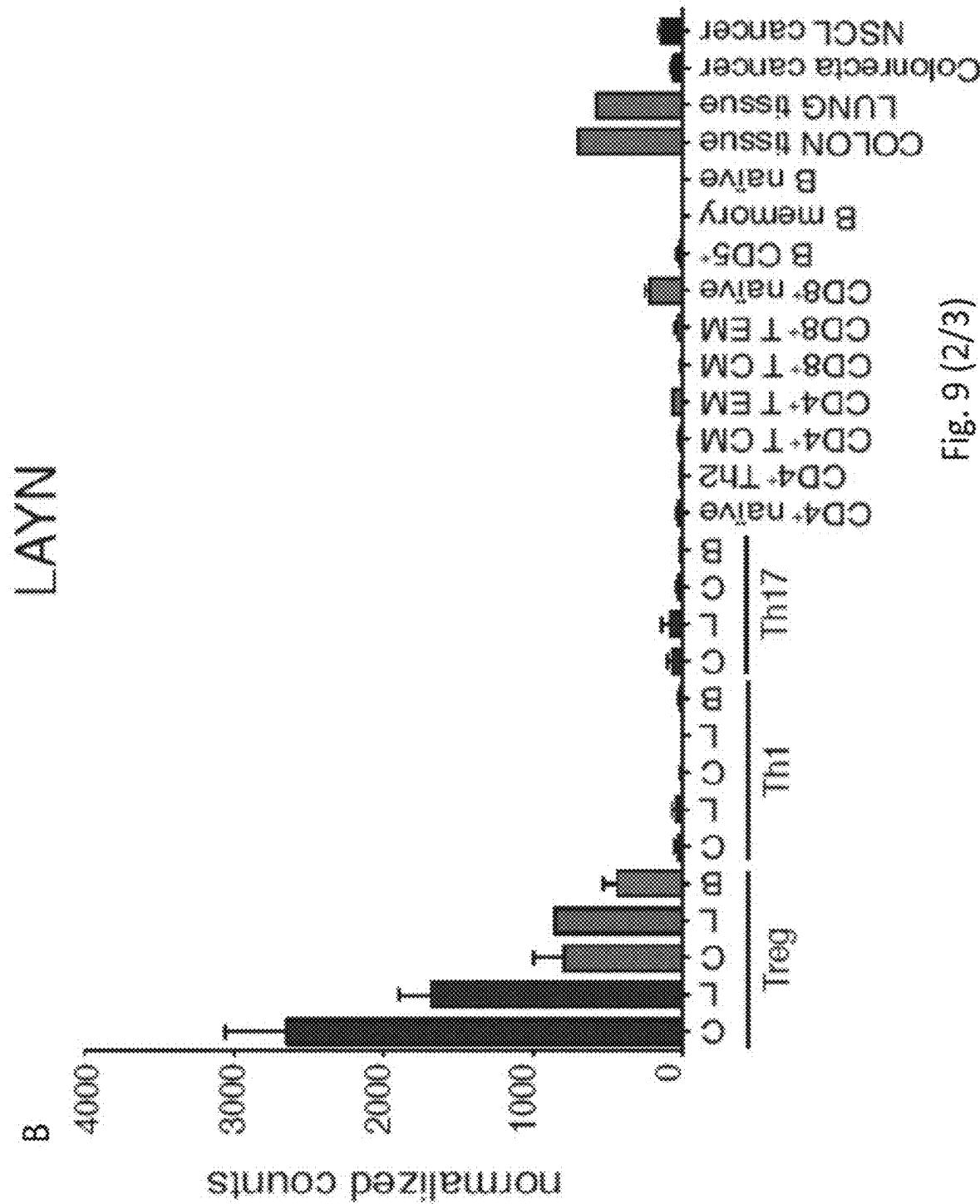
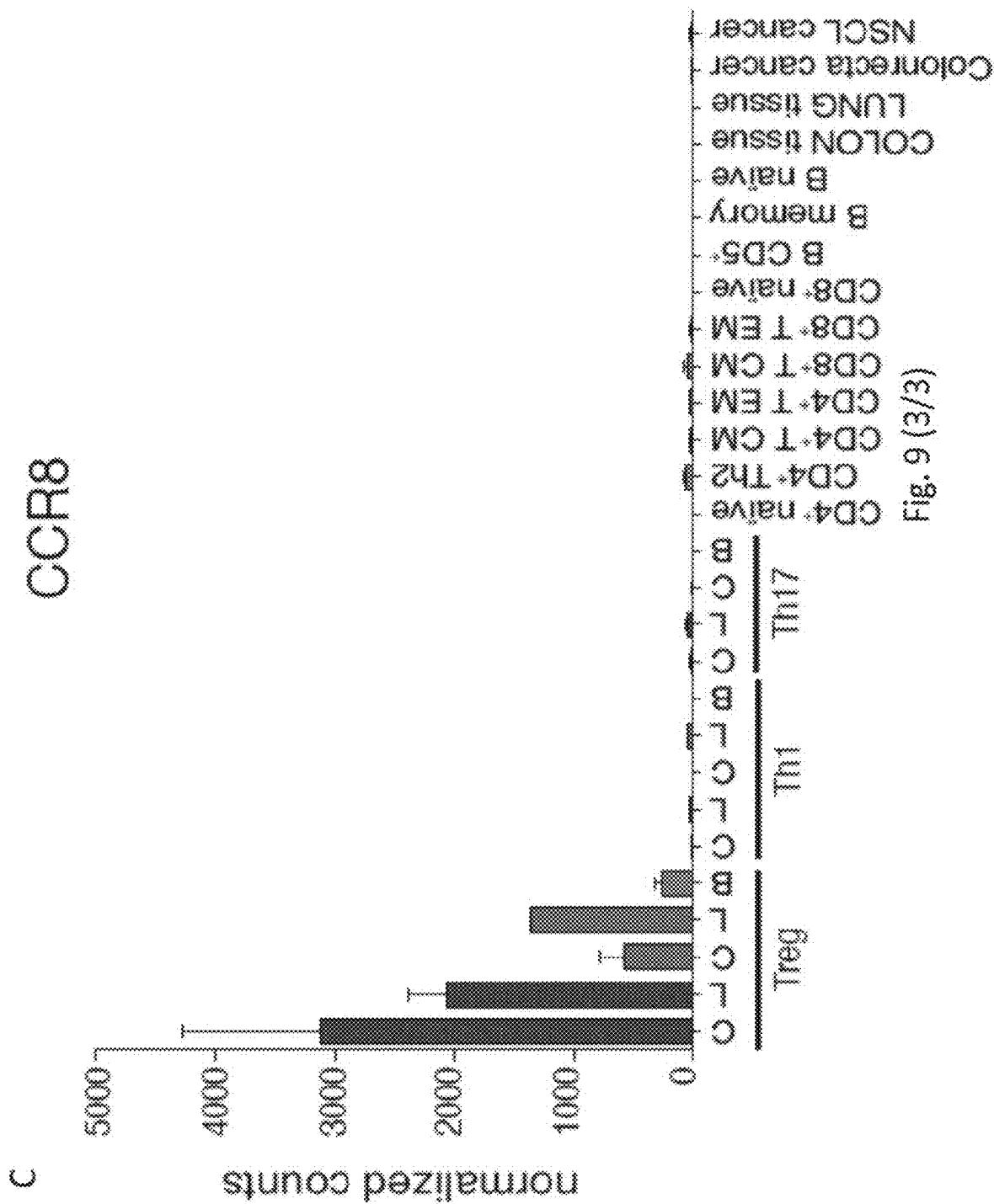


Fig.8







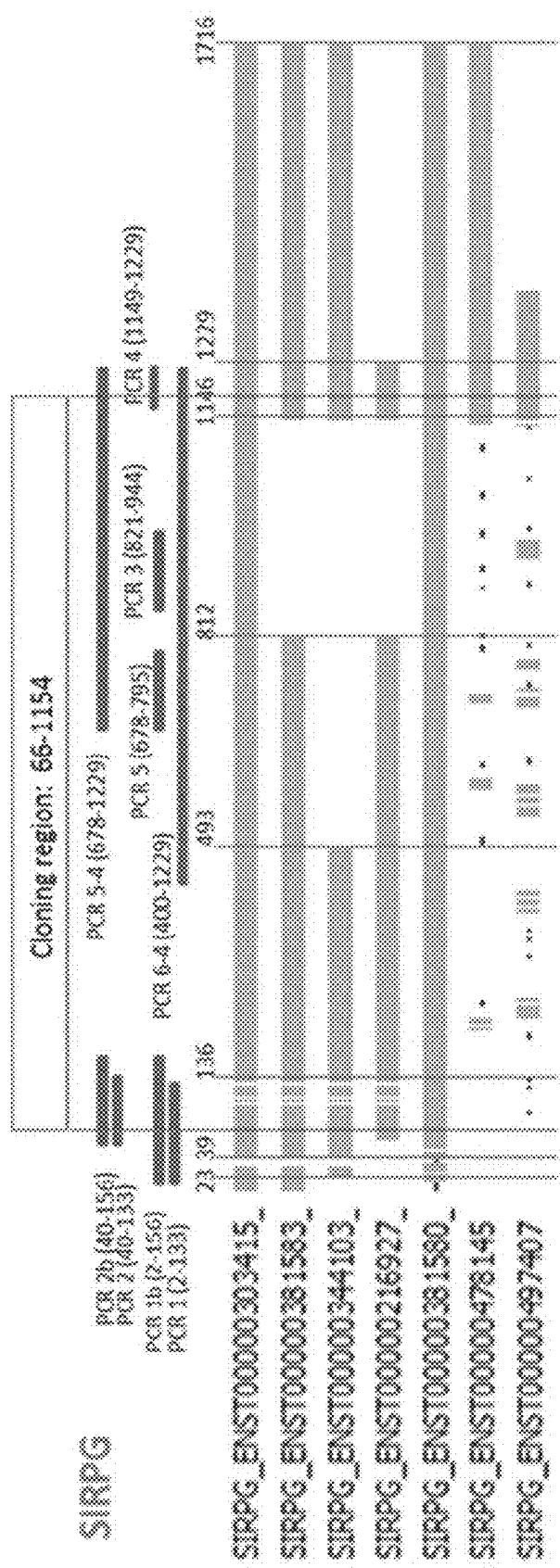
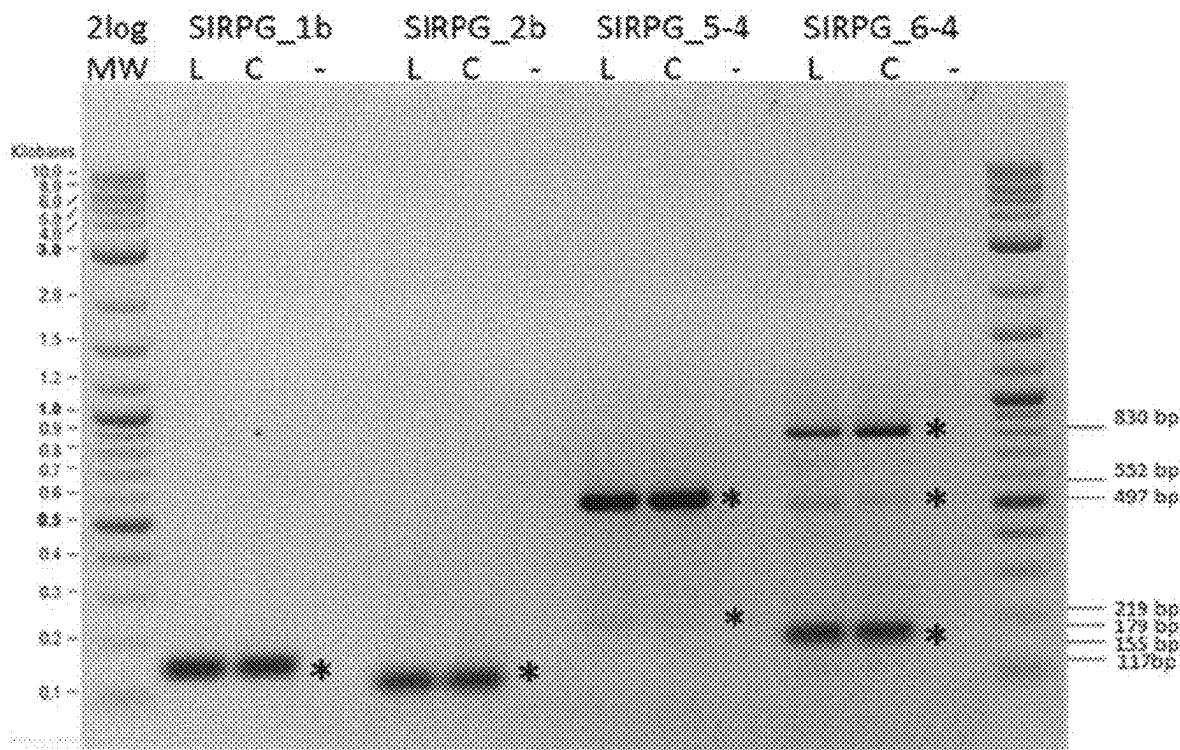


Fig. 10 (1/2)



Schematization of the expected size (bp) for each PCR designed on the SIRPG annotated transcript isoforms				
Transcript Code	PCR1b	PCR2b	PCRS-4	PCR6-4
ENST00000303415	155 bp	117 bp	552 bp	830 bp
ENST00000381583	155 bp	117 bp	219 bp	497 bp
ENST00000344103	-	117 bp	-	179 bp
ENST00000216927	-	-	219 bp	497 bp
ENST00000381580	-	-	552 bp	830 bp
ENST00000478145	-	-	-	-
ENST00000497407	-	-	-	-
Genomic DNA control	8388 bp	8350 bp	6100 bp	18924 bp

Fig. 10 (2/2)

MARKERS SELECTIVELY DEREGLATED IN TUMOR-INFILTRATING REGULATORY T CELLS

RELATED APPLICATIONS

[0001] This application is a continuation of U.S. application Ser. No. 18/295,965, filed Apr. 5, 2023, which is a continuation of U.S. application Ser. No. 16/301,805, filed Nov. 15, 2018, which is a national stage filing under 35 U.S.C. § 371 of International Application Serial No. PCT/EP2017/061642, filed May 15, 2017, the contents of each of which is incorporated herein by reference in their entirety.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

[0002] The contents of the electronic sequence listing (C158570000US02-SEQ-JRV.xml; Size: 953,347 bytes; and Date of Creation: Jan. 24, 2025) is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0003] The present invention relates to a molecule able to modulate the expression and/or function of at least one marker that is selectively deregulated in tumor-infiltrating regulatory T cell or to a molecule capable of specifically binding to at least one marker that is selectively deregulated in tumor-infiltrating regulatory T cell and inducing antibody-dependent cell-mediated cytotoxicity (ADCC) for use in the prevention and/or treatment of cancer or for use in a method for in vivo depleting tumor-infiltrating regulatory T cell in a subject or for use in a method to enhance tumor immunity in a subject and relative pharmaceutical composition.

BACKGROUND OF THE INVENTION

[0004] The combination of genetic mutations and epigenetic modifications that are peculiar to all tumors generate antigens that T and B lymphocytes can use to specifically recognize tumor cells (Jamal-Hanjani et al., 2013). It is increasingly clear that T lymphocytes recognizing tumor derived peptides presented by major histocompatibility complex (MHC) molecules play a central role in immunotherapy and in conventional chemo-radiotherapy of cancer (Galluzzi et al., 2015). In fact, anti-tumor T cell responses arise in cancer patients but are disabled upon tumor progression by suppressive mechanisms triggered by the interplay between malignant cells and the tumor microenvironment (Munn and Bronte, 2015). The tumor-dependent immunosuppressive mechanisms depend on the integrated action of infiltrating leukocytes and lymphocytes that upregulate a range of modulatory molecules, collectively called immune checkpoints, whose function is only partially characterized (Pardoll, 2012). Therefore, the search for agonists of co-stimulatory complexes or antagonists of inhibitory molecules to potentiate antigen-specific T cell responses is a primary goal of current anti-tumor research (Sharma and Allison, 2015; Zitvogel et al., 2013). Indeed, clinical trials have unequivocally shown that the blockade of immune checkpoints unleashes the spontaneous anti-tumor immune responses in such a powerful way that it has created a paradigm shift in cancer therapy (Sledzinska et al., 2015; Topalian et al., 2015).

[0005] Amongst the immune checkpoints targeted by blocking strategies, CTLA-4 has been one of the first to be translated into therapeutic applications.

[0006] Anti-CTLA-4 monoclonal antibodies (mAb) showed remarkable success in metastatic melanoma, and more recently in non-small-cell lung cancer, prostate cancer, renal cell carcinoma, urothelial carcinoma and ovarian cancer (Carthon et al., 2010; Hodi et al., 2010; van den Eertwegh et al., 2012; Yang et al., 2007). However, the fraction of patients that do not respond remains high, prompting a deeper investigation of the mechanisms underpinning the modulation of immune responses by tumors. Recent experimental evidence showed that anti-CTLA-4 mAb efficacy depends on Fc γ R mediated depletion of CD4 $^{+}$ regulatory T cells (Treg cells) within the tumor microenvironment (Peggs et al., 2009; Selby et al., 2013; Simpson et al., 2013; Twyman-Saint Victor et al., 2015). Treg cells, which are physiologically engaged in the maintenance of immunological self-tolerance and immune homeostasis (Josefowicz et al., 2012; Sakaguchi et al., 2008), are potent suppressors of effector cells and are found at high frequencies in various types of cancers (Fridman et al., 2012; Nishikawa and Sakaguchi, 2010). Interestingly, Treg cells adapt their transcriptional program to the various cytokines to which they are exposed in the inflammatory milieu (Campbell and Koch, 2011). This versatility is controlled by transcription factors generally associated with the differentiation of other effector CD4 $^{+}$ T cell subsets, resulting in various Treg cell populations with unique features and immunomodulatory functions (Duhen et al., 2012; Geginat et al., 2014). Moreover, Treg cells infiltrating non-lymphoid tissues are reported to exhibit unique phenotypes and transcriptional signatures, as they can display functions beyond their well-established suppressive roles, such as metabolic modulation in adipose tissue (Cipolletta et al., 2012) or regulation of tissue repair in skeletal muscle (Burzyn et al., 2013) and in lung tissue (Arpaia et al., 2015).

[0007] Treg cells depletion has been reported to increase anti-tumor specific immune responses and to reduce tumor burden (Marabelle et al., 2013; Teng et al., 2010; Walter et al., 2012).

[0008] Although promising clinical results have been achieved with Treg cell depleting strategies, some relevant issues are to be addressed, for a safer, more effective and wider clinical application of these therapies. First, severe autoimmunity can occur following systemic Treg cells depletion (Nishikawa and Sakaguchi, 2010), which could be avoided if selective depletion of tumor infiltrating Treg cells were feasible. A second issue concerns the specificity of targeting, indeed Treg cells share with effector lymphocytes most of the molecules targeted for therapy, which can possibly deplete also the tumor-specific effector cells. Therefore, the molecular characterization of Treg cells at different tumor sites should help to better define therapeutic targets through a better description of their signature molecules and of the network that regulates Treg cell functions in the tumor microenvironment.

[0009] Non-small-cell lung cancer (NSCLC) and colorectal cancer (CRC) are the two most frequent cancers in both genders (Torre et al., 2015). NSCLC has the worst prognosis due to its high mortality rate even in early stages. Although CRC survival rate is highly dependent on the tumor stage at diagnosis, about 50% of patients will progress to metastatic cancer (Gonzalez-Pons and Cruz-Correia, 2015). Both

tumors have been targeted with therapies based on monoclonal antibodies to checkpoint inhibitors, but the outcomes were different. While remarkable clinical success has been obtained in NSCLC, evidence of durable response in CRC is scarce with the exception of mismatch repair-deficient CRC lesions (Jacobs et al., 2015; Kroemer et al., 2015; Le et al., 2015).

[0010] Then there is still need for agents that target tumor infiltrating Treg cells for the treatment and/or prevention of cancer.

SUMMARY OF THE INVENTION

[0011] Tumor-infiltrating regulatory T lymphocytes (Treg) can suppress effector T cells specific for tumor antigens. Since new anti-cancer immunotherapies aim at unleashing effector T cells by targeting immune-checkpoints, deeper molecular definitions of tumor-infiltrating-lymphocytes could offer new therapeutic opportunities. Transcriptomes of T helper 1(Th1), Th17 and Treg cells infiltrating colorectal or non-small-cell lung cancers were compared to transcriptomes of the same subsets from normal tissues, and validated at the single cell level. The inventors found tumor-infiltrating Treg cells are highly suppressive, upregulate several immune-checkpoints, and express on the cell surface specific signature molecules such as interleukin-1 receptor 2 (IL1R2), programmed death (PD)-1 Ligand1, PD-1 Ligand2, and CCR8 chemokine which were not previously described on Treg cells. Remarkably, high expression in whole tumor samples of Treg signature genes, such as LAYN, MAGEH1 or CCR8, correlated with poor prognosis. The invention provides new insights into the molecular identity and functions of human tumor-infiltrating Treg cells, and define new potential targets for tumor immunotherapy.

[0012] In the present invention, the inventors provide a comprehensive transcriptome analysis of human CD4⁺ Treg cells and effector cells (Th1 and Th17) infiltrating NSCLC or CRC and their matched normal tissues.

[0013] Inventors defined molecular signatures of tumor-infiltrating Treg cells in these two cancer types and confirmed the relevance of these signatures by single-cell analyses. These data could help a better understanding of Treg functional role at tumor sites and pave the way to the identification of therapeutic targets for more specific and safer modulation of Treg cells in cancer therapy.

[0014] The inventors' findings provide new insights on the inhibitory mechanisms of Treg cells and offer precise targets for cancer immunotherapy.

[0015] Then the present invention provides a molecule able to modulate the expression and/or function of at least one marker that is selectively deregulated in tumor-infiltrating regulatory T cells for use in the prevention and/or treatment of said tumor.

[0016] Preferably, the molecule according to the invention is capable of specifically binding to said at least one marker and inducing antibody-dependent cell-mediated cytotoxicity (ADCC).

[0017] Said molecule is preferably able to selectively deplete tumor-infiltrating regulatory T cells.

[0018] Said molecule is preferably selected from the group consisting of:

[0019] a) an antibody or a fragment thereof;

[0020] b) a polypeptide;

[0021] c) a small molecule;

[0022] d) a polynucleotide coding for said antibody or polypeptide or a functional derivative thereof;

[0023] e) a polynucleotide, such as antisense construct, antisense oligonucleotide, RNA interference construct or siRNA,

[0024] e) a vector comprising or expressing the polynucleotide as defined in d) or e);

[0025] f) a host cell genetically engineered expressing said polypeptide or antibody or comprising the polynucleotide as defined in d) or e).

[0026] Preferably, the marker is selected from the group consisting of at least one marker disclosed in the following Table VIII.

TABLE VIII

MARKER NAME	ENSEMBL_release87	ENTREZ_ID release108
FUCA2	ENSG00000001036	2519
ICA1	ENSG00000003147	3382
TTC22	ENSG00000006555	55001
COX10	ENSG00000006695	1352
IL32	ENSG00000008517	9235
ETV7	ENSG00000010030	51513
ATP2C1	ENSG00000017260	27032
FAS	ENSG00000026103	355
ARNTL2	ENSG00000029153	56938
IKZF2	ENSG00000030419	22807
PEX3	ENSG00000034693	8504
MAT2B	ENSG00000038274	27430
TSPAN17	ENSG00000048140	26262
COL9A2	ENSG00000049089	1298
TNFRSF9	ENSG00000049249	3604
FOXP3	ENSG00000049768	50943
NFE2L3	ENSG00000050344	9603
LIMA1	ENSG00000050405	51474
TNIP3	ENSG00000050730	79931
LY75	ENSG00000054219	4065
ZNF280C	ENSG00000056277	55609
YIPF1	ENSG00000058799	54432
NFYC	ENSG00000066136	4802
ISOC1	ENSG00000066583	51015
PHKA1	ENSG00000067177	5255
ACSL4	ENSG00000068366	2182
MAST4	ENSG00000069020	375449
LMCD1	ENSG00000071282	29995
TFRC	ENSG00000072274	7037
PANX2	ENSG00000073150	56666
FNDC3B	ENSG00000075420	64778
REXO2	ENSG00000076043	25996
TP73	ENSG00000078900	7161
LXN	ENSG00000079257	56925
CEACAM1	ENSG00000079385	634
IL12RB2	ENSG00000081985	3595
GSK3B	ENSG00000082701	2932
TDRD3	ENSG00000083544	81550
RRAGB	ENSG00000083750	10325
STARD7	ENSG00000084090	56910
SSH1	ENSG00000084112	54434
NCOA1	ENSG00000084676	8648
MGST2	ENSG00000085871	4258
ACOX3	ENSG00000087008	8310
AURKA	ENSG00000087586	6790
TPX2	ENSG00000088325	22974
ANKRD10	ENSG00000088448	55608
FKBP1A	ENSG00000088832	2280
SIRPG	ENSG00000089012	55423
BIRC5	ENSG00000089685	332
RGS1	ENSG00000090104	5996
DPYSL2	ENSG00000092964	1808
WHRN	ENSG00000095397	25861
CENPM	ENSG00000100162	79019
SEPT3	ENSG00000100167	55964
NCF4	ENSG00000100365	4689

TABLE VIII-continued

MARKER NAME	ENSEMBL_release87	ENTREZ_ID release108
CSF2RB	ENSG00000100368	1439
IL2RB	ENSG00000100385	3560
CNIH1	ENSG00000100528	10175
ZMYND8	ENSG00000101040	23613
MAP1LC3A	ENSG00000101460	84557
PIGU	ENSG00000101464	128869
NXT2	ENSG00000101888	55916
SMS	ENSG00000102172	6611
NDFIP2	ENSG00000102471	54602
ACP5	ENSG00000102575	54
NFAT5	ENSG00000102908	10725
CYB5B	ENSG00000103018	80777
IL21R	ENSG00000103522	50615
LAPTM4B	ENSG00000104341	55353
IL7	ENSG00000104432	3574
NCALD	ENSG00000104490	83988
ERI1	ENSG00000104626	90459
EBI3	ENSG00000105246	10148
PLA2G4C	ENSG00000105499	8605
CDK6	ENSG00000105810	1021
HOXA1	ENSG00000105991	3198
GLCCI1	ENSG00000106415	113263
MINPP1	ENSG00000107789	9562
ACTA2	ENSG00000107796	59
WSB1	ENSG00000109046	26118
CLNK	ENSG00000109684	116449
HTATIP2	ENSG00000109854	10553
CTSC	ENSG00000109861	1075
VWA5A	ENSG00000110002	4013
DCPS	ENSG00000110063	28960
SLC35F2	ENSG00000110660	54733
FOXM1	ENSG00000111206	2305
RAD51AP1	ENSG00000111247	10635
RASAL1	ENSG00000111344	8437
VDR	ENSG00000111424	7421
FAM184A	ENSG00000111879	79632
DNPH1	ENSG00000112667	10591
KIF20A	ENSG00000112984	10112
SEC24A	ENSG00000113615	10802
KAT2B	ENSG00000114166	8850
PPM1G	ENSG00000115241	5496
IL1R2	ENSG00000115590	7850
IL1R1	ENSG00000115594	3554
IL1RL2	ENSG00000115598	8808
IL1RL1	ENSG00000115602	9173
UXS1	ENSG00000115652	80146
SLC25A12	ENSG00000115840	8604
THADA	ENSG00000115970	63892
PARK7	ENSG00000116288	11315
LEPR	ENSG00000116678	3953
GADD45A	ENSG00000116717	1647
KIF14	ENSG00000118193	9928
MREG	ENSG00000118242	55686
HSDL2	ENSG00000119471	84263
F1VCR2	ENSG00000119686	55640
CD274	ENSG00000120217	29126
SOCS2	ENSG00000120833	8835
TNFRSF8	ENSG00000120949	943
RDH10	ENSG00000121039	157506
LAX1	ENSG00000122188	54900
TWIST1	ENSG00000122691	7291
ZWINT	ENSG00000122952	11130
CIT	ENSG00000122966	11113
ACOT9	ENSG00000123130	23597
IKZF4	ENSG00000123411	64375
HJURP	ENSG00000123485	55355
METTL8	ENSG00000123600	79828
TOX2	ENSG00000124191	84969
GTSF1L	ENSG00000124196	149699
SOX4	ENSG00000124766	6659
TM9SF2	ENSG00000125304	9375
HS3ST3B1	ENSG00000125430	9953
EML2	ENSG00000125746	24139
MGME1	ENSG00000125871	92667

TABLE VIII-continued

MARKER NAME	ENSEMBL_release87	ENTREZ_ID release108
IGFLR1	ENSG00000126246	79713
DLGAP5	ENSG00000126787	9787
HIVEP3	ENSG00000127124	59269
LRRK61	ENSG00000127399	65999
TST	ENSG00000128311	7263
STRIP2	ENSG00000128578	57464
MYO5C	ENSG00000128833	55930
FOXA1	ENSG00000129514	3169
ITFG1	ENSG00000129636	81533
KLHDC7B	ENSG00000130487	113730
TRAF3	ENSG00000131323	7187
MCCC2	ENSG00000131844	64087
GRSF1	ENSG00000132463	2926
SYT11	ENSG00000132718	23208
SLC41A1	ENSG00000133065	254428
ATP13A3	ENSG00000133657	79572
MICAL2	ENSG00000133816	9645
IL2RA	ENSG00000134460	3559
CABLES1	ENSG00000134508	91768
RFK	ENSG00000135002	55312
HAVCR2	ENSG00000135077	84868
CGA	ENSG00000135346	1081
FAIM2	ENSG00000135472	23017
EGLN1	ENSG00000135766	54583
ARHGEF4	ENSG00000136002	50649
SLC41A2	ENSG00000136052	84102
FLNB	ENSG00000136068	2317
RCBTB1	ENSG00000136144	55213
TMOD1	ENSG00000136842	7111
TPMT	ENSG00000137364	7172
CASP1	ENSG00000137752	834
NUSAP1	ENSG00000137804	51203
ADAM10	ENSG00000137845	102
ZNF280D	ENSG00000137871	54816
HADHB	ENSG00000138029	3032
CEP55	ENSG00000138180	55165
ENTPD1	ENSG00000138185	953
NAB1	ENSG00000138386	4664
HECW2	ENSG00000138411	57520
CD27	ENSG00000139193	939
CDH24	ENSG00000139880	64403
RAB15	ENSG00000139998	376267
ETFA	ENSG00000140374	2108
KSR1	ENSG00000141068	8844
PCTP	ENSG00000141179	58488
SECTM1	ENSG00000141574	6398
EVA1B	ENSG00000142694	55194
WDTC1	ENSG00000142784	23038
CTTNBP2NL	ENSG00000143079	55917
CASQ1	ENSG00000143318	844
SNAP47	ENSG00000143740	116841
STAC	ENSG00000144681	6769
ARL6IP5	ENSG00000144746	10550
ADPRH	ENSG00000144843	141
PAM	ENSG00000145730	5066
RNF145	ENSG00000145860	153830
TTBK1	ENSG00000146216	84630
TMEM140	ENSG00000146859	55281
CHST7	ENSG00000147119	56548
CHRNA6	ENSG00000147434	8973
MKI67	ENSG00000148773	4288
PTPRJ	ENSG00000149177	5795
ZC3H12C	ENSG00000149289	85463
NCAM1	ENSG00000149294	4684
INPP1	ENSG00000151689	3628
JAKMIP1	ENSG00000152969	152789
GTF3C6	ENSG00000155115	112495
RHOC	ENSG00000155366	389
SLC16A1	ENSG00000155380	6566
BATF	ENSG00000156127	10538
CXCL13	ENSG00000156234	10563
SH3RF2	ENSG00000156463	153769
NPTN	ENSG00000156642	27020
CCNB2	ENSG00000157456	9133

TABLE VIII-continued

MARKER NAME	ENSEMBL_release87	ENTREZ_ID release108
RNF207	ENSG00000158286	388591
AHCYL2	ENSG00000158467	23382
PTGIR	ENSG00000160013	5739
CALM3	ENSG00000160014	808
TMPRSS3	ENSG00000160183	64699
FCR3	ENSG00000160856	115352
PAQR4	ENSG00000162073	124222
ZG16B	ENSG00000162078	124220
JAK1	ENSG00000162434	3716
DIRAS3	ENSG00000162595	9077
ACTG2	ENSG00000163017	72
SGPP2	ENSG00000163082	130367
NEURL3	ENSG00000163121	93082
CTLA4	ENSG00000163599	1493
ICOS	ENSG00000163600	29851
RYBP	ENSG00000163602	23429
KIF15	ENSG00000163808	56992
TMEM184C	ENSG00000164168	55751
C5orf63	ENSG00000164241	401207
PTTG1	ENSG00000164611	9232
MELK	ENSG00000165304	9833
FAAH2	ENSG00000165591	158584
PRDX3	ENSG00000165672	10935
Hprt1	ENSG00000165704	3251
CACNB2	ENSG00000165995	783
TPP1	ENSG00000166340	1200
AKIP1	ENSG00000166452	56672
ACAA2	ENSG00000167315	10449
GNG8	ENSG00000167414	94235
GNG4	ENSG00000168243	2786
CX3CR1	ENSG00000168329	1524
AHCYL1	ENSG00000168710	10768
TSPN5	ENSG00000168785	10098
PGM2	ENSG00000169299	55276
CRADD	ENSG00000169372	8738
UGP2	ENSG00000169764	7360
ZNF282	ENSG00000170265	8427
GLB1	ENSG00000170266	2720
SMAD1	ENSG00000170365	4086
SPATA24	ENSG00000170469	202051
PRKCDPB	ENSG00000170955	112464
TADA3	ENSG00000171148	10474
RBKS	ENSG00000171174	64080
NETO2	ENSG00000171208	81831
LRG1	ENSG00000171236	116844
FAM98B	ENSG00000171262	283742
CHST11	ENSG00000171310	50515
ECEL1	ENSG00000171551	9427
BCL2L1	ENSG00000171552	598
MALT1	ENSG00000172175	10892
ZMAT3	ENSG00000172667	64393
CORO1B	ENSG00000172725	57175
CYP7B1	ENSG00000172817	9420
HPSE	ENSG00000173083	10855
VANGL1	ENSG00000173218	81839
GLRX	ENSG00000173221	2745
TRIB1	ENSG00000173334	10221
CD7	ENSG00000173762	924
HAP1	ENSG00000173805	9001
FBXO45	ENSG00000174013	200933
CHST2	ENSG00000175040	9435
RMI2	ENSG00000175643	116028
SLC35E3	ENSG00000175782	55508
ZBTB38	ENSG00000177311	253461
ZBED2	ENSG00000177494	79413
PARD6G	ENSG00000178184	84552
GLDC	ENSG00000178445	2731
AKAP5	ENSG00000179841	9495
CCR8	ENSG00000179934	1237
PAK2	ENSG00000180370	5062
YIPF6	ENSG00000181704	286451
TIGIT	ENSG00000181847	201633
CREB3L2	ENSG00000182158	64764
XKRX	ENSG00000182489	402415

TABLE VIII-continued

MARKER NAME	ENSEMBL_release87	ENTREZ_ID release108
CADM1	ENSG00000182985	23705
LHFP	ENSG00000183722	10186
CSF1	ENSG00000184371	1435
PTP4A3	ENSG00000184489	11156
CDCA2	ENSG00000184661	157313
OSBP2	ENSG00000184792	23762
METTL7A	ENSG00000185432	25840
SPATC1	ENSG00000186583	375686
TNFRSF4	ENSG00000186827	7293
TNFRSF18	ENSG00000186891	8784
TMPRSS6	ENSG00000187045	164656
GCNT1	ENSG00000187210	2650
MAGEH1	ENSG00000187601	28986
NHS	ENSG00000188158	4810
IL17REL	ENSG00000188263	400935
ADAT2	ENSG00000189007	134637
NEMP2	ENSG00000189362	100131211
SPATS2L	ENSG00000196141	26010
NTNG2	ENSG00000196358	84628
MYL6B	ENSG00000196465	140465
ARHGEF12	ENSG00000196914	23365
MAP3K5	ENSG00000197442	4217
PDGFA	ENSG00000197461	5154
PDCD1LG2	ENSG00000197646	80380
TOR4A	ENSG00000198113	54863
HIBCH	ENSG00000198130	26275
ZNF334	ENSG00000198185	55713
NTRK1	ENSG00000198400	4914
TMA16	ENSG00000198498	55319
WDHD1	ENSG00000198554	11169
FAM19A2	ENSG00000198673	338811
F5	ENSG00000198734	2153
GK	ENSG00000198814	2710
INPP5F	ENSG00000198825	22876
LAYN	ENSG00000204381	143903
CARD16	ENSG00000204397	114769
TBC1D8	ENSG00000204634	11138
CD177	ENSG00000204936	57126
LEPROT	ENSG00000213625	54741
SEC14L6	ENSG00000214491	730005
TRIM16	ENSG00000221926	10626
LTA	ENSG00000226979	4049
PROB1	ENSG00000228672	389333
AF165138.7	ENSG00000243440	NA
USP51	ENSG00000247746	158880
CARD17	ENSG00000255221	440068
DOC2B	ENSG00000272636	8447
C17orf96	ENSG00000273604	100170841
SSTR3	ENSG00000278195	6753
AC019206.1	ENSG00000279229	NA

wherein each of said marker name is characterized by “Ensembl gene id” and includes all of therein disclosed isoform protein sequences.

[0027] Each gene of table VIII is characterized by its Ensembl Gene accession number (ENSG), retrievable in the public database EnsEMBL (<http://www.ensembl.org/>) and by its Entrez Gene ID, retrievable in the public database NCBI (<https://www.ncbi.nlm.nih.gov/>), if present.

[0028] Preferably the marker is selected from the group consisting of: a transmembrane protein, a cytokine, an epigenetic factor, a kinase phosphatase or a transcription factor.

[0029] More preferably, the marker is a transmembrane protein selected from the group of SEQ ID NO:1-661, even more preferably, the marker is selected from the group

consisting of: LAYN (SEQ ID NOS:1-9), CCR8 (SEQ ID Nos:10-11), IL21R (SEQ ID Nos: 12-14), IL1 R2 (SEQ ID Nos:206-209), LY75 (SEQ ID NO: 78), SIRPG (SEQ ID Nos:122-126), CD177 (SEQ ID Nos:651-653), CD7 (SEQ ID Nos:549-554), FCRL3 (SEQ ID Nos:452-457), CADM1 (SEQ ID Nos: 570-583), NTNG2 (SEQ ID Nos:621-622), CSF2RB (SEQ ID Nos:134-137), SECTMI (SEQ ID Nos: 349-356), TSPAN5 (SEQ ID Nos:497-503), TMPRSS3 (SEQ ID Nos:448-451), TMPRSS6 (SEQ ID Nos:605-611), METTL7A (SEQ ID Nos:600-604), THADA (SEQ ID Nos: 237), NDIFP2 (SEQ ID Nos:148-151), CHRNA6 (SEQ ID Nos:392-394), or from the group consisting of:

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LAYN (SEQ ID NOS: 1-9
[>ENSG00000204381_ENST00000375614_ESP00000364764_LAYN

MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRRGTQRPCYKVIYFHDTSRRLNFEEAKEACR

RDGGQLVSIESEDEQKLIKEKFIEENLLPSDGFHWIGLRRREEQSNSTACQDLYAWTDGSISQFRN

WYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKYSDEKPAVPSREAE

GEETELTPVLPTEETQEEAKTFKESREAALNLAYILIPSIPLLLLVVTTVVCVWWICRKRKRE

QPDPSKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDLKNISFRVCSGEATPDDMSCD

YDNMAVNPSSEGFVTLVSVEGFVTNDIYEFPSPDQMGRSKESGWVENEIYGY* (SEQ ID NO: 1)

>ENSG00000204381_ENST00000375615_ESP00000364765_LAYN

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGTQRPCYKVIYFHDTSRRLNF

EEAKEACRRDGGQLVSIESEDEQKLIKEKFIEENLLPSDGFHWIGLRRREEQSNSTACQDLYAWTD

GSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKYSDEKPA

VPSREAEGEETELTPVLPTEETQEEAKTFKESREAALNLAYILIPSIPLLLLVVTTVVCVWWIC

RKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVNVIRKQSEADLAETRPDLKNISFRVCSGEATP

DDMSCDYDNMAVNPSSEGFVTLVSVEGFVTNDIYEFPSPDQMGRSKESGWVENEIYGY*

(SEQ ID NO: 2)

>ENSG00000204381_ENST00000436913_ESP00000392942_LAYN

MVTSGLGS GG VRRNKAIAQPARTFMLGLMAAYHNL EKPAVPSREAEGEETELTPVLPTEETQEE

DAKKTFKESREAALNLAYILIPSIPLLLLVVTTVVCVWWICRKRKREQPDPSTKKQHTIWPSPHQ

GNSPDLEVNVIRKQSEADLAETRPDLKNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFVTLV

SVESGFVTNDIYEFPSPDQMGRSKESGWVENEIYGY* (SEQ ID NO: 3)

>ENSG00000204381_ENST00000525126_ESP00000434328_LAYN

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGTQRPCYKVIYFHDTSRRLNF

EEAKEACRRDGGQLVSIESEDEQKLIKEKFIEENLLPSDGFHWIGLRRREEQSNSTACQDLYAWTD

GSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKYSDEKPA

VPSREAEGEETELTPVLPTEETQEEAKTFKESREAALNLAYILIPSIPLLLLVVTTVVCVWWIC

RKRQKTAARP* (SEQ ID NO: 4)

>ENSG00000204381_ENST00000525866_ESP00000434300_LAYN

MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRRGTQRPCYKVIYFHDTSRRLNFEEAKEACR

RDGGQLVSIESEDEQKLIKEKFIEENLLPSDGFHWIGLRRREEQSNSTACQDLYAWTDGSISQFRET

SSSF* (SEQ ID NO: 5)

>ENSG00000204381_ENST00000528924_ESP00000486561_LAYN

MVTSGLGS GG VRRNKAIAQPARTFMLGLMAAYHNL EKPAVPSREAEGEETELTPVLPTEETQEE

DAKKTFKESREAALNLAYILIPSIPLLLLVVTTVVCVWWICRK (SEQ ID NO: 6)

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>ENSG00000204381_ENST00000530962_ENSP00000431627_LAYN
MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAEGEETELTPVLPETQE
EDAKKTFKESREAALNLAYILIPSIPLLLLVVTTVVVCWWICRK (SEQ ID NO: 7)

>ENSG00000204381_ENST00000533265_ENSP00000434972_LAYN
MRPGTALQAVLLAVLLVGLRAATGRLLSGQPVCRGQTQRPCYKVIYFHDTSRRLNFEEAKEACR
RDGGQLSIESEDEQKLIKEFIENLLPSDGFwigLRRREEQNSNSTACQDLYAQTDGSISQFRN
WYVDEPSCGSECVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAE
GEETELTPVLPETQEEDAKKTFKESREAALNLAYILIPSIPLLLLVVTTVVVCWWICRKRQKT
GAARP* (SEQ ID NO: 8)

>ENSG00000204381_ENST00000533999_ENSP00000432434_LAYN
MYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDEKPAVPSREAE (SEQ ID NO: 9)] ,
CCR8 (SEQ ID Nos:10-11

[>ENSG0000179934_ENST00000326306_ENSP00000326432_CCR8
MDYTLDSLVTVDYYDPDFSSPCDAELIQTNGKLLLAVFYCLLFVFSLLGNSLVILVLVVCKKL
RSITDVYLLNLALS DLLFVFSPPFQTYLLDQWVFGTVMCKVVGFYIYGFYSSMFFITLMSVDR
YLAVVHavyALKVRTIRMGTTLCLAWLTAIMATIPLLVFYQVASEDGVLQCYSFYNQQTLKW
KIFTNFKMNIILGLLIPPTIFMPCYIKILHQLKRCQHNKTKAIRLVLIIVVIASLLFWVPFNVLPLTS
LHSMHILDGCSISQQLTYATHVTEIIISFTHCVCNPVIYAFVGEKFKKHLSEIFQKCSQIFNYLGRQ
MPRESCEKSSSCQQHSSRSSSVDYIL* (SEQ ID NO: 10)

>ENSG0000179934_ENST00000414803_ENSP00000390104_CCR8
MDYTLDSLVTVDYYDPDFSSPCDAELIQTNDLLSAGPVGVWDNCNVQSGVWLLLHWLLQOH
VFHHPHECGQVPGCCPCRVCVKGEDDQDGHNAVPGSMANHYGYHPIASVLPGL* (SEQ ID
NO: 11)] ,
IL21R (SEQ ID Nos: 12-14

[>ENSG0000103522_ENST00000337929_ENSP00000338010_IL21R
MPRGWAAPLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTWTQDQEELKDEAT
SCSLHRSAHNATHATYTCHMDVFHMADDIFSVNITDQSGNYSQECGSFLAESIKPAPPFNVT
TFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRK
DSSYELQVRAGPMGSSYQGTWSEWSDPVIQFTQSEELKEGWNPHLLLLLIVFIPAFWSLKT
HPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGWPSPEVPSTLEVYSCHP
PRSPAKRLQLTELQEPAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTLDAEG
PCTWPCSCEDDGYPALDLDAGLEPSPGLEDPPLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLP
PLADGEDWAGGLPWGRSPGGVSESEAGSPLAGLDMTDFDSFGVGSDCSSPVECDFTSPGDEGP
PRSylRQWVVI PPPPLSSPGPQAS* (SEQ ID NO: 12)

>ENSG0000103522_ENST00000395754_ENSP00000379103_IL21R
MPRGWAAPLLLLLQGGWGCPDLVCYTDYLQTVICILEMWNLHPSTLTWTQDQEELKDEAT
SCSLHRSAHNATHATYTCHMDVFHMADDIFSVNITDQSGNYSQECGSFLAESIKPAPPFNVT
TFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRK
HPLWRLWKKIWAVPSPERFFMPLYKGCSGDFKKWVGAPFTGSSLELGWPSPEVPSTLEVYSCHP
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PRSPAKRLQLTELQEPAAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG
PCTWPCSCEDDGYPALLDAGLEPSPGLEDPPLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKP
PLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMTFDSFGVGSDCSSPVECDFTSPGDEGP
PRSYLRQWVVI PPPPLSSPGPQAS* (SEQ ID NO: 13)

>ENSG00000103522_ENST00000564089_ENSP00000456707_IL21R

MPRGWAAPLLLLLQQGGWGCPLDVCYTDYLQTVICILEMWNLHPSTLTWTQDQYEELKDEAT
SCSLHRSAHNATHATYTCHMDVPHFMADDIFSVNITDQSGNYSQECSFLLAESIKPAPPFNTV
TFSGQYNI SWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKRLLISVDSRSVSLLPLEFRK
DSSYELQVRAGPMGSSYQGTWSEWSDPVI FQTQSEELKEGWNPHLLLLLIVVPIPAPWSLKT
HPLWRLWKKI WAVPSPERFFMPLYKGCGDFKKWVGAPFTGSSLELGWSPEVPSTLEVYSCHP
PRSPAKRLQLTELQEPAAELVESDGVPKPSFWPTAQNSGGSAYSEERDRPYGLVSIDTVTVLDAEG
PCTWPCSCEDDGYPALLDAGLEPSPGLEDPPLDAGTTVLSCGCVSAGSPGLGGPLGSLLDRLKP
PLADGEDWAGGLPWGGRSPGGVSESEAGSPLAGLDMTFDSFGVGSDCSSPVECDFTSPGDEGP
PRSYLRQWVVI PPPPLSSPGPQAS* (SEQ ID NO: 14)].

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[0030] Said cytokine is preferably selected from the group of consisting of: IL32 (SEQ ID Nos: 19-30), IL7 (SEQ ID Nos: 168-174), EB13 (SEQ ID NO: 175), SECTMI (SEQ ID Nos: 349-356), CSF1 (SEQ ID Nos: 585-592) and LTA (SEQ ID Nos: 657-658).

[0031] Said epigenetic factor is preferably selected from the group of consisting of: TDRD3 (SEQ ID NO: 712-718), KAT2B (SEQ ID NO:719), FOXA1 (SEQ ID Nos: 720-721) and RCBTB1 (SEQ ID Nos: 722-723).

[0032] Said kinase phosphatase is preferably selected from the group of consisting of: GSK3B (SEQ ID Nos: 724-725), SSH1 (SEQ ID NOS:111-112), CDK6 (SEQ ID Nos: 726-727), MINPP1 (SEQ ID Nos:181-183), PTPRJ (SEQ ID Nos: 395-400), CALM3 (SEQ ID Nos: 728-734) and PTP4A3 (SEQ ID Nos: 593-598).

[0033] Said transcription factor is preferably selected from the group of consisting of: VDR (SEQ ID NO:204), ZNF334 (SEQ ID Nos: 736-741), CREB3L2 (SEQ ID Nos: 565-567), ETV7 (SEQ ID NO:31 or 32), SOX4 (SEQ ID NO:735), TWIST1 (SEQ ID Nos: 743-745), TP73 (SEQ ID Nos: 746-756), FOXP3, NFE2L3 (SEQ ID NO:76), ARNTL2 (SEQ ID Nos: 757-764), BATF (SEQ ID Nos: 765-766), PTTG1 (SEQ ID Nos: 767-770), HIVEP3 (SEQ ID Nos: 771-772), FOXA1 (SEQ ID Nos: 720-721), ZBTB38 (SEQ ID NO:561), FOXM1 (SEQ ID Nos: 773-778), TADA3 (SEQ ID Nos: 779-782), NFAT5 (SEQ ID NO:160, 783-791, 742).

[0034] In a preferred embodiment, the marker is MAGEH1 (SEQ ID NO: 708 or 709)

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[MAGEH1_Entrez:28986_ENSG00000187601_ENST00000342972_ENSP00000343706
ATGCCCTGGGGACGAAAGAGTCGGCGCCCGTAATGCGAGAGCCGCAGAAGAGAACCGC
AACATCGAAAATCAGGCCTCAGAGGCCCTCCGAGAACCCCTATGGCCGCCTGTGGTAGC
GAGCACCCCCGAAGACGACTGAGCGGCCCCGAGGAAGACCCGAGCACTCCAGAGGAGGC
CTCTACCACCCCTGAAGAACGCTCGAGCACTGCCAACGACAAAAGCCTTCAGTCCCCGGA
GCAATTTCAGGGCACCAAGAAAAGTCTCCTGATGTCTATATTAGCGCTCATCTTCATCATG
GGCACACAGCGCCAAGGAAGCTCTGGCTGGAAAGTGCTGGGAAGTTAGGAATGCAGCCTG
GACGTAGCACAGCATCTTGGAGATCCGAAGAAGATCGTACAGAACAGAGTTGTGCGCAG
AGGGTACCTGATTATAACCGTGCCCCGTAGCAGTCCGGTGGAGTATGAGTTCTCTGGG
GGCCCGAGCACACGTGGAATCGAGCAAATGAAAGTCATGCATTGGCAAGGGTCG
TAACCGATGCTCTAAAGACTGGCCTGTAATTATGACTGGGATTGGACGATGATGCAGAGG
TTGAGGCTATCCTCAATTAGGTCTAGGGTTATCCGCCCTTAA (SEQ ID NO: 708)

MPRGRKSRRRNARAAEENNNRKIQASEASETPMAASVVAESTPDDLSGPEEDPSTPEEASTP
EEASSTAQAQKPSVPRSNSQGKTSLLMSILALIFIMGNSAKEALVWKVLGKLMQPGRQHSIFG

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DPKKIVTEEFVRRGYLIYKPVPRSSPVEFFWGPRAHVESSKLKVMHFVARVRNRCSKDWPCN

YDWDSDDAEVEAILNSGARGYSAP* (SEQ ID NO: 709)].

[0035] In the present invention, the tumor is preferably a solid or liquid tumor. Preferably, the solid tumor is selected from the group consisting of: non-small cell lung cancer, colorectal cancer, breast cancer, gastric cancer.

[0036] In a preferred embodiment of the invention, the tumor is a metastasis, preferably a bone, a brain or a liver metastasis.

[0037] Preferably, the metastasis derives from colon rectal cancer or non-small-cell lung cancer.

[0038] Another object of the invention is the above defined molecule for use in a method for in vivo depleting tumor-infiltrating regulatory T cells in a subject or for use in a method to enhance tumor immunity in a subject.

[0039] Another object of the invention is a pharmaceutical composition comprising the molecule as defined above and at least one pharmaceutically acceptable carrier.

[0040] A further object of the invention is a pharmaceutical composition comprising the molecule as above defined, for use in the prevention and/or treatment of tumor or for use in a method for in vivo depleting tumor-infiltrating regulatory T cell in a subject or for use in a method to enhance tumor immunity in a subject.

[0041] The pharmaceutical composition according to the invention may further comprise a therapeutic agent, preferably the therapeutic agent in an anti-tumoral agent.

[0042] Another object of the invention is an in vitro method for diagnosing and/or assessing the risk of developing and/or prognosing and/or for monitoring the progression and/or for monitoring the efficacy of a therapeutic treatment and/or for the screening of a therapeutic treatment of a tumour in a subject comprising the steps of:

[0043] a) detecting at least one of the marker as above defined in an isolated biological sample obtained from the subject and

[0044] b) comparing with respect to a proper control.

[0045] Another object of the invention is an in vitro or ex-vivo method for diagnosing and/or assessing the risk of developing and/or prognosing and/or for monitoring the progression and/or for monitoring the efficacy of a therapeutic treatment and/or for the screening of a therapeutic treatment of a tumour in a subject as above defined, wherein the marker to be detected is at least one of the marker selected from the group consisting of: LAYN, MAGEH1 and CCR8.

[0046] Preferably the above method is for prognosing of colorectal cancer or non-small cell lung cancer in a subject and comprises the steps of:

[0047] a) detecting at least one of the marker selected from the group consisting of: LAYN, MAGEH1 and CCR8 in an isolated biological sample obtained from the subject and

[0048] b) comparing with respect to a proper control,

[0049] wherein an amount of said at least one marker in the isolated biological sample obtained from the subject higher than the control amount indicates that the subject has a poor prognosis.

[0050] In the above method, preferably step a) comprises measuring the amount of the marker or of fragments thereof

or of the polynucleotide coding for said protein (DNA or mRNA) or of fragments thereof in said isolated biological sample obtained from the subject and step b) comprises comparing the measured amount of step a) with a proper control amount.

[0051] Preferably, the in vitro method for monitoring the progression and/or for monitoring the efficacy of a therapeutic treatment of a tumour, as above defined, comprises the steps of:

[0052] a) measuring the alteration of the amount or the alteration of the activity of the above markers or of fragments thereof or of the polynucleotide coding for said protein or fragments thereof in said isolated biological sample obtained from the subject and

[0053] b) comparing the measured alteration of step a) with a proper control alteration.

[0054] Another object of the invention is a method for the treatment and/or prevention of tumor comprising administering to a subject the molecule as above defined.

[0055] A further object is a method for identifying a molecule acting as an anti-tumoral, comprising the steps of:

[0056] assaying candidate molecules for their binding specificity to the at least one marker as above defined;

[0057] selecting molecules having a specific binding activity to the at least one marker as above defined;

[0058] testing such specific binding molecules for their capacity of inhibiting proliferation and/or inducing an apoptotic response in a cell system,

[0059] preferably by selectively depleting tumor-infiltrating regulatory T cell, more preferably by inducing antibody-dependent cell-mediated cytotoxicity (ADCC).

[0060] Preferably, the biological sample is a fluid, a cell or a tissue sample, more preferably said sample is plasma or serum.

[0061] The term "biological sample" encompasses a clinical sample, and also includes tissue obtained by surgical resection, tissue obtained by biopsy, cells in culture, cell supernatants, cell lysates, tissue samples, organs, bone marrow, blood, plasma, serum, and the like.

[0062] A "sample" in the context of the present teachings refers to any biological sample that is isolated from a subject. A sample can include, without limitation an aliquot of body fluid, whole blood, serum, plasma, solid tissue samples such as tissue biopsies, or tissue cultures or cells derived therefrom and the progeny thereof, synovial fluid, lymphatic fluid, ascites fluid, and interstitial or extracellular fluid. The term "sample" also encompasses the fluid in spaces between cells, including gingival crevicular fluid, bone marrow, cerebrospinal fluid (CSF), saliva, mucous, sputum, semen, sweat, urine, or any other bodily fluids. "Blood sample" can refer to whole blood or any fraction thereof, including serum and plasma. Samples can be obtained from a subject by means including but not limited to venipuncture, excretion, ejaculation, massage, biopsy, needle aspirate, lavage, scraping, surgical incision, or intervention or other means known in the art. The definition also includes samples that have been manipulated in any way

after their procurement, such as by treatment with reagents; washed; or enrichment for certain cell populations, such as cancer cells or samples in which regulatory T cells, are isolated and then analyzed. The definition also includes sample that have been enriched for particular types of molecules, e.g., nucleic acids, polypeptides, etc.

[0063] Another object of the invention is a kit for carrying out the above methods, comprising

[0064] means to measure the amount or the activity of the above markers or of fragments thereof and/or means to measure the amount of the polynucleotide coding for said protein or of fragments thereof and optionally,

[0065] control means.

[0066] Any combination of the above markers is comprised within the present invention.

[0067] Preferred combinations of markers are LAYN and MAGEH1; LAYN and CCR8; CCR8 and MAGEH1; LAYN, MAGEH1 and CCR8.

[0068] Preferably, the above polynucleotide is an RNAi inhibitor, preferably selected from the group consisting of: siRNA, miRNA, shRNA, stRNA, snRNA, and antisense nucleic acid, or a functional derivative thereof.

[0069] A comparative analysis of gene expression arrays from CD4+ T cells infiltrating NSCLC and CRC revealed Treg-specific expression of 328 markers as listed in Table IV. Manipulation of Treg cells via these markers can therefore be used to enhance immunotherapy of cancer.

[0070] The expression "molecule able to modulate" and "modulator" are herein interchangeable.

[0071] By the term "modulator" it is meant a molecule that effects a change in the expression and/or function of at least one marker as above defined.

[0072] The change is relative to the normal or baseline level of expression and/or function in the absence of the modulator, but otherwise under similar conditions, and it may represent an increase (e.g. by using an inducer or activator) or a decrease (e.g. by using a suppressor or inhibitor) in the normal/baseline expression and/or function. In the context of the present invention, a "modulator" is a molecule which may suppress or inhibit the expression and/or function of at least one marker that is selectively deregulated in tumor-infiltrating regulatory T cell for use in the prevention and/or treatment of cancer.

[0073] By the term "suppressor or inhibitor" or a "molecule which (selectively) suppresses or inhibits" it is meant a molecule that effects a change in the expression and/or function of the target.

[0074] In the context of the present invention, a "modulator" is a molecule which may induce or activate the expression and/or function of at least one marker that is selectively deregulated in tumor-infiltrating regulatory T cell for use in the prevention and/or treatment of cancer.

[0075] The change is relative to the normal or baseline level of expression and/or function in the absence of the modulator, but otherwise under similar conditions, and it may represent an increase (e.g. by using an inducer or activator) or a decrease (e.g. by using a suppressor or inhibitor) in the normal/baseline expression and/or function.

[0076] The suppression or inhibition of the expression and/or function of the target may be assessed by any means known to the skilled in the art. The assessment of the expression level or of the presence of the target is preferably performed using classical molecular biology techniques

such as (real time Polymerase Chain Reaction) qPCR, microarrays, bead arrays, RNase protection analysis or Northern blot analysis or cloning and sequencing.

[0077] The assessment of target function is preferably performed by in vitro suppression assay, whole transcriptome analysis, mass spectrometry analysis to identify proteins interacting with the target.

[0078] In the context of the present invention, the target (or the marker) may be the gene, the mRNA, the cDNA, or the encoded protein thereof, including fragments, derivatives, variants, isoforms, etc. Preferably, the marker is characterized by its Accession numbers (i.e. NCBI Entrez ID; Ensembl Gene accession number (ENSG), Ensembl transcript accession number (ENST) and Ensembl protein accession number (ENSP), retrievable in the public database EnsEMBL (<http://www.ensembl.org>) and/or amino acid and nucleotide sequences, herein disclosed.

[0079] In the context of the present invention, the term "treat" (or "treated", "treatment", etc.) when referred to CD4+ T cell, means e.g. the exposure of the cell to an exogenous modulator as above defined. The overexpression may be obtained e.g. by infecting the cells with a viral vector expressing the molecule of the invention. The inhibition of marker expression may e.g. be obtained by transfection with polynucleotide, as e.g. with siRNAs.

[0080] The term "treat" may also mean that the cells are manipulated in order to overexpress or silence the marker. The overexpression or the silencing may be obtained e.g. by genetically modifying the cells.

[0081] Control means can be used to compare the amount or the increase of amount of the marker defined to a proper control. The proper control may be obtained for example, with reference to known standard, either from a normal subject or from normal population, or from T cells different from tumour infiltrating regulatory T cells or regulatory T cells. The means to measure the amount of at least one marker as above defined are preferably at least one antibody, functional analogous or derivatives thereof. Said antibody, functional analogous or derivatives thereof are specific for said marker.

[0082] In the context of the present invention, the antibody is preferably selected from the group consisting of an intact immunoglobulin, a Fv, a scFv (single chain Fv fragment), a Fab, a F(ab)2, an "antibody-like" domain, an "antibody-mimetic domain", a single antibody domain (VH domain or VL domains), a multimeric antibody, recombinant or synthetic antigen-binding fragments, a peptide or a proteolytic fragment containing the epitope binding region. The terms "antibody" and "immunoglobulin" can be used interchangeably and are herein used in the broadest sense and encompass various antibodies and antibody mimetics structures, including but not limited to monoclonal antibodies, polyclonal antibodies, multispecific antibodies (e.g., bispecific antibodies), chimeric antibodies, nanobodies, antibody derivatives, antibody fragments, anticalins, DARPins, affibodies, affilins, affimers, affitins, alphabodies, avimers, fynomers, monobodies and other binding domains, so long as they exhibit the desired antigen-binding activity.

[0083] The term immunoglobulin also includes "conjugate" thereof. In the context of the present invention "conjugate" in relation to the antibody of the invention includes antibodies (or fragments thereof) conjugated with a substance (a compound, etc.) having a therapeutic activity, e.g. anti-tumor activity and/or cell-killing activity or a cytotoxic

agents such as various A chain toxins, ribosomes inactivating proteins, and ribonucleases; bispecific antibodies designed to induce cellular mechanisms for killing tumors (see, for example, U.S. Pat. Nos. 4,676,980 and 4,954,617). The conjugate may be formed by previously preparing each of the aforementioned antibody molecule and the aforementioned substance having anti-tumor activity and/or cell-killing activity, separately, and then combining them (immunoconjugate) or by ligating a protein toxin used as such a substance having anti-tumor activity and/or cell-killing activity to an antibody gene on a gene according to a genetic recombination technique, so as to allow it to express as a single protein (a fusion protein) (immunotoxin).

[0084] An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds.

[0085] Examples of antibody fragments include but are not limited to Fv, Fab, Fab', Fab'-SH, F(ab')2; diabodies; linear antibodies; single-chain antibody molecules (e.g. scFv); and multispecific antibodies formed from antibody fragments. VH or VL Fvs are also called "Nanobodies".

[0086] The term "antibody mimetics" refers to those organic compounds or binding domains that are not antibody derivatives but that can bind specifically an antigen like antibodies do.

[0087] They include anticalins, DARPins, affibodies, affilins, affimers, affitins, alphabodies, avimers, fynomers, monobodies and others.

[0088] The term "chimeric" antibody refers to an antibody in which a portion of the heavy and/or light chain is derived from a particular source or species, while the remainder of the heavy and/or light chain is derived from a different source or species.

[0089] The terms "full length antibody," "intact antibody," and "whole antibody" are used herein interchangeably to refer to an antibody having a structure substantially similar to a native antibody structure or having heavy chains that contain an Fc region as defined herein.

[0090] In a preferred embodiment, the kit of the invention comprises:

[0091] a solid phase adhered antibody specific for said compound;

[0092] detection means of the ligand specific-marker complex.

[0093] Alternatively, the reagents can be provided as a kit comprising reagents in a suspension or suspendable form, e.g. reagents bound to beads suitable for flow cytometry, preferably magnetic beads coated with antibody capture. The instructions may comprise instructions for conducting an antibody-based flow cytometry assay.

[0094] Detection means are preferably means able to detect and/or measure the amount of the described markers, e.g. means able to detect the complex antigen-antibody, as enzyme conjugated secondary antibodies, luminescent substrates, magnetic beads coated with antibody capture, customized dried antibody cocktails and/or columns with size filter cartridges and/or combined with specific antibody filter (SAF).

[0095] In an embodiment, the method further comprises selecting a therapeutic regimen based on the analysis. In an embodiment, the method further comprises determining a treatment course for the subject based on the analysis. Other means may be e.g. specific primers and probes for RT PCR.

The kits according to the invention can further comprise customary auxiliaries, such as buffers, carriers, markers, etc. and/or instructions for use.

[0096] In the context of the present invention the term "detecting" may be intended also as "measuring the amount" or "measuring the alteration". In the case of a method or a kit for assessing the risk and/or diagnosing and/or prognosis of a tumour, the proper control may be a sample taken from a healthy patient or from a patient affected by another disorder or pathology, and the proper control amount or activity may be the amount or activity of the same protein or polynucleotide measured in a sample taken from a healthy patient or from a patient affected by another disorder or pathology.

[0097] In the case of a method or a kit for monitoring the progression of a tumour, the progress of the cancer is monitored and the proper control may be a sample taken from the same subject at various times or from another patient, and the proper control amount or activity may be the amount or activity of the same protein or polynucleotide measured in a sample taken from the same subject at various times or from another patient.

[0098] In the case of a method or a kit for monitoring the efficacy of a therapeutic treatment, the proper control may be a sample taken from the same subject before initiation of the therapy or taken at various times during the course of the therapy and the proper control amount or activity may be the amount or activity of the same protein or polynucleotide measured in a sample taken from the same subject before initiation of the therapy or taken at various times during the course of the therapy.

[0099] In the case of a method or a kit for the screening of a therapeutic treatment, the proper control may be a sample taken from subjects without treatment and from subjects treated with a substance that is to be assayed or from subjects treated with a reference treatment and the proper control amount or activity may be the average of the amounts or activity of the same protein or polynucleotide measured in samples taken from subjects without treatment and from subjects treated with a substance that is to be assayed or from subjects treated with a reference treatment. In this case, if the amount or activity of MAGEH1 and/or LAYN and/or CCR8 or polynucleotides thereof in the isolated biological sample obtained from the subject is lower or equal than the control amount or activity, it may indicate that the tested substance is effective for the treatment of the tumour.

[0100] In the present invention, the expression "measuring the amount" can be intended as measuring the amount (or the activity) or concentration or level of the respective protein and/or mRNA thereof and/or DNA thereof, preferably semi-quantitative or quantitative.

[0101] Measurement of a protein can be performed directly or indirectly. Direct measurement refers to the amount or concentration measure of the marker, based on a signal obtained directly from the protein, and which is directly correlated with the number of protein molecules present in the sample. This signal—which can also be referred to as intensity signal—can be obtained, for example, by measuring an intensity value of a chemical or physical property of the marker. Indirect measurements include the measurement obtained from a secondary component (e.g., a different component from the gene expression

product) and a biological measurement system (e.g. the measurement of cellular responses, ligands, "tags" or enzymatic reaction products).

[0102] The term "amount", as used in the description refers but is not limited to the absolute or relative amount of proteins and/or mRNA thereof and/or DNA thereof, and any other value or parameter associated with the same or which may result from these. Such values or parameters comprise intensity values of the signal obtained from either physical or chemical properties of the protein, obtained by direct measurement; for example, intensity values in an immunoassay, mass spectroscopy or a nuclear magnetic resonance. [0103] Additionally, these values or parameters include those obtained by indirect measurement, for example, any of the measurement systems described herein. Methods of measuring mRNA and DNA in samples are known in the art. To measure nucleic acid levels, the cells in a test sample can be lysed, and the levels of mRNA in the lysates or in RNA purified or semi-purified from lysates can be measured by any variety of methods familiar to those in the art. Such methods include hybridization assays using detectably labeled DNA or RNA probes (i.e., Northern blotting) or quantitative or semi-quantitative RT-PCR methodologies using appropriate oligonucleotide primers. Alternatively, quantitative or semi-quantitative in situ hybridization assays can be carried out using, for example, tissue sections, or unlysed cell suspensions, and detectably labeled (e.g., fluorescent, or enzyme-labeled) DNA or RNA probes. Additional methods for quantifying mRNA include RNA protection assay (RPA), cDNA and oligonucleotide microarrays, representation difference analysis (RDA), differential display, EST sequence analysis, and serial analysis of gene expression (SAGE).

[0104] If by comparing the measured amount or activity of the above markers or of the polynucleotide coding for said protein with the amount or activity obtained from a control sample, the amount or the activity of said marker in the sample isolated from the subject corresponds to a higher value, the subject may present cancer or go towards an aggravation of said disease.

[0105] If by comparing the measured amount or activity of the above markers or of the polynucleotide coding for said protein with the amount or the activity obtained from a control sample, the amount or the activity of said marker in the sample isolated from the subject corresponds to a similar or lower value, the subject may be not affected by cancer or go toward an amelioration of cancer, respectively.

[0106] Alternatively, the expression "detecting" or "measuring the amount" is intended as measuring the alteration of the molecule. Said alteration can reflect an increase or a decrease in the amount or activity of the molecules as above defined. An increase of the protein or of the activity of the marker or of the polynucleotide coding for said marker can be correlated to an aggravation of cancer. A decrease of the protein or of the activity of said marker or of the polynucleotide coding for said protein can be correlated to an amelioration of cancer or to recovery of the subject.

[0107] The expression "marker" is intended to include also the corresponding protein encoded from said marker orthologous or homologous genes, functional mutants, functional derivatives, functional fragments or analogues, isoforms, splice variants thereof.

[0108] When the expression "marker" is referred to genes, it is intended to include also the corresponding orthologous

or homologous genes, functional mutants, functional derivatives, functional fragments or analogues, isoforms thereof.

[0109] As used herein "fragments" refers to polynucleotides having preferably a length of at least 1000 nucleotides, 1100 nucleotide, 1200 nucleotides, 1300 nucleotides, 1400 nucleotides, 1500 nucleotides.

[0110] As used herein "fragments" refers to polypeptides having preferably a length of at least amino acids, more preferably at least 15, at least 17 amino acids or at least 20 amino acids, even more preferably at least 25 amino acids or at least 37 or 40 amino acids, and more preferably of at least 50, or 100, or 150 or 200 or 250 or 300 or 350 or 400 or 450 or 500 amino acids.

[0111] The term "polynucleotide" also refers to modified polynucleotides.

[0112] As used herein, the term "vector" refers to an expression vector, and may be for example in the form of a plasmid, a viral particle, a phage, etc. Such vectors may include bacterial plasmids, phage DNA, baculovirus, yeast plasmids, vectors derived from combinations of plasmids and phage DNA, viral DNA such as vaccinia, adenovirus, lentivirus, fowl pox virus, and pseudorabies. Large numbers of suitable vectors are known to those of skill in the art and are commercially available.

[0113] The polynucleotide sequence, preferably the DNA sequence in the vector is operatively linked to an appropriate expression control sequence(s) (promoter) to direct mRNA synthesis. As representative examples of such promoters, one can mention prokaryotic or eukaryotic promoters such as CMV immediate early, HSV thymidine kinase, early and late SV40, LTRs from retrovirus, and mouse metallothionein-1. The expression vector may also contain a ribosome binding site for translation initiation and a transcription vector.

[0114] The vector may also include appropriate sequences for amplifying expression. In addition, the vectors preferably contain one or more selectable marker genes to provide a phenotypic trait for selection of transformed host cells such as dihydro folate reductase or neomycin resistance for eukaryotic cell culture, or such as tetracycline or ampicillin resistance in *E. coli*.

[0115] As used herein, the term "host cell genetically engineered" relates to host cells which have been transduced, transformed or transfected with the polynucleotide or with the vector described previously. As representative examples of appropriate host cells, one can cite bacterial cells, such as *E. coli*, *Streptomyces*, *Salmonella typhimurium*, fungal cells such as yeast, insect cells such as SF9, animal cells such as CHO or COS, plant cells, etc. The selection of an appropriate host is deemed to be within the scope of those skilled in the art from the teachings herein. Preferably, said host cell is an animal cell, and most preferably a human cell.

[0116] The introduction of the polynucleotide or of the vector described previously into the host cell can be effected by method well known from one of skill in the art such as calcium phosphate transfection, DEAE-Dextran mediated transfection, electroporation, lipofection, microinjection, viral infection, thermal shock, transformation after chemical permeabilisation of the membrane or cell fusion.

[0117] The polynucleotide may be a vector such as for example a viral vector.

[0118] The polynucleotides as above defined can be introduced into the body of the subject to be treated as a nucleic

acid within a vector which replicates into the host cells and produces the polynucleotides or the proteins.

[0119] Suitable administration routes of the pharmaceutical composition of the invention include, but are not limited to, oral, rectal, transmucosal, intestinal, enteral, topical, suppository, through inhalation, intrathecal, intraventricular, intraperitoneal, intranasal, intraocular and parenteral (e.g., intravenous, intramuscular, intramedullary, and subcutaneous). An additional suitable administration route includes chemoembolization. Other suitable administration methods include injection, viral transfer, use of liposomes, e.g. cationic liposomes, oral intake and/or dermal application.

[0120] In certain embodiments, a pharmaceutical composition of the present invention is administered in the form of a dosage unit (e.g., tablet, capsule, bolus, etc.).

[0121] For pharmaceutical applications, the composition may be in the form of a solution, e.g. an injectable solution, emulsion, suspension or the like. The carrier may be any suitable pharmaceutical carrier. Preferably, a carrier is used which is capable of increasing the efficacy of the RNA molecules to enter the target cells. Suitable examples of such carriers are liposomes.

[0122] The modulator as above defined is administered in a pharmaceutically effective dosage, which in the case of polynucleotides may be in the range of 0.001 pg/kg body weight to 10 mg/kg body weight depending on the route of administration and the type or severity of the disease.

[0123] The term "pharmaceutical composition" refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. In the present invention the term "effective amount" shall mean an amount which achieves a desired effect or therapeutic effect as such effect is understood by those of ordinary skill in the art. In the present invention, the antibody may be administered simultaneously or sequentially with another therapeutic treatment, that may be a chemotherapy or radiotherapy. The invention provides formulations comprising a therapeutically effective amount of an antibody as disclosed herein, a buffer maintaining the pH in the range from about 4.5 to about 8.5, and, optionally, a surfactant. The formulations are typically for an antibody as disclosed herein, recombinant or synthetic antigen-binding fragments thereof of the invention as active principle concentration from about 0.1 mg/ml to about 100 mg/ml. In certain embodiments, the antibody, recombinant or synthetic antigen-binding fragments thereof concentration is from about 0.1 mg/ml to 1 mg/ml; preferably from 1 mg/ml to 10 mg/ml, preferably from 10 to 100 mg/ml.

[0124] Therapeutic formulations of the antibody/antibodies can be prepared by mixing the antibody having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed., 1980), in the form of lyophilized formulations or aqueous solutions.

[0125] Pharmaceutical compositions containing the antibody of the present invention may be manufactured by processes well known in the art, e.g., using a variety of well-known mixing, dissolving, granulating, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes. Proper formulation is dependent upon the route of administration chosen. Parenteral routes are preferred in many aspects of the invention.

[0126] For injection, including, without limitation, intravenous, intramuscular and subcutaneous injection, the compounds of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as physiological saline buffer or polar solvents including, without limitation, a pyrrolidone or dimethylsulfoxide.

[0127] Formulations for injection may be presented in unit dosage form, e.g. in ampoules or in multi-dose containers. Useful compositions include, without limitation, suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain adjuncts such as suspending, stabilizing and/or dispersing agents. Pharmaceutical compositions for parenteral administration include aqueous solutions of a water soluble form, such as, without limitation, a salt of the active compound. Additionally, suspensions of the active compounds may be prepared in a lipophilic vehicle. Suitable lipophilic vehicles include fatty oils such as sesame oil, synthetic fatty acid esters such as ethyl oleate and triglycerides, or materials such as liposomes. Aqueous injection suspensions may contain substances that increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Optionally, the suspension may also contain suitable stabilizers and/or agents that increase the solubility of the compounds to allow for the preparation of highly concentrated solutions. Alternatively, the active ingredient may be in powder form for constitution with a suitable vehicle, e.g., sterile, pyrogen-free water, before use. For administration by inhalation, the antibody of the present invention can conveniently be delivered in the form of an aerosol spray using a pressurized pack or a nebulizer and a suitable propellant. The antibody may also be formulated in rectal compositions such as suppositories or retention enemas, using, e.g., conventional suppository bases such as cocoa butter or other glycerides. In addition to the formulations described previously, the antibody may also be formulated as depot preparations. Such long acting formulations may be administered by implantation (for example, subcutaneously or intramuscularly) or by intramuscular injection. The compounds of this invention may be formulated for this route of administration with suitable polymeric or hydrophobic materials (for instance, in an emulsion with a pharmacologically acceptable oil), with ion exchange resins, or as a sparingly soluble derivative such as, without limitation, a sparingly soluble salt. Additionally, the antibody may be delivered using a sustained-release system, such as semi-permeable matrices of solid hydrophobic polymers containing the therapeutic agent. Other delivery systems such as liposomes and emulsions can also be used.

[0128] A therapeutically effective amount refers to an amount of compound effective to prevent, alleviate or ameliorate cancer or cancer recurrence symptoms. Determination of a therapeutically effective amount is well within the capability of those skilled in the art, especially in light of the disclosure herein. For any antibody used in the invention, the therapeutically effective amount can be estimated initially from *in vitro* assays. Then, the dosage can be formulated for use in animal models so as to achieve a circulating concentration range that includes the effective dosage. Such information can then be used to more accurately determine dosages useful in patients. The amount of the composition that is administered will depend upon the parent molecule included therein.

[0129] Generally, the amount used in the treatment methods is that amount which effectively achieves the desired

therapeutic result in mammals. Naturally, the dosages of the various compounds can vary somewhat depending upon the compound, rate of in vivo hydrolysis, etc. In addition, the dosage, of course, can vary depending upon the dosage form and route of administration. The range set forth above is illustrative and those skilled in the art will determine the optimal dosing of the compound selected based on clinical experience and the treatment indication. Moreover, the exact formulation, route of administration and dosage can be selected by the individual physician in view of the patient's condition and of the most effective route of administration (e.g., intravenous, subcutaneous, intradermal). Additionally, toxicity and therapeutic efficacy of the antibody and other therapeutic agent described herein can be determined by standard pharmaceutical procedures in cell cultures or experimental animals using methods well-known in the art.

[0130] It is contemplated that the treatment will be given for one or more cycles until the desired clinical and biological result is obtained. The exact amount, frequency and period of administration of the compound of the present invention will vary, of course, depending upon the sex, age and medical condition of the patient as well as the severity and type of the disease as determined by the attending clinician.

[0131] The modulator of the present invention may comprise a single type of modulator or a plurality of different modulators.

[0132] The function of a regulatory T-cell may be inhibited by inhibiting markers activity and/or expression or by decreasing the number of cells positive for such markers in a T-cell population (for example by binding at least one of the above marker and inducing antibody-dependent cell-mediated cytotoxicity (ADCC)). Inhibiting the function of regulatory T-cells in an organism may be used to enhance the immune T-cell response in those circumstances where such a response is desirable, such as in a patient suffering from cancer.

[0133] When treating a cancer patient with an inhibitory agent that binds to marker protein or mRNA, one may optionally co-administer an anti-tumor vaccine or therapy. Such vaccines may be directed to isolated antigens or to groups of antigens or to whole tumor cells. It may be desirable to administer the inhibitory agent with chemotherapeutic agents or together with radiotherapy.

[0134] Treatment with multiple agents need not be done using a mixture of agents but may be done using separate pharmaceutical preparations. The preparations need not be delivered at the same exact time, but may be coordinated to be delivered to a patient during the same period of treatment, i.e. within a week or a month or each other.

[0135] Thus a composition comprising two active ingredients may be constituted in the body of the patient. Any suitable anti-tumor treatment can be coordinated with the treatments of the present invention targeted to the markers. Similarly, if treating patients with infections, other anti-infection agents can be coordinated with the treatment of the present invention targeted to the markers. Such agents may be small molecule drugs, vaccines, antibodies, etc.

[0136] The number of marker+ cells in a T-cell population can be modified by using an antibody or other agent that selectively binds to the marker. marker+ cells represent an enriched population of regulatory T-cells that can be introduced back into the original source of the T-cells or into another compatible host to enhance regulatory T-cell func-

tion. Alternatively, the marker-cells represent a population of T-cells deficient in regulatory T-cell activity that can be reintroduced into the original source of the T-cells or another compatible host to inhibit or reduce regulatory T-cell function while retaining general T-cell activity.

[0137] Any desired means for either increasing or decreasing (modulating) marker activity can be used in the methods of the invention. This includes directly modulating the function of marker protein, modulating marker signal transduction, and modulating expression of marker in T-cells by modulating either transcription or translation or both. Those means which selectively modulate marker activity are preferred over nonselective modulators.

[0138] Also, those inhibitory means which create a transient marker deficiency in a population of T-cells which then return to normal levels of marker activity may be preferred for treating a temporary T-cell deficiency. The transiently deficient T-cells may be used to reconstitute a diminished T-cell population with T-cells that will be genetically normal with respect to the marker. Modulation of marker activity can be performed on cells in vitro or in whole animals, in vivo. Cells which are treated in vitro can be administered to a patient, either the original source of the cells or an unrelated individual.

[0139] To inhibit the function of the marker (antagonist), marker antibodies or small molecule inhibitors can be used. Antibodies or antibody fragments that are useful for this purpose will be those that can bind to the marker and block its ability to function. Such antibodies may be polyclonal antibodies, monoclonal antibodies, chimeric antibodies, humanized antibodies, single-chain antibodies, soluble MHC class II molecules, antibody fragments, etc.

[0140] Antibodies generated against marker polypeptides can be obtained by direct injection of the marker polypeptides into an animal or by administering marker polypeptides to an animal, preferably a nonhuman. The antibody so obtained will then bind the marker polypeptides itself. In this manner, even a sequence encoding only a fragment of the marker polypeptide can be used to generate antibodies binding the whole native marker polypeptide.

[0141] For preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples include the hybridoma technique (Kohler and Milstein, 1975, *Nature*, 256: 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor et al., 1983, *Immunology Today* 4: 72), and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole, et al; 1985, in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96). Techniques described for the production of single chain antibodies (U.S. Pat. No. 4,946,778) can be readily used to produce single chain antibodies to marker polypeptides. Also, transgenic mice may be used to express humanized antibodies to immunogenic marker polypeptides. To enhance or activate the function of the marker, any agent which increases the level of the marker or the activity of existing marker in the T-cell may be used. Such agents may be identified using the screening assays described below. Expression vectors encoding the marker can also be administered to increase the gene dosage. The expression vectors can be plasmid vectors or viral vectors, as are known in the art. Any vector can be chosen by the skilled in the art for particularly desirable properties. In the context of the present invention, the term "polynucleotide" includes DNA mol-

ecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA, siRNA, shRNA) and analogues of the DNA or RNA generated using nucleotide analogues. The polynucleotide may be single-stranded or double-stranded. The polynucleotide may be synthesized using oligonucleotide analogues or derivatives (e.g., inosine or phosphorothioate nucleotides).

[0142] The RNAi inhibitors as above defined are preferably capable of hybridizing to all or part of specific target sequence. Therefore, RNAi inhibitors may be fully or partly complementary to all of or part of the target sequence

[0143] The RNAi inhibitors may hybridize to the specified target sequence under conditions of medium to high stringency.

[0144] An RNAi inhibitors may be defined with reference to a specific sequence identity to the reverse complement of the sequence to which it is intended to target. The antisense sequences will typically have at least about 75%, preferably at least about 80%, at least about 85%, at least about 90%, at least about 95% or at least about 99% sequence identity with the reverse complements of their target sequences.

[0145] The term polynucleotide and polypeptide also includes derivatives and functional fragments thereof.

[0146] In the context of the present invention, the at least one gene or marker as above defined is preferably characterized by at least one of the sequence identified by its Ensembl Gene ID or NCBI Accession Numbers, as disclosed in Tables VIII or VI, or by at least one of the SEQ ID No. 1-709.

[0147] The term gene herein also includes corresponding orthologous or homologous genes, isoforms, variants, allelic variants, functional derivatives, functional fragments thereof.

[0148] The expression "protein" is intended to include also the corresponding protein encoded from a corresponding orthologous or homologous genes, functional mutants, functional derivatives, functional fragments or analogues, isoforms thereof.

[0149] The term "analogue" as used herein referring to a protein means a modified peptide wherein one or more amino acid residues of the peptide have been substituted by other amino acid residues and/or wherein one or more amino acid residues have been deleted from the peptide and/or wherein one or more amino acid residues have been deleted from the peptide and/or wherein one or more amino acid residues have been added to the peptide. Such addition or deletion of amino acid residues can take place at the N-terminal of the peptide and/or at the C-terminal of the peptide.

[0150] A "derivative" may be a nucleic acid molecule, as a DNA molecule, coding the polynucleotide as above defined, or a nucleic acid molecule comprising the polynucleotide as above defined, or a polynucleotide of complementary sequence. In the context of the present invention the term "derivatives" also refers to longer or shorter polynucleotides and/or polypeptides having e.g. a percentage of identity of at least 41%, 50%, 60%, 65%, 70% or 75%, more preferably of at least 85%, as an example of at least 90%, and even more preferably of at least 95% or 100% with the sequences herein mentioned or with their complementary sequence or with their DNA or RNA corresponding sequence. The term "derivatives" and the term "polynucleotide" also include modified synthetic oligonucleotides. The modified synthetic oligonucleotide are preferably LNA (Locked Nucleic Acid), phosphoro-thiolated oligos or meth-

ylated oligos, morpholinos, 2'-O-methyl, 2'-O-methoxyethyl oligonucleotides and cholesterol-conjugated 2'-O-methyl modified oligonucleotides (antagonists).

[0151] The term "derivative" may also include nucleotide analogues, i.e. a naturally occurring ribonucleotide or deoxyribonucleotide substituted by a non-naturally occurring nucleotide.

[0152] The term "derivatives" also includes nucleic acids or polypeptides that may be generated by mutating one or more nucleotide or amino acid in their sequences, equivalents or precursor sequences. The term "derivatives" also includes at least one functional fragment of the polynucleotide.

[0153] In the context of the present invention "functional" is intended for example as "maintaining their activity".

[0154] In the context of the present invention, the vector as above defined is preferably selected from the group consisting of: plasmids, viral vectors and phages, more preferably the viral vector is a lentiviral vector.

[0155] In the context of the present invention, the host cell as above defined is preferably selected from the group consisting of: bacterial cells, fungal cells, insect cells, animal cells, plant cells, preferably being an animal cell.

[0156] Compositions comprising a mixture of antibodies which specifically bind to the marker(s); and an anti-cancer vaccine can be made in vitro. Preferably the composition is made under conditions which render it suitable for use as a pharmaceutical composition.

[0157] Pharmaceutical compositions may be sterile and pyrogen-free. The components of the composition can also be administered separately to a patient within a period of time such that they are both within the patient's body at the same time. Such a time-separated administration leads to formation of the mixture of antibodies and vaccine within the patient's body. If the antibody and vaccine are to be administered in a time-separated fashion, they may be supplied together in a kit. Within the kit the components may be separately packaged or contained. Other components such as excipients, carriers, other immune modulators or adjuvants, instructions for administration of the antibody and the vaccine, and injection devices can be supplied in the kit as well. Instructions can be in a written, video, or audio form, can be contained on paper, an electronic medium, or even as a reference to another source, such as a website or reference manual.

[0158] Anti-marker antibodies of the invention can be used to increase the magnitude of anti-cancer response of the cancer patient to the anti-cancer vaccine or anti-cancer therapy.

[0159] It can also be used to increase the number of responders in a population of cancer patients. Thus the antibodies can be used to overcome immune suppression found in patients refractory to anti-cancer vaccines or treatment. The anti-cancer vaccines can be any that are known in the art, including, but not limited to whole tumor cell vaccines, isolated tumor antigens or polypeptides comprising one or more epitopes of tumor antigens.

[0160] Expression of marker in T-cells can be modulated at the transcriptional or translational level. Agents which are capable of such modulation can be identified using the screening assays described below.

[0161] Translation of marker mRNA can be inhibited by using ribozymes, antisense molecules, small interference RNA (siRNA; See Elbashir, S. M. et al., "Duplexes of

21-nucleotide RNAs mediate RNA interference in cultured mammalian cells", *Nature* 411: 494-498 (2001)) or small molecule inhibitors of this process which target marker mRNA.

[0162] Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5'coding portion of the polynucleotide sequence, which codes for the mature polypeptides of the present invention, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix—see Lee et al., *Nucl. Acids Res.*, 6: 3073 (1979); Cooney et al., *Science*, 241: 456 (1988); and Dervan et al., *Science*, 251: 1360 (1991)), thereby preventing transcription and the production of the marker. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into the marker polypeptide (Antisense—Okano, *J. Neurochem.*, 56: 560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, Fla. (1988)). The oligonucleotides described above can also be delivered to cells by antisense expression constructs such that the antisense RNA or DNA may be expressed in vivo to inhibit production of the marker. Such constructs are well known in the art. Antisense constructs, antisense oligonucleotides, RNA interference constructs or siRNA duplex RNA molecules can be used to interfere with expression of the marker.

[0163] Typically, at least 15, 17, 19, or 21 nucleotides of the complement of marker mRNA sequence are sufficient for an antisense molecule. Typically at least 19, 21, 22, or 23 nucleotides of marker are sufficient for an RNA interference molecule. Preferably an RNA interference molecule will have a 2 nucleotide 3' overhang. If the RNA interference molecule is expressed in a cell from a construct, for example from a hairpin molecule or from an inverted repeat of the desired marker sequence, then the endogenous cellular machinery will create the overhangs. siRNA molecules can be prepared by chemical synthesis, in vitro transcription, or digestion of long dsRNA by Rnase III or Dicer. These can be introduced into cells by transfection, electroporation, or other methods known in the art. (See Hannon, G J, 2002, RNA Interference, *Nature* 418:244-251; Bernstein E et al., 2002, The rest is silence. *RNA* 7:1509-1521; Hutvagner G et al., 2002, RNAi: Nature harbors a double-strand. *Curr. Opin. Genetics & Development* 12: 225-232, 2002, A system for stable expression of short interfering RNAs in mammalian cells. *Science* 296: 550-553; Lee N S, Dohjima T, Bauer G, Li H, Li M-J, Ehsani A, Salvaterra P, and Rossi J. (2002). Expression of small interfering RNAs targeted against HIV-1 rev transcripts in human cells. *Nature Biotechnol.* 20: 500-505; Miyagishi M, and Taira K. (2002). U6-promoter-driven siRNAs with four uridine 3' overhangs efficiently suppress targeted gene expression in mammalian cells. *Nature Biotechnol.* 20: 497-500; Paddison P J, Caudy A A, Bernstein E, Hannon G J, and Conklin D S. (2002). Short hairpin RNAs (shRNAs) induce sequence-specific silencing in mammalian cells. *Genes & Dev.* 16: 948-958; Paul C P, Good P D, Winer I, and Engelke D R. (2002). Effective expression of small interfering RNA in human cells. *Nature Biotechnol.* 20: 505-508; Sui G, Soohoo C, Affar E-B, Gay F, Shi Y, Forester W C, and Shi Y. (2002). A DNA vector-

based RNAi technology to suppress gene expression in mammalian cells. *Proc. Natl. Acad. Sci. USA* 99 (6): 5515-5520; Yu J-Y, DeRuiter S L, and Turner D L. (2002). RNA interference by expression of short-interfering RNAs and hairpin RNAs in mammalian cells. *Proc. Natl. Acad. Sci. USA* 99 (9): 6047-6052).

[0164] In addition to known modulators, additional modulators of markers activity that are useful in the methods of the invention can be identified using two-hybrid screens, conventional biochemical approaches, and cell-based screening techniques, such as screening candidate molecules for an ability to bind to marker or screening for compounds which inhibit marker activity in cell culture.

[0165] This provides a simple in vitro assay system to screen for marker activity modulators. The method may identify agents that directly interact with and modulate the marker, as well as agents that indirectly modulate marker activity by affecting a step in the marker signal transduction pathway.

[0166] Cell-based assays employing cells which express the marker can employ cells which are isolated from mammals and which naturally express the marker. Alternatively, cells which have been genetically engineered to express the marker can be used. Preferably the genetically engineered cells are T-cells.

[0167] Agents which modulate the marker activity by modulating the markergene expression can be identified in cell based screening assays by measuring amounts of the marker protein in the cells in the presence and absence of candidate agents. The marker protein can be detected and measured, for example, by flow cytometry using anti-marker specific monoclonal antibodies. Marker mRNA can also be detected and measured using techniques known in the art, including but not limited to Northern blot, RT-PCR, and array hybridization.

[0168] In accordance with the teachings of the invention, marker inhibitors may be administered to an organism to increase the number of T-cells in the organism. This method may be useful for treating organisms suffering from conditions resulting in a low T-cell population.

[0169] Such conditions include disorders involving unwanted cellular invasion or growth, such as tumor growth or cancer. Marker inhibitors may also be useful when administered in combination with conventional therapeutics to treat T-cell proliferation sensitive disorders.

[0170] For instance, a tumor, which is a T-cell proliferation sensitive disorder, is conventionally treated with a chemotherapeutic agent which functions by killing rapidly dividing cells. The marker inhibitors of the invention when administered in conjunction with a chemotherapeutic agent enhance the tumoricidal effect of the chemotherapeutic agent by stimulating T-cell proliferation to enhance the immunological rejection of the tumor cells.

[0171] In accordance with the teachings of the invention, marker activators (agonists) or expression enhancers may be administered to an organism to decrease the number of T-cells, in particular tumor-infiltrating regulatory T cells, in the organism and thereby decrease deleterious T-cell activity. The methods of the invention may be applied to any organism which contains T-cells that express the marker. This includes, but is not limited to, any mammal and particularly includes humans and mice.

[0172] When methods of the invention are carried out in vivo, the effective amount of the marker modulator used will

vary with the particular modulator being used, the particular condition being treated, the age and physical condition of the subject being treated, the severity of the condition, the duration of the treatment, the nature of the concurrent therapy (if any), the specific route of administration and similar factors within the knowledge and expertise of the health practitioner. For example, an effective amount can depend upon the degree to which an individual has abnormally depressed levels of T cells.

[0173] When administered, the pharmaceutical preparations of the invention are applied in pharmaceutically-acceptable amounts and in pharmaceutically-acceptably compositions.

[0174] Such preparations may routinely contain salt, buffering agents, preservatives, compatible carriers, and optionally other therapeutic agents. When used in medicine, the salts should be pharmaceutically acceptable, but non-pharmaceutically acceptable salts may conveniently be used to prepare pharmaceutically-acceptable salts thereof and are not excluded from the scope of the invention. Such pharmacologically and pharmaceutically-acceptable salts include, but are not limited to those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic, and the like. Also, pharmaceutically-acceptable salts can be prepared as alkaline metal or alkaline earth salts, such as sodium, potassium or calcium salts. Marker modulators may be combined, optionally, with a pharmaceutically-acceptable carrier. The term "pharmaceutically-acceptable carrier" as used herein means one or more compatible solid or liquid filler, diluents or encapsulating substances which are suitable for administration into a human. The term "carrier" denotes an organic or inorganic ingredient, natural or synthetic, with which the active ingredient is combined to facilitate the application. The components of the pharmaceutical compositions also are capable of being co-mingled with the molecules of the present invention, and with each other, in a manner such that there is no interaction which would substantially impair the desired pharmaceutical efficacy.

[0175] The pharmaceutical compositions may contain suitable buffering agents, including: acetic acid in a salt; citric acid in a salt; boric acid in a salt; and phosphoric acid in a salt. The pharmaceutical compositions also may contain, optionally, suitable preservatives, such as: benzalkonium chloride; chlorobutanol; parabens and thimerosal.

[0176] Compositions suitable for parenteral administration conveniently comprise a sterile aqueous preparation of the anti-inflammatory agent, which is preferably isotonic with the blood of the recipient. This aqueous preparation may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents.

[0177] The sterile injectable preparation also may be a sterile injectable solution or suspension in a non-toxic parenterally-acceptable diluent or solvent, for example, as a solution in butane diol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose any bland fixed oil may be employed including synthetic mono- or di-glycerides. In addition, fatty acids such as oleic acid may be used in the preparation of injectables.

[0178] Carrier formulation suitable for oral, subcutaneous, intravenous, intramuscular, etc. administrations can be found in Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa.

[0179] A variety of administration routes are available. The particular mode selected will depend, of course, upon the particular drug selected, the severity of the condition being treated and the dosage required for therapeutic efficacy. The methods of the invention, generally speaking, may be practiced using any mode of administration that is medically acceptable, meaning any mode that produces effective levels of the active compounds without causing clinically unacceptable adverse effects. Such modes of administration include oral, rectal, topical, nasal, interdermal, or parenteral routes.

[0180] The term "parenteral" includes subcutaneous, intravenous, intramuscular, or infusion.

[0181] Intravenous or intramuscular routes are not particularly suitable for long-term therapy and prophylaxis. They could, however, be preferred in emergency situations. Oral administration will be preferred because of the convenience to the patient as well as the dosing schedule. The pharmaceutical compositions may conveniently be presented in unit dosage form and may be prepared by any of the methods well-known in the art of pharmacy. All methods include the step of bringing the active agent into association with a carrier which constitutes one or more accessory ingredients. In general, the compositions are prepared by uniformly and intimately bringing the active agent into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary, shaping the product. Compositions suitable for oral administration may be presented as discrete units, such as capsules, tablets, lozenges, each containing a predetermined amount of the active agent. Other compositions include suspensions in aqueous liquids or non-aqueous liquids such as a syrup, elixir or an emulsion.

[0182] Other delivery systems can include time-release, delayed release or sustained release delivery systems. Such systems can avoid repeated administrations of the active agent, increasing convenience to the subject and the physician. Many types of release delivery systems are available and known to those of ordinary skill in the art. They include polymer base systems such as poly (lactide-glycolide), copolyoxalates, polycaprolactones, polyesteramides, polyorthoesters, polyhydroxybutyric acid, and polyanhydrides.

[0183] Microcapsules of the foregoing polymers containing drugs are described in, for example, U.S. Pat. No. 5,075,109. Delivery systems also include non-polymer systems that are: lipids including sterols such as cholesterol, cholesterol esters and fatty acids or neutral fats such as mono-di- and tri-glycerides; hydrogel release systems; sylvatic systems; peptide based systems; wax coatings; compressed tablets using conventional binders and excipients; partially fused implants; and the like. Specific examples include, but are not limited to: (a) erosional systems in which the anti-inflammatory agent is contained in a form within a matrix such as those described in U.S. Pat. Nos. 4,452,775, 4,667,014, 4,748,034 and 5,239,660 and (b) diffusional systems in which an active component permeates at a controlled rate from a polymer such as described in U.S. Pat. Nos. 3,832,253, and 3,854,480. In addition, pump-based hardware delivery systems can be used, some of which are adapted for implantation.

[0184] Use of a long-term sustained release implant may be particularly suitable for treatment of chronic conditions. Long-term release, are used herein, means that the implant is constructed and arranged to deliver therapeutic levels of the active ingredient for at least 30 days, and preferably 60 days. Long-term sustained release implants are well-known to those of ordinary skill in the art and include some of the release systems described above. While the invention has been described with respect to specific examples including presently preferred modes of carrying out the invention, those skilled in the art will appreciate that there are numerous variations and permutations of the above described systems and techniques that fall within the spirit and scope of the invention as set forth in the appended claims.

[0185] The invention will be illustrated by means of non-limiting examples in reference to the following figures.

[0186] FIG. 1. Purification, functional characterization and expression of immune checkpoints in tumor infiltrating cells.

[0187] (A) Representation of the sorting strategy of Treg cells infiltrating tumor or normal tissue.

[0188] (B) Representative flow cytometry plots showing suppressive activity of Treg cells isolated from tumor (NSCLC or CRC), normal lung and blood of the same patient. 4×10^5 carboxyfluorescein diacetate succinimidyl ester (CFSE)-labeled CD4+ naïve T cells from healthy donors were cocultured with an equal number of Treg cells for 4 days with a CD3-specific mAb and CD1c+CD11c+ dendritic cells. Percentage of proliferating cells are indicated. Data are representative of three independent experiments.

[0189] (C) Z-score normalized RNA-seq expression values of immunecheckpoints genes are represented as a heatmap. Cell populations are reported in the upper part of the graph, while gene names have been assigned to heatmap rows. Hierarchical clustering results are shown as a dendrogram drawn on the left side of the matrix. Colon tissues are indicated as C, lung tissues as L and peripheral blood as B. See also FIG. 6.

[0190] FIG. 2. Differential expression analysis identifies co-regulated genes in tumor infiltrating Treg cells

[0191] Z-score normalized expression values of genes that are preferentially expressed in tumor-infiltrating Tregs (Wilcoxon Mann Whitney test $p < 2.2 \times 10^{-16}$) over the listed cell subsets are represented as boxed plots. Colon tissues are indicated as C, lung tissues as L and peripheral blood as B.

[0192] FIG. 3. Single cell analysis of tumor infiltrating Treg cells

[0193] (A) Schematic representation of the experimental workflow. Experiments were performed on Treg cells infiltrating CRC, NSCLC, or isolated from peripheral blood of healthy donors (PB); five samples were collected for each tissue.

[0194] (B) Percentage of co-expression of signature genes with FOXP3 and IL2RA is depicted.

[0195] (C) Expression levels of the signature genes classified by the percentage of co-expression are represented as box plot.

[0196] (D) Expression distribution (violin plots) in Treg cells infiltrating CRC, NSCLC or PB. Plots representing the ontology classes of receptors, signaling and enzymatic activity, cytokine activity and transcription factors are shown (Wilcoxon Mann Whitney test $p < 0.05$). Gray scale gradient

indicates the percentage of cells expressing each gene in Treg cells isolated from the three compartments.

[0197] (E) Gene expression analysis of tumor Treg signature genes in different tumor types. Expression values are expressed as $\log_2(2^{-\Delta Ct})$.

[0198] FIG. 4. Expression of tumor-infiltrating Treg cells protein signatures in CRC and NSCLC samples.

[0199] (A and B) Representative flow cytometry plots for tumor normal tissue infiltrating Treg cells and peripheral blood Treg cells analyzed for the expression of the indicated proteins.

[0200] FIG. 5. Prognostic value of signature transcripts of tumor infiltrating Treg cells.

[0201] (A) Kaplan-Meier survival curve comparing the high and low expression of the tumor Treg signature transcripts (CCR8, MAGEH1, LAYN) normalized to the CD3G for the CRC ($n=177$) and NSCLC ($n=263$) studies. Univariate analysis confirmed a significant difference in overall survival curve comparing patients with high and low expression. Statistical significance was determined by the log-rank test. (CRC: $p=0.05$ for CCR8, $p=1.48 \times 10^{-3}$ for MAGEH1, $p=2.1 \times 10^{-4}$ for LAYN; NSCLC: $p=0.0125$ for CCR8, $p=0.035$ for MAGEH1, $p=0.0131$ for LAYN) Each table depicts the Kaplan Meier estimates at the specified time points. (B) Expression distributions of CCR8, MAGEH1 and LAYN according to tumor staging at the time of surgery in the cohort of CRC patients. See also FIG. 9.

[0202] FIG. 6 related to FIG. 1. Transcriptome analysis of tumor infiltrating lymphocytes.

[0203] (A) Representation of the sorting strategy of Treg cells infiltrating colorectal tumor or normal tissue.

[0204] (B) RNA-seq expression values (normalized counts) of FOXP3, TBX21 and RORC in CD4+ Th1, Th17 and Treg cells from CRC (C), NSCLC (L) or peripheral blood (PB) of healthy donors.

[0205] (C) RNA-seq normalized counts data for selected immune checkpoints and their ligands are shown as histogram plot. Cell population names are reported in the lower part of each graph, while gene names are shown in the upper part.

[0206] FIG. 7 related to FIG. 3. Single-cell analysis of tumor infiltrating Treg cells.

[0207] Assessment of CD4+ Treg, Th1, Th17, Th2, CD8+ T cells and B cell markers expression (percentage of expressing cells) in single Treg cells purified from NSCLC and CRC.

[0208] FIG. 8 related to FIG. 4. Comparison of BATF expression in CD4+ Treg vs Th17 cells.

[0209] BATF expression levels (RNA-seq normalized counts data) in CD4+ Treg and Th17 subsets isolated from tumor tissue or peripheral blood

[0210] FIG. 9 related to FIG. 5. Expression levels of tumour-infiltrating Treg signature genes.

[0211] RNA-seq normalized counts data of three tumour-infiltrating Treg signature genes (MAGEH1 (panel A), LAYN (panel B) and CCR8 (panel C)) across listed cell populations.

[0212] FIG. 10. Results of RT-PCR analysis done on cDNA from Tumor infiltrating Treg cells (L=NSCLC, C=CRC, -ntc) with specific primers able to discriminate the different transcript isoforms annotated for SIRPG.

DETAILED DESCRIPTION OF THE
INVENTION

Experimental Procedures

Human Primary Tissues

[0213] Primary human lung or colorectal tumors and non-neoplastic counterparts were obtained respectively from fifteen and fourteen patients who underwent surgery for therapeutic purposes at Fondazione IRCCS Ca' Granda, Policlinico or San Gerardo Hospitals (Italy).

[0214] Records were available for all cases and included patients' age at diagnosis, gender, smoking habit (for lung cancer patients), clinicopathological staging (Sobin et al., 2009), tumor histotype and grade (Table II). No patient received palliative surgery or neoadjuvant chemo- and/or radiotherapy. Informed consent was obtained from all patients, and the study was approved by the Institutional Review Board of the Fondazione IRCCS Ca' Granda (approval n. 30/2014).

[0215] Non-small-cell lung cancer (NSCLC) were cut into pieces and single-cell suspensions were prepared by using the Tumor Dissociation Kit, human and the gentleMACSTM Dissociator (Miltenyi Biotech cat. 130-095-929) according to the accompanying standard protocol. Cell suspensions were then isolated by ficoll-hypaque density-gradient centrifugation (Amersham Bioscience). Colorectal cancer (CRC) specimens were cut into pieces and incubated in DTT 0.1 mM (Sigma-Aldrich) for 10 min, then extensively washed in HBSS (Thermo Scientific) and incubated in 1 mM EDTA (Sigma-Aldrich) for 50 min at 37° C. in the presence of 5% CO₂. They were then washed and incubated in type D collagenase solution 0.5 mg/mL (Roche Diagnostic) for 4 h at 37° C. Supernatants containing tumor infiltrating lymphocytes were filtered through 100 µm cell strainer, centrifuged and fractionated 1800×g for 30 min at 4° C. on a four-step gradient consisting of 100%, 60%, and 40% and 30% Percoll solutions (Pharmacia). The T cell fraction was recovered from the inter-face between the 60% and 40% Percoll layers.

[0216] CD4 T cell subsets were purified by FACS sorting using the following fluorochrome conjugated antibodies: anti-CD4 APC/Cy7 (Biolegend clone OKT4), anti-CD27 Pacific Blue (Biolegend, clone M-T271), anti-IL7R PE (Miltenyi, clone MB15-18C9), anti-CD25 PE/Cy7 (eBioscience, clone BC96), anti-CXCR3 PE/Cy5 (BD, clone 1C6/ CXCR3), anti-CCR6 APC (Biolegend, clone G034E3) and anti-CCR5 FITC (Biolegend, clone j418F1) using a FACSAria II (BD).

Flow Cytometry

[0217] To validate surface marker expression cells were directly stained with the following fluorochrome-conjugated antibodies and analyzed by flow cytometry: anti-CD4 (Biolegend, clone OKT4); anti-PD-L2 (Biolegend, Clone CL24F.10C12); anti-CD127 (eBioscience, clone RDR5); anti-BATF (eBioscience, clone MBM7C7), anti-GITR (eBioscience, clone eBIOAITR), anti-CD25 (Miltenyi, clone 4E3) and anti 4-1BB (eBioscience clone 4B4) anti CCR8(Biolegend clone L263G8) anti CD30 (eBioscience, clone Ber-H2) anti PD-L1 (Biolegend clone 29E.2A3) anti TIGIT (eBioscience, clone MBSA43) anti IL1 R2 (R and D

clone 34141) IL21R (Biolegend clone 2G1-K12) anti OX40 (Biolegend clone Ber-ACT35). Intracellular staining was performed using eBioscience Foxp3 staining kit according to the manufacturer's protocol (eBioscience cat 00-5523-00). Briefly cells were harvested and fixed for 30 min in fixation/permeabilization buffer at 4° C., and then stained with anti-FOXP3 antibody (eBioscience, clone 236A/E7) and anti-BATF (eBioscience clone MBM7C7) in permeabilisation buffer for 30 min at 4° C. Cells were then washed two times, resuspended in FACS washing buffer and analyzed by flow cytometry.

Suppression Assay.

[0218] 4×10⁴ carboxyfluorescein diacetate succinimidyl ester (CFSE)-labeled (1 µM) responders Naive⁺ T cells from healthy donors were cocultured with different E/T ratio with unlabeled CD127⁻CD25^{low}CD4⁺ T cells sorted from TILs or PBMCs of patients with CRC or NSCLC, using FACS Aria II (BD Biosciences), in the presence of CD11c⁺CD1c⁺ dendritic cells as antigen-presenting cells and 0.5 mg/ml anti-CD3 (OKT3) mAb. Proliferation of CFSE-labeled cells was assessed by flow cytometry after 96 hr culture. RNA Isolation and RNA Sequencing

[0219] RNA from tumor-infiltrating lymphocytes was isolated using mirVana Isolation Kit.

[0220] Residual contaminating genomic DNA was removed from the total RNA fraction using Turbo DNA-free (Thermo Fisher). The RNA yields were quantified using the QuantiFluor RNA System (Promega) and the RNA quality was assessed by the Agilent 2100 Bioanalyzer (Agilent). Libraries for Illumina sequencing were constructed from 50 ng of total RNA with the Illumina TruSeq RNA Sample Preparation Kit v2 (Set A). The generated libraries were loaded on to the cBot (Illumina) for clustering on a HiSeq Flow Cell v3. The flow cell was then sequenced using a HiSeq 2500 in High Output mode (Illumina). A paired-end (2×125) run was performed.

RNA-Seq Data Analysis

[0221] Raw .fastq files were analyzed using FastQC v0.11.3, and adapter removal was performed using cutadapt 1.8. Cutadapt is run both for reverse and forward sequences with default parameters [-anywhere <adapter1>-anywhere <adapter2>-overlap 10-times 2-mask-adapter]. Adapter sequences used for libraries preparation are

Adapter1:

(SEQ ID NO: 710)
AGATCGGAAGAGCACACGTCTGAAGTCACNNNNNATCTCGTATG

CCGTCTTCTGCTTG

Adapter2:

(SEQ ID NO: 711)
AGATCGGAAGAGCGTCGTAGGGAAAGAGTGTAGATCTCGGTGGTCGCC

GTATCATT

[0222] Trimming was performed on raw reads using Trimmomatic (Bolger et al., 2014): standard parameters for phred33 encoding were used: ILLUMINA_CLIP (LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15), MINLEN parameter was set to 50.

[0223] Mapping and quantification: reads mapping to the reference genome (GRCh38) was performed on quality-checked and trimmed reads using STAR 2.4.1c: [STAR-genomeDir <index_star>-runThreadN <cpu_number>-readFilesIn <trimmed>_R1.fastq.gz<trimmed>_R2_P.fastq.gz-readFilesCommand zcat]. The reference annotation is Ensembl v80. The overlap of reads with annotation features found in the reference .gtf was calculated using HT-seq v0.6.1. The output computed for each sample (raw read counts) was then used as input for DESeq2 analysis. Raw counts were normalized using DESeq2's function 'rlog', and normalized counts were used to perform and visualize Principal Component Analysis (PCA) results (using DESeq2's 'plotPCA' function).

[0224] Differential expression analysis: differential expression analyses of tumor-infiltrating CD4+ Treg/Th1/Th17 subsets vs. CD4+ Treg/Th1/Th17 from PBMC were performed using DESeq2. Upregulated/downregulated genes were selected for subsequent analyses if their expression values were found to exceed the threshold of 0.05 FDR (Benjamini-Hochberg correction).

Capturing of Single Cells, Preparation of cDNA and Single-Cell PCR

[0225] Treg cells from 5 CRC and 5 NSCLC specimens were isolated as previously described (See also Table II). Single cells were captured on a microfluidic chip on the C1 System (Fluidigm) and whole-transcriptome amplified. cDNA was prepared on chip using the SMARTer Ultra Low RNA kit (Clontech). Cells were loaded onto the chip at a concentration of 3-5E5 cells/ml, stained for viability (LIVE/DEAD cell viability assay; Thermo Fisher) and imaged by phase-contrast and fluorescence microscopy to assess the number and viability of cells per capture site. Only single, live cells were included in the analysis. For qPCR experiments, harvested cDNA was pre-amplified using a 0.2 \times pool of primers prepared from the same gene expression assays to be used for qPCR.

[0226] Pre-amplification allows for multiplex sequence-specific amplification 78 targets. In detail, a 1.25 μ l aliquot of single cell cDNA was pre-amplified in a final volume of 5 μ l using 1 μ l of PreAmp Master Mix (Fluidigm) and 1.25 μ l pooled TaqMan assay mix (0.2 \times). cDNA went through amplification by denaturing at 95° C. for 15 s, and annealing and amplification at 60° C. for 4 min for 20 cycles. After cycling, pre-amplified cDNA was diluted 1:5 by adding μ l TE Buffer to the final 5 μ l reaction volume for a total volume of 25 μ l. Single-cell gene expression experiments were performed using the 96 \times 96 quantitative PCR (qPCR) DynamicArray microfluidic chips (Fluidigm). A 2.25 μ l aliquot of amplified cDNA was mixed with 2.5 μ l of TaqMan Fast Advanced Master Mix (Thermo Fisher) and 0.25 μ l of Fluidigm's "sample loading agent," then inserted into one of the chip "sample" inlets. A 2.5 μ l aliquot of each 20 \times TaqMan assay was mixed with 2.5 μ l of Fluidigm's "assay loading agent" and individually inserted into one of the chip "assay" inlets. Samples and probes were loaded into 96 \times 96 chips using an IFC Controller HX (Fluidigm), then transferred to a BioMark real-time PCR reader (Fluidigm) following manufacturer's instructions. A list of the 78 TaqMan assays used in this study is provided below.

TABLE V

Related to FIG. 3.
List of TaqMan Probes and assay number
used in RT-qPCR single-cell experiments
Taqman Assays Numbers

Gene Name	Assay Number	Gene Name	Assay Number
BCL2L1	Hs00235329_m1	ACP5	Hs00356261_m1
EOS	Hs00223842_m1	BATF	Hs00232390_m1
AHCYL1	Hs00198382_m1	SLC35F2	Hs00233850_m1
NFE2L3	Hs00852569_m1	LAX1	Hs00214948_m1
IL12RB2	Hs00155486_m1	CCR8	Hs00174764_m1
CD177	Hs00360669_m1	ADPRH	Hs00153890_m1
OX40	HS00937194_g1	IKZF2	Hs00212361_m1
METTL7A	Hs00204042_m1	C5F2RB	Hs00166144_m1
ENTPD1	HS00969339_m1	NDFIP2	Hs00324851_m1
NFAT5	Hs00232437_m1	CADM1	Hs00942508_m1
CT9C	Hs00175188_m1	ICOS	Hs00359999_m1
SSH1	Hs00368014_m1	COL9A2	Hs00156712_m1
TMEM184C	Hs00217311_m1	LTA	Hs00236874_m1
HTATIP2	Hs03091727_m1	MAGEH1	Hs00371974_s1
HSDL2	Hs00953689_m1	IL21R	Hs00222310_m1
FOXP3	Hs01085834_m1	S6TR3	Hs01066399_m1
IL2RA	Hs00907778_m1	RNF145	Hs01066399_m1
LIMA1	Hs01033646_m1	LAPTM4B	Hs00363282_m1
NAB1	Hs00428619_m1	GRSF1	Hs00909877_m1
ACSL4	Hs00244871_m1	ANKRD10	Hs00214321_m1
ERI1	Hs00405251_m1	NPTN	Hs01033353_m1
FKEP1A	Hs00356621_g1	HS3ST3B1	Hs00797512_s1
LEPROT	Hs00956627_s1	TRAFF3	Hs00936781_m1
NETO2	Hs00983152_m1	RRAGB	Hs01099787_m1
VDR	Hs00172113_m1	ZBTB3S	Hs00257315_s1
CSF1	Hs00174164_m1	TIGIT	Hs00545087_m1
GITR	Hs00188346_m1	TFRC	Hs00951083_m1
IL1R2	Hs01030384_m1	JAK1	Hs01026982_m1
IL1R1	Hs00991010_m1	KSR1	Hs00300134_m1
LAYN	Hs00379511_m1	ZNF202	Hs00411965_m1
THADA	Hs00736554_m1	PTPRJ	Hs01119326_m1
CTLA4	Hs00175480_m1	CHRNA6	Hs02563909_s1
CHST2	Hs01921028_s1	IL2RB	Hs01081597_m1
CHST7	Hs00219871_m1	TBX21	Hs00203436_m1
LRBA	Hs01032231_m1	RORC	Hs01076112_m1
ETV7	Hs00903229_m1	CXCR5	Hs00540548_s1
LY75	Hs00982383_m1	CD8A	Hs00233520_m1
ADAT2	Hs00699339_m1	CD8B	Hs00174762_m1
GCNT1	Hs00155243_m1	PTGDR2	Hs00173717_m1
CASP1	Hs00354836_m1	CD19	Hs01047410_g1

[0227] Single-cell data analysis: The Quality Threshold in the BioMark™ Analysis software is a qualitative tool designed to measure the "quality" of each amplification curve. Basically, each amplification curve is compared to an ideal exponential curve and as the quality score approaches 1 the closer it is to ideal. The further the curve is from ideal, its quality score approaches 0. The default cutoff of 0.65 is an arbitrary value set by Fluidigm. Any curve above 0.65 passes. Any curve below, fails. Baseline correction was set on Linear (Derivative)[default]. Ct Threshold Method was set on Auto (Detectors). This method independently calculates a threshold for each detector on a chip. For clustering and downstream analysis, raw Cts have been converted to Log 2Exp by using a Limit of Detection (LOD) of 35, which corresponds to the last PCR cycle. Co-expression analysis has been performed by considering both CRC and NSCLC samples on those genes for which both FOXP3 and IL2RA were co-expressed at least to 2%. Gene's levels above the background were depicted as violin plots after log 2 scale transformation by ggplot2 (v. 2.1.10). The violin color gradient is the percentage of cells that are expressing the gene of interest and the upper bound of the color scale is the maximum percentage of cells that express a gene of the whole geneset.

[0228] Procedure for the removal of transcripts whose expression values are affected by the ‘dropout’ effect. Single-cell qPCR data are inherently noisy, and due the limitations of current technologies the expression patterns of a certain number of genes may be affected by the ‘dropout effect’. Inventors performed a gene selection procedure in order to take into account this ‘dropout’ effect and discard those genes whose expression values cannot be reliably used in a binary comparison (tumor-peripheral vs blood). Inventors fitted a number of parametric distributions to the ratios of detected genes on the total number of tumor cells (both NSCLC and CRC) and selected the reciprocal inverse Gaussian continuous random variable as best fit.

[0229] Inventors then calculated the median value of the fitted distribution and discarded those genes whose detection ratio is less than this threshold value (at least 8.4% of detection). Inventors reasoned that these genes are more likely to be affected by the ‘dropout’ effect. With this threshold inventors selected 45 genes for which a non-parametric T-test (Wilcoxon Mann Whitney test $p < 0.05$) has been performed (by comparing tumor vs. peripheral blood samples).

Meta Analysis Kaplan-Meier and Stage Correlation

[0230] Statistical analysis was performed by using the R survival package (Therneau T. 2013). Survival times were calculated as the number of days from initial pathological diagnosis to death, or the number of days from initial pathological diagnosis to the last time the patient was reported to be alive. The Kaplan-Meier (KM) was used to compare the high and low expression levels of the tumor-Treg cell signature transcripts in either CRC (GSE17536) and NSCLC (GSE41271) patients. For both studies annotation was normalized to four tumor stages (1,2,3,4). For study GSE41271 five patients were excluded due to incomplete or inaccurate annotation (GSM1012883, GSM1012884, GSM1012885, GSM1013100, GSM1012888), retaining a total of two hundred and sixty three patients. Patients from both studies were labeled as ‘High’ ‘Low’ whether or not their relative expression values exceeded a decision boundary (mean of the samples). Inventors define \bar{x}_{ij} to denote the relative expression of the gene i for the n samples of the study normalized to the CD3 level:

$$\bar{x}_{ij} = \frac{x_{ij}}{x_{CD3G,j}}; \quad i = (CCR8, MAGEH1, LAYN) \quad j = 1, 2, \dots, n \text{ samples}$$

[0231] To classify a patient, a threshold on the \bar{x}_{ij} is required and defined as

$$T_{(Upper, Lower)} = \text{median}(\bar{x}_{ij}) \pm \frac{\sigma(\bar{x}_{ij})}{10}$$

where $T_{(Upper, Lower)}$ represent the upper and lower extreme of the decision boundary:

$$\begin{cases} \bar{x}_{ij} > T_{Upper, High} \\ \bar{x}_{ij} < T_{Lower, Low} \\ T_{Upper} \leq \bar{x}_{ij} \leq T_{Lower} \text{ excluded} \end{cases}$$

[0232] Inventors examined the prognostic significance of tumor Treg cells transcripts by using log-rank statistics; a p-value of less than 0.05 was considered statistically significant. Since the log-rank test resulted in a p-value of less than 0.05, a post stage comparison by means of box plot representation was performed in order to evaluate the correlation degree between the expression level of the transcripts and tumor stages in the cohort of CRC patients. The annotation was normalized to four tumor stages (1,2,3,4).

ACCESSION NUMBERS

[0233] The accession numbers for the present data are as follows: ENA: PRJEB11844 for RNA-seq tumor and tissue infiltrating lymphocytes; ArrayExpress: E-MTAB-2319 for RNA-seq human lymphocytes datasets; ArrayExpress: E-MTAB-513 for Illumina Human BodyMap 2.0 project; GEO: GSE50760 for RNA-seq datasets CRC; GEO: GSE40419 for RNA-seq datasets NSCLC; GEO: GSE17536 for CRC expression profiling by array; and GEO: GSE41271 for NSCLC expression profiling by array.

Prediction of Surface-Exposed and Membrane-Associated Proteins

[0234] The probability of surface exposure of the proteins encoded by the genes of interest was determined by a combination of four different cell localization prediction algorithms: Yloc (Briesemeister et al, 2010), TMHMM (<http://www.cbs.dtu.dk/services/TMHMM/>), SignalP (<http://www.cbs.dtu.dk/services/SignalP/>) and Phobius (KAI et al., 2007). In particular Yloc is a interpretable system offering multiple predictive models in animal version; inventors used both YLoc-LowRes predicting into 4 location (nucleus, cytoplasm, mitochondrion, secretory pathway) and Yloc-HighRes predicting into 9 locations (extracellular space, plasma membrane, nucleus, cytoplasm, mitochondrion, endoplasmic reticulum, peroxisome, Golgi apparatus, and lysosome).

[0235] TMHMM and SignalP were developed by the bioinformatic unit of the technical University of Denmark for the prediction of transmembrane helices and the presence and location of signal peptide cleavage sites in amino acid sequences, respectively. Phobius is a combined transmembrane topology and signal peptide predictor.

RT-PCR Analysis of Transcript Isoforms Expressed by Tumor-Infiltrating Regulatory T Cells (Treg Cells)

[0236] Total RNA was extracted from tumor Treg cells (NSCLC or CRC) using mIRCURY RNA isolation kit (Exiqon) and 1 μ g was reverse transcribed with iScript reverse transcription supermix (BIORAD). Afterwards, 25 ng of cDNA were amplified with DreamTaq Green PCR Master Mix (ThermoScientific) using multiple gene-specific primers able to discriminate the different isoforms. PCR products were run on agarose gel. The expression of specific transcripts was assessed based on the expected band size.

Results

Tumor Infiltrating Tregs Cells Upregulate Immune Checkpoints and are Highly Suppressive

[0237] To assess the gene expression landscape of tumor infiltrating CD4 $^{+}$ T cells, the inventors isolated different CD4 $^{+}$ lymphocytes subsets from two different tumors,

NSCLC and CRC, from the adjacent normal tissues, and from peripheral blood samples. From all these tissues, the inventors purified by flow cytometry (FIGS. 1A and 6A and 6B) CD4⁺ Treg (36 samples from 18 individuals), Th1 (30 samples from 21 individuals) and Th17 (22 samples from 14 individuals) cells (Table I and Table II).

TABLE I
Purification and RNA-Sequencing of Human Primary Lymphocyte Subsets

Tissue	Subset	Sorting Phenotype	Number of Samples	Mapped Reads (M)
NSCLC	CD4 ⁺ Treg	CD4 ⁺ CD127 ⁻ CD25 ⁺	8	587
	CD4 ⁺ Th1	CD4 ⁺ CXCR3 ⁺ CCR6 ⁻	8	409
	CD4 ⁺ Th17	CD4 ⁺ CCR6 ⁺ CXCR3 ⁻	6	206
CRC	CD4 ⁺ Treg	CD4 ⁺ CD127 ⁻ CD25 ⁺	7	488
	CD4 ⁺ Th1	CD4 ⁺ CXCR3 ⁺ CCR6 ⁻	5	266
	CD4 ⁺ Th17	CD4 ⁺ CCR6 ⁺ CXCR3 ⁻	5	308

TABLE 1-continued

Purification and RNA-Sequencing of Human Primary Lymphocyte Subsets

Tissue	Subset	Sorting Phenotype	Number of Samples	Mapped Reads (M)
Lung (normal tissue)	CD4 ⁺ Treg	CD4 ⁺ CD127 ⁻ CD25 ⁺	1 (pool of 6)	73
	CD4 ⁺ Th1	CD4 ⁺ CXCR3 ⁺ CCR6 ⁻	1 (pool of 6)	76
Colon (normal tissue)	CD4 ⁺ Treg	CD4 ⁺ CD127 ⁻ CD25 ⁺	7	404
	CD4 ⁺ Th1	CD4 ⁺ CXCR3 ⁺ CCR6 ⁻	6	352
	CD4 ⁺ Th17	CD4 ⁺ CCR6 ⁺ CXCR3 ⁻	6	284
PB (healthy donor)	CD4 ⁺ Treg	CD4 ⁺ CD127 ⁻ CD25 ⁺	8	259
	CD4 ⁺ Th1	CD4 ⁺ CXCR3 ⁺ CCR6 ⁻	5	70
	CD4 ⁺ Th17	CD4 ⁺ CCR6 ⁺ CXCR3 ⁻	5	77

For each cell subsets profiled by RNA-seqencing tissue of origin, surface marker combinations used for sorting, number of profiled samples, as well as number of mapped sequencing reads are indicated. M, million; CRC, colorectal cancer; NSCLC, non-small cell lung cancer; PB, peripheral blood.

TABLE II

Table II related to Table I. Patients information and histological analysis.

For each cell subset profiled by RNA-seqencing, patient records are shown including: age at diagnosis, gender, smoking habit (for lung cancer patients), clinicopathological staging (TNM classification) tumor histotype and grade. For Treg cell isolated for qPCR experiment the same information are available, including also the number of live cells captured from each tumor and available for single-cell analysis.

NSCLC PATIENTS LIST (RNA SEQUENCING)	(T)Th1	(T)Th17	(T)Treg	(H)Th1	(H)Th17	(H)Treg	SMOKE HABIT	STATUS	GENDER
PATIENT1			SQ_0342				PREVIOUS SMOKER >15 y	ALIVE	M
PATIENT2			SQ_0339				PREVIOUS SMOKER <15 y	ALIVE	M
PATIENT3	SQ_0365	SQ_0375					PREVIOUS SMOKER <15 y	ALIVE	M
PATIENT4	SQ_0366	SQ_0374	SQ_0341				PREVIOUS SMOKER >15 y	ALIVE	M
PATIENT5	SQ_0364	SQ_0373		SQ_0350		SQ_0351	SMOKER	DEAD	M
PATIENT6	SQ_0358		SQ_0336	SQ_0350		SQ_0351	PREVIOUS SMOKER <15 y	ALIVE	M
PATIENT7	SQ_0363	SQ_0376	SQ_0334	SQ_0350		SQ_0351	PREVIOUS SMOKER <15 y	ALIVE	M
PATIENT8	SQ_0357		SQ_0337	SQ_0350		SQ_0351	PREVIOUS SMOKER <15 y	ALIVE WITH RELAPSE	M
PATIENT9	SQ_0404	SQ_0408	SQ_0398	SQ_0350		SQ_0351	SMOKER <15 y	ALIVE	F
PATIENT10	SQ_0403	SQ_0407	SQ_0396	SQ_0350		SQ_0351	PREVIOUS SMOKER >15 y	ALIVE	F

NSCLC PATIENTS LIST (RNA SEQUENCING)	AGE(y)	HISTO-TYPE MAJOR	ADCA SUBTYPE (PRE-DOMINANT)	GRADE	pTNM: T	pTNM: N	pTNM: M	STAGE
PATIENT1	84	SCC		G3	2b	0	0	IIA
PATIENT2	83	SCC		G3	2a	0	0	IB
PATIENT3	72	SCC		G3	2	2	0	IIIA
PATIENT4	79	SCC		G3	2a	0	0	IB

TABLE II-continued

Table II related to Table I. Patients information and histological analysis.

For each cell subset profiled by RNA-sequencing, patient records are shown including: age at diagnosis, gender, smoking habit (for lung cancer patients), clinicopathological staging (TNM classification) tumor histotype and grade. For Treg cell isolated for qPCR experiment the same information are available, including also the number of live cells captured from each tumor and available for single-cell analysis.

PATIENT5	66	SCC	G3	3	2	0	IIIA
PATIENT6	71	SCC	G3	4	1	0	IIIA
PATIENT7	78	SCC	G3	2b	1	0	IB
PATIENT8	77	ADCA	SOLID	G3	2	2	0
PATIENT9	69	ADCA	SOLID	G3	1a	0	IA
PATIENT10	77	ADCA	ACINAR	G3	1a	0	IA
NSCLC = Non Small Cell Lung Cancer ADC = Adenocarcinoma SCC = Squamous Cell Carcinoma (T) = Tumor Sample (H) = Healthy Tissue							

TUMOR INFILTRATING TREG FROM NSCLC (SINGLE CELL qPCR)	SMOKE HABIT	STATUS	GENDER	AGE(y)	HISTO-TYPE MAJOR	ADCA SUBTYPE PREDOMINANT
PATIENT1	NEVER SMOKER	ALIVE	F	65	ADCA	ACINAR and PAPILLARY
PATIENT2	PREVIOUS SMOKER <15 y	ALIVE	M	62	ADCA	SOLID
PATIENT3	NEVER SMOKER	ALIVE	F	63	ADCA	ACINAR
PATIENT4	SMOKER	ALIVE	M	66	SCC	
PATIENT5	SMOKER	ALIVE	M	68	SCC	

TUMOR INFILTRATING TREG FROM NSCLC (SINGLE CELL qPCR)	GRADE	pTNM: T	pTNM: N	pTNM: M	STAGE	CAPTURED SINGLE CELLS
PATIENT1	G2	2a	0	0	IB	71
PATIENT2	G2	1b	0	0	IA	61
PATIENT3	G1	1a	0	0	IA	44
PATIENT4	G2	2a	0	0	IB	55
PATIENT5	G3	1b	0	0	IA	55
NSCLC = Non Small Cell Lung Cancer ADC = Adenocarcinoma SCC = Squamous Cell Carcinoma (T) = Tumor Sample (H) = Healthy Tissue						

CRC PATIENTS LIST (RNA SEQUENCING)	(T) Th1	(T) Th17	(T) Treg	(H) Th1	(H) Th17	(H) Treg	GENDER
PATIENT1			SQ_0389	SQ_0386	SQ_0387	SQ_0388	M
PATIENT2	SQ_0427	SQ_0434				SQ_0418	F
PATIENT3	SQ_0423	SQ_0436	SQ_0411				M
PATIENT4	SQ_0426	SQ_0437	SQ_0413	SQ_0428	SQ_0439	SQ_0417	M
PATIENT5	SQ_0425		SQ_0412	SQ_0429	SQ_0441	SQ_0422	M
PATIENT6	SQ_0424		SQ_0415	SQ_0431	SQ_0442	SQ_0421	M
PATIENT7		SQ_0435	SQ_0416	SQ_0432	SQ_0438	SQ_0420	F
PATIENT8			SQ_0414				F
PATIENT9		SQ_0433		SQ_0430	SQ_0440	SQ_0419	M

CRC PATIENTS LIST (RNA SEQUENCING)	AGE(y)	HISTO-TYPE MAJOR	GRADE	pTNM: T	pTNM: N	pTNM: M	STAGE
PATIENT1	76	ADC	G2	3	1A	0	IIIB
PATIENT2	68	ADC	G2	3	0	0	IIA
PATIENT3	80	ADC	G2	4B	1B	0	IIIB

TABLE II-continued

Table II related to Table I. Patients information and histological analysis.

For each cell subset profiled by RNA-sequencing, patient records are shown including: age at diagnosis, gender, smoking habit (for lung cancer patients), clinicopathological staging (TNM classification) tumor histotype and grade. For Treg cell isolated for qPCR experiment the same information are available, including also the number of live cells captured from each tumor and available for single-cell analysis.

PATIENT4	79	ADC	G2	3	1A	0	IIIB
PATIENT5	78	ADC	G2	3	0	0	IIA
PATIENT6	69	MUC	—	3	1B	0	IIIB
		ADC					
PATIENT7	84	ADC	G2	4B	0	0	IIC
PATIENT8	75	MUC	—	3	1C	0	IIIB
		ADC					

ADC G2 2
 ADC = Adenocarcinoma
 MUC ADC = Mucinous Adenocarcinoma
 CRIB ADC = Cribriform Adenocarcinoma
 (T) = Subsets purified from Tumor Sample
 (H) = Subsets purified from Healthy Tissue

TUMOR INFILTRATING TREG FROM CRC (SINGLE CELL qPCR)	GENDER	AGE(y)	HISTO- TYPE MAJOR	GRADE	pTNM: T
PATIENT1	M	64	ADC	2	3
PATIENT2	M	59	CRIB	—	3
			ADC		
PATIENT3	F	75	MUC	—	4A
			ADC		
PATIENT4	M	71	ADC	1	3
PATIENT5	M	64	ADC	2	3

TUMOR INFILTRATING TREG FROM CRC (SINGLE CELL qPCR)	pTNM: N	pTNM: M	STAGE	CAPTURED SINGLE CELLS
PATIENT1	0	0	IIA	62
PATIENT2	0	0	IIA	66
PATIENT3	2B	0	IIIC	65
PATIENT4	0	0	IIA	63
PATIENT5	0	0	IIA	64

ADC = Adenocarcinoma
 MUC ADC = Mucinous Adenocarcinoma
 CRIB ADC = Cribrous Adenocarcinoma
 (T) = Subsets purified from Tumor Sample
 (H) = Subsets purified from Healthy Tissue

CRC: colorectal cancer;
 NSCLC: non-small cell lung cancer;
 (T): Tumor Sample;
 (H): Healthy Tissue;
 ADC: Adenocarcinoma;
 SCC: Squamous Cell Carcinoma;
 MUC ADC: Mucinous Adenocarcinoma

[0238] To assess Treg cell function, inventors tested their suppressor activity and showed that Treg cells infiltrating either type of tumor tissues have a remarkably stronger suppressive activity *in vitro* compared to Treg cells isolated from the adjacent normal tissue and peripheral blood of the same patients (FIG. 1B).

[0239] The polyadenylated RNA fraction extracted from the sorted CD4+ Treg, Th1, and Th17 cells was then analyzed by pair-end RNA sequencing obtaining about 4 billion mapped “reads” (Table 1). First, inventors interrogated RNA-sequencing data of CD4+ T cells infiltrating

both CRC and NSCLC and their matched normal tissues, to quantitate mRNA expression of known immune checkpoints and their ligands. Second, inventors analyzed RNA-seq data of CRC and NSCLC, as well as of normal colon and lung samples.

[0240] Inventors found that several immune checkpoints and their ligands transcripts were strikingly upregulated in tumor infiltrating Treg cells compared to both normal tissue and peripheral blood-derived Treg cells, as well as to T and B lymphocyte subsets purified from peripheral blood mono-nuclear cells (PBMCs) (FIGS. 10C and 60 and Table III).

GENE NAME	Treg_Tumor_Infiltrating_CRC	Treg_Tumor_Infiltrating_NSCLC	Treg_Tissue_Infiltrating_Colon	Treg_Tissue_Infiltrating_Lung	Treg_healthy_Peripheral_Blood
ADORA2A	14.69	24.06	17.97	44.84	18.52
BTLA	554.04	742.11	389.51	208.76	108.2
BTLN2 (BTLN2)	0	0.14	0.29	0	0.75
C10orf54 (VISTA)	779.38	872.36	555.47	1405.63	1111.37
CD160	58.39	38.24	51.87	34.54	36.55
CD200	268.39	283.21	282.05	104.64	99.59
CD200R1	95.89	136.08	81.36	349.99	59.03
CD244	34.46	31.21	29.59	128.35	47.8
CD27	710.13	1068.55	583.58	496.38	468.93
CD274 (PD-L1)	1050.94	645.66	576.59	390.71	120.19
CD276	16.85	72.3	10.44	65.98	3.61
CD28	4770.41	4585.17	5446.29	3687.01	5179.32
CD40	112.04	161.29	80.64	93.3	34.71
CD40LG	135.51	143.07	360.09	418.55	104.22
CD44	13049.36	8518.98	13513.69	19851	16013.71
CD48	346.61	489.78	494.58	594.83	1523.63
CD70	426.35	269.38	318.97	249.48	101.67
CD80	632.12	483.34	318.48	269.06	114.41
CD86	29.52	78.86	52.72	278.86	3.87
CTLA4	6798.82	10378.3	4810.74	5340.06	4806.23
HAVCR2 (TIM-3)	577.57	633.27	265.84	487.62	49.81
HHLA2	3.41	3.66	4.47	9.28	12.7
ICOS	6830.94	7339.08	4119.2	5211.71	3398.28
ICOSLG (B7RP1)	58.02	8.86	59.13	33.5	76.5
IDO1	3.86	83.81	9.51	5.15	2.36
IDO2	0.22	2.25	1.41	5.15	1.58
KIR3DL1 (KIR)	0.38	0.43	0.28	4.64	0.9
LAG3	705.14	1956.22	2181.52	1505.63	127.02
LAIR1	277.06	194.09	551.94	874.72	346.22
LGALS9 (Galectin-9)	1175.81	1530.47	1160.89	1593.26	592.56
NRP1	7.38	36.24	8.89	106.7	8.59
PDCD1LG2 (PD-L2)	214.51	223.04	61.89	25.77	12.12
PDCD1 (PD1)	467.22	496.56	405.01	676.27	111.26
TIGIT	14821.45	14747.79	10986.74	4901.41	4611.14
TMIGD2	28.38	16.64	78.3	75.77	71.27
TNFRSF14 (HVEM)	2230.85	2677.32	2297.43	2675.7	2274.82
TNFRSF18 (GITR)	4038.86	4078.14	2871.78	3071.57	333.36
TNFRSF25	5236.86	4188.61	4986.56	5111.71	3587.58
TNFRSF4 (OX40)	4222.16	4642.56	2873.16	2992.18	400.56
TNFRSF8 (CD30)	155.59	430.23	115.57	208.24	30.89
TNFRSF9 (4-1BB)	2921.72	3128.82	898.69	1739.13	502.86
TNFSF14 (LIGHT)	148.57	183.77	223.49	421.12	105.12
TNFSF15	1.58	3.75	0.89	25.77	1.23
TNFSF18	0.4	1.11	0.53	0	0.45
TNFSF4 (OX40LG)	110.82	136.82	100.95	98.97	16.33
TNFSF9 (CD137L)	26.79	19.48	19.72	29.9	7.41
VTCN1 (B7-H4)	1.12	4.49	1.48	1.55	2.65

[0241] RNA-seq normalized counts data for selected immune checkpoints genes and their ligands in all the subsets analyzed.

[0242] These findings highlight the specific expression patterns of immune checkpoints and their ligands in tumor infiltrating Treg and effector cells and suggest that their functional relevance should be investigated directly at tumor sites.

Tumor-Infiltrating Treg Cells Express a Specific Gene Signature

[0243] The inventors then asked whether tumor infiltrating Treg cells could be defined by specific gene expression patterns.

[0244] To identify signature transcripts of tumor-infiltrating Treg cells, the inventors included in the expression pattern analyses the transcriptome dataset they previously obtained from different T and B lymphocyte subsets purified from PBMCs (Ranzani et al., 2015). In so doing, the inventors obtained a signature of 328 transcripts whose expression is higher in tumor infiltrating Treg cells (Wilcoxon Mann Whitney test $p < 2.2 \times 10^{-16}$) (FIG. 2, and Table IV compared to the other lymphocyte subsets purified from non-tumoral tissues and from PBMCs of healthy or neoplastic patients.

Gene Name	Treg_Tumor_Infiltrating_CRC	Treg_Tumor_Infiltrating_NSCLC	Treg_Tissue_Infiltrating_Colon	Treg_Tissue_Infiltrating_Lung	Treg healthy Peripheral Blood
AC019206.1	15.41	8.72	12.89	12.04	29.46
ACAA2	305.76	499.02	497.41	526.58	614.28
ACOT9	918.3	803.71	1361.82	2180.66	1272.07
ACOX3	183.48	384.73	469.06	506.97	439.27
ACP5	267.7	837.72	859.77	1872.29	1483.27
ACSL4	1154.87	1384.88	1903.56	2170.94	2043.91
ACTA2	86.65	270.74	108.76	234.86	232.15
ACTG2	10.69	6.16	22.68	21.11	36.14
ADAM10	2378.26	3051.7	2545.29	3600.38	3167.56
ADAT2	927.45	1272.17	1214.4	2094.25	3103.21
ADPRH	136.34	460.61	352.57	836.7	718.74
AHCYL1	914.19	1271.5	1269.55	1835.94	1711.94
AHCYL2	305.15	570.67	525.24	790.1	856.25
AKAP5	174.24	264	358.75	709.28	535.97
AKIP1	261.47	273.85	225.25	436.84	360.48
ANKRD10	2251.92	3433.73	2805.08	4192.8	4672.81
ARHGEF12	1371.05	2064.05	1536.04	3069.77	2637.79
ARHGEF4	19.42	71.47	28.87	195.02	252.84
ARL6IP5	3008.69	4385.74	4051.43	4983.16	4712.48
ARNTL2	20.4	201.3	281.95	560.77	445.13
ATP13A3	3776.14	4020.7	4688.02	6688.94	6967.94
ATP2C1	1491.87	1399.81	1553.57	2029.41	1819.78
AURKA	24.56	50.12	79.89	66.37	87.07
BATF	820.97	3325.93	1698.92	5052.64	2727.65
BCL2L1	212.64	478.8	537.61	554.11	892.28
BIRC5	14.74	20.27	20.62	25.03	44.99
C17orf96	19	174.31	159.79	239.88	377.03
C5orf63	146.45	201.44	112.88	228.2	357.09
CABLES1	59.04	196.68	125.77	473.94	386.73
CACNB2	67.43	50.49	40.21	169.83	105.62
CADM1	113.76	602.72	115.46	1766.12	901.32
CALM3	2474.48	2829.3	2675.18	2954.03	4107.03
CARD16	370.31	696.36	493.29	1220.7	823.89
CARD17	41.87	96.94	54.12	101.19	132.95
CASP1	925.29	1453.84	1521.09	2028.95	1980.45
CASQ1	52.11	31.21	24.74	135.08	174.95
CCNB2	18.28	27.62	34.02	51.57	58.08
CCR8	255.66	578.27	1355.63	3127.33	2069.11
CD177	2.36	204.74	299.99	718.58	470.27
CD27	468.93	583.58	496.38	710.13	1068.55
CD274	120.19	576.59	390.71	1050.94	645.66
CD7	1622.12	6900.01	2829.82	9053.96	6919.59
CDCA2	19.24	35.09	49.48	68.21	49.95
CDH24	57.67	57.11	89.69	148.93	105.02
CDK6	602.97	2175.36	2463.85	3580.4	3238.58
CEACAM1	360.01	340.84	326.28	381.79	732.86
CENPM	43.72	39.12	61.85	72.94	61.32
CEP55	56.18	88.17	223.71	220.17	273.64
CGA	1.08	13.59	22.68	334.28	9.73
CHRNA6	14.46	218.49	67.52	336.38	504.28
CHST11	1822.7	2085.92	2806.11	2790.19	2535.23
CHST2	75.46	218.75	156.7	458.24	604.97
CHST7	141.3	341.87	426.79	1087.21	333.3
CIT	89.25	105.13	155.15	150.2	262.67
CLNK	153.06	288.36	248.96	340.12	528.54
CNIH1	1028.31	1005.46	935.03	2336.95	1101.87
COL9A2	149.87	278.77	357.72	889.47	805.72

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Gene Name	Treg_Infiltrating_CRC	Treg_Infiltrating_NSCLC	Treg_Infiltrating_Colon	Treg_Infiltrating_Lung	Treg_healthy_Peripheral_Blood
CORO1B	481.34	667.37	861.83	774.65	1040.47
COX10	305.31	399.33	397.93	447.17	612.29
CRADD	77.04	155.66	277.31	394.31	306.61
CREB3L2	739.04	1289.66	1415.94	2984.54	2590.37
CSF1	313.09	1629.13	1609.75	2204.79	3288.67
CSF2RB	1069.75	1275.49	1290.69	2036.76	2531.99
CTLA4	4806.23	4810.74	5340.06	6798.82	10378.3
CTSC	1026.76	2196.93	2514.88	3030.74	2767.27
CTTNBP2NL	85	200.53	248.45	500.75	267.16
CX3CR1	9.57	63.99	123.71	341.79	293.28
CXCL13	1.07	255.23	1145.33	1270.98	11433.26
CYB5B	714.26	1129.39	947.4	1156.4	1221.22
CYP7B1	9.83	210.33	29.38	186.99	161.17
DCPS	153.25	210.26	210.82	191.31	271.71
DFNB31	561.87	1636.56	1727.79	4251.83	2526.15
DIRAS3	1.9	4.59	3.61	26.01	35.64
DLGAP5	7.89	14.46	20.62	27.41	49.7
DNPH1	160.15	650.05	321.13	683.55	576.77
DOC2B	10.47	3.42	5.15	14.23	238.86
DPYSL2	208.98	189.08	580.4	591.32	618.42
EBI3	7.47	103.59	56.7	148.96	200.74
ECEL1	3.7	150.7	34.02	199.17	794.51
EGLN1	977.29	969.32	1021.11	1381.2	1271.06
EML2	861.51	1601.25	1643.25	2156.04	1957.43
ENTPD1	752.88	2078.17	1447.38	4321.79	4162.57
ERI1	354.33	862.86	932.45	1200.06	1070.15
ETFA	414.08	586.15	534.01	615.35	689.14
ETV7	93.62	511.26	361.85	728.85	1111.55
EVA1B	21.39	35.63	26.8	42.86	47.36
F5	2343.39	2346.94	2499.41	4868.41	4729.97
FAAH2	244.19	431.76	209.27	737.44	699.42
FAIM2	15.05	33.47	57.21	69.26	117.28
FAM184A	192.41	742.47	525.24	706.33	891.02
FAM19A2	311.38	204.56	302.57	264.46	748.09
FAM98B	314.26	664.69	491.22	698.92	657.42
FAS	2337.14	5167.46	2712.81	5982.39	3656.21
FBXO45	460.56	783.06	631.43	964.13	894.23
FCR3	1161.64	1997.02	938.63	3281.36	2699.01
FKBP1A	733.83	1240.62	1174.19	1377.67	1578.09
FLNB	1671.04	1363.04	1394.81	3395.38	2307.44
FLVCR2	69.84	579.55	388.13	744.8	528.01
FNDC3B	377.47	501.27	506.17	1111.07	531.12
FOXA1	2.7	11.87	17.01	70.68	18.22
FOXM1	56.39	74.94	108.24	88.16	125.31
FOXP3	6586.98	10713.12	6060.66	13483.77	11472.41
FUCA2	107.56	175.46	160.82	249.54	315.45
GADD45A	745.14	1431.9	884.51	3681.24	1396.98
GCNT1	99.22	632.16	608.75	1133.62	845.83
GK	637.31	1994.73	2430.34	5200.55	2065.35
GLB1	563.96	819.22	873.17	1077.84	854.94
GLCCI1	1557.57	3211.73	1753.04	3189.77	2909.06
GLDC	19.25	20.56	25.26	31.21	74.61
GLRX	1213.06	1251.64	1512.85	1764.61	1872
GNG4	5.08	79.18	64.43	197.1	343.93
GNG8	11.94	63.28	10.82	67.63	175.16
GRSF1	1277.4	1725.67	1397.9	2899.76	2343.4
GSK3B	1099.5	1267.18	1208.73	1333.16	1454.67
GTF3C6	313.17	579.04	445.86	617.48	597.55
GTSF1L	13.67	20.36	15.46	44.6	99.03
HADHB	1179.61	1207.14	1287.59	1396.89	1521.16
HAP1	92.39	180.51	74.22	292.97	577
HAVCR2	49.81	265.84	487.62	577.57	633.27
HECW2	17.63	98.93	38.66	111.21	177.5
HIBCH	124.32	290.04	226.8	348.34	332.88
HIVEP3	358.34	649.68	893.27	1091.96	1316.89
HJURP	8.55	18.52	15.98	27.13	39.99
HOXA1	16.66	15.22	14.95	25.57	44.75
HPRT1	442.58	532.66	542.25	811.75	724.15
HPSE	248.88	676.54	515.45	674.09	754.04
HS3ST3B1	1222.43	1930.88	1980.87	2609.49	2431.83
HSDL2	242.56	611.72	285.56	785.27	921.97
HTATIP2	567.61	1439.29	997.4	3285.86	1576.24

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Gene Name	Treg_Infiltrating_CRC	Treg_Infiltrating_NSCLC	Treg_Infiltrating_Colon	Treg_Infiltrating_Lung	Treg_healthy_Peripheral_Blood
ICA1	94.65	371.57	113.91	487.68	411.64
ICOS	3398.28	4119.2	5211.71	6830.94	7339.08
IGFLR1	67.43	78.13	92.78	108.12	185.13
IKZF2	6061.48	6317.6	4919.45	9983.52	8551.49
IKZF4	1422.66	2362.49	1258.21	3745.25	3958.19
IL12RB2	120.8	369.84	509.78	835.92	877.51
IL17REL	9.74	23.21	34.02	52.62	57.04
IL1R1	506.51	9670.81	2766.42	7852.18	5585.89
IL1R2	41.72	1225.4	526.79	2117.34	1793.21
IL1RL1	17.37	135.26	44.33	715.42	71.67
IL1RL2	8.65	76.53	28.35	74.81	59.47
IL21R	708.61	1355.83	1715.93	3092.3	3514.36
IL2RA	5244.31	9685.38	5627.68	11454.42	12731.31
IL2RB	6716.4	14249.6	12502.75	17733	18564.35
IL32	4332.08	13202.73	9755.92	11766.98	13883.45
IL7	117.66	230.78	165.97	257.71	178.1
INPP1	124.25	497.01	312.88	458.2	487.93
INPPSF	787.92	2172.55	830.9	2189.48	1549.46
ISOC1	233.44	329.49	400.5	514.43	335.93
ITFG1	313.34	324.11	402.05	396.94	511.86
JAK1	10779.78	11919.66	10072.4	17755.9	11521.32
JAKMIP1	291.14	387.49	1063.89	756.36	953.47
KAT2B	3145.05	3910.01	4756.57	5520.88	4632.76
KIF14	20.18	25.43	31.96	36.73	59.61
KIF15	20.64	29.67	51.03	41.9	68.63
KIF20A	9.84	14.93	7.22	20.97	32.72
KLHDC7B	131.39	211.42	188.65	245.3	394.73
KSR1	837.87	1569.86	1176.77	2241.36	1847.72
LAPTM4B	86.42	369.78	181.44	938.88	738.38
LAX1	1135.24	1155.91	1406.15	1721.7	1854.78
LAYN	441.73	796.76	859.25	2650.24	1681.25
LEPR	58.77	130.22	129.38	137.47	237.88
LEPROT	614.73	860.55	676.79	1044.66	1296.13
LHFPL	1.58	10.38	9.79	18.09	63.16
LIMA1	404.55	727.57	1017.5	1064.46	1570.15
LMCD1	115.76	104.74	112.37	257.92	404.7
LOC388813	7.42	45.99	28.87	86.3	60.63
LRG1	17.67	61.54	46.39	71.6	78.3
LRRC61	98.78	291.45	138.66	292.51	314.79
LTA	214.07	516.57	270.61	351.26	747.01
LXN	67.37	91.06	75.77	114.23	133.43
LY75	249.92	970.85	680.91	1302.79	1624.82
MAGEH1	461.13	1349.51	448.96	2800.36	3719.29
MALT1	3362.14	3568.46	2743.74	5892.86	4776.24
MAP1LC3A	70.92	110.44	119.07	272.07	169.3
MAP3K5	1865.12	2189.99	1787.06	2822.55	2265.54
MAST4	1053.08	2239.36	2198.39	3373.36	1855.42
MAT2B	2305.62	4050.5	2959.2	4435.41	4159.25
MCCC2	737.75	875.78	873.69	1018.1	1245.79
MELK	28.77	50.08	83.5	72.28	83.06
METTL7A	280.99	442.99	385.04	845.09	1671.74
METTL8	318.99	882.21	377.82	880.99	1413.12
MGME1	236.76	332.08	342.77	400.19	552.69
MGST2	54.22	87.18	69.59	147.04	148.13
MICAL2	354.6	1601.79	1813.35	1910.22	3188.92
MINPP1	85.19	204.32	211.85	243.22	290.02
MKI67	192.68	206.77	518.03	372.61	650.04
MREG	120.75	119.91	226.28	229.41	325.33
MYL6B	122.13	182.71	107.73	174.22	252.52
MYO5C	95.68	122.36	157.21	130.81	347.49
NAB1	508.21	973.74	1261.31	1831.77	1227.51
NCALD	111.73	163.32	272.67	283.43	370.26
NCAM1	7.88	58.27	39.69	207.45	213.23
NCF4	509.63	630.55	880.39	894.67	1176.84
NCOA1	2088.38	2062.57	1941.7	2367.54	2618.11
NDFIP2	77.99	529.73	618.54	829.53	987.25
NEMP2	382.56	478.4	475.76	565.18	634.41
NETO2	145.84	559.95	773.69	1490.82	1137.73
NEURL3	4.04	29.74	12.37	24.02	35.49
NFAT5	2075.17	3880.92	3923.6	4786.04	5295.06
NFE2L3	279.28	590.19	560.29	743.24	1114.26

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Gene Name	Treg_Infiltrating_CRC	Treg_Infiltrating_NSCLC	Treg_Infiltrating_Colon	Treg_Infiltrating_Lung	Treg_Peripheral_Blood
NFYC	588.49	713.51	756.16	733.52	798.27
NHS	7.27	18.73	55.15	60.16	159.44
NPTN	525.86	838.02	897.91	1007.87	969.1
NTNG2	117.04	296.81	534.52	669.43	1001.58
NTRK1	20.85	27.9	155.15	88.29	161.78
NUSAP1	199.28	266.11	445.86	635.51	365.17
NXT2	221.6	263.39	226.8	285.15	302.01
OSBP2	111.03	89.82	127.83	195.47	244.93
PAK2	4621.62	6173.86	5024.6	7194.78	6376.28
PAM	582.52	904.05	1069.56	1365.03	1631.64
PANX2	3.7	76.02	15.46	97.12	71.72
PAQR4	16.99	46.54	62.37	92.6	65.27
PARD6G	55.86	172.18	249.99	546.52	182.4
PARK7	1271.06	1563.96	1283.47	1764.8	1764.91
PCTP	49.2	173.47	163.4	253.27	270.62
PDCD1LG2	12.12	61.89	25.77	214.51	223.04
PDGFA	6.19	38.74	159.79	154.17	153.03
PEX3	179.31	239.78	205.66	326.61	291.17
PGM2	316.91	419.51	454.63	471.89	487.85
PHKA1	8.59	19.98	28.87	107.79	109.7
PIGU	147.54	205.18	184.53	220.25	265.12
PLA2G4C	22.16	128.81	65.98	245.65	159.6
PPM1G	1974.96	2324.16	2563.85	2751.69	2598.5
PRDX3	466.56	854.12	745.34	890.58	1052.67
PRKCDBP	4.45	6.8	19.07	28.51	27.92
PROB1	53.7	140.39	109.79	177.19	272.89
PTGIR	96.17	147.61	107.21	214.61	449.25
PTP4A3	134.06	262.63	463.39	340.08	667.84
PTPRJ	2654.92	3999.84	5584.38	6101.63	7239.3
PTTG1	211.97	198.56	236.59	302.53	335.68
RAB15	160.6	470.25	302.05	420.06	519.4
RAD51AP1	29.89	46.33	40.21	49.23	51.73
RASAL1	18.87	53.37	50	87.38	238.78
RBKS	67.62	56.45	133.5	141.16	85.46
RCBTB1	1154.33	1312.01	1131.41	1960.76	1384.84
RDH10	194.04	311.58	467.51	658.5	1448.57
REXO2	487.9	832.35	648.44	852.58	987.43
RFK	378.31	396.91	292.26	460.78	452.8
RGS1	16547.6	15176.27	18057.75	23425.18	17168.17
RHOC	78.07	230.17	207.21	317.85	290.86
RMI2	19.46	76.58	39.69	70.44	73.47
RNF145	1625.11	3074.78	2117.47	4417.29	3266.94
RNF207	41.75	469.3	314.94	723.56	765.87
RRAGB	281.49	274.98	196.9	384.81	506.1
RYBP	1861.27	2273.72	2496.32	3178.31	2818.02
SEC14L6	6.42	86.23	27.32	179.47	274.97
SEC24A	718	917.25	1157.7	1259.04	1062.95
SECTM1	69.01	1347.35	725.75	2354.1	1511.04
SEPT3	15.6	59.23	49.48	149.11	244.4
SGPP2	428.14	656.73	364.94	1001.71	809.92
SH3RF2	20.9	18.3	65.98	98.4	196.34
SIRPG	433.99	605.49	317	575.41	1245.12
SLC16A1	947.47	1385.08	1532.43	2050.74	1460.73
SLC25A12	246.72	323.6	423.18	406.15	498.91
SLC35E3	385.3	451.16	370.09	582.86	653.13
SLC35F2	378.22	795.55	688.64	1130.81	880.5
SLC41A1	1194.29	1119.86	1164.92	1401.41	1630.88
SLC41A2	13.45	356.73	114.95	482.48	395.27
SMAD1	15.34	53.93	30.41	63.54	87.46
SMS	565.6	760.65	719.57	818.12	735.99
SNAP47	310.71	503.77	577.82	690.31	696.18
SOCS2	245.77	405.76	463.39	605.25	611.78
SOX4	128.76	244.57	218.04	1205.78	715.01
SPATA24	38.86	77.02	36.6	66.43	94.41
SPATC1	7.97	10.96	19.59	61.51	55.84
SPATS2L	366.98	891.61	1172.13	1430.11	1531.61
SSH1	1890.01	3432.55	2771.06	4390.36	4552.26
SSTR3	230.28	248.12	341.74	240.77	901.25
STAC	11.63	48.36	39.69	75.94	71.4

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Gene Name	Treg_Infiltrating_CRC	Treg_Infiltrating_NSCLC	Treg_Infiltrating_Colon	Treg_Infiltrating_Lung	Treg_healthy_Peripheral_Blood
STARD7	2415.01	3185.95	3024.66	3809.46	3445.47
STRIP2	103.39	1002.96	540.19	716.49	1192.77
SYT11	1078.51	1733.37	2080.36	2110.18	2818.39
TADA3	677.14	893.74	852.04	880.43	1189.01
TBC1D8	53.89	374.1	265.97	817.36	1087.39
TDRD3	461.34	383.25	520.09	584.64	643.84
TFRC	3608.04	4612.18	5640.05	8107.35	10082.21
THADA	1102.51	1505.13	1467.48	3472.21	3171.99
TIGIT	4611.14	10986.74	4901.41	14821.45	14747.79
TM9SF2	2048.03	2689.14	2665.91	2935.98	3358.4
TMA16	172.88	180.92	137.11	304.24	192.53
TMEM140	273.98	640.28	574.73	917.16	691
TMEM184C	520.19	508.83	599.98	1170.37	519.43
TMOD1	14.75	72.22	32.47	150.93	89.62
TMPRSS3	70.84	352.78	321.64	540.8	1106.85
TMPRSS6	113.53	548.87	265.97	698.41	985.34
TNFRSF18	333.36	2871.78	3071.57	4038.86	4078.14
TNFRSF4	400.56	2873.16	2992.18	4222.16	4642.56
TNFRSF8	30.89	115.57	208.24	155.59	430.23
TNFRSF9	502.86	898.69	1739.13	2921.72	3128.82
TNIP3	28.73	485.83	213.91	324.53	419.8
TOR4A	141.27	291.3	346.9	358.98	326.51
TOX2	237.46	860.48	490.71	861.08	1264.13
TP73	7.86	31.27	39.69	78.27	93.99
TPMT	357.13	354.93	305.66	480.15	519.82
TPP1	2589.92	6024.92	4380.81	7164.96	6236.83
TPX2	106.25	89.08	184.02	150.35	202.77
TRAF3	1140.85	3231.25	2706.11	4078.84	3554.01
TRIB1	927.27	1820.64	1482.95	2402.58	1469.85
TRIM16	160.05	115.2	121.13	240.55	210.13
TSPAN17	709.59	1721.26	1322.64	1685.38	1865.69
TSPAN5	372.4	1167.46	723.69	1230.67	1398.7
TST	3.8	26.32	26.8	39.78	41.65
TTBK1	13.41	164.27	99.48	380.69	460.64
TTC22	237.9	386.91	323.19	483.96	451.61
TWIST1	4.21	94.46	21.65	95.32	195.78
UGP2	1950.41	3283.79	2562.82	3399.18	2864.71
USP51	48.1	133.95	28.87	233.48	291.46
UXS1	1661.1	2156.16	1600.47	2614.66	1914.74
VANGL1	97.19	192.58	248.96	263.46	289.05
VDR	123	992.41	1771.6	2616.68	3656.18
VWA5A	426.29	550.67	373.7	604.53	739.57
WDHD1	101.74	126.37	140.2	136.76	193.58
WDTC1	1220.3	3855.35	2029.33	4398.54	3774.61
WSB1	2837.49	3876.77	4697.29	5090.18	5383.33
XKRX	16.06	71.84	90.2	115.05	101.81
YIPF1	310.29	351.68	285.04	354.44	456.27
YIPF6	342.01	687.07	705.14	1078.09	793.2
ZBED2	87.53	94.86	522.15	230.51	1238.63
ZBTB38	1986.89	5405.41	3134.97	6174.05	4680.43
ZC3H12C	123.76	159.39	518.54	1191.95	985.54
ZG16B	3.42	17.03	15.46	32.31	32.59
ZMAT3	529.91	925.46	822.66	1077.17	1234.3
ZMYND8	585.94	675.31	711.84	850.29	1131.01
ZNF280C	181.86	444.81	326.28	635.21	467.78
ZNF280D	698.54	973.93	616.48	1061.55	1290.04
ZNF282	374.36	1273.4	2253.55	2562.43	3165.99
ZNF334	6.95	26.52	17.53	40.03	100.33
ZWINT	60.55	73.28	101.03	87.1	105.4

[0245] Altogether, the data show that Treg cells display the most pronounced differences in transcripts expression among CD4+ T cell subsets infiltrating normal and tumor tissues.

[0246] The inventors defined a subset of signature genes that describe the specific gene expression profile of tumor infiltrating Treg cells.

Gene Signature of Tumor-Infiltrating Treg Cells is Present in Primary and Metastatic Human Tumors

[0247] The inventors then looked at the single cell level for the differential expression profile of signature genes of tumor infiltrating Treg cells. The inventors isolated CD4+ T cells from CRC and 5 NSCLC tumor samples as well as from 5 PBMCs of healthy individuals (Table II), purified Treg cells, and using an automated microfluidic system (C1

Fluidigm) captured single cells (a total of 858 Treg cells: 320 from CRC and 286 from NSCLC; 252 from PBMCs of healthy individuals). The inventors then assessed by high throughput RT-qPCR (Biomark HD, Fluidigm) the expression of 79 genes selected among the highly expressed (>10 FKPM) tumor Treg cell signature genes (FIGS. 3A, 3C and 7). Notably, it was found that the vast majority (75 over 79; 95%) of the tumor-infiltrating Treg cell signatures were co-expressed with bona fide Treg cell markers (i.e., FOXP3+ and IL2RA) (FIG. 3B). The percentage of co-expression between these Treg cell markers and the 79 genes selected among the tumor-infiltrating-Treg-cell signature genes ranged between 81% of TIGIT and 0.59% of CGA (FIG. 3B). The expression of Treg signature genes in the RNA-seq of the whole Treg cell population correlated with the percentage of single cells expressing the different genes (FIG. 3C). In order to reduce the “drop-out” effect of the single cell data (i.e., events in which a transcript is detected in one cell but not in another one because the transcript is ‘missed’ during the reverse-transcription step) (Kharchenko et al., 2014), a threshold (median value t=8.4%) was defined based on the expression distribution for each transcript and discarded genes below this threshold. The forty-five signature transcripts of tumor infiltrating Treg cells detected above this threshold were in most cases significantly over-expressed in Treg cells from both tumors (39 over 45, 87%; Wilcoxon Mann Whitney test p<0.05) or in one tumor type (43 over 45, 96%; FIG. 3D). Homogeneity of the purified tissue infiltrating Treg cells can be affected by the carry-over of cells from other lymphocyte subsets. To quantitate this possible contamination, the single cell RT-qPCR analyses of Treg cells was performed including markers specific for other lymphocytes subsets (i.e., Th1, Th2, Th17, TfH, CD8 T cells, B cells) (FIG. 7). Our data showed that only a very low fraction of the purified single cells displayed markers of lymphocytes subsets different from Treg cells (FIG. 7).

[0248] The overlap between the signature genes in the CRC and NSCLC infiltrating Treg cells (FIG. 2) prompted us to assess whether this signature were also enriched in Treg cells infiltrating other tumors. RNA was thus extracted from Treg cells infiltrating breast cancer, gastric cancer, brain metastasis of NSCLC, and liver metastasis of CRC. It was found by RT-qPCR that tumor infiltrating Treg signatures genes were mostly upregulated also in these tumors (FIG. 3E).

[0249] Overall these data show that the tumor-infiltrating Treg cell signature genes are co-expressed at single cell level with FOXP3 and IL2RA and that several primary and metastatic human tumors express the tumor-infiltrating Treg cell signature.

Gene Signature of Tumor Infiltrating Treg Cells is Translated in a Protein Signature

[0250] The inventors then assessed at the single cell level by flow cytometry the protein expression of ten representative signature genes present in CRC and NSCLC infiltrating Treg cells, adjacent normal tissues, and patients PBMCs. Of the ten proteins, two are proteins (OX40 and TIGIT) whose relevance for Treg cells biology has been demonstrated (Joller et al., 2014; Voo et al., 2013), seven are proteins (BATF, CCR8, CD30, IL-1 R2, IL-21R, PDL-1 and PDL-2) whose expression has never been described in tumor-infiltrating Treg cells, and one protein, 4-1BB, is a co-stimulatory receptor expressed on several hematopoietic cells, whose expression on Treg cells has been shown to mark antigen-activated cells (Schoenbrunn et al., 2012). Our findings showed that all these proteins were upregulated (FIGS. 4A and 4B), at different extent, in tumor infiltrating Treg cells compared to the Treg cells resident in normal tissues.

[0251] Altogether, our data show there is a molecular signature of tumor infiltrating Treg cells, which can be detected both at the mRNA and at the protein levels.

Expression of Tumor Treg Signature Genes is Negatively Correlated with Patients Survival

[0252] In an attempt to correlate our findings with clinical outcome, the inventors asked whether the expression of the tumor-Treg signature transcripts correlated with disease prognosis in CRC and NSCLC patients. The inventors therefore interrogated for expression of Treg signature genes transcriptomic datasets obtained from resected tumor tissues of a cohort of 177 CRC patients (GSE17536 (Smith et al., 2010) and of a cohort of 263 NSCLC patients (GSE41271—(Sato et al., 2013), and correlated high and low gene expression levels with the 5-years survival data. Among those genes whose expression is highly enriched in tumor infiltrating Treg cells, LAYN, MAGEH1 and CCR8 were selected as they are the three genes more selectively expressed (FIG. 9A-C). To normalize for differences in T cell densities within the resected tumor tissues, the inventors used the ratio between expression of the selected signature genes and CD3G. Remarkably, it was found that high expression of the three signature genes is in all cases correlated with a significantly reduced survival (FIG. 5A). Interestingly, it was also observed that expressions of the three signature genes increased with tumor staging of CRC patients (FIG. 5B).

[0253] In conclusion, high expression in the whole tumor samples of three genes (LAYN, MAGEH1 and CCR8) that are specifically and highly expressed in tumor infiltrating Treg cells, correlates with a poor prognosis in both NSCLC and CRC patients.

Selection of Potential Targets Specifically Over-Expressed on the Surface of Tumor-Infiltrating Treg

[0254] All annotated protein isoforms encoded by the 328 genes and retrievable in the public database EnsEMBL (<http://www.ensembl.org>) were simultaneously analysed with the four prediction algorithms and genes encoding at least one isoform predicted to be surface exposed were considered as potential targets.

[0255] Out of 328 genes, 193 encode for at least one potential cell surface protein isoform on the basis of at least one of the four predictors. The list of protein isoforms predicted to be membrane-associated is reported in Table VI.

TABLE VI

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
LAYN	Layilin	ENSG00000204381	ENST00000375614	ENSP00000364764	1
			ENST00000375615	ENSP00000364765	2
			ENST00000436913	ENSP00000392942	3
			ENST00000525126	ENSP00000434328	4
			ENST00000525866	ENSP00000434300	5
			ENST00000528924	ENSP00000486561	6
			ENST00000530962	ENSP00000431627	7
			ENST00000533265	ENSP00000434972	8
			ENST00000533999	ENSP00000432434	9
			ENST00000564089	ENSP00000456707	10
CCR8	C—C chemokine receptor type 8	ENSG00000179934	ENST00000326306	ENSP00000326432	11
IL21R	Interleukin-21 receptor	ENSG00000103522	ENST00000414803	ENSP00000390104	12
			ENST00000337929	ENSP00000338010	13
			ENST00000395754	ENSP00000379103	14
FUCA2	Plasma alpha-L-fucosidase	ENSG00000001036	ENST00000002165	ENSP0000002165	15
ICA1	Islet cell autoantigen 1	ENSG00000003147	ENST00000407906	ENSP00000386021	16
			ENST00000261643	ENSP00000261643	17
COX10	Protoheme IX farnesyltransferase, mit.	ENSG00000006695			18
IL32	Interleukin-32	ENSG00000008517	ENST00000008180	ENSP00000008180	19
			ENST00000396890	ENSP00000380099	20
			ENST00000525228	ENSP00000431740	21
			ENST00000525377	ENSP00000433866	22
			ENST00000530890	ENSP00000433747	23
			ENST00000534507	ENSP00000431775	24
			ENST00000548246	ENSP00000447979	25
			ENST00000548476	ENSP00000449483	26
			ENST00000548807	ENSP00000448354	27
			ENST00000551513	ENSP00000449147	28
ETV7	Transcription factor ETV7	ENSG00000010030	ENST00000552356	ENSP00000446978	29
			ENST00000552936	ENSP00000447033	30
ATP2C1	Calcium-transporting ATPase type 2C member 1	ENSG00000017260	ENST00000339796	ENSP00000342260	31
			ENST00000627426	ENSP00000486712	32
FAS	Fatty acid synthase	ENSG00000026103	ENST00000328560	ENSP00000329664	33
			ENST00000359644	ENSP00000352665	34
			ENST00000422190	ENSP00000402677	35
			ENST00000428331	ENSP00000395809	36
			ENST00000504381	ENSP00000425320	37
			ENST00000504571	ENSP00000422489	38
			ENST00000504612	ENSP00000425228	39
			ENST00000504948	ENSP00000423330	40
			ENST00000505072	ENSP00000427625	41
			ENST00000505330	ENSP00000423774	42
			ENST00000507194	ENSP00000427087	43
			ENST00000507488	ENSP00000421326	44
			ENST00000508297	ENSP00000421261	45
			ENST00000508532	ENSP00000424783	46
			ENST00000508660	ENSP00000424930	47
			ENST00000509662	ENSP00000426849	48
			ENST00000510168	ENSP00000427461	49
			ENST00000513801	ENSP00000422872	50
			ENST00000515854	ENSP00000422890	51
			ENST00000533801	ENSP00000432956	52
			ENST00000352159	ENSP00000345601	53
			ENST00000355279	ENSP00000347426	54
			ENST00000355740	ENSP00000347979	55
			ENST00000357339	ENSP00000349896	56
			ENST00000479522	ENSP00000424113	57
			ENST00000484444	ENSP00000420975	58
			ENST00000488877	ENSP00000425159	59
			ENST00000492756	ENSP00000422453	60
			ENST00000494410	ENSP00000423755	61
			ENST00000612663	ENSP00000477997	62
PEX3	Peroxisomal biogenesis factor 3	ENSG00000034693	ENST00000367591	ENSP00000356563	63
TSPAN17	Tetraspanin-17	ENSG00000048140	ENST00000367592	ENSP00000356564	64
			ENST00000298564	ENSP00000298564	65
			ENST00000310032	ENSP00000309036	66
			ENST00000503030	ENSP00000425975	67
			ENST00000503045	ENSP00000425212	68

TABLE VI-continued

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
COL9A2	Collagen alpha-2(IX) chain	ENSG00000049089	ENST00000504168	ENSP00000423957	69
			ENST00000507471	ENSP00000423610	70
			ENST00000508164	ENSP00000422053	71
			ENST00000515708	ENSP00000426650	72
NFE2L3	Nuclear factor erythroid 2-related factor 3	ENSG00000050344	ENST00000372736	ENSP00000361821	73
			ENST00000372748	ENSP00000361834	74
			ENST00000417105	ENSP00000388493	75
TNIP3	TNFAIP3-interacting prot.3	ENSG00000050730	ENST00000515036	ENSP00000424284	77
LY75 YIPF1	Lymphocyte antigen 75 Protein YIPF1	ENSG00000054219 ENSG00000058799	ENST00000263636	ENSP00000263636	78
			ENST0000072644	ENSP0000072644	79
ISOC1	Isochorismatase domain-containing protein 1	ENSG00000066583	ENST00000371399	ENSP00000360452	80
			ENST00000412288	ENSP00000416507	81
			ENST00000464950	ENSP00000432266	82
			ENST00000173527	ENSP00000173527	83
			ENST00000514194	ENSP00000421273	84
ACSL4	Long-chain-fatty-acid-CoA ligase 4	ENSG00000068366	ENST00000340800	ENSP00000339787	85
			ENST00000469796	ENSP00000419171	86
			ENST00000469857	ENSP00000423077	87
			ENST00000502391	ENSP00000425408	88
			ENST00000504980	ENSP00000421425	89
MAST4	Microtubule-assoc.serine/threonine-protein kinase 4	ENSG00000069020	ENST00000508092	ENSP00000425378	90
			ENST00000434115	ENSP00000396765	91
			ENST000004395842	ENSP00000379183	98
LMCD1	LIM and cysteine-rich domains protein 1	ENSG00000071282	ENST00000402472	ENSP00000384148	99
			ENST00000336824	ENSP00000338523	100
			ENST00000415807	ENSP00000411242	101
TFRC	Transferrin receptor protein 1	ENSG00000072274	ENST00000416957	ENSP00000389094	102
			ENST00000421757	ENSP00000408496	103
			ENST00000423424	ENSP00000392471	104
PANX2	Pannexin-2	ENSG00000073150	ENST00000262345	ENSP00000262345	105
			ENST00000371000	ENSP00000360039	106
			ENST00000441640	ENSP00000400959	107
FNDC3B	Fibronectin type III domain-containing protein 3B	ENSG00000075420	ENST00000541374	ENSP00000445276	108
			ENST00000544434	ENSP00000442443	109
			ENST00000337288	ENSP00000338030	110
STARD7	StAR-related lipid transfer protein 7, mitochondrial	ENSG00000084090	ENST00000514423	ENSP00000446652	111
			ENST00000548522	ENSP00000448586	112
			ENST00000265498	ENSP00000265498	113
SSH1	Protein phosphatase Slingshot homolog 1	ENSG00000084112	ENST00000503816	ENSP00000423008	114
			ENST00000506797	ENSP00000424278	115
			ENST00000616265	ENSP00000482639	116
MGST2	Microsomal glutathione S-transferase 2	ENSG00000085871	ENST00000514423	ENSP00000427321	117
			ENST00000614856	ENSP00000482758	120
			ENST00000618612	ENSP00000478093	121
ACOX3	Peroxisomal acyl-coenzyme A oxidase 3	ENSG00000087008	ENST00000612074	ENSP00000480846	119
			ENST00000303415	ENSP00000305529	123
			ENST00000344103	ENSP00000342759	124
ANKRD10	Ankyrin repeat domain-containing protein 10	ENSG00000088448	ENST00000381580	ENSP00000370992	125
			ENST00000381583	ENSP00000370995	126
			ENST00000381583	ENSP00000370995	126
FKBP1A	Peptidyl-prolyl cis-trans isomerase FKBP1A	ENSG00000088832	ENST00000618612	ENSP00000478093	121
			ENST00000216927	ENSP00000216927	122
			ENST00000303415	ENSP00000305529	123
SIRPG	Signal-regulatory protein gamma	ENSG00000089012	ENST00000344103	ENSP00000342759	124
			ENST00000381580	ENSP00000370992	125
			ENST00000381583	ENSP00000370995	126

TABLE VI-continued

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
WHRN	Whirlin	ENSG00000095397	ENST00000374059	ENSP00000363172	127
CENPM	Centromere protein M	ENSG00000100162	ENST00000215980	ENSP00000215980	128
			ENST00000402338	ENSP00000384731	129
			ENST00000402420	ENSP00000384132	130
			ENST00000404067	ENSP00000384814	131
			ENST00000407253	ENSP00000384743	132
NCF4	Neutrophil cytosol factor 4	ENSG00000100365	ENST00000447071	ENSP00000414958	133
CSF2RB	Cytokine receptor common subunit beta	ENSG00000100368	ENST00000262825	ENSP00000262825	134
			ENST00000403662	ENSP00000384053	135
			ENST00000406230	ENSP00000385271	136
			ENST00000421539	ENSP00000393585	137
CNIH1	Protein cornichon homolog 1	ENSG00000100528	ENST00000216416	ENSP00000216416	138
			ENST00000395573	ENSP00000378940	139
			ENST00000553660	ENSP00000452457	140
			ENST00000554683	ENSP00000452466	141
			ENST00000556113	ENSP00000451142	142
			ENST00000557659	ENSP00000451640	143
			ENST00000557690	ENSP00000451852	144
PIGU	Phosphatidylinositol glycan anchor biosynthesis class U protein	ENSG00000101464	ENST00000217446	ENSP00000217446	145
			ENST00000374820	ENSP00000363953	146
			ENST00000438215	ENSP00000395755	147
NDFIP2	NEDD4 family-interacting protein 2	ENSG00000102471	ENST00000218652	ENSP00000218652	148
			ENST00000487865	ENSP00000419200	149
			ENST00000612570	ENSP00000480798	150
			ENST00000620924	ENSP00000480881	151
ACP5	Tartrate-resistant acid phosphatase type 5	ENSG00000102575	ENST00000218758	ENSP00000218758	152
			ENST00000412435	ENSP00000392374	153
			ENST00000433365	ENSP00000413456	154
			ENST00000589792	ENSP00000468685	155
			ENST00000590420	ENSP00000468509	156
			ENST00000590832	ENSP00000465127	157
			ENST00000591319	ENSP00000464831	158
			ENST00000592828	ENSP00000468767	159
NFAT5	Nuclear factor of activated T-cells 5	ENSG00000102908	ENST00000567990	ENSP00000455115	160
CYB5B	Cytochrome b5 type B	ENSG00000103018	ENST00000307892	ENSP00000308430	161
			ENST00000512062	ENSP00000423679	162
			ENST00000568237	ENSP00000464102	163
LAPTM4B	Lysosomal-associated transmembrane protein 4B	ENSG00000104341	ENST00000445593	ENSP00000402301	164
			ENST00000517924	ENSP00000429868	165
			ENST00000521545	ENSP00000428409	166
			ENST00000619747	ENSP00000482533	167
IL7	Interleukin-7	ENSG00000104432	ENST00000263851	ENSP00000263851	168
			ENST00000379113	ENSP00000368408	169
			ENST00000518982	ENSP00000430272	170
			ENST00000520215	ENSP00000428364	171
			ENST00000520269	ENSP00000427750	172
			ENST00000520317	ENSP00000427800	173
			ENST00000541183	ENSP00000438922	174
EBI3	Interleukin-27 subunit beta	ENSG00000105246	ENST00000221847	ENSP00000221847	175
PLA2G4C	Cytosolic phospholipase A2 gamma	ENSG00000105499	ENST00000595161	ENSP00000469528	176
			ENST00000595487	ENSP00000471328	177
			ENST00000596352	ENSP00000471759	178
			ENST00000598488	ENSP00000468972	179
GLCCI1	Glucocorticoid-induced transcript 1 protein	ENSG00000106415	ENST00000430798	ENSP00000396171	180
MINPP1	Multiple inositol polyphosphate phosphatase 1	ENSG00000107789	ENST00000371994	ENSP00000361062	181
			ENST00000371996	ENSP00000361064	182
			ENST00000536010	ENSP00000437823	183
WSB1	WD repeat and SOCS box-containing protein 1	ENSG00000109046	ENST00000581440	ENSP00000462737	184
			ENST00000582208	ENSP00000463621	185
			ENST00000583193	ENSP00000462595	186
			ENST00000583742	ENSP00000462365	187
HTATIP2	Oxidoreductase HTATIP2	ENSG00000109854	ENST00000419348	ENSP00000392985	188
			ENST00000530266	ENSP00000436548	189
			ENST00000532081	ENSP00000432107	190
			ENST00000532505	ENSP00000432338	191

TABLE VI-continued

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
CTSC	Dipeptidyl peptidase 1	ENSG00000109861	ENST00000227266	ENSP00000227266	192
			ENST00000524463	ENSP00000432541	193
			ENST00000527018	ENSP00000432556	194
			ENST00000528020	ENSP00000433229	195
			ENST00000529974	ENSP00000433539	196
VWA5A	von Willebrand factor A domain-containing protein 5A	ENSG00000110002	ENST00000392744	ENSP00000376501	197
			ENST00000392748	ENSP00000376504	198
			ENST00000456829	ENSP00000407726	199
SLC35F2	Solute carrier family 35 member F2	ENSG00000110660	ENST00000375682	ENSP00000364834	200
			ENST00000525071	ENSP00000434307	201
			ENST00000525815	ENSP00000436785	202
			ENST00000532513	ENSP00000433783	203
VDR SEC24A	Vitamin D3 receptor Protein transport protein Sec24A	ENSG00000111424	ENST00000547065	ENSP00000449074	204
			ENSG00000113615	ENST00000398844	205
IL1R2	Interleukin-1 receptor type 2	ENSG00000115590	ENST00000332549	ENSP00000330959	206
			ENST00000393414	ENSP00000377066	207
IL1R1	Interleukin-1 receptor type 1	ENSG00000115594	ENST00000441002	ENSP00000414611	208
			ENST00000457817	ENSP00000408415	209
			ENST00000409288	ENSP00000386478	210
			ENST00000409329	ENSP00000387131	211
			ENST00000409589	ENSP00000386555	212
			ENST00000409929	ENSP00000386776	213
			ENST00000410023	ENSP00000386380	214
			ENST00000413623	ENSP00000407017	215
			ENST00000422532	ENSP00000390349	216
			ENST00000424272	ENSP00000415366	217
			ENST00000428279	ENSP00000410461	218
			ENST00000430171	ENSP00000408101	219
			ENST00000442590	ENSP00000393296	220
			ENST00000450319	ENSP00000411627	221
			ENST00000452403	ENSP00000401646	222
			ENSG00000115598	ENST00000264257	223
			ENST00000421464	ENSP00000387611	224
			ENST00000441515	ENSP00000413348	225
IL1RL1	Interleukin-1 receptor-like 1	ENSG00000115602	ENST00000233954	ENSP00000233954	226
			ENST00000311734	ENSP00000310371	227
			ENST00000404917	ENSP00000384822	228
			ENST00000409584	ENSP00000386618	229
			ENST00000427077	ENSP00000391120	230
UXS1	UDP-glucuronic acid decarboxylase 1	ENSG00000115652	ENST00000447231	ENSP00000409437	231
			ENST00000283148	ENSP00000283148	232
			ENST00000409501	ENSP00000387019	233
			ENST00000441952	ENSP00000416656	234
			ENST00000457835	ENSP00000399316	235
SLC25A12	Calcium-binding mitochondrial carrier protein Aralar1	ENSG00000115840	ENST00000426896	ENSP00000413968	236
			ENST00000473053	ENSP00000399316	237
THADA	Thyroid adenoma-associated protein	ENSG00000115970	ENST00000403856	ENSP00000385469	238
			ENST00000406510	ENSP00000384025	239
LEPR	Leptin receptor	ENSG00000116678	ENST00000344610	ENSP00000340884	240
			ENST00000349533	ENSP00000330393	241
			ENST00000371058	ENSP00000360097	242
			ENST00000371059	ENSP00000360098	243
			ENST00000371060	ENSP00000360099	244
			ENST00000406510	ENSP00000384025	245
			ENST00000616738	ENSP00000483390	246
MREG	Melanoregulin	ENSG00000118242	ENST00000263268	ENSP00000263268	247
			ENST00000620139	ENSP00000484431	248
FLVCR2	Feline leukemia virus subgroup C receptor-related protein 2	ENSG00000119686	ENST00000238667	ENSP00000238667	249
			ENST00000539311	ENSP00000443439	250
			ENST00000553341	ENSP00000452584	251
			ENST00000553587	ENSP00000451603	252
			ENST00000554580	ENSP00000451781	253
			ENST00000555027	ENSP00000452453	254
			ENST00000555058	ENSP00000451104	255
			ENST00000556856	ENSP00000452468	256

TABLE VI-continued

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
SOCS2	Suppressor of cytokine signaling 2	ENSG00000120833	ENST00000548537 ENST00000549510	ENSP00000448709 ENSP00000474888	255 256
RDH10	Retinol dehydrogenase 10	ENSG00000121039	ENST00000240285 ENST00000519380 ENST00000521928	ENSP00000240285 ENSP00000428132 ENSP00000429727	257 258 259
LAX1	Lymphocyte transmembrane adapter 1	ENSG00000122188	ENST00000367217 ENST00000442561	ENSP00000356186 ENSP00000406970	260 261
ZWINT	ZW10 interactor	ENSG00000122952	ENST00000489649	ENSP00000473330	262
ACOT9	Acyl-coenzyme A thioesterase 9, mitochondrial	ENSG00000123130	ENST00000336430 ENST00000379303 ENST00000494361	ENSP0000036580 ENSP00000368605 ENSP00000420238	263 264 265
TM9SF2	Transmembrane 9 superfamily member 2	ENSG00000125304	ENST00000376387	ENSP00000365567	266
HS3ST3B1	Heparan sulfate glucosamine 3-O-sulfotransferase 3B1	ENSG00000125430	ENST00000360954 ENST00000466596	ENSP00000354213 ENSP00000436078	267 268
EML2	Echinoderm microtubule-associated protein-like 2	ENSG00000125746	ENST00000245925 ENST00000586195 ENST00000586405 ENST00000586770 ENST00000587152 ENST00000587484 ENST00000588272 ENST00000588308 ENST00000589876 ENST00000590018 ENST00000590043 ENST00000590819 ENST00000591721 ENST00000592853 ENST00000593255	ENSP00000245925 ENSP00000465339 ENSP00000465885 ENSP00000465786 ENSP00000468312 ENSP00000465994 ENSP00000466100 ENSP00000468329 ENSP00000464789 ENSP00000468373 ENSP00000464804 ENSP00000464950 ENSP00000468470 ENSP00000468383 ENSP00000467941	269 270 271 272 273 274 275 276 277 278 279 280 281 282 283
MGME1	Mitochondrial genome maintenance exonuclease 1	ENSG00000125871	ENST00000377704 ENST00000377709 ENST00000377710	ENSP00000366933 ENSP00000366938 ENSP00000366939	284 285 286
IGFLR1	IGF-like family receptor 1	ENSG00000126246	ENST00000246532 ENST00000588018 ENST00000588992 ENST00000591277 ENST00000591748 ENST00000592537 ENST00000592693 ENST00000592889	ENSP00000246532 ENSP00000468545 ENSP00000465962 ENSP00000468644 ENSP00000476009 ENSP00000466181 ENSP00000474913 ENSP00000467750	287 288 289 290 291 292 293 294
MYO5C	Unconventional myosin-Vc	ENSG00000128833	ENST00000261839	ENSP00000261839	295
ITFG1	T-cell immunomodulatory protein	ENSG00000129636	ENST00000320640 ENST00000544001 ENST00000563730 ENST00000565262 ENST00000565940	ENSP00000319918 ENSP00000441062 ENSP00000455630 ENSP00000457665 ENSP00000459192	296 297 298 299 300
SYT11	Synaptotagmin-11	ENSG00000132718	ENST00000368324	ENSP00000357307	301
SLC41A1	Solute carrier family 41 member 1	ENSG00000133065	ENST00000367137	ENSP00000356105	302
ATP13A3	Probable cation-transporting ATPase 13A3	ENSG00000133657	ENST00000256031 ENST00000429136 ENST00000439040 ENST00000446356 ENST00000457986 ENST00000619199	ENSP00000256031 ENSP00000402550 ENSP00000416508 ENSP00000410767 ENSP00000406234 ENSP00000482200	303 304 305 306 307 308
MICAL2	Protein-methionine sulfoxide oxidase MICAL2	ENSG00000133816	ENST00000379612	ENSP00000368932	309
CABLES1	CDK5 and ABL1 enzyme substrate 1	ENSG00000134508	ENST00000256925 ENST00000579963	ENSP00000256925 ENSP00000464435	310 311
HAVCR2	Hepatitis A virus cellular receptor 2	ENSG00000135077	ENST00000307851 ENST00000522593	ENSP00000312002 ENSP00000430873	312 313

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
CGA	Chromogranin-A	ENSG00000135346	ENST00000369582	ENSP00000358595	314
			ENST00000610310	ENSP00000482232	315
			ENST00000625577	ENSP00000486666	316
			ENST00000627148	ENSP00000486024	317
			ENST00000630630	ENSP00000487300	318
FAIM2	Protein lifeguard 2	ENSG00000135472	ENST00000320634	ENSP00000321951	319
			ENST00000547871	ENSP00000449360	320
			ENST00000550195	ENSP00000447715	321
			ENST00000550635	ENSP00000449711	322
			ENST00000550890	ENSP00000450132	323
			ENST00000552669	ENSP00000446771	324
			ENST00000552863	ENSP00000449957	325
ARHGEF4	Rho guanine nucleotide exchange factor 4	ENSG00000136002	ENST00000392953	ENSP00000376680	326
SLC41A2	Solute carrier family 41 member 2	ENSG00000136052	ENST00000258538	ENSP00000258538	327
NUSAP1	Nucleolar and spindle-associated protein 1	ENSG00000137804	ENST00000557840	ENSP00000453428	329
ADAM10	Disintegrin and metalloproteinase domain-containing protein 10	ENSG00000137845	ENST00000559046	ENSP00000452725	330
			ENST00000260408	ENSP00000260408	331
			ENST00000396136	ENSP00000456542	332
			ENST00000402627	ENSP00000386056	333
			ENST00000439637	ENSP00000391930	334
			ENST00000461408	ENSP00000481779	335
			ENST00000558004	ENSP00000452704	336
			ENST00000559053	ENSP00000453952	337
			ENST00000561288	ENSP00000452639	338
HADHB	Trifunctional enzyme subunit beta, mitochondrial	ENSG00000138029	ENST00000545822	ENSP00000442665	339
CD27	CD27 antigen	ENSG00000139193	ENST00000266557	ENSP00000266557	340
			ENST00000267383	ENSP00000267383	341
CDH24	Cadherin-24	ENSG00000139880	ENST00000397359	ENSP00000380517	342
			ENST00000487137	ENSP00000434821	343
			ENST00000554034	ENSP00000452493	344
			ENST00000610348	ENSP00000478078	345
			ENST00000560309	ENSP00000453753	347
ETFA	Electron transfer alpha, mitochondrial flavoprotein subunit	ENSG00000140374	ENST00000560044	ENSP00000452942	346
KSR1 SECTM1	Kinase suppressor of Ras 1 Secreted and transmembrane protein 1	ENSG00000141068	ENST00000580163	ENSP00000463204	348
			ENST00000269389	ENSP00000269389	349
			ENST00000580437	ENSP00000463904	350
			ENST00000581691	ENSP00000463114	351
			ENST00000581864	ENSP00000464111	352
			ENST00000581954	ENSP00000464385	353
			ENST00000582290	ENSP00000462294	354
			ENST00000582563	ENSP00000463120	355
			ENST00000583093	ENSP00000462563	356
			ENST00000270824	ENSP00000270824	357
EVA1B CTTNBP2NL	Protein eva-1 homolog B CTTNBP2 N-terminal-like protein	ENSG00000142694	ENST00000271277	ENSP00000271277	358
			ENST00000441739	ENSP00000390976	359
CASQ1 ARL6IP5	Calsequestrin-1 PRA1 family protein 3	ENSG00000143318	ENST00000368078	ENSP00000357057	360
			ENST00000273258	ENSP00000273258	361
ADPRH	[Protein ADP-ribosylarginine] hydrolase	ENSG00000144843	ENST00000478935	ENSP00000420138	362
			ENST00000484921	ENSP00000419374	363
			ENST00000485444	ENSP00000419021	364
			ENST00000481816	ENSP00000419703	369
			ENST00000304400	ENSP00000306100	370
			ENST00000345721	ENSP00000302544	371
			ENST00000346918	ENSP00000282992	372
PAM	Peptidyl-glycine alpha-amidating monooxygenase	ENSG00000145730	ENST00000348126	ENSP00000314638	373
			ENST00000438793	ENSP00000396493	374
			ENST00000455264	ENSP00000403461	375
			ENST00000504691	ENSP00000424203	376
			ENST00000505654	ENSP00000421569	377

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
RNF145	RING finger protein 145	ENSG00000145860	ENST00000506006	ENSP00000423611	378
			ENST00000509832	ENSP00000423763	379
			ENST00000511477	ENSP00000421823	380
			ENST00000511839	ENSP00000426448	381
			ENST00000512073	ENSP00000420851	382
			ENST00000274542	ENSP00000274542	383
			ENST00000424310	ENSP00000409064	384
			ENST00000518802	ENSP00000430955	385
			ENST00000519865	ENSP00000430397	386
			ENST00000520638	ENSP00000429071	387
TMEM140	Transmembrane protein 140	ENSG00000146859	ENST00000521606	ENSP00000430753	388
			ENST00000611185	ENSP00000482720	389
CHST7	Carbohydrate sulfotransferase 7	ENSG00000147119	ENST00000276055	ENSP00000276055	390
CHRNA6	Neuronal acetylcholine receptor subunit alpha-6	ENSG00000147434	ENST00000276410	ENSP00000276410	392
			ENST00000533810	ENSP00000434659	393
			ENST00000534622	ENSP00000433871	394
			ENST00000418331	ENSP00000400010	395
			ENST00000440289	ENSP00000409733	396
			ENST00000527952	ENSP00000435618	397
			ENST00000534219	ENSP00000432686	398
			ENST00000613246	ENSP00000477933	399
			ENST00000615445	ENSP00000479342	400
			ENST00000316851	ENSP00000318472	401
PTPRJ	Receptor-type tyrosine-protein phosphatase eta	ENSG00000149177	ENST00000401611	ENSP00000384055	402
			ENST00000524916	ENSP00000478072	403
			ENST00000526322	ENSP00000479687	404
			ENST00000528158	ENSP00000486241	405
			ENST00000528590	ENSP00000480269	406
			ENST00000529356	ENSP00000482205	407
			ENST00000531044	ENSP00000484943	408
			ENST00000531817	ENSP00000475074	409
			ENST00000533073	ENSP00000486406	410
			ENST00000613217	ENSP00000479353	411
			ENST00000615112	ENSP00000480797	412
			ENST00000615285	ENSP00000479241	413
			ENST00000618266	ENSP00000477835	414
			ENST00000619839	ENSP00000480132	415
			ENST00000620046	ENSP00000482852	416
			ENST00000621128	ENSP00000481083	417
			ENST00000621518	ENSP00000477808	418
			ENST00000621850	ENSP00000480774	419
INPP1	Inositol polyphosphate 1-phosphatase	ENSG00000151689	ENST00000413239	ENSP00000391415	420
			ENST00000444194	ENSP00000404732	421
			ENST00000451089	ENSP00000410662	422
			ENST00000458193	ENSP00000412119	423
JAKMIP1	Janus kinase and protein 1	ENSG00000152969	ENST00000409021	ENSP00000386711	424
			ENST00000409371	ENSP00000387042	425
RHOC	microtubule-interacting Rho-related GTP-binding protein RhoC	ENSG00000155366	ENST00000468093	ENSP00000431392	426
			ENST00000484280	ENSP00000434310	427
			ENST00000528831	ENSP00000432209	428
SLC16A1	Monocarboxylate transporter 1	ENSG00000155380	ENST00000369626	ENSP00000358640	429
			ENST00000429288	ENSP00000397106	430
			ENST00000443580	ENSP00000399104	431
			ENST00000458229	ENSP00000416167	432
			ENST00000538576	ENSP00000441065	433
CXCL13	C—X—C motif chemokine 13	ENSG00000156234	ENST00000286758	ENSP00000286758	434
			ENST00000359120	ENSP00000352028	435
SH3RF2	Putative E3 ubiquitin-protein ligase SH3RF2	ENSG00000156463	ENST00000511217	ENSP00000424497	436
			ENST00000345330	ENSP00000290401	437
			ENST00000351217	ENSP00000342958	438
			ENST00000562924	ENSP00000456349	439
NPTN	Neuroplastin	ENSG00000156642	ENST00000563691	ENSP00000457028	440
			ENST00000565325	ENSP00000457470	441

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
AHCYL2	Adenosylhomocysteinase 3	ENSG00000158467	ENST00000466924	ENSP00000419346	442
PTGIR	Prostacyclin receptor	ENSG00000160013	ENST00000291294 ENST00000594275	ENSP00000291294 ENSP00000469408	443 444
			ENST00000596260	ENSP00000468970	445
			ENST00000597185	ENSP00000470566	446
			ENST00000598865	ENSP00000470799	447
TMPRSS3	Transmembrane protease serine 4	ENSG00000160183	ENST00000291532 ENST00000398397 ENST00000398405	ENSP00000291532 ENSP00000381434 ENSP00000381442	448 449 450
			ENST00000433957	ENSP00000411013	451
FCRL3	Fc receptor-like protein 3	ENSG00000160856	ENST00000368184 ENST00000368186 ENST00000477837 ENST00000485028	ENSP00000357167 ENSP00000357169 ENSP00000433430 ENSP00000434331	452 453 454 455
			ENST00000492769	ENSP00000435487	456
			ENST00000496769	ENSP00000473680	457
PAQR4	Progesterin and adipoQ receptor family member 4	ENSG00000162073	ENST00000293978 ENST00000318782 ENST00000572687 ENST00000574988	ENSP00000293978 ENSP00000321804 ENSP00000459418 ENSP00000458683	458 459 460 461
			ENST00000576565	ENSP00000460326	462
ZG16B	Zymogen granule protein 16 homolog B	ENSG00000162078	ENST00000382280 ENST00000570670 ENST00000571723 ENST00000572863	ENSP00000371715 ENSP00000460793 ENSP00000458847 ENSP00000461740	463 464 465 466
SGPP2	Sphingosine-1-phosphate phosphatase 2	ENSG00000163082	ENST00000321276	ENSP00000315137	467
NEURL3	E3 ubiquitin-protein ligase NEURL1B	ENSG00000163121	ENST00000310865	ENSP00000479456	468
KIF15	Kinesin-like protein KIF15	ENSG00000163808	ENST0000043580 ENST00000438321	ENSP00000480933 ENSP00000406939	469 470
TMEM184C	Transmembrane protein 184C	ENSG00000164168	ENST00000296582 ENST00000505999 ENST00000508208	ENSP00000296582 ENSP00000421159 ENSP00000425940	471 472 473
C5ORF63	Glutaredoxin-like protein C5orf63	ENSG00000164241	ENST00000296662 ENST00000508527 ENST00000509733 ENST00000535381	ENSP00000453964 ENSP00000475157 ENSP00000475415 ENSP00000454153	474 475 476 477
			ENST00000606042 ENST00000606937	ENSP00000475733 ENSP00000475810	478 479
			ENST00000607731	ENSP00000476160	480
MELK	Maternal embryonic leucine zipper kinase	ENSG00000165304	ENST00000495529 ENST00000536329 ENST00000536987 ENST00000543751	ENSP00000487536 ENSP00000443550 ENSP00000439184 ENSP00000441596	481 482 483 484
			ENST00000626154	ENSP00000486558	485
FAAH2	Fatty-acid amide hydrolase 2	ENSG00000165591	ENST00000374900	ENSP00000364035	486
TPP1	Alpha-tocopherol transfer protein	ENSG00000166340	ENST00000299427 ENST00000436873 ENST00000528571 ENST00000528657	ENSP00000299427 ENSP00000398136 ENSP00000434647 ENSP00000435001	487 488 489 490
CX3CR1	CX3C chemokine receptor 1	ENSG00000168329	ENST00000358309 ENST00000399220 ENST00000412814 ENST00000435290	ENSP00000351059 ENSP00000382166 ENSP00000408835 ENSP00000394960	491 492 493 494
			ENST00000541347 ENST00000542107	ENSP00000439140 ENSP00000444928	495 496
TSPAN5	Tetraspanin-5	ENSG00000168785	ENST00000305798 ENST00000505184 ENST00000508798 ENST00000511651	ENSP00000307701 ENSP00000423916 ENSP00000421808 ENSP00000426248	497 498 499 500
			ENST00000511800 ENST00000515287	ENSP00000422548 ENSP00000423504	501 502
			ENST00000515440	ENSP00000422351	503

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
UGP2	UTP--glucose-1-uridylyltransferase phosphate	ENSG00000169764	ENST00000467999 ENST00000496334	ENSP00000418642 ENSP00000420760	504 505
GLB1	Beta-galactosidase	ENSG00000170266	ENST00000307363 ENST00000307377 ENST00000399402 ENST00000415454 ENST00000436768 ENST00000438227 ENST00000440656 ENST00000446732 ENST00000450835	ENSP00000306920 ENSP00000305920 ENSP00000382333 ENSP00000411813 ENSP00000387989 ENSP00000401250 ENSP00000411769 ENSP00000407365 ENSP00000403264	506 507 508 509 510 511 512 513 514
SPATA24	Spermatogenesis-associated protein 24	ENSG00000170469	ENST00000514983	ENSP00000423424	515
RBKS	Ribokinase	ENSG00000171174	ENST00000449378	ENSP00000413789	516
NETO2	Neuropilin and toll-like protein 2	ENSG00000171208	ENST00000303155 ENST00000562435 ENST00000562559 ENST00000563078 ENST00000564667	ENSP00000306726 ENSP00000455169 ENSP00000454213 ENSP00000456818 ENSP00000457133	517 518 519 520 521
LRG1	Leucine-rich alpha-2-glycoprotein	ENSG00000171236	ENST00000306390	ENSP00000302621	522
FAM98B	Protein FAM98B	ENSG00000171262	ENST00000491535 ENST00000559431	ENSP00000453166 ENSP00000453926	523 524
CHST11	Carbohydrate sulfotransferase 11	ENSG00000171310	ENST00000303694 ENST00000546689 ENST00000547956	ENSP00000305725 ENSP00000448678 ENSP00000449093	525 526 527
ECEL1	Endothelin-converting enzyme-like 1	ENSG00000171551	ENST00000304546 ENST00000409941	ENSP00000450004 ENSP00000386333	528 530
BCL2L1	Bcl-2-like protein 1	ENSG00000171552	ENST00000307677 ENST00000376055	ENSP00000302564 ENSP00000365223	531 532
MALT1	Mucosa-associated lymphoid tissue lymphoma translocation protein 1	ENSG00000172175	ENST00000345724 ENST00000348428 ENST00000591792	ENSP00000304161 ENSP00000319279 ENSP00000467222	533 534 535
CYP7B1	25-hydroxycholesterol 7-alpha-hydroxylase	ENSG00000172817	ENST00000310193	ENSP00000310721	537
HPSE	Heparanase	ENSG00000173083	ENST00000311412 ENST00000405413 ENST00000507150 ENST00000508891 ENST00000509906 ENST00000512196 ENST00000513463	ENSP00000308107 ENSP00000384262 ENSP00000426139 ENSP00000421827 ENSP00000421038 ENSP00000423265 ENSP00000421365	538 539 540 541 542 543 544
VANGL1	Vang-like protein 1	ENSG00000173218	ENST00000310260 ENST00000355485 ENST00000369509 ENST00000369510	ENSP00000310800 ENSP00000347672 ENSP00000358522 ENSP00000358523	545 546 547 548
CD7	T-cell antigen CD7	ENSG00000173762	ENST00000312648 ENST00000578509 ENST00000581434 ENST00000582480 ENST00000583376 ENST00000584284	ENSP00000312027 ENSP00000464565 ENSP00000464546 ENSP00000464182 ENSP00000463489 ENSP00000463612	549 550 551 552 553 554
HAP1	Huntingtin-associated protein 1	ENSG00000173805	ENST00000455021	ENSP00000397242	555
FBXO45	F-box/SPRY domain-containing protein 1	ENSG00000174013	ENST00000440469	ENSP00000389868	556
CHST2	Carbohydrate sulfotransferase 2	ENSG00000175040	ENST00000309575	ENSP00000307911	557
RM12	RecQ-mediated genome instability protein 2	ENSG00000175643	ENST00000572173	ENSP00000461206	558
SLC35E3	Solute carrier family 35 member E3	ENSG00000175782	ENST00000398004 ENST00000431174	ENSP00000381089 ENSP00000403769	559 560
ZBTB38	Zinc finger and BTB domain-containing protein 38	ENSG00000177311	ENST00000503809	ENSP00000422051	561

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
YIPF6	Protein YIPF6	ENSG00000181704	ENST00000374622	ENSP00000363751	562
			ENST00000451537	ENSP00000401799	563
			ENST00000462683	ENSP00000417573	564
CREB3L2	Cyclic AMP-responsive element-binding protein 3-like protein 2	ENSG00000182158	ENST00000330387	ENSP00000329140	565
			ENST00000420629	ENSP00000402889	566
			ENST00000456390	ENSP00000403550	567
XKRX	XK-related protein 2	ENSG00000182489	ENST00000372956	ENSP00000362047	568
			ENST00000468904	ENSP00000419884	569
CADM1	Cell adhesion molecule 1	ENSG00000182985	ENST00000331581	ENSP00000329797	570
			ENST00000452722	ENSP00000395359	571
			ENST00000536727	ENSP00000440322	572
			ENST00000537058	ENSP00000439817	573
			ENST00000540951	ENSP00000445375	574
			ENST00000542447	ENSP00000439176	575
			ENST00000542450	ENSP00000442001	576
			ENST00000543540	ENSP00000439847	577
			ENST00000545380	ENSP00000442387	578
			ENST00000612235	ENSP00000483648	579
			ENST00000612471	ENSP00000483793	580
			ENST00000616271	ENSP00000484516	581
			ENST00000621043	ENSP00000482840	582
			ENST00000621709	ENSP00000482924	583
LHFP	Lipoma HMGIC fusion partner	ENSG00000183722	ENST00000379589	ENSP00000368908	584
CSF1	Macrophage colony-stimulating factor 1	ENSG00000184371	ENST00000329608	ENSP00000327513	585
			ENST00000357302	ENSP00000349854	586
			ENST00000369801	ENSP00000358816	587
			ENST00000369802	ENSP00000358817	588
			ENST00000420111	ENSP00000407317	589
			ENST00000488198	ENSP00000433837	590
			ENST00000525659	ENSP00000431547	591
			ENST00000527192	ENSP00000434527	592
			ENST00000329397	ENSP00000332274	593
			ENST00000349124	ENSP00000331730	594
PTP4A3	Protein tyrosine phosphatase type IVA 3	ENSG00000184489	ENST00000520105	ENSP00000428758	595
			ENST00000521578	ENSP00000428976	596
			ENST00000523147	ENSP00000428725	597
			ENST00000524028	ENSP00000430332	598
			ENST00000445781	ENSP00000411497	599
OSBP2	Oxysterol-binding protein 2	ENSG00000184792	ENST00000445781	ENSP00000411497	599
METTL7A	Methyltransferase-like protein 7A	ENSG00000185432	ENST00000332160	ENSP00000331787	600
			ENST00000547104	ENSP00000447542	601
			ENST00000548553	ENSP00000448785	602
			ENST00000550097	ENSP00000448286	603
			ENST00000550502	ENSP00000450239	604
TMPRSS6	Transmembrane protease serine 6	ENSG00000187045	ENST00000346753	ENSP00000334962	605
			ENST00000381792	ENSP00000371211	606
			ENST00000406725	ENSP00000385453	607
			ENST00000406856	ENSP00000384964	608
			ENST00000423761	ENSP00000400317	609
			ENST00000429068	ENSP00000392433	610
			ENST00000442782	ENSP00000397691	611
			ENST00000376730	ENSP00000365920	612
			ENST00000442371	ENSP00000415454	613
			ENST00000444201	ENSP00000390703	614
GCNT1	Beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase	ENSG00000187210	ENST00000342972	ENSP00000343706	615
			ENST00000442371	ENSP00000415454	613
MAGEH1	Melanoma-associated antigen H1	ENSG00000187601	ENST00000342972	ENSP00000343706	615
NEMP2	Nuclear envelope integral membrane protein 2	ENSG00000189362	ENST00000343105	ENSP00000340087	616
			ENST00000409150	ENSP00000386292	617
			ENST00000414176	ENSP00000404283	618
			ENST00000421038	ENSP00000410306	619
			ENST00000444545	ENSP00000403867	620
			ENST0000040761	ENSP00000403867	620
NTNG2	Netrin-G2	ENSG00000196358	ENST00000372179	ENSP00000361252	621
PDGFA	Platelet-derived growth factor subunit A	ENSG00000197461	ENST00000393229	ENSP00000376921	622
			ENST00000354513	ENSP00000346508	623
			ENST00000402802	ENSP00000383572	624
			ENST00000405692	ENSP00000383889	625
				ENSP00000384673	626

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Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
PDCD1LG2	Programmed cell death 1 ligand 2	ENSG00000197646	ENST00000397747	ENSP00000380855	627
TOR4A	Torsin-4A	ENSG00000198113	ENST00000357503	ENSP00000350102	628
HIBCH	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	ENSG00000198130	ENST00000392333	ENSP00000376145	629
NTRK1	High affinity nerve growth factor receptor	ENSG00000198400	ENST00000358660	ENSP00000351486	631
			ENST00000368196	ENSP00000357179	632
			ENST00000392302	ENSP00000376120	633
			ENST00000497019	ENSP00000436804	634
			ENST00000524377	ENSP00000431418	635
FAM19A2	Protein FAM19A2	ENSG00000198673	ENST00000416284	ENSP00000393987	636
			ENST00000548780	ENSP00000449310	637
			ENST00000549379	ENSP00000447584	638
			ENST00000549958	ENSP00000447280	639
			ENST00000550003	ENSP00000449457	640
			ENST00000551449	ENSP00000449632	641
			ENST00000551619	ENSP00000447305	642
			ENST00000552075	ENSP00000449516	643
F5	Coagulation factor V	ENSG00000198734	ENST00000367796	ENSP00000356770	644
			ENST00000367797	ENSP00000356771	645
GK	Glycerol kinase	ENSG00000198814	ENST00000378943	ENSP00000368226	646
			ENST00000427190	ENSP00000401720	647
			ENST00000488296	ENSP00000419771	648
INPP5F	Phosphatidylinositol phosphatase SAC2	ENSG00000198825	ENST00000490818	ENSP00000487706	649
CD177	CD177 antigen	ENSG00000204936	ENST00000378012	ENSP00000367251	651
			ENST00000607855	ENSP00000483817	652
			ENST00000618265	ENSP00000479536	653
LEPROT	Leptin Receptor Overlapping Transcript	ENSG00000213625	ENST00000371065	ENSP00000360104	654
TRIM16	Tripartite motif-containing protein 16	ENSG00000221926	ENST00000613538	ENSP00000483521	655
LTA	Lymphotoxin-alpha	ENSG00000226979	ENST00000418386	ENSP00000413450	657
			ENST00000434752	ENSP00000403495	658
PROB1	Proline-rich basic protein 1	ENSG00000228672	ENST00000434752	ENSP00000416033	659
SSTR3	Somatostatin receptor type 3	ENSG00000278195	ENST00000610913	ENSP00000480971	660
CEACAM1	Carcinoembryonic antigen-related cell adhesion molecule 1	ENSG00000079385	ENST00000161559	ENSP00000161559	662
			ENST00000352591	ENSP00000244291	663
			ENST00000358394	ENSP00000351165	664
			ENST00000403444	ENSP00000384709	665
			ENST00000403461	ENSP00000384083	666
			ENST00000471298	ENSP00000472633	667
			ENST00000599389	ENSP00000471918	668
			ENST00000600172	ENSP00000471566	669
CTLA4	Cytotoxic T-lymphocyte protein 4	ENSG00000163599	ENST00000295854	ENSP00000295854	670
			ENST00000302823	ENSP00000303939	671
			ENST00000427473	ENSP00000409707	672
			ENST00000472206	ENSP00000417779	673
TIGIT	T-cell immunoreceptor with Ig and ITIM domains	ENSG00000181847	ENST00000383671	ENSP00000373167	674
			ENST00000461158	ENSP00000418917	675
			ENST00000481065	ENSP00000420552	676
			ENST00000484319	ENSP00000419706	677
			ENST00000486257	ENSP00000419085	678
IL2RA	Interleukin-2 receptor subunit alpha	ENSG00000134460	ENST00000256876	ENSP00000256876	679
			ENST00000379954	ENSP00000369287	680
			ENST00000379959	ENSP00000369293	681
ENTPD1	Ectonucleoside triphosphate diphosphohydrolase 1	ENSG00000138185	ENST00000371205	ENSP00000360248	682
			ENST00000371207	ENSP00000360250	683
			ENST00000453258	ENSP00000390955	684
			ENST00000483213	ENSP00000489333	685
			ENST00000543964	ENSP00000442968	686
			ENST00000635076	ENSP00000489250	687
ICOS	Inducible T-cell costimulator	ENSG00000163600	ENST00000316386	ENSP00000319476	688
			ENST00000435193	ENSP00000415951	689
TNFRSF4	Tumor necrosis factor receptor superfamily member 4	ENSG00000186827	ENST00000379236	ENSP00000368538	690

TABLE VI-continued

Gene name	Description	ENSG ID release87	ENST ID	ENSP ID	SEQ ID No of the aa sequence of the protein isoform
TNFRSF18	Tumor necrosis factor receptor superfamily member 18	ENSG00000186891	ENST00000328596	ENSP00000328207	691
			ENST00000379265	ENSP00000368567	692
			ENST00000379268	ENSP00000368570	693
			ENST00000486728	ENSP00000462735	694
TNFRSF8	Tumor necrosis factor receptor superfamily member 8	ENSG00000120949	ENST00000263932	ENSP00000263932	695
			ENST00000417814	ENSP00000390650	696
			ENST00000514649	ENSP00000421938	697
CD274	Programmed cell death 1 ligand 1	ENSG00000120217	ENST00000381573	ENSP00000370985	698
IL2RB	Interleukin-2 receptor subunit beta	ENSG00000100385	ENST00000381577	ENSP00000370989	699
			ENST00000216223	ENSP00000216223	700
			ENST00000429622	ENSP00000402685	701
TNFRSF9	Tumor necrosis factor receptor superfamily member 9	ENSG00000049249	ENST00000445595	ENSP00000401020	702
			ENST00000453962	ENSP00000403731	703
			ENST00000377507	ENSP00000366729	704
IKZF2	Zinc finger protein Helios	ENSG00000030419	ENST00000474475	ENSP00000465272	705
			ENST00000615230	ENSP00000478699	706
			ENST00000442445	ENSP00000390045	707

[0256] Genes of table VI are characterized by their Ensembl Gene accession number (ENSG), retrievable in the public database EnsEMBL (<http://www.ensembl.org>). Each related protein isoform is characterized by an Ensembl transcript accession number (ENST) and an Ensembl protein accession number (ENSP).

Identification of Transcript Isoforms Expressed by Tumor-Treg Cells

[0257] An important aspect to be verified in the selection of potential targets of tumor-T reg is that the protein isoforms predicted to be surface exposed/membrane associated by the cell localization algorithms are indeed expressed in tumor Treg cells. Thus, total RNA was extracted from tumor Treg cells isolated from NSCLC or CRC samples and subjected to RT-PCR using specific primer pairs able to discriminate the different isoforms annotated for each gene. Exemplificative results of protein isoforms predicted to be surface exposed and detected in tumor T reg cells is reported in Table VII. Moreover, an example of RT-PCR analysis carried out for SIRPG is reported in FIG. 10.

TABLE VII

GENE SYMBOL	Representative examples of transcripts detected in tumor-infiltrating Treg cells
CCR8	ENST00000326306
LAYN	ENST00000375614 and/or ENST00000533265 and/or ENST00000375615 and/or ENST00000525126
CD7	ENST00000312648 and/or ENST00000584284
CXCL13	ENST00000286758
FCRL3	ENST00000492769 and/or ENST00000368184 and/or ENST00000368186 and/or ENST00000485028
IL1R2	ENST00000332549 and/or ENST00000393414
IL21R	ENST00000337929 and/or ENST00000395754 and/or ENST00000564089

TABLE VII-continued

Representative examples of transcripts detected in tumor-infiltrating Treg cells	
GENE SYMBOL	Surface predicted isoform detected in Tumor Treg cells
NTNG2	ENST00000393229
SIRPG	ENST00000303415 and/or ENST00000216927 and/or ENST00000344103 and/or ENST00000381580 and/or ENST00000381583
TSPAN5	ENST00000305798 and/or ENST00000505184
TMPRSS3	ENST00000291532
TMPRSS6	ENST00000406725 and/or ENST00000406856
NDFIP2	ENST00000218652

Discussion

[0258] Diversity of tumor infiltrating Treg cells should be fully elucidated to understand their functional relevance and prognostic significance in different types of cancer, and to possibly improve the therapeutic efficacy of Treg cell modulation through the selective depletion of tumor infiltrating Treg cells. The transcriptome analysis performed on CRC- and NSCLC-infiltrating T cells showed that tumor-infiltrating Treg cells are different from both circulating and normal tissue-infiltrating Tregs, suggesting that the tumor microenvironment influences specific gene expression in Treg cells. Our findings further support the view that Treg cells from different tissues are instructed by environmental factors to display different gene expression profiles (Panduro et al., 2016). Indeed the list of signature genes includes a number of molecules that are consistently upregulated in tumor infiltrating Treg cells isolated from different tumor types, and these signature genes would have not been identified if the inventors had not profiled specifically tumor infiltrating Treg cells. It was found tumor-infiltrating-Treg signature genes are not only largely shared between CRC and NSCLC infiltrating cells, but are also conserved in breast and gastric cancers as well as in CRC and NSCLC metastatic tumors (in liver and brain respectively) suggesting that expression of

these genes is a common feature of tumor infiltrating Treg cells that may correlate with Treg cells specific function within the tumor microenvironment. Although our knowledge on the function of immune checkpoints on lymphocytes is still incomplete, agonist or antagonist monoclonal antibodies targeting checkpoints are in clinical development. Interestingly, it has been found that some of these checkpoints (such as GITR, OX40, TIGIT, LAG-3 and TIM-3) and some of their ligands (such as OX40LG, Galectin-9, CD70) are upregulated also in tumor infiltrating Treg cells, and this fact should be taken into account in interpreting clinical results with checkpoint inhibitors. Indeed, it is likely that assessment of the expression of checkpoints and of their ligands on the various subsets of tumor infiltrating lymphocytes will help to elucidate conflicting results and provide the rationale for combination therapies. Therefore, expression pattern of checkpoints should be evaluated both in tumor infiltrating lymphocytes and in tumor cells. Single-cell analysis on selected tumor Treg signature genes confirmed the whole transcriptomic data and provided information on the expression frequency of these genes. Tumor infiltrating Treg cells express with high frequency genes that are associated with increased suppressor activity, such as the well characterized OX40, CTLA4 and GITR. Moreover, there are a number of interesting and less expected genes the specific expression of which was validated also at the protein level. For example, IL-1 R2 upregulation could be another mechanism that tumor resident Treg cells employ to dampen anti-tumor immune responses through the neutralization of IL-1 β function on effector cells. PD-L1 and PD-L2 expression has been recently reported on activated T cells or APCs (Boussiotis et al., 2014; Lesterhuis et al., 2011; Messal et al., 2011) but, to the best of our knowledge, neither PD-L2 nor PD-L1 expression has ever been reported in Treg cells, and our finding that they are overexpressed in tumor infiltrating Treg cells adds an additional level of complexity to the PD1/PD-Ls immunomodulatory axis within the tumor microenvironment. BATF is a transcription factor that has been mainly associated to Th17 development and CD8 $^{+}$ T cells differentiation (Murphy et al., 2013). Our findings show that BATF transcript is upregulated in tumor infiltrating Treg cells more than in tumor infiltrating Th17 cells (FIG. 8). Interestingly, expression of BATF in CD8 $^{+}$ T cells is induced by IL-21 (Xin et al., 2015), and it was found that IL21R is highly expressed in tumor-infiltrating Treg cells (FIG. 4).

[0259] It was showed that tumor infiltrating Treg cells express high amounts of 4-1 BB (CD137) a marker of TcR mediated activation (Schoenbrunn et al., 2012) and have shown they display very high suppressor function on effector T cell proliferation. It could be that expression of the signature genes correlated with the enhanced suppressive ability and so contributed to the establishment of a strong immunosuppressive environment at tumor sites. A corollary to our findings would have that increased number of Treg cells in the tumor environment should associate with a worst clinical outcome. In fact, when LAYN, MAGEH1 and CCR8 (which represent three of the most enriched genes in tumor infiltrating Treg cells) are highly detected in whole tumor samples there is a significant worsening of the 5 years survival of both CRC and NSCLC patients. Although, the functional roles in Treg cells of LAYN, a transmembrane protein with homology to c-type lectin (Borowsky and Hynes, 1998), and of MAGEH1, a member of the Melanoma

Antigen Gene family (Weon and Potts, 2015) are unknown, the high expression of the chemokine receptor CCR8 is instead intriguing. Indeed CCL18, the ligand of CCR8 (Islam et al., 2013), is highly expressed in different tumors including NSCLC (Chen et al., 2011; Schutyser et al., 2005). The high specificity of CCR8 expression on tumor infiltrating Treg cells suggests it could be a new interesting therapeutic target to inhibit Treg cells trafficking to tumor sites, without disturbing recruitment of other effector T cells that do not express CCR8. Considerable efforts have been recently put in the development of sophisticated bioinformatics approaches that exploit lymphocyte gene expression data to understand the immune-modulatory networks at tumor sites, to predict clinical responses to immune-therapies, and to define novel therapeutic targets (Bindea et al., 2013a; Bindea et al., 2013b; Gentles et al., 2015). The data here presented represent the first comprehensive RNA-sequencing analysis performed on tumor-infiltrating human CD4 $^{+}$ Treg, Th1 and Th17 cells. Our findings highlight the relevance of assessing gene expression patterns of lymphocyte at tumor-sites and suggest that generation of more transcriptomic data of tumor-infiltrating lymphocyte subsets purified from different cancer types may contribute to a better understanding of the dynamics underlying immune modulation in the tumor microenvironment. Moreover, our data represent a resource to generate and validate novel hypotheses that will increase our knowledge on tumor infiltrating Treg cell biology and should lead to the identification of new therapeutic targets.

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SEQUENCE LISTING

Sequence total quantity: 791

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 source 1..374
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 organism = Homo sapiens

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 EACRRDGQL VSIESEDEQK LIEKPIENLL PSDGDFWIGL RRREEKQSNS TACQDLYAWT 120
 DGSISQFRNW VSVDEPSCGSE VCVMYHQPSS APAGIGGPYMFQ FQWNNDRCNM KNNFICKYSD 180
 EKPAVPSREA EGEETELTPP VLPEETQEDAK KTFKESREAA AALNLAYILILI PSIPLLLL 240
 VTTVVCWWI CRKRKREQPD PSTKKQHTIW PSPHQGNSPD LEVYNVIRKQ SEADLAETRP 300
 DLKNISFRVC SGEATPDDMS CDYDNMAVNP SESGFVTLVS VESGFVTNDI YEFSPDQMGR 360
 SKESGWVENE IYGY 374

SEQ ID NO: 2 moltype = AA length = 382
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 source 1..382
 mol_type = protein
 organism = Homo sapiens

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 RLNFEEAKEA CRRDGQLVS IESEDEQKLI EKFIENLLPS DGDFWIGLRR REEKQSNSTA 120
 CQDLYAWTDG SISQFRNWVY DEPSCGSEVC VVMYHQPSAP AGIGGPYMFQ WNDDRCNMKN 180
 NFICKYSEK PAVPSREAAEG EETELTPVPL PEETQEEADAK KTFKESREAA LNLAYILIPS 240
 IPPLLLLVT TVVCWWICR KRKRKREQPDPS TKKQHTIWPS PHQGNSPDLE VYNVIRKQSE 300
 ADLAETRPDL KNISFRVC SGEATPDDMSCD YDNMAVNPSE SGFVTLVSVE SGFVTNDIYE 360
 FSPDQMGRSK ESGWVENEIY GY 382

SEQ ID NO: 3 moltype = AA length = 229
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 mol_type = protein
 organism = Homo sapiens

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 QHTIWPSPHQ GNPDLEVYN VIRKQSEADL AETRPDLKNI SFRVCSGEAT PDDMSCDYDN 180
 MAVNPSESGF VTLVSVESGF VTNDIYEFS DQMGRSKESG WVENEIYGY 229

SEQ ID NO: 4 moltype = AA length = 270
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 mol_type = protein
 organism = Homo sapiens

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 CQDLYAWTDG SISQFRNWVY DEPSCGSEVC VVMYHQPSAP AGIGGPYMFQ WNDDRCNMKN 180
 NFICKYSEK PAVPSREAAEG EETELTPVPL PEETQEEADAK KTFKESREAA LNLAYILIPS 240
 IPPLLLLVT TVVCWWICR KRQKTGAARP 270

SEQ ID NO: 5 moltype = AA length = 134
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 mol_type = protein
 organism = Homo sapiens

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 DGSISQFRRET SSSF 134

SEQ ID NO: 6 moltype = AA length = 108
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 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 6
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SEQ ID NO: 7      moltype = AA length = 109
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source          Location/Qualifiers
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mol_type = protein
organism = Homo sapiens
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mol_type = protein
organism = Homo sapiens
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mol_type = protein
organism = Homo sapiens
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VVCKKLRSIT DLYVLLNLALS DLLFVFSFPF QTYYLLDQWV FGTVMCKVVS GFYYIGFYSS 120
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LQCYSFYNQQ TLKWKIFTNF KMNLIGLLIP FTIFMFCYIK ILHQLKRCQN HNKTKAIRLV 240
LIVVIASLLF WVPFNVLFL TSLHSMHILD GCSISQQLTY ATHVTEIIISF THCCVNPVIY 300
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source          Location/Qualifiers
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organism = Homo sapiens
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organism = Homo sapiens
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APPFNVTVTF SGQYNIISWRS DYEDPAFYML KGKLQYELQY RNRRGDPWAVS PRRKLISVDS 180
RSVSLPLEF RKDSSYELQV RAGPMPGSSY QGTWSEWSDP VIFQTQSEEL KEGWNPHLLL 240
LLLVLVIVEIP AFWSLKHPL WRLWKKIWA VSPERFFFML YKGCSGDFKK WVGAFTGSS 300
LELGPWSPEV PSTLEVYSCB PPRSPAKRLQ LTELQEPAAEL VESDGVPKPS FWPTAQNSGG 360
SAYSEERDRP YLVLSIDTVT VLDAEGPCTW PCSCEDDGEP ALDDLADLEP SPGLEDPPLL 420
AGTTVLSGCGC VSAGSPGLGG PLGSSLDRLK PPLADGEDWA GGLPWGRSP GGVSESEAGS 480
PLAGLDMTF DSGFGVGSDCS SPVECDFTSP GDEGPPRSYL RQWVVIPPL SSPGPQAS 538

SEQ ID NO: 13     moltype = AA length = 538
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source          Location/Qualifiers
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organism = Homo sapiens
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SAYSEERDRP YGLVSIDTVT VLDAEGPCTW PCSCEDDGYP ALLDADGLEP SPGLEDPILL	420
AGTTVLS CGC VSAGSPGLGG PLGSLLDRLK PPLADGEDWA GGLPWGRSP GGVSESEAGS	480
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organism = Homo sapiens	
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RSVSLPLEF RKDSSYELQV RAGPMPGSSY QGTWSENSDP VIFQTQSEEL KEGWNPHLLL	240
LLLLVIVFIP AFWSLKHPL WRLWKKIHAV PSPERFFMPL YKGCSDFKK WVGAPFTGSS	300
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SAYSEERDRP YGLVSIDTVT VLDAEGPCTW PCSCEDDGYP ALLDADGLEP SPGLEDPILL	420
AGTTVLS CGC VSAGSPGLGG PLGSLLDRLK PPLADGEDWA GGLPWGRSP GGVSESEAGS	480
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organism = Homo sapiens	
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WGVSFSVPSFG SEFWWYWQK EKIPKYVEFM KDNYPPSPFKY EDFGPIFLAK FFNANQWADI	120
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YSLFEWHPFL FLEDESSSFH KRQFPVSKTL PELYELVNYY QPEVLWSDGD GGAPDQYWN	240
TGFLAWLYNE SPVRGTVVTN DRWLGASICK HGGFYTCSDR YNPGHLLPHK WENCMТИDKL	300
SWGYRREAGI SDYLTIEELV KQLVETVSCG GNLLMNIGPT LDGTISVVFE ERLRQMGSWL	360
KVNGEAIYET HTWRSQNDTV TPDVWYTSKPK KEKLVYAIFL KWPTSGQFLF GHPKAILGAT	420
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organism = Homo sapiens	
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ELFHHSIQRTE LDLSKAIVLY QKRICFLSQE ENELGKFLRS QGFQDKTRAG KMMQATGKAL	120
CFSQQRLAL RNPLCRFHQE VETFRHRAIS DTWLTVNRM E QCRTEYRGAL LWMKDVSQEL	180
DPDLYKQMEK FRKVQTQVRL AKKNFDKLM DVCQKVDLLG ASRCNLSSHM LATYQTTLLH	240
FWEKTSHTMA AIHESFKGYQ PYEFTTLKVN KLEGPLENLE KSKVLFISQA KSIAESIIIP	300
GLRMLKRELC PQQSLFLSFF LSFFFFFFF TAGFNTMRI YCNPKARI	350
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organism = Homo sapiens	
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TCCAVPGVAI LTGPNPLTG ALGLFNIFLY TCCYTPLKRI SIANTWVGAV VGAIPVMGW	300
TAATGSLDAF AFLLGGILYS WQFPHFNALS WGLREDYSRG GYCMMSVTHP GLCRVALRH	360
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SFCCSLSELF M	131
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VALVHAVQAL WKQFQSFC CS LSELFMSSF Q SYGATRGARR SMCFPKVLS D MKKLKARMV	240
MILLPTSAQGL GAWVSACDTE DTVGHLGPWR DKDPALWCQL CLSSQHQAI E RFYDKM QNAE	300
SGRGQVMSSL AELEDDFKEG YLETVAAYYE EQHPELTPPLL EKERDGLRCR GNRSPVPDVE	360
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VQALWKQFQS FCCSLSELF M SSFQSYGAPR GDKEELTPQK CSEPQSSK	168
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KERDGLRCRG NRSPVPDVDED PATEEPGESF CDKVMRWFQA MLQRLQTWWH GVLAWVKEKV 180
VALVHAVQAL WKQFQSFC CS LSELFMSSFQ SYGAPRGDKE ELTPQKCSEP QSSK 234

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organism = Homo sapiens
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KERDGLRCRG NRSPVPDVDED PATEEPGESF CDKVMRWFQA MLQRLQTWWH GVLAWVKEKV 180
VALVHAVQAL WKQFQSFC CS LSELFMSSFQ SYGAPRGDKE ELTPQKCSEP 225

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organism = Homo sapiens
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GNRSPVPDVDE DPATEEPGES FCDKVMRWFQ AMLQRLQTWWH HGVLAWVKEK VVALVHAVQA 180
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VQALWKQFQS FCCSLSELF M SSFQSYGAPR GDKEELTPQK CSEPOQSSK 168

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organism = Homo sapiens
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TEEPGESFCD KVMRWFQAML QRLQTWWHG V LAWVKEKVA LVHAVQALWK QFQSFCCSLS 180
ELFMSSFQSY GAPRGDKEEL TPQKCSEPQSK 212

SEQ ID NO: 31      moltype = AA  length = 317
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organism = Homo sapiens
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VCVPFFGGIF RLKPTQHQS VPPEEVGTGPS QMDTRRGHLL QPPDPGLTSN FGHLDDPGLA 180
RWTPGKEESL NLCHCAELGC RTQGVCSFP A MPQAPIDGRI ADCRLLWDYV YQLLLDTRYE 240
PYIKWEDKD A KIFRVVDPNG LARLWGNHKN RVNMITYEKMS RALRHYYKLN IIKKEPGQKL 300
LFRNGLQLIF IFIWSFQ 317

SEQ ID NO: 32      moltype = AA  length = 262
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organism = Homo sapiens
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PGQKLLFRNG LQLIFIFIWS FQ	262
SEQ ID NO: 33 moltype = AA length = 888	
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LMGKPTEGAL IALAMKGMLD GLQQDYIRKA EYPFSSEQKW MAVKCVHRTQ QDRPEICFMK	480
GAYEIQVIKYC TTYSQSKQTL TLTQQQRDVY QOEKARMGSA GLRVLALASG PELGQLTFLG	540
LVGIIDPPRT GVKEAVTLLI ASGSVIKMIT GDSQETAVAI ASRLGLYSKT SQSVSGEEID	600
AMDVQQLSQI VPVKAVFYRA SPRHKMKIIK SLQKNGSVVA MTGDGVNDAV ALKAADIGVA	660
MGQTGTDVCK EAADMILVDD DFQTIMSAIE EGKGIYNNNIK NFVRFQLSTS IAALTLSLA	720
TLMNFPNPLN AMQILWINII MDGPPAQSLG VEPVDKDVR KPPRNWKDSI LTKNLILKIL	780
VSSIIIVCGT LFVFWRELRD NVITPRDTTM TFTCFVFFDM FNALSSRSQT KSVFEIGLCS	840
NRMFCYAVLG SIMGQLLVIY FPPLQKVFQF ESLSILDLLF LLGLTSSVCI VAEIKKVER	900
SRKEKIQKHVS STSSSFLEVW LWERSGQQLV EIHPHLETGL PLTEDVSCV	949
SEQ ID NO: 34 moltype = AA length = 949	
FEATURE Location/Qualifiers	
source 1..949	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 34 MKVARFQKIP NGENETMIPV LTSKKASELP VSEVASILOA DLQNLNKCE VSHRRAFHW	60
NEFDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DDAVSITVAI LIVVTVAFVQ	120
EYRSEKSLEE LSCLVPPECH CVREGKLEHT LARDLVPGDT VCLSGDRVP ADLRLFEAVD	180
LSIDESLLTG ETPCSKVTA PQPAATNGDL ASRSNIAFMG TLVRGKAKG VVIGTGENSE	240
FGEVFKMMQA EEAQKPLQK SMDLLGQLS FYSFQIIGII MLVGWLLGKD ILEMFTISVS	300
LAVAAIPEGL PIVVTTLAL GVMRMVKRA IVKKLPIVET LGCCNVICSD KTGTLTKNEM	360
TVTHIFTSRG LHAEVTVGKY NQFGEVIVDG DVVHGFYNPA VRSLIVEAGCV CNDAVIRNNT	420
LMGKPTEGAL IALAMKGMLD GLQQDYIRKA EYPFSSEQKW MAVKCVHRTQ QDRPEICFMK	480
GAYEIQVIKYC TTYSQSKQTL TLTQQQRDVY QOEKARMGSA GLRVLALASG PELGQLTFLG	540
LVGIIDPPRT GVKEAVTLLI ASGSVIKMIT GDSQETAVAI ASRLGLYSKT SQSVSGEEID	600
AMDVQQLSQI VPVKAVFYRA SPRHKMKIIK SLQKNGSVVA MTGDGVNDAV ALKAADIGVA	660
MGQTGTDVCK EAADMILVDD DFQTIMSAIE EGKGIYNNNIK NFVRFQLSTS IAALTLSLA	720
TLMNFPNPLN AMQILWINII MDGPPAQSLG VEPVDKDVR KPPRNWKDSI LTKNLILKIL	780
VSSIIIVCGT LFVFWRELRD NVITPRDTTM TFTCFVFFDM FNALSSRSQT KSVFEIGLCS	840
NRMFCYAVLG SIMGQLLVIY FPPLQKVFQF ESLSILDLLF LLGLTSSVCI VAEIKKVER	900
SRKEKIQKHVS STSSSFLEVW LWERSGQQLV EIHPHLETGL PLTEDVSCV	949
SEQ ID NO: 35 moltype = AA length = 939	
FEATURE Location/Qualifiers	
source 1..939	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 35 MKVARFQKIP NGENETMIPV LTSKKASELP VSEVASILOA DLQNLNKCE VSHRRAFHW	60
NEFDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DDAVSITVAI LIVVTVAFVQ	120
EYRSEKSLEE LSCLVPPECH CVREGKLEHT LARDLVPGDT VCLSGDRVP ADLRLFEAVD	180
LSIDESLLTG ETPCSKVTA PQPAATNGDL ASRSNIAFMG TLVRGKAKG VVIGTGENSE	240
FGEVFKMMQA EEAQKPLQK SMDLLGQLS FYSFQIIGII MLVGWLLGKD ILEMFTISVS	300
LAVAAIPEGL PIVVTTLAL GVMRMVKRA IVKKLPIVET LGCCNVICSD KTGTLTKNEM	360
TVTHIFTSRG LHAEVTVGKY NQFGEVIVDG DVVHGFYNPA VRSLIVEAGCV CNDAVIRNNT	420
LMGKPTEGAL IALAMKGMLD GLQQDYIRKA EYPFSSEQKW MAVKCVHRTQ QDRPEICFMK	480
GAYEIQVIKYC TTYSQSKQTL TLTQQQRDVY QOEKARMGSA GLRVLALASG PELGQLTFLG	540
LVGIIDPPRT GVKEAVTLLI ASGSVIKMIT GDSQETAVAI ASRLGLYSKT SQSVSGEEID	600
AMDVQQLSQI VPVKAVFYRA SPRHKMKIIK SLQKNGSVVA MTGDGVNDAV ALKAADIGVA	660
MGQTGTDVCK EAADMILVDD DFQTIMSAIE EGKGIYNNNIK NFVRFQLSTS IAALTLSLA	720
TLMNFPNPLN AMQILWINII MDGPPAQSLG VEPVDKDVR KPPRNWKDSI LTKNLILKIL	780
VSSIIIVCGT LFVFWRELRD NVITPRDTTM TFTCFVFFDM FNALSSRSQT KSVFEIGLCS	840
NRMFCYAVLG SIMGQLLVIY FPPLQKVFQF ESLSILDLLF LLGLTSSVCI VAEIKKVER	900
SRKEKIQKHVS STSSSFLEVW LWERSGQQLV EIHPHLETGL PLTEDVSCV	939
SEQ ID NO: 36 moltype = AA length = 919	
FEATURE Location/Qualifiers	
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mol_type = protein	

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		organism = Homo sapiens
SEQUENCE: 36		
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EYRSEKSLEE LSKLVPPECH CVREGKLEHT LARDLVPGD T VCLSVGDRVP ADLRLFEAVD	180	
LSDIDESLTG ETTPCSKVTA PQPAATNGDL ASRSNIAFMG TLVRGKAKG VVIGTGENSE	240	
FGEVFKMMQA EEAAPKTPLQK SMDLLGKQLS FYSGIIGIGI MLVGWLLGKD ILEMFTISVS	300	
LAVAAIPEGL PIVVTVTAL GVMMRKVRA IVKLPPIVET LGCCNVICSD KTGTTLTKNEM	360	
TVTHIFTSRG LHAEVTVGVY NQFGEVIVDG DVVHGFYVNP A SRIVEAGCV CNDAVIRNNT	420	
LMGKPTEGAL I ALAMKMGDL GLQGYIRKA EYPFSSEQKW MAVKCVHRTQ QDRPEICFMK	480	
GAYEQVIKYC TTYSQSKQTL TLTQQRDVY QQEKARMGS A GLRVLA LASG PELQLTFLG	540	
LVGIIDPPRT GVKEAVTLL ASGVSIKMIT GDSQETAVAI ASRLGLYSK SQSVSCEEID	600	
AMDVQQLSQI VPVKAVAFYRA SPRHKMKIIK SLQKNGSVVA MTGDPVNDAV ALKAADIGVA	660	
MQGTGTDVCK EAADMILVDD DFQTMISAIE EGKGIYNNNIK NFVFRFQLSTS IAALTLISLA	720	
TLMNFPNPLN MDGPPAQSGLN VEPVDKDVRN KPPRNWKDSI LTKNLKIL	780	
VSSIIIIVCGT LFVFWRELRD NVITPRDTTM TFTCFVFFDM FNALSSRSQT KSVFEGILCS	840	
NRMFICYAVLG SIMGQLLVY FPPLQKVFQFT ESLSILDLLF LLGLTSSVCI VAEIICKVER	900	
SREKIQKHVS STSSSPLEV	919	
SEQ ID NO: 37	moltype = AA length = 944	
FEATURE	Location/Qualifiers	
source	1..944	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 37		
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SELPVSEVAS ILQFKNPLM LLLASAVISV LMHQFDDAVS ITVAILIVVT VAFVQEYRSE	120	
KSLEELSKLV PPECHCVREG KLEHTLARDL VP GDPDTVCLSV GDRVPADRLR FEAVLSDIDE	180	
SSLTGETTPC SKVTAPQPA A TNQDLASRSN IAFMGTLCR GKAKGVVIGT GENSEFGEVF	240	
KMMQAEAEAPK TPLQKSMMDL GKQKSFYFSFG II GIIMLVGW LLGKDILEMF TISVSLAVAA	300	
IPEGLPIVV TPLQKSMMDL GKQKSFYFSFG II GIIMLVGW LLGKDILEMF TISVSLAVAA	360	
FTSDGLHAEV TVGVYQFGE VIVDGVVHVG FYNPAVSRIE EAGCVCNDAV IRNNTLMGKP	420	
TEGALIALAM KMGLDGLQQD YIRKAEYFPF SEQKWMWAKC VR HRTQQDRPE ICFMKGAYEQ	480	
VIKYCTTYQS KGQTLTLLTQQ QRDVYQEQKA RMGSAGLRLV ALASGPFLGQ LTFLGLVGII	540	
DPPRTGKVEA VTTLIASGV S IKMGTDSQE TAVAIASRLG LYSKTSQSVS GEEIDAMDQ	600	
QLSQIVPKVA VFYRASPRHK MKIIKSLQKN GS VVAMTGDG V NDVALVKA DIGVAMGQTC	660	
TDVCKEAADM ILVDDDFQTL MSAIEEGKG YNNIKNFVRF QLSTSIAALT LISLATLMNF	720	
PNPLNAMQIL WINIIMDGPP AQSLGVEPV D KVIRKPPR WKDSILTKNL ILKILVSSII	780	
IVCGTLFVFW RELRDNVITP RD TFCVFFDM FNALSSRSQT KSVFEGILCS	840	
YAVLGSIMGQ LLVIYFPPLQ VKFQTESLSI LDLLFLLGLT SSVCIVAEII KKVERSREKI	900	
QHVSSTSS FLEVWLWERS GQQLVEIHPH L ETGLPLTEDV VSCV	944	
SEQ ID NO: 38	moltype = AA length = 215	
FEATURE	Location/Qualifiers	
source	1..215	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 38		
VTVTALGVM RMVKKRAIVK KLPIVETLGC CNVICSDKTG TLTKNEMVT HIFTSDFGLHA	60	
EVTGVGVYNQF GEIVDGDVV HGFYNPVSR IVEAGCVCND AVIRNNTLMG KPTEGALIAL	120	
AMKMGLDGLQ QDYIRKAEYP FSSEQKWMV KCVHRTQDQR PEICFMKGAY EQVIKYCTTY	180	
QSKGQTLTLLT QQORDVYQEQ KAR MGSA GLR VYLVF	215	
SEQ ID NO: 39	moltype = AA length = 903	
FEATURE	Location/Qualifiers	
source	1..903	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 39		
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TVAI LIVVT A FVQEYRSEK SLEELSKLV PECCHCVREGK LEHTLARDL PGDTVCLSV	120	
DRVPA DRLRF EAVDLSIDES SLTGETTPCS KVTAPQPAAT NGDLASRSN AFMGTLCR	180	
KAKGVVIGTG ENSEFGEVFK MMQAEAEAPK PLQKSMMDL GKQKSFYFSFG IGIIMLVWL	240	
LGKDILEMF ISVSLAVAAI PEGLPIVV TV ALGVMR MV KKRAIVKLP I VETLGCCNV	300	
ICSDKTGTLT KNEMVT THIF TSDGLHAEV TVGVYQFGEV IDGDVVHGF YNP AVSRIE	360	
AGCVCNDAVI RNNTLMGKP EGALIALAMK MG LDGLQODY IRKA EYFSS EQKWMVAKCV	420	
HRTQQRPEI CFMKGAYEQV IKYCTTYQS GQTLTLLTQQ RDVYQEQKAR MGSAGLRLVA	480	
LA SGPELQL TFLGLVGIID PPRTGVKEAV TTLIASGVSI KMITGDSQET AVAIASRLGL	540	
YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV FYRASPRHKM KIIKSLQKNG SVVAMTGDGV	600	
NDAVALKAAD IGVAMGQTGT DVCKEAADMI LV DDDFQTIM SAIEEGKGY NN KNFVRFQ	660	
LSTSIAALT L ISLATLMNFP NP LNAMQILW INI IMDGPPA QSLGV EFPV D V I R K P PR NW	720	
KDSILTKNLI LKILVSSIII VCGTLFVFW EL RDNVITP DTTMFTFCV FFDMFNALSS	780	
RSQTKSVEI GLCSNRMFCY AVLGSIMGQ LVIYFPPLQK VQTE SLSIL DLLFLLGLTS	840	
SV CIVAEII K VERSREKI QHVSSTSSSF LEVWLWERSG QQLVEIHPHL ETGLPLTEDV	900	
SCV	903	

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SEQ ID NO: 40	moltype = AA length = 903
FEATURE	Location/Qualifiers
source	1..903
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 40	
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SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQEYRSEK SLEELSKLPV 120	
PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPAIDLRLF EAVDLSIDES SLTGETTPCS 180	
KVTAPQPAAT NGDLASRSNI AFMGTIVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAAPIKT 240	
PLQKSMDLLG KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVT 300	
TLALGVMRMV KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360	
GVGYNQFGEV IVDGDVVHGF YNPRAVSRIVE AGCVCNDAVI RNNNTLMGKPT EGALIALAMK 420	
MGLDGLQDY IRKAEYPFSS EQKWMMAVKCV HRTQCDRPEI CFMKGAYEQV IKYCTTYQSK 480	
GQTLLTQQQ RDVYQQEKAR MGSAGLRLVA LASGPTELQGL TFLGLVGIIID PPRTRGVKEAV 540	
TTLIASGVSI KMITGDSQET AVAIASRLGL YSKTSQSWSG EEIDAMDVQQ LSQIVPKVAV 600	
FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660	
LVDDDFQTIM SAIEEGKGIVY NNIKNFVRFQ LSTSIAALTL ISLATLMNFP NPLNAMQILW 720	
INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780	
ELRDNVITPR DTTMTFTCFV FFDMFNALSS RSQTKSVFPI GLCSNRMFCY AVLGSIMGQL 840	
LVIYFPPLQK VFQTESLSIL DLLFLGLTS SVCIVAEIIK KVERSREKIQ KHVSSTSSSF 900	
LEV	903
SEQ ID NO: 41	moltype = AA length = 120
FEATURE	Location/Qualifiers
source	1..120
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 41	
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NEFDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DDAVSITVAI LIVVTVAFVQ 120	
SEQ ID NO: 42	moltype = AA length = 953
FEATURE	Location/Qualifiers
source	1..953
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 42	
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SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI SQFKNPLIML 120	
LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQEYRSEK SLEELSKLPV PECHCVREGK 180	
LEHTLARDLV PGDTVCLSVG DRVPAIDLRLF EAVDLSIDES SLTGETTPCS KVTAPQPAAT 240	
NGDLASRSNI AFMGTIVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAAPIKT PLQKSMDLLG 300	
KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVT TLALGVMRMV 360	
KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT GVGYNQFGEV 420	
IVDGDVVHGF YNPRAVSRIVE AGCVCNDAVI RNNNTLMGKPT EGALIALAMK MGLDGLQDY 480	
IRKAEYPFSS EQKWMMAVKCV HRTQCDRPEI CFMKGAYEQV IKYCTTYQSK GQTLLTQQQ 540	
RDVYQQEKAR MGSAGLRLVA LASGPTELQGL TFLGLVGIIID PPRTRGVKEAV TTLIASGVSI 600	
KMITGDSQET AVAIASRLGL YSKTSQSWSG EEIDAMDVQQ LSQIVPKVAV FYRASPRHKM 660	
KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI LVDDDFQTIM 720	
SAIEEGKGIVY NNIKNFVRFQ LSTSIAALTL ISLATLMNFP NPLNAMQILW INIIMDGPPA 780	
QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR ELRDNVITPR 840	
DTTMTFTCFV FFDMFNALSS RSQTKSVFPI GLCSNRMFCY AVLGSIMGQL LVIYFPPLQK 900	
VFQTESLSIL DLLFLGLTS SVCIVAEIIK KVERSREKIQ KHVSSTSSSF LEV	953
SEQ ID NO: 43	moltype = AA length = 50
FEATURE	Location/Qualifiers
source	1..50
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 43	
LVDDDFQTIM SAIEEGKGIVY NNIKNFVRFQ LSTFCGSILL WMDPQLRALE	50
SEQ ID NO: 44	moltype = AA length = 973
FEATURE	Location/Qualifiers
source	1..973
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 44	
MDSLLPPSRV SYFKKYPLHA IRRYLSTLRN QRAEEQVARF QKIPNGENET MIPVLTSKKA 60	
SELPVSEVAS ILQADLQNGL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI SQFKNPLIML 120	
LLASAVISVL MHQFDDAVSI TVAILIVTV AFVQEYRSEK SLEELSKLPV PECHCVREGK 180	
LEHTLARDLV PGDTVCLSVG DRVPAIDLRLF EAVDLSIDES SLTGETTPCS KVTAPQPAAT 240	
NGDLASRSNI AFMGTIVRCG KAKGVVIGTG ENSEFGEVFK MMQAEAAPIKT PLQKSMDLLG 300	
KQLSFYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGLPIVVT TLALGVMRMV 360	
KKRAIVKKLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT GVGYNQFGEV 420	

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IVDGDVVHGF YNPAVSRIVE AGCVCNDAVI RNNTLMGKPT EGALIALAMK MGLDGLQQDY	480
IRKAEGYFPSS EOKWMAVKV HRTQDRPEI CFMKGAYEQV IKYCTTYQSK GQTLLTQQQ	540
RDVYQQEKAR MGSAGLRLVA LASGPELGQL TFLGLVGIID PPRTGVKEAV TTLIASGVSI	600
KMITGDSQET AVAIASRLGL YSKTSQSVSQ EEDAMDVOQ LSQIVPKVAV FYRASPRHKM	660
KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEAADMI LVDDDFQTIM	720
SAIEEGKGIY MNINKFVRFQ LSTSIAALT ISLATLMNPF NPLNAMQILW INIIMDGPPA	780
QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR ELRDNVITPR	840
DTTMTFTCFV FFDMFNALSS RSQTKSVFEI GLCSNRMPYC AVLGSIMGQL LVIYPPPLQK	900
Vfqteslsil DLLFLLGLTS SVCIVAEIIK KVERSREKIQ KHVWLWERSG QQLVEIHPHL	960
ETGLPLTEDV SCV	973
 SEQ ID NO: 45	moltype = AA length = 82
FEATURE Location/Qualifiers	
source 1..82	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 45	
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SQFKNPMLM LLASAVISVL MH	82
 SEQ ID NO: 46	moltype = AA length = 919
FEATURE Location/Qualifiers	
source 1..919	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 46	
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NEPDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DDAVSITVVAI LIVVTVAFVQ	120
EYRSEKSLEE LSKLVPPECH CVREGKLEHT LARDLVPGDT VCLSVGDRV ADLRLFEAVD	180
LSIDESLLTG ETTPCSKVTA PQPAATNGDL ASRSNIAFMG TLVRCGKAKG VVIGTGENSE	240
FGEVFKMMQA EAAPKPLQK SMDLLGKQLS FYSGFIIGII MLVGWLLGKD ILEMFTISVS	300
LAVAAIPEGI PIVVTVTAL GVMRMVKKRA IVKKLPIVET LGCCNVICSD KTGTLTKNEM	360
TVTHIFTSDEG LHAEVTVGKY NQFGEVIVDG DVVHGFYNPNA VSRIEAGCV CNDAVIRNN	420
LMGKPTEGAL IALAMKMGD GLQDQDYIRKA EYPFSSEQKW MAVKCVHRTQ QDRPEICFMK	480
GAYEQVIKYC TTYSKGQTL TLTQSKQRDVY QOEKARMGSA GLRVLAASG PELGQLTFLG	540
LVGIIDPPRT CVKEAVTTLI ASGVSIMKIT GDSQETAVAI ASRLGLYSKT SQSVSCEEID	600
AMDVQQLSQI VPKVAVFYRA SPRHKMKIIK SLQKNGSVVA MTGDGVNDAV ALKAADIGVA	660
MGQTGTDVCK EAADMILVDD DFQTIMSAIE EGKGIYNNNIK NFVFRQLSTS IAALTLISLA	720
TLMNFPNPLN AMQIILWINII MDGPPAQSLSG VEPVDKDVR KPPRNWKDSI LTKNLILKIL	780
VSSIIIVCGT LFVFWRELRD NVITPRDTTM TFTCFVFFDM FNALSSRSQ KSVFEIGLCS	840
NRMFPCAYAVLG SIMGQLLVYI FPPLQKVQFT ESLSILDLLF LLGLTSSVCI VAEIICKVER	900
SREKIQKHVS STSSSPLEV	919
 SEQ ID NO: 47	moltype = AA length = 314
FEATURE Location/Qualifiers	
source 1..314	
mol_type = protein	
organism = Homo sapiens	
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VIKYCTTYQSK KGQTLTQQ QRDVYQQEKA RMGSAGLRS RLGLYSKTSQ SVSCEEIDAM	120
DVQQLSQIVPA KVAVFYRASP RHMKMKISSL QKNGSVVAMT GDGVNDVAL KAADIGVAMG	180
QTGTDVCKEA ADMILVDDDF QTIMSAIEG KGIIYNNNIKF VRFQLSTSIA ALTLISLATL	240
MNFPNPLNAM QILWINIIMD GPPAQSLGVE PVDKDVIRKP PRNWKDSILT KNLILKILVS	300
SIIIVCGTLF VFWR	314
 SEQ ID NO: 48	moltype = AA length = 102
FEATURE Location/Qualifiers	
source 1..102	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 48	
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NEFDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DD	102
 SEQ ID NO: 49	moltype = AA length = 919
FEATURE Location/Qualifiers	
source 1..919	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 49	
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EYRSEKSLEE LSKLVPPECH CVREGKLEHT LARDLVPGDT VCLSVGDRV ADLRLFEAVD	180
LSIDESLLTG ETTPCSKVTA PQPAATNGDL ASRSNIAFMG TLVRCGKAKG VVIGTGENSE	240
FGEVFKMMQA EAAPKPLQK SMDLLGKQLS FYSGFIIGII MLVGWLLGKD ILEMFTISVS	300

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TVTHIFTSRD	LHAEATGVNG	NQFGEVIVDG	DVUVHGFYNPNA	VSSRIVEAGCV	CNDAVIRNTK	420
LMGKPTEGAL	IHALAMKGMLD	GLQDDYIRKA	EYFPSSQECKW	MAVKCVHRTO	QDRPICEFMK	480
GAYEQVKVYKC	TTYQSKGQTL	TLTQOQRDYY	QOEKARMGSA	GLRVLALASG	PELGOLTFGL	540
LVGIIDPPTR	GVKEAVTTLI	ASGVSIKMIT	GDSQETAVAI	ASRLGYLSKT	SQSVEGEEID	600
AMDVQQLSQQI	VPKVAVFYRA	SPRHKMKIIK	SLOQNGNSVVA	MTGDGVNDAV	ALKADIGVA	660
MQCTQDTDVCK	EAADMILVDD	DFQTIMSAIE	EGKKIYNNKK	NFVRQFLQSTS	IAALTLISLA	720
TLMNFPNPLN	AMQILWINII	MDGPPAQSLG	VEPVDKDVIR	KPPRNWKDSI	LTKNLILKIL	780
VSSIFIIVCGT	LFVFWRERLD	NVITPRTDTM	TFTCFVFEDM	FNALSSRSQT	KSVFEIIGLCS	840
NRMFICYAVLG	SIMGQLLVII	FPPLQKVFQT	ESLSILDLLF	LLGLTSSVCI	VAEIIKKVER	900
SEKRIQKHVS	STSSSKFLEV					919

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SEQ ID NO: 50          moltype = AA    length = 923
FEATURE                Location/Qualifiers
source                 1..923
                      mol_type = protein
                      organism = Homo sapiens
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SEQ ID NO: 51 moltype = AA length = 131
FEATURE Location/Qualifiers
source 1..131
mol_type = protein
organism = Homo sapiens

SEQ ID NO: 52 moltype = AA length = 888
FEATURE Location/Qualifiers
source 1..888
mol_type = protein
organism = Homo sapiens

	organism = homo sapiens
SEQUENCE: 52	
MKVARFQKIP NGENETMIPV LTSKKASELP VSEVASILQA DLQNGLNKCE VSHRRAFHGW	60
NEFDISEDEP LWKKYISQFK NPLIMLLAS AVISVLMHQF DDAVSITVAI LIVVTVAFVQ	120
EYRSEKSLEE LSKLVPCKVE CRVERGKLEHT LARDLVPGDT VCLSVGRDRV ADLRLFEAVD	180
LSIDESLTLT ETTPCSKVTA PQPAATNGDL ASRSNIAFMGLV TLVRCKGAKG VVIGTGENSE	240
FEVGEVKIMMQA EEAKPTPLQK SMDDLLGQKLFS FYSGFGIIIGI MLVGVWLLGKD ILEMPLITSVS	300
LAVAIAIPEGL PIVVTVTLLA GVMRMVVKRA IVKKLPIVET LGCCNVICSD KTGTTLKNEM	360
TVTHIPTSDG LHAEVITVGVY NQFGEVIBDG DVVHGFYNPNA VSRIEAGCV CNDAVIRNNT	420
LMGKPTEGAL IALAMKMGDL GLQDQDYIRKA EYPFSSEQKW MAVKCVHRTO QDRPEICFMNT	480
GAYEQIVIKYC TTYSQKGQLT TLTQQQRDVY QOEKARMGSA GLRVLLASLG PELGQTLFLG	540
LVGIIIDPPRT GVKEAVTTLI ASGVSIKMT GDSQETAVAI ASRGLIYLSKT SQSVGSEEID	600
AMDVQQLSQI VPKVAVFYRA SPRHKMKIIK SLQKNGSVA MTGDGVNDAV ALKAADIGVA	660
MQQTGTDVCK EAADMILVDD DFQTIMSAIE EGKGIYNNIK NFVRFOLSTS IAAATLISLA	720
TLMNPFPNMLN AMQIILWINII MDDGPPAQSGLG VEVPVDKDVIR KPPRNWKDSI LTKNLILKIL	780
VSSIIIIVCGT LPFVFWRELND NVITPRDTTM TFTCFEVPPDM FNALSSRSQT KSVFEGLCS	840
NRMFCYAVLG SIMGOLLVVI FPFLPKOYFVT ESLSILGLAL GEEWTAAAG	880

SEQ ID NO: 53 moltype = AA length = 233
FEATURE Location/Qualifiers
source 1..233
mol_type = protein
organism Homo sapiens

organism = *Homo sapiens*

SEQUENCE: 53	MLGIWTLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHGDQFCH	60
	PTCOPPGERKA RDCTVNGDDE CDPVCPEGKE YTDKAHEFSK CRRCRLCDEG HGLEVINECT	120
	PTCOPPGERKA DNEFGTCTTC EYEDCCTGTEK UHLLKFTETP CTNTKGKHEEGS RGNLWGLSL	180

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LLPIPLIVWV KRKEVQKTCR KHRKENQGSH ESPTLNPETV AINLSDYFLF FRC	233
SEQ ID NO: 54	moltype = AA length = 220
FEATURE	Location/Qualifiers
source	1..220
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 54	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSKK CRRCRLCDEG HGLEVEINCT	120
RTQNTKCRCK PNFFCNSTVC EHCDPCTKCE HGIIKECTLT SNTKCKEEGS RSNLGWLCLL	180
LLPIPLIVWV KRKEVQKTCR KHRKENQGSH ESPTLNPMILT	220
SEQ ID NO: 55	moltype = AA length = 335
FEATURE	Location/Qualifiers
source	1..335
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 55	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSKK CRRCRLCDEG HGLEVEINCT	120
RTQNTKCRCK PNFFCNSTVC EHCDPCTKCE HGIIKECTLT SNTKCKEEGS RSNLGWLCLL	180
LLPIPLIVWV KRKEVQKTCR KHRKENQGSH ESPTLNPETV AINLSDVDLS KYITTIAGVM	240
TLSQVKGFVR KNGVNNEAKID EIKNDNVQDT AEQKVQLLRN WHQLHGKREA YDTLIKDLKK	300
ANLCTLAEKI QTIIILKDIS DSENSNFRNE IQSLV	335
SEQ ID NO: 56	moltype = AA length = 314
FEATURE	Location/Qualifiers
source	1..314
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 56	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSKK CRRCRLCDEG HGLEVEINCT	120
RTQNTKCRCK PNFFCNSTVC EHCDPCTKCE HGIIKECTLT SNTKCKEEVK RKEVQKTCRK	180
HRKENQGSHE STPLNPETVA INLSDVDLSK YITTIAGVMT LSQVKGFVRK NGVNNEAKIDE	240
IKNNDNVQDTA BQKVQLLRNW HQLHGKKEAY DTLIKDLKK NLCTLAEKIQ TIILKDITS	300
SENSNFRNEI QSLV	314
SEQ ID NO: 57	moltype = AA length = 86
FEATURE	Location/Qualifiers
source	1..86
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 57	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPDVNME SSRNAHSPAT PSAKRK	86
SEQ ID NO: 58	moltype = AA length = 103
FEATURE	Location/Qualifiers
source	1..103
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 58	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPDVNME SSRNAHSPAT PSAKRKDPL TWGGFVFFFC QFH	103
SEQ ID NO: 59	moltype = AA length = 149
FEATURE	Location/Qualifiers
source	1..149
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 59	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSKK CRRCRLCDEG HDVNMESSRN	120
AHSPATPSAK RKDPDLTWGG FVFFFCQFH	149
SEQ ID NO: 60	moltype = AA length = 132
FEATURE	Location/Qualifiers
source	1..132
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 60	
MLGIWTLLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHDGQFCH	60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSKK CRRCRLCDEG HDVNMESSRN	120
AHSPATPSAK RK	132

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SEQ ID NO: 61      moltype = AA  length = 149
FEATURE
source          Location/Qualifiers
1..149
mol_type = protein
organism = Homo sapiens
SEQUENCE: 61
MLGIWTLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHHDGQFCH 60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSSK CRRCRLCDEG HDVNMESSRN 120
AHSPATPSAK RKDPDLTWGG FVFFFCQFH 149

SEQ ID NO: 62      moltype = AA  length = 244
FEATURE
source          Location/Qualifiers
1..244
mol_type = protein
organism = Homo sapiens
SEQUENCE: 62
MLGIWTLPL VLTSVARLSS KSVNAQVTDI NSKGLELRKT VTTVETQNLE GLHHHDGQFCH 60
KPCPPGERKA RDCTVNGDEP DCVPCQEGKE YTDKAHFSSK CRRCRLCDEG HGLEVEINCT 120
RTQNTKCRCK PNFFCNSTVC EHCDPCTKCE HGIIKECTLT SNTKCKEEGS RSNLGWLCLL 180
LLPIPLIVWV KRKEVQKTCR KHRKENQGSH ESPTLNPMES CSIAQAGVQG CNHGSLOPQS 240
PGLK 244

SEQ ID NO: 63      moltype = AA  length = 373
FEATURE
source          Location/Qualifiers
1..373
mol_type = protein
organism = Homo sapiens
SEQUENCE: 63
MLRSVWNFLK RHKKKCIFLG TVLGGVYILG KYGOKKIREI QEREAAEYIA QARROYHFES 60
NQRTCNMTVL SMLPTLREAL MQQLNSESLSLT ALLKNRPSNK LEIWEDLKII SFTRSTVAVY 120
STCMVLVLLR VQLNIIGGYI YLDNAAVGKN GTTILAPPDV QQYLSSIQH LLGDGLTELJ 180
TVIKQAVQKV LGSVSLKHS LSLDLEQKLK EIRNLVEQHK SSSWINKDGS KPLLCHYMP 240
DEETPLAVQA CGLSPRDIT ICKLNNETRDM LESPDFSTVL NTCLNRGFSR LLDNMAEFFR 300
PTEQDLQHGN SMNSLSSVSL PLAIIPIVN GQIHSVCSET PSHFVQDLTT MEQVKDFAAN 360
VYEAFSTPQQ LEK 373

SEQ ID NO: 64      moltype = AA  length = 182
FEATURE
source          Location/Qualifiers
1..182
mol_type = protein
organism = Homo sapiens
SEQUENCE: 64
MLRSVWNFLK RHKKKCIFLG TVLGVLMSLMP TLREALMQOL NSESLTALLK NRPSNKLEIW 60
EDLKIISFTR STVAVYSTCM LVVLLRVQLN IIGGYIYLDN AAVGKNGTTI LAPPDVQQY 120
LSSIQHLLGD GLTELITVIK QAVQKVLGSV SLKHSLSLLD LEQKLKEIRN LVEQHKSSW 180
IN 182

SEQ ID NO: 65      moltype = AA  length = 188
FEATURE
source          Location/Qualifiers
1..188
mol_type = protein
organism = Homo sapiens
SEQUENCE: 65
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWF SVFLGLIIFL ELATGILAFV FKDWIRDQLN 60
LFINNNVKAY RDDIDLQNL DFAQEYEDVL NTQCGYDVRL KLELEQQGFI HTKGCVGQFE 120
KWLQDNLLIVV AGVFMGIAL QVPLWPHVPL PLPGPPSLSP HLSSVLQIFG ICLAQNLVSD 180
IKAVKANW 188

SEQ ID NO: 66      moltype = AA  length = 332
FEATURE
source          Location/Qualifiers
1..332
mol_type = protein
organism = Homo sapiens
SEQUENCE: 66
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWF LGALFLAIGL WAWGEKGVLS NISALTDLGG 60
LDPVWLFFFVVV GGVMSVLGFA GCIGALRENT FLLKFFSVFL GLIFFLELAT GILAFVFKDW 120
IRDQLNLFIN NNNVKAYRDDI DLQNLIDFAQ EYWSCCGARG PNDWNLNIIYF NCTDLNPSRE 180
RCGVPFSCCV RDPAEDVLNT QCGYDVRLKL VRGELEQQGF IHTKGCVGQF EKWLQDNLIV 240
VAGVFMGIAL LQIFGICLAQ NLVSDIKAVK ANWSKWNNDF ENHWLPTTIS EVLSTAGPQQ 300
NSLTGAPGPB PPSRHVFFGL GGLYPEPTFK NW 332

SEQ ID NO: 67      moltype = AA  length = 58
FEATURE
source          Location/Qualifiers
1..58
mol_type = protein

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SEQUENCE: 67          organism = Homo sapiens
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWV SAGCWEPCSW LSASGPGVRR AFSRTSQR      58

SEQ ID NO: 68          moltype = AA length = 309
FEATURE          Location/Qualifiers
source           1..309
mol_type = protein
organism = Homo sapiens

SEQUENCE: 68          moltype = AA length = 309
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWV LGALFLAIGL WAWGEKGVL NISALTDLGG 60
LDPVWLFWVV GGVMsvLGFA GCIGALRENT FLLKFDWIRD QLNLFINNN KAYRDIIDLQ 120
NLIDFAQEYWW SCGGARGPND WNLNIYFNCT DLNPSRERC VPFSCCVRD P AEDVLNTQCG 180
YDVRKLVRG ELEQQGFIHT KGCVGQFEKW LDQNLIVVAG VFMGIALLQI FGICLAQNLV 240
SDIKAVKANW SKWNDDFENH WLPTTISEVL STAGPQQNSL TGAPGPAPP RHVFFGLGGL 300
YPEPTFKNW                                         309

SEQ ID NO: 69          moltype = AA length = 257
FEATURE          Location/Qualifiers
source           1..257
mol_type = protein
organism = Homo sapiens

SEQUENCE: 69          moltype = AA length = 257
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWV LGALFLAIGL WAWGEKGVL NISALTDLGG 60
LDPVWLFWVV GGVMsvLGFA GCIGALRENT FLLKFLATGI LAFVFKDWIR DQLNLFINNN 120
VKAYRDDIDL QNLIDFAQEY WSCCGARGPN DWNLNIYFNC TDLNPSRERC GVPFSCCVRD 180
PAEDVLNTQC GYDVRKLREL EQQGFIHTKG CVGQFEKWQ DNLIIVVAGVF MGIALLQIFG 240
ICLAQNLVSD IKAVKAN                                         257

SEQ ID NO: 70          moltype = AA length = 203
FEATURE          Location/Qualifiers
source           1..203
mol_type = protein
organism = Homo sapiens

SEQUENCE: 70          moltype = AA length = 203
XGKHQHFQEP EVGCCGKYFL FGFNIVFWFS VFLGLIFFLE LATGILAFVF KDWIRDQLNL 60
FINNNVKAYR DDIDLQNLID FAQEYWSCCG ARGPNDWNLN IYFNCTDLNP SRERCGVPF 120
CCVRDPAEDV LNTQCGYDVR LKLELEQQGF IHTKGCVGQF EKWLQDNLIV VAGVFMGIAL 180
LQIFGICLAQ NLVSDIKAVK ANW                                         203

SEQ ID NO: 71          moltype = AA length = 329
FEATURE          Location/Qualifiers
source           1..329
mol_type = protein
organism = Homo sapiens

SEQUENCE: 71          moltype = AA length = 329
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWV LGALFLAIGL WAWGEKGVL NISALTDLGG 60
LDPVWLFWVV GGVMsvLGFA GCIGALRENT FLLKFFSVL GLIFFLELAT GILAFVFKDW 120
IRDQLNLFIN NNVKAYRDDI DLQNLIDFAQ EYWSCCGARG PNDWNLNIF NCTDLNPSRE 180
RCGVPFSCCV RDPAEDVLNT QCQGYDVRKL ELEQQGFIHT KGCVGQFEKW LDQNLIVVAG 240
VFMGIALLQI FGICLAQNLV SDIKAVKANW SKWNDDFENH WLPTTISEVL STAGPQQNSL 300
TGAPGPAPP RHVFFGLGGL YPEPTFKNW                                         329

SEQ ID NO: 72          moltype = AA length = 263
FEATURE          Location/Qualifiers
source           1..263
mol_type = protein
organism = Homo sapiens

SEQUENCE: 72          moltype = AA length = 263
MPGKHQHFQE PEVGCCGKYF LFGFNIVFWV LGALFLAIGL WAWGEKGVL NISALTDLGG 60
LDPVWLFWVV GGVMsvLGFA GCIGALRENT FLLKFFSVL GLIFFLELAT GILAFVFKDW 120
IRDQLNLFIN NNVKAYRDDI DLQNLIDFAQ EYWSCCGARG PNDWNLNIF NCTDLNPSRE 180
RCGVPFSCCV RDPAEDVLNT QCQGYDVRKL ELEQQGFIHT KGCVGQFEKW LDQNLIVVAG 240
VFMGIALLQI FGICLAQNLQ EME                                         263

SEQ ID NO: 73          moltype = AA length = 83
FEATURE          Location/Qualifiers
source           1..83
mol_type = protein
organism = Homo sapiens

SEQUENCE: 73          moltype = AA length = 83
MAATASPRS LLVLLQVVVL ALAQIRGPPG ERGPPGPPGP PGVPGSDGID GPPGPVGLPG 60
EIGIRGPKGD PGPDGPSGPP GPP                                         83

SEQ ID NO: 74          moltype = AA length = 689
FEATURE          Location/Qualifiers

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source          1..689
               mol_type = protein
               organism = Homo sapiens

SEQUENCE: 74
MAAAATASPRS LLVLLQVVVL ALAQIRGPPG ERGPPGPPG PGVPGSDGID GDNGPPGKAG 60
PPGPKGEPK AGPDGPDGKF GIDGLTGAKG EPGPMGIPGV KGQPGPLPGRP GLPGPGFAGP 120
PGPPGPVGLP GEIGIRGPKG DPGDPGSPGP PGPPGKPGP GTIQGLEGSA DFLCPTNCPP 180
GMKGPPGLQG VKGHAGKRG1 LGDPGHQGKP GPKGDVAGSG EQGIPGPGP QGIRGYPGMA 240
GPKGETGPHG YKGMVGAIGA TGPPGEEGPR GPPGRAGEKG DEGSPGIRGP QGITGPKGAT 300
GPPGINGKD TPGTGPMKGS AGQAGQPGSP GHQGLAGVPG QPGTGGPGP QGEPGPQGLP 360
GFPGPPGKEGP EPGPGRGEIGP QGIMQKGQDQ GERGPVGQGP PQCRQGPKE QGPPGIPGPQ 420
GLPGVKDGK SPGKTGPRGE VGDPGVAGLGP GEKEKEGEG PEGPKQQQGV RGEPCYPGPs 480
GDAGAPVGQG YPGPPGPRGL AGNRGVPQGP GRQGVEGRDA TDQHIVDVAL KMLQEQLAEV 540
AVSAKREALG AVGMMGPPGP PGPGPYPGKQ GPHGHPGPRG VPGIVGAVGQ IGNNTGPKGKR 600
GEKGDPGEVG RGHPGMPGP GIPGLPGRGP QAINKGDR GSPGAPGEAG RPGLPGPVGL 660
PGCEPEAACL GASAYASARL TEPGSIKG 689

SEQ ID NO: 75      moltype = AA length = 226
FEATURE
source          Location/Qualifiers
               1..226
               mol_type = protein
               organism = Homo sapiens

SEQUENCE: 75
XSPFRGPPGA AGARRGPPGE RGPPGPPGPP GVPGSDGIDG DNGPPGKAGP PGPKGEKGKA 60
GPDGPDGKPG IDGLTGAKGE PGPMGIPGVK QGPGLPGRP LPGPGFAGPP GPPGPVGLPG 120
EIGIRGPKGD PGDPGSPGP GPPGKPGPRG TIQGLEGSAD FLCPTNCPP MKGPPGLQGV 180
KGHAGKRGIL GDPGHQGKPG PKGDVGASGE QGIPGPQGPQ GIRGYP 226

SEQ ID NO: 76      moltype = AA length = 694
FEATURE
source          Location/Qualifiers
               1..694
               mol_type = protein
               organism = Homo sapiens

SEQUENCE: 76
MKHLKRWWSA GGGLLHLLTL LSLAGLVRDL DLYLLLPPPT LLQDELLFLG GPASSAYALS 60
PFSASGGWGR AGHLHPKGRE LDPAAPPEGQ LLREVRALGV PFVPRTSVDA WLVHSVAAGS 120
ADEAHGLLGA AAASSTGGAG ASVDDGGSQAV QGGGGDPRAA RSGPLDAGEE EKAPAEPTAQ 180
VPDAGGCASE ENGVLRKHE AVDHSSQHEE NEERVSQAKE NSLQQNDDE NKIAEKPDWE 240
AEKTTERNE RHRLNGTDTSF SLEDNGRTS SOPENSLLEGI SLGDIPLPGS ISDGGMNSSAH 300
YHVNFSQAIIS QDVNLHEAIL CTPNNTFRRD PTARTSQSQE PFLQLNSHTT NPEQTLPGTN 360
LTGFPLSVDN HMRNLTSQDL LYLDLINITD EINLMSLATE DNFDPIDVSQ LFDEPDSDSG 420
LSLDSSHNNT SVIKSNSSHS VCDEGAIGYC TDHESSHHHD LEGAVGGYYP EPSKLCHLDQ 480
SDSDFHDLT FQHVFHNHTY HLQPTAPEST SEPFPPWPQKS QKIRSYLED TDRNLSRDEQ 540
RAKALHIPKFS VDEIVGMPVD FSNSMLSRYY LTDLQVSLIR DIRRRGKNKV AAQNCRKRL 600
DIILNLEDDV CNLQAKETL KREQAQCNCNA INIMKQKLHD LYHDIFSRLL DDQGRPVNP 660
HYALQCTHDG SILIVPKELV ASGHKKETQK GKRK 694

SEQ ID NO: 77      moltype = AA length = 86
FEATURE
source          Location/Qualifiers
               1..86
               mol_type = protein
               organism = Homo sapiens

SEQUENCE: 77
CNCGLVFLHQ DPWVPTGPGA VQKQREHPPD YQWYALDQLP PDVQHKANES AILSTACFYG 60
LVRPPRSGLY KLSYNQNPTS ILIKYT 86

SEQ ID NO: 78      moltype = AA length = 1722
FEATURE
source          Location/Qualifiers
               1..1722
               mol_type = protein
               organism = Homo sapiens

SEQUENCE: 78
MRTGWATPRR PAGLMLLFW FFDLAEPSGR AANDPFTIVH GNTGKCIKPV YGWIVADDCCD 60
ETEDKLWKWV SQHRLFHLHS QKCLGLDITK SVNELRMFSC DSSAMLWWKC EHHSLYGAAR 120
YRLALKDGHG TAISNASDWV KGGGSEESLC DQPYHEIYTR DGNSYGRPCE FPFLIDGTWH 180
HDCILDDEDS GPWCATTLNV EYDRKGICL KPENGCEDNW EKNEQFGSCY QFNTQTAWS 240
KEAYVSCCNQ GADLLSINSA AELTYLKEKE GIAKIFWIGL NQLYSARGWE WSDHKPLNFL 300
NWDPDRPSAP TIGGSSCARM DAESGLWQSF SCEAQLPVVC RKPLNNNTVEL TDVWWTYSDTR 360
CDAGWLPNNG FCYLLVNESI SWDKAHAKCK AFSSDLISIH SLADVEVVVT KLHNEDIKEE 420
VWIGLKNINI PTLFQWSDGT EVTLYWDEN EPNVYPNKT NCVSYLGEGL QWKVQSCEEK 480
LKYVCKRKGE KLNDASSDKM CPPDEGWKRH GETCYK1YED EVPFGTNCL TITSRFEQEY 540
LNDLMKKYDK SLRKYFWTGL RDVDSCGEYN WATVGGRRAA VTFSWNWFLE PASPGGCVAM 600
STGKSVGKWE VKDCRSFKAL SICKKMSGPL GPEEASPKPD DPCPEGWQSF PASLSCYKVF 660
HAERIVRKRN WEEAERFCQA LG AHLSSFSH VDEIKEFLHF LTDQFSQHWH LWIGLNKRSP 720
DLQGSWQWSD RTPVSTIIMP NEFQDYDIR DCAAVKVFHR PWRRGWHFYD DREFIYLRRPF 780
ACDTKLEWVC QIPKGRTPKT PDWYNPDRAG IHGPPLIIEG SEYWFWADLH LNYEEAVLYC 840

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ASNHSFLATI	TSFVGLKAIK	NKIANISGDG	QKWWIRISEW	PIDDHFTYSR	YPWHRFPVTF	900
GEECLYMSAK	TWLIDLGKPT	DCSTKLKPIC	EKYNVSSLEK	YSPDSAAKVQ	CSEOWIPFQN	960
KCFLKIKPVS	LTFSQASDTC	HSYGGTLPSV	LSQIEQDFIT	SLLPDMEATL	WIGLRWTAYE	1020
KINKWTDNRE	LTYSNFHPLL	VSGRLRIPEN	FFFEESRYHC	ALILNLQKSP	FTGTWNFTSC	1080
SERHFVSLCQ	KYSEVKSRQT	LQNASETVKY	LNNLYKIIPK	TLTWHSAKRE	CLKSNMQLVS	1140
ITDPYQQAFQ	SVQALLHHNS	LWIGLFSQDD	ELNFGWSDGK	RLHFSRWAET	NGQLEDCVVL	1200
DTDGEFWKTV	CNDNQPGAI	YYSGNTEKE	VKPVDSVKCP	SPVLNTPWIP	FQNCCYNFII	1260
TKNRHMATTQ	DEVHTKCQKL	NPKSHILSIR	DEKENNFVLE	QLLYFNYMAS	WVMLGITYRN	1320
KSLMWFDKTP	LSYTHWRAGR	PTIKNEKFLA	GLSTDGFWDI	QTFKVIEEA	YFHQHSILAC	1380
KIEMVDYKEE	YNTTLPQFMP	YEDIYYSVIQ	KKVTWYEALN	MCSQSGGHLA	SVHNONGQLF	1440
LEDIVKRDGF	LEDIVKRDGF	GSESSWHD	GSTFDYIPWK	GOTSPGNCVL	LDPKGTVKHE	1500
KCNSVKDGA	CYKPTKSKKL	SRLTYSSRCP	AAKEENGSRWI	QYKGHCYKSD	QALHSFSEAK	1560
KLC SKDHSA	TIVSIKDEDE	NKFVSRMLMRE	NNNITMRVWL	GLSQHSVDQS	WSWLDGSSEVT	1620
FVKWENKSKS	GVGRCSMLIA	SNETWKVBC	EHGFGRVVCK	VPLGPDYTAI	AIIIVATLSIL	1680
VLMGGGLIWF	FQRHRLHLAG	FSSVRYAQGV	NEDEIMLPSF	HD		1722

SEQ ID NO: 79	moltype = AA	length = 306				
FEATURE	Location/Qualifiers					
source	1..306					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 79						
MAAVDDLQFE	EFGNAATS LT	ANPDATTVN	EDPGETPKHQ	PGSPRGSGRE	EDDELLGNDD	60
SDKTELLAGQ	KKSSPFWT	FE YYQTFDVT	D YQVFDRIKGS	LLPIP GKNFV	R LYI RSNPDL	120
YGF PWICATL	VFAIAISGNL	SNFLIHLGEK	TYHYVPEFRK	VSIAATIIYA	YAWLVPLALW	180
GFLMWRNSKV	MNIVSYSFLE	IVCVYGYSLF	IYIPTAILWI	IPQKAVRWIL	VMIALGSGS	240
LIA MTFWPAV	REDNRRVALA	TIVTIVLHM	LLSVGCLAYF	FDAPEMDHLP	TTTATPNQTV	300
AAAKSS						306

SEQ ID NO: 80	moltype = AA	length = 123				
FEATURE	Location/Qualifiers					
source	1..123					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 80						
MWRNSKVMNI	VSYSFLEIVC	VYGYSLFIYI	PTAILWIIPQ	KAVRWILVMI	ALGISGSSLLA	60
MTFWPAVRED	NRRVALATIV	TIVLHM	LLSVGCLAYF	PEMDHLP	ATPNQTVAAA	120
KSS						123

SEQ ID NO: 81	moltype = AA	length = 217				
FEATURE	Location/Qualifiers					
source	1..217					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 81						
MAAVDDLQFE	EFGNAATS LT	ANPDATTVN	EDPGETPKHQ	PGSPRGSGRE	EDDELLGNDD	60
SDKTELLAGQ	KKSSPFWT	FE YYQTFDVT	D YQVFDRIKGS	LLPIP GKNFV	R LYI RSNPDL	120
YGF PWICATL	VFAIAISGNL	SNFLIHLGEK	TYHYVPEFRK	VSIAATIIYA	YAWLVPLALW	180
GFLMWRNSKV	MNIVSYSFLE	IVCVYGYSLF	IYIPTAILWI	IPQKAVRWIL	VMIALGSGS	240
LIA MTFWPAV	REDNRRVALA	TIVTIVLHM	LLSVGCLAYF	FDAPEMDHLP	TTTATPNQTV	300
AAAKSS						217

SEQ ID NO: 82	moltype = AA	length = 306				
FEATURE	Location/Qualifiers					
source	1..306					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 82						
MAAVDDLQFE	EFGNAATS LT	ANPDATTVN	EDPGETPKHQ	PGSPRGSGRE	EDDELLGNDD	60
SDKTELLAGQ	KKSSPFWT	FE YYQTFDVT	D YQVFDRIKGS	LLPIP GKNFV	R LYI RSNPDL	120
YGF PWICATL	VFAIAISGNL	SNFLIHLGEK	TYHYVPEFRK	VSIAATIIYA	YAWLVPLALW	180
GFLMWRNSKV	MNIVSYSFLE	IVCVYGYSLF	IYIPTAILWI	IPQKAVRWIL	VMIALGSGS	240
LIA MTFWPAV	REDNRRVALA	TIVTIVLHM	LLSVGCLAYF	FDAPEMDHLP	TTTATPNQTV	300
AAAKSS						306

SEQ ID NO: 83	moltype = AA	length = 298				
FEATURE	Location/Qualifiers					
source	1..298					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 83						
MAAAEPAVLA	LPNAGAGGAG	APSGTVPVL	CFSVFARPSS	VPHGAGYELL	IQKFLSLYGD	60
QIDMHRKFVV	QLFAEEWGQY	VDLPGF	AVS ERCKVRLVPL	QIQLTTLGNL	TPSSTVF FCC	120
DMQERFRPAI	KYFGDIISVG	QRLLQGARIL	GIPVIVTEQY	PKGLGTVQE	IDLTGVKLVL	180
PTKFKFSMVLP	EVEAALAEIP	GVRSVLFGV	ETHVCIQQT	LA LELVGRGV	EV HIVADATSSR	240
SMMDRMFALE	RLARTGIIVT	TSEAVLLQLV	ADKDHPKFKE	I QNLIKASAP	ESGLLSKV	298

SEQ ID NO: 84	moltype = AA	length = 188
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FEATURE	Location/Qualifiers
source	1..188
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 84	
MAAAEPAVLA LPNSGAGGAG APSTVVPVLF CFSVFARPSS VPHGAGYELL IQKFLSLYGD	60
QIDMHRKFVV QLFAEEWGQY VDLPKGFAVS ERCKLTTLGN LTPSSTVFC CDMQERFRPA	120
IKYFGDIIISV GQRLLQGARI LGIPVIVTEQ YPKGLGSTVQ EIDLTVVKLV LPKTKFMSVL	180
PEVEAALA	188
SEQ ID NO: 85	moltype = AA length = 711
FEATURE	Location/Qualifiers
source	1..711
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 85	
MKLKLNVLTI ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDKPGSPYR	60
SVTHFDLSAV IDIPGADTLK KLFDHAVSKF GKKDSLGTRE ILSEENEMQP NGKVFKKLIL	120
GNYKWMNLYLE VNRRVNNFGS GLTALGLPK NTIAIFCETR AEWMIAAQTC FKYNFPLVTL	180
YATLGKEAVV HGLNESEASY LITSVELLES KLKTALLDIS CVKHIIYVDN KAINKAEYPE	240
GFEIHSMSVQ EELGSNPENL GIPPSRPTPS DMAIVMYTSG STGRPKGVMM HHSNLIAGMT	300
GCERIPIGLG PKDTYIGYL P LAHVELTAE ISCFTYGCRI GYSSPLTLSD QSSKIKKGSK	360
GDCTVLKPTL MAAVPEIMDR IYKVNMSKVQ EMNYIQKTLF KIGYDYKLEQ IKKGYDAPLC	420
NLLLFKKVKA LLGGNVRMML SGGAPLSPQT HRFMNVCFC PIGQQGYLTE SCGAGTVTEV	480
TDYTTGRVGA PLICCEIQLK DWQEGGYTIN DKPNPRGEIV IGGQNISMGY FKNEEKTAED	540
YSVDENGORW FCTGDIGEFH PDGCLQIIDR KKDLVQLQAG EYVSLGKVEA ALKNCPLIDN	600
ICAFAKSDQS YVISFVVPNQ KRLTLLAQOK GVEGTWVDIC NNPAAMEAEIL KEIREANAM	660
KLERFEIPIK VRLSPEPWTP ETGLVTDASF LKRKELRNHY LKDIERMYGG K	711
SEQ ID NO: 86	moltype = AA length = 711
FEATURE	Location/Qualifiers
source	1..711
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 86	
MKLKLNVLTI ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDKPGSPYR	60
SVTHFDLSAV IDIPGADTLK KLFDHAVSKF GKKDSLGTRE ILSEENEMQP NGKVFKKLIL	120
GNYKWMNLYLE VNRRVNNFGS GLTALGLPK NTIAIFCETR AEWMIAAQTC FKYNFPLVTL	180
YATLGKEAVV HGLNESEASY LITSVELLES KLKTALLDIS CVKHIIYVDN KAINKAEYPE	240
GFEIHSMSVQ EELGSNPENL GIPPSRPTPS DMAIVMYTSG STGRPKGVMM HHSNLIAGMT	300
GCERIPIGLG PKDTYIGYL P LAHVELTAE ISCFTYGCRI GYSSPLTLSD QSSKIKKGSK	360
GDCTVLKPTL MAAVPEIMDR IYKVNMSKVQ EMNYIQKTLF KIGYDYKLEQ IKKGYDAPLC	420
NLLLFKKVKA LLGGNVRMML SGGAPLSPQT HRFMNVCFC PIGQQGYLTE SCGAGTVTEV	480
TDYTTGRVGA PLICCEIQLK DWQEGGYTIN DKPNPRGEIV IGGQNISMGY FKNEEKTAED	540
YSVDENGORW FCTGDIGEFH PDGCLQIIDR KKDLVQLQAG EYVSLGKVEA ALKNCPLIDN	600
ICAFAKSDQS YVISFVVPNQ KRLTLLAQOK GVEGTWVDIC NNPAAMEAEIL KEIREANAM	660
KLERFEIPIK VRLSPEPWTP ETGLVTDASF LKRKELRNHY LKDIERMYGG K	711
SEQ ID NO: 87	moltype = AA length = 54
FEATURE	Location/Qualifiers
source	1..54
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 87	
MKLKLNVLTI ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDK	54
SEQ ID NO: 88	moltype = AA length = 145
FEATURE	Location/Qualifiers
source	1..145
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 88	
MKLKLNVLTI ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDKPGSPYR	60
SVTHFDLSAV IDIPGADTLK KLFDHAVSKF GKKDSLGTRE ILSEENEMQP NGKVFKKLIL	120
GNYKWMNLYLE VNRRVNNFGS GLTAL	145
SEQ ID NO: 89	moltype = AA length = 126
FEATURE	Location/Qualifiers
source	1..126
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 89	
MKLKLNVLTI ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDKPGSPYR	60
SVTHFDLSAV IDIPGADTLK KLFDHAVSKF GKKDSLGTRE ILSEENEMQP NGKVFKKLIL	120
GNYKWM	126

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SEQ ID NO: 90	moltype = AA length = 128
FEATURE	Location/Qualifiers
source	1..128
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 90	
MKLKLNVLTI	ILLPVHLLIT IYSALIFIPW YFLTNAKKKN AMAKRIKAKP TSDKPGSPYR 60
SVTHFDSLAV	IDIPGADTLK KLFDAVSKF GKKDSLGTRE ILSEENEMQP NGKVFKKLIL 120
GNYKWMNY	128
SEQ ID NO: 91	moltype = AA length = 80
FEATURE	Location/Qualifiers
source	1..80
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 91	
NLVRMRSQAL	GQSAPSLTAS LKELSLPRRG SLIDSQKWNC LVKRSLSPTP SSPGSPCSPL 60
LAPHFWSPVC	PNAGRTSPLG 80
SEQ ID NO: 92	moltype = AA length = 58
FEATURE	Location/Qualifiers
source	1..58
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 92	
MAKVAKDLNP	GVKKMSLGQL QSARGVACLG CKGTCSGFEP HSWRDCSTWS SSPRRSSQ 58
SEQ ID NO: 93	moltype = AA length = 760
FEATURE	Location/Qualifiers
source	1..760
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 93	
MMDQARSAFS	NLFGGEPLSY TRFSLARQVD GDNSHVEMKL AVDEEENADN NTKANVTKPK 60
RCSGSICYGT	IAIVVFPLIG FMIGYLGYCK GVEPKTECER LAGTESPVRE EPGEDFPAAR 120
RLYWDDLKRM	LSEKLDSTDF TGTIKLNNEN SYVPREAGSQ KDENLALYVE NQFREFKLSK 180
VWRDQHFKI	QVKDSAQNSV IIVDKNGRLV YLVENPGGYV AYSKAATVTG KLVHANFGTK 240
KDFEDLYTPV	NGSIVIVRAG KITFAEKVAN AESLNAIGVL IYMDQTKEPI VNAELSFVGH 300
AHLGTDGPY	PGFPSPFNHTQ FPPPSRSSGLP NIPVQTISRA AAEKLFGNME GDCPSDWKTD 360
STCRMVTS	KNVKLTVSNSV LKEKILNIF GVIKGFEVDPD HYVVVGAQRD AWGPGAAKSG 420
VGTALLLKL	QMFSDMVLKD GFQPSRSIIIF ASWSAGDFGS VGATEWLEGY LSSLHLKAFT 480
YINLDKAVLG	TSNFKVSASP LLYTLIEKTM QNVKHPVTGQ FLYQDSNWAS KVEKLTLDNA 540
APPFLAYSGI	PAVSFCFCED TDYPYLGTTM DTYKELIERI PELNKVARAA AEVAGQFVIK 600
LTHDVELNL	YERYNSQLLS FVRDLNQYRA DIKEMGLSLQ WLYSARGDFF RATSRLLTDF 660
GNAEKTDRFV	MKKLNDRVMR VEYHFLSPVY SPKESPFRHV FWGSGSHTLP ALLENLKLK 720
QNNGAFNETL	PRNQLALATW TIQGAANALS GDVWDIDNEF 760
SEQ ID NO: 94	moltype = AA length = 760
FEATURE	Location/Qualifiers
source	1..760
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 94	
MMDQARSAFS	NLFGGEPLSY TRFSLARQVD GDNSHVEMKL AVDEEENADN NTKANVTKPK 60
RCSGSICYGT	IAIVVFPLIG FMIGYLGYCK GVEPKTECER LAGTESPVRE EPGEDFPAAR 120
RLYWDDLKRM	LSEKLDSTDF TGTIKLNNEN SYVPREAGSQ KDENLALYVE NQFREFKLSK 180
VWRDQHFKI	QVKDSAQNSV IIVDKNGRLV YLVENPGGYV AYSKAATVTG KLVHANFGTK 240
KDFEDLYTPV	NGSIVIVRAG KITFAEKVAN AESLNAIGVL IYMDQTKEPI VNAELSFVGH 300
AHLGTDGPY	PGFPSPFNHTQ FPPPSRSSGLP NIPVQTISRA AAEKLFGNME GDCPSDWKTD 360
STCRMVTS	KNVKLTVSNSV LKEKILNIF GVIKGFEVDPD HYVVVGAQRD AWGPGAAKSG 420
VGTALLLKL	QMFSDMVLKD GFQPSRSIIIF ASWSAGDFGS VGATEWLEGY LSSLHLKAFT 480
YINLDKAVLG	TSNFKVSASP LLYTLIEKTM QNVKHPVTGQ FLYQDSNWAS KVEKLTLDNA 540
APPFLAYSGI	PAVSFCFCED TDYPYLGTTM DTYKELIERI PELNKVARAA AEVAGQFVIK 600
LTHDVELNL	YERYNSQLLS FVRDLNQYRA DIKEMGLSLQ WLYSARGDFF RATSRLLTDF 660
GNAEKTDRFV	MKKLNDRVMR VEYHFLSPVY SPKESPFRHV FWGSGSHTLP ALLENLKLK 720
QNNGAFNETL	PRNQLALATW TIQGAANALS GDVWDIDNEF 760
SEQ ID NO: 95	moltype = AA length = 81
FEATURE	Location/Qualifiers
source	1..81
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 95	
MMDQARSAFS	NLFGGEPLSY TRFSLARQVD GDNSHVEMKL AVDEEENADN NTKANVTKPK 60
RCSGSICYGT	IAIVVFPLIG C 81

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SEQ ID NO: 96      moltype = AA length = 118
FEATURE          Location/Qualifiers
source           1..118
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 96
AAAECVAGQFV 1KLTTHDVELN LDYERYNSQL LSFVRDLNQY RADIKEMLGS LQWLYSARGD 60
FFRATSLRTT DFGNAEKTDR FVMKKLNDRV MREGPQMMLL LTDARPSNHF LSPLLRLH 118

SEQ ID NO: 97      moltype = AA length = 643
FEATURE          Location/Qualifiers
source           1..643
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 97
MHHLLEQSAD MATALLAGEK LRELILPGAQ DDKAGALAAL LLQLKLELPF DRVVTIGTVL 60
VPILLVTLVF TKNFAEPIY CYTPHNFTRD QALYARGYCW TELRDALPGV DASLWPSLFE 120
HKPLPYALLA FAAIMVVPAL GWEFLASTRL TSELINFLQI IDNCYHRAAE GRAPKIEKQI 180
QSKGPGITER EKREIIENAE KEKSPEQNLF EKYLERGRS NFLAKLYLAR HVLILLLSAV 240
PISYLCTYYA TQKQNEFTCA LGASPDGAAG AGPAVRVSCK LPSVQLQRII AGVDIVLVC 300
MNLIILVNLI HLFIFRKSNF IFDKLHKVGI KTRRQWRRSQ FCDINILAMF CNENRDHIKS 360
LNRLDFITNE SDLMDYDNVR QLLAALAQSII HDATPTVRSN GVQTVDPSAN PAEPDGAEP 420
PVVKRPRKKM KWIPTSNPLP QPFKEPLAIM RVENSAEKP KPARRKTATD TLIAPLLDRS 480
AHHYKGGGGD PGPGPAPAPA PPPAPDKKHA RHFSLDVHPY ILGTKKAKAE AVPAALPASR 540
SQEGGFLSQA EDCGLGLAPA PIKDAPLPEK EIPYPTEPAR AGLPSGGPFH VRSPAAAPAV 600
APLTPASLGK AEPLTILSRN ATHPLLHINT LSSSPPSTSR ERS 643

SEQ ID NO: 98      moltype = AA length = 677
FEATURE          Location/Qualifiers
source           1..677
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 98
MHHLLEQSAD MATALLAGEK LRELILPGAQ DDKAGALAAL LLQLKLELPF DRVVTIGTVL 60
VPILLVTLVF TKNFAEPIY CYTPHNFTRD QALYARGYCW TELRDALPGV DASLWPSLFE 120
HKPLPYALLA FAAIMVVPAL GWEFLASTRL TSELINFLQI IDNCYHRAAE GRAPKIEKQI 180
QSKGPGITER EKREIIENAE KEKSPEQNLF EKYLERGRS NFLAKLYLAR HVLILLLSAV 240
PISYLCTYYA TQKQNEFTCA LGASPDGAAG AGPAVRVSCK LPSVQLQRII AGVDIVLVC 300
MNLIILVNLI HLFIFRKSNF IFDKLHKVGI KTRRQWRRSQ FCDINILAMF CNENRDHIKS 360
LNRLDFITNE SDLMDYDNVR QLLAALAQSII HDATPTVRSN GVQTVDPSAN PAEPDGAEP 420
PVVKRPRKKM KWIPTSNPLP QPFKEPLAIM RVENSAEKP KPARRKTATD TLIAPLLDRS 480
AHHYKGGGGD PGPGPAPAPA PPPAPDKKHA RHFSLDVHPY ILGTKKAKAE AVPAALPASR 540
SQEGGFLSQA EDCGLGLAPA PIKDAPLPEK EIPYPTEPAR AGLPSGGPFH VRSPAAAPAV 600
APLTPASLGK AEPLTILSRN ATHPLLHINT LYEARREEEDG GPRPLQDVGD LIAIPAPQQI 660
LIATFDEPRT VVSTVEF 677

SEQ ID NO: 99      moltype = AA length = 77
FEATURE          Location/Qualifiers
source           1..77
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 99
MATALLAGEK LRELILPGAQ DDKAGALAAL LLQLKLELPF DRVVTIGTVL VPILLVTLVF 60
TKNFAGWTLF SGWSWDWL 77

SEQ ID NO: 100     moltype = AA length = 1204
FEATURE          Location/Qualifiers
source           1..1204
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 100
MYVTMMMTDQ IPLELPLLNL GEVAMMPHLV NGDAAQQVIL VQVNPGETFT IRAEDGTLQC 60
IQGPAAEVPMN SPNGSIPPIH VPPGYISQVI EDSTGVRRV VTPQSFECYP PSYPSAMSPT 120
HHPLPPYLTHH PHFIHNSHTA YYPPVTGPGD MPQQFFFQHQH LPHTIYGEQE IIPFYGMSTY 180
ITREDQYSKPK PHKLLKDRQI DRQNRLNSPP SSIYKSSCTP YVNGYKGKHS GGSGGGGS 240
GPGIKKTERR ARSSPKNSDS DLQYELEVK RVQDILSGIE KPQVSNIQAR AVVLSWAPPV 300
GLSCGPHGSL SFYPSYEVAL SDKGRDGKYK IIYSGEELEC NLKDLRPATD YHVRVYAMY 360
SVKGSCSEPV SFTTHSCAPE CPFPKLAHR SKSSLTLQWK APIDNGSKIT NYLLEWDENG 420
RNNSGFRQCFF GSQKHCKLTT LCPAMGYTFR LAARNDIGTS GYSQEVVCYT LGNIPQMPSA 480
PRLVRAGITW VTLQWSKPEG CSPEEVITYT LEIQEDEDN LFHPKYTGED LTCTVKNLKR 540
STQYKFLRTA SNTEGKSCPS EVLVCTTSPD RPGPPTRPLV KGPVTSHGFS VKWDPKDN 600
GSEILKYLLE ITDGNSEANQ WEVAYSGSAT EYTFTHLKGK TLYKLACCI STGGHSQCSE 660
SLPVVRTLSIA PGQCRPRVL GRPKHKEVHL EWDVPAESG CEVSEYSVEM TEPEPDVASEV 720
YHGPELECTV GNLLPGTVYR FRVRALNDGG YGPYSDVSEI TTAAGPPGQC KAPCISCTPD 780
GCVLVGVWESP DSSGADISEY RLEWGEDEES LELIYHGTDT RFEIRDLLPA AQYCCRLQAF 840
NQAGAGPYSE LVLCQTPASA PDPVSTLCVL EEEPLDAYPD SPSACLVLNW EEPCCNNGSEI 900

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LAYTIDLGDT	SITVGNTTMH	VMKDLLPETT	YRIRIQAINE	IGAGPFSQFI	KAKTRPLPPL	960
PPLECAAG	PQSLKLKWGD	SNSKTHAAED	IVYTLQLEDR	NKRFISIYRG	PSHTYKVQRL	1020
TEFTCYSFRI	QAASEAGEGP	FSETYTFSTT	KSVPPTIKAP	RVTQLEGNSC	EILWETVPSM	1080
KGDPVNLYLQ	VLVGRESEYK	QVYKGEEATF	QISGLQTNTD	YRFRVCACRR	CLDTSQELSG	1140
AFSPSAAFVL	QRSEVMLTGD	MGSLDDPKMK	SMMPTDEQFA	AIIVLGFATL	SILFAFILQY	1200
FLMK						1204

SEQ ID NO: 101	moltype = AA	length = 1204
FEATURE	Location/Qualifiers	
source	1..1204	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 101						
MYVTMAMMTDQ	IPLELPPLLN	GEVAMMPHLV	NGDAAAQQVIL	VQVNPGETFT	IRAEDGTLQC	60
IQGPAEVPM	SPNGSIPPI	VPPGYISQVI	EDSTGVRRV	VTPQSPECYP	PSYPSAMSPT	120
HHLPPYLTHH	PHFIHNSHTA	YYPPVTGPGD	MPPQFFPOHH	LPHTIYGEQE	IIPFYGMSTY	180
ITREDQYSKP	PHKKLKDRQI	DRQNRLNSPP	SSIYKSSCTT	VYNGYKGHS	GGSGGGGSGS	240
GPGIKKTERR	ARSSPKSND	DQYELEVK	RVQDILSGIE	KPQVSNIQAR	AVVLSWAPPV	300
GLSCGPHGSL	SFPYSYEVAL	SDKGRDGKYK	IIYSGEELEC	NLKDLRPATD	YHVRVYAMYN	360
SVKGSCSEPV	SFTTHSCAPE	CPFPKLAHR	SKSSLTLQWK	APIDNGSKIT	NYLLEWDEGK	420
RNSGFRQCFF	GSQKHCKLTK	LCPAMGYTFR	LAARNDIGTS	GYSEVVVCYT	LGNIPQMPSA	480
PRLVRAGITW	VTLQWSKPEG	CSPEEVITYT	LEIQEDEDEND	LFHPKYTGED	LTCTVKNLKR	540
STQYKFRLTA	SNTEGKSCPS	EVLVCTTSPD	RPGPPTRPLV	KGPVTSHGFS	VKWDPPKDNG	600
GSEILKYLLE	ITDGNSEANQ	WEVAYSGSAT	EYTFTHLKG	TLYKLRACCI	STGGHSQCSE	660
SLPVRTLTLIA	PGQCRPPRVL	GRPKHKEVHL	EWDPASESG	CEVSEYSVEM	TEPEDVADEV	720
YHGPELECTV	CNLLPGTVYR	FRVRALNDGG	YGPYSDVSEI	TTAAGPPGQC	KAPCISCTPD	780
GCVLVGVWESP	DSSGADISEY	RLEWGDEEES	LELIYHGTD	RFEIRDLLPA	AQYCCRLQAF	840
NQAGAGPYSE	LVLCQTPASA	PDPVSTLCVL	EEEPLDAYPD	SPSACLVLNW	EEPCNNNGSEI	900
LAYTIDLGDT	SITVGNTTMH	VMKDLLPETT	YRIRIQAINE	IGAGPFSQFI	KAKTRPLPPL	960
PPLECAAG	PQSLKLKWGD	SNSKTHAAED	IVYTLQLEDR	NKRFISIYRG	PSHTYKVQRL	1020
TEFTCYSFRI	QAASEAGEGP	FSETYTFSTT	KSVPPTIKAP	RVTQLEGNSC	EILWETVPSM	1080
KGDPVNLYLQ	VLVGRESEYK	QVYKGEEATF	QISGLQTNTD	YRFRVCACRR	CLDTSQELSG	1140
AFSPSAAFVL	QRSEVMLTGD	MGSLDDPKMK	SMMPTDEQFA	AIIVLGFATL	SILFAFILQY	1200
FLMK						1204

SEQ ID NO: 102	moltype = AA	length = 1204
FEATURE	Location/Qualifiers	
source	1..1204	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 102						
MYVTMAMMTDQ	IPLELPPLLN	GEVAMMPHLV	NGDAAAQQVIL	VQVNPGETFT	IRAEDGTLQC	60
IQGPAEVPM	SPNGSIPPI	VPPGYISQVI	EDSTGVRRV	VTPQSPECYP	PSYPSAMSPT	120
HHLPPYLTHH	PHFIHNSHTA	YYPPVTGPGD	MPPQFFPOHH	LPHTIYGEQE	IIPFYGMSTY	180
ITREDQYSKP	PHKKLKDRQI	DRQNRLNSPP	SSIYKSSCTT	VYNGYKGHS	GGSGGGGSGS	240
GPGIKKTERR	ARSSPKSND	DQYELEVK	RVQDILSGIE	KPQVSNIQAR	AVVLSWAPPV	300
GLSCGPHGSL	SFPYSYEVAL	SDKGRDGKYK	IIYSGEELEC	NLKDLRPATD	YHVRVYAMYN	360
SVKGSCSEPV	SFTTHSCAPE	CPFPKLAHR	SKSSLTLQWK	APIDNGSKIT	NYLLEWDEGK	420
RNSGFRQCFF	GSQKHCKLTK	LCPAMGYTFR	LAARNDIGTS	GYSEVVVCYT	LGNIPQMPSA	480
PRLVRAGITW	VTLQWSKPEG	CSPEEVITYT	LEIQEDEDEND	LFHPKYTGED	LTCTVKNLKR	540
STQYKFRLTA	SNTEGKSCPS	EVLVCTTSPD	RPGPPTRPLV	KGPVTSHGFS	VKWDPPKDNG	600
GSEILKYLLE	ITDGNSEANQ	WEVAYSGSAT	EYTFTHLKG	TLYKLRACCI	STGGHSQCSE	660
SLPVRTLTLIA	PGQCRPPRVL	GRPKHKEVHL	EWDPASESG	CEVSEYSVEM	TEPEDVADEV	720
YHGPELECTV	CNLLPGTVYR	FRVRALNDGG	YGPYSDVSEI	TTAAGPPGQC	KAPCISCTPD	780
GCVLVGVWESP	DSSGADISEY	RLEWGDEEES	LELIYHGTD	RFEIRDLLPA	AQYCCRLQAF	840
NQAGAGPYSE	LVLCQTPASA	PDPVSTLCVL	EEEPLDAYPD	SPSACLVLNW	EEPCNNNGSEI	900
LAYTIDLGDT	SITVGNTTMH	VMKDLLPETT	YRIRIQAINE	IGAGPFSQFI	KAKTRPLPPL	960
PPLECAAG	PQSLKLKWGD	SNSKTHAAED	IVYTLQLEDR	NKRFISIYRG	PSHTYKVQRL	1020
TEFTCYSFRI	QAASEAGEGP	FSETYTFSTT	KSVPPTIKAP	RVTQLEGNSC	EILWETVPSM	1080
KGDPVNLYLQ	VLVGRESEYK	QVYKGEEATF	QISGLQTNTD	YRFRVCACRR	CLDTSQELSG	1140
AFSPSAAFVL	QRSEVMLTGD	MGSLDDPKMK	SMMPTDEQFA	AIIVLGFATL	SILFAFILQY	1200
FLMK						1204

SEQ ID NO: 103	moltype = AA	length = 71
FEATURE	Location/Qualifiers	
source	1..71	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 103						
MYVTMAMMTDQ	IPLELPPLLN	GEVAMMPHLV	NGDAAAQQVIL	VQVNPGETFT	IRAEDGTLQC	60
IQDEVVKRAC D						71

SEQ ID NO: 104	moltype = AA	length = 71
FEATURE	Location/Qualifiers	
source	1..71	
	mol_type = protein	

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SEQUENCE: 104	organism = Homo sapiens
MYVTMMMTDQ IPLELPPLLN GEVAMMPHLV NGDAQQVIL VQVNPGETFT IRAEDGTLQC	60
IQDEVVKRAC D	71
 SEQ ID NO: 105	moltype = AA length = 862
FEATURE Location/Qualifiers	
source 1..862	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 105	
MAHTFRGCSL AFMFIITWLL IKAKIDACKR GDVTVKPSHV ILLGSTVNIT CSLKPRQGCF	60
HYSSRRNKLIL YKFDRRINFH HGHSLSNSQVT GLPLGTTLFV CKLACINSDE IQICGAEIFV	120
GAVAPEQPQNL SCIQKGEQGT VACTWERGRD THLYTEYTLQ LSGPKNLWTWQ KQCKDIYCDY	180
LDFGINLTPE SPESNFTAKV TAVNSLGSSS SLPSTFTFLD IVRPLPPWDI RIKFQKASVS	240
RCTLYWRDEG LVLLNRLRYR PSNSRLWNMV NVTKAKGRHD LLDLKPFTEY EFQISSKLHL	300
YKGWSWDWSE SLRAQTPEEE PTGMLDVWYM KRHIDYSRQQ ISLFWKNLNV SEARGKILHY	360
QVTLQELTGG KAMTNQNTGH TSWTIVIPRT GNWAVAVSAA NSKGSSLPTR INIMNLCEAG	420
LLAPRQVSAN SEGMDNILVT WQPPRKDPSA VQEYVVVEWRE LHPGGDTQVP LNWLRSRPYN	480
V SALISENIK SYICYEIRVY ALSGDQGGCS SILGNSHKHA PLSPGHINAI TEEKGSILIS	540
WNSIPVQEQM GCLHYRIW KERDSNSQPQ LCEIPYRVSQ NSHPINSLQP RVTYVLWMTA	600
LTAAGESSHG NEREFCLOQGE ANWMAFVAPS ICIAIIMVGI FSTHYFQQKV FVLLAALRPQ	660
WCSREIPDPA NSTCAKKYPI AEEKTQLPLD RLLIDWPTE DPEPLVISEV LHQVTPVFRH	720
PPCSNWPKRE KGQHQASE KDMMHASSP PPPRALQAES RQLVLDLYKVL ESRGSDPKPE	780
NPACPWTVLP AGDLPHTHDGY LPSNIDDLPS HEAPLADSLE ELEPQHISLS VFPSSSLHPL	840
TFSCGDKLTL DQLKMRCDSL ML	862
 SEQ ID NO: 106	moltype = AA length = 659
FEATURE Location/Qualifiers	
source 1..659	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 106	
MAHTFRGCSL AFMFIITWLL IKAKIDACKR GDVTVKPSHV ILLGSTVNIT CSLKPRQGCF	60
HYSSRRNKLIL YKFDRRINFH HGHSLSNSQVT GLPLGTTLFV CKLACINSDE IQICGAEIFV	120
GAVAPEQPQNL SCIQKGEQGT VACTWERGRD THLYTEYTLQ LSGPKNLWTWQ KQCKDIYCDY	180
LDFGINLTPE SPESNFTAKV TAVNSLGSSS SLPSTFTFLD IVRPLPPWDI RIKFQKASVS	240
RCTLYWRDEG LVLLNRLRYR PSNSRLWNMV NVTKAKGRHD LLDLKPFTEY EFQISSKLHL	300
YKGWSWDWSE SLRAQTPEEE PTGMLDVWYM KRHIDYSRQQ ISLFWKNLNV SEARGKILHY	360
QVTLQELTGG KAMTNQNTGH TSWTIVIPRT GNWAVAVSAA NSKGSSLPTR INIMNLCEAG	420
LLAPRQVSAN SEGMDNILVT WQPPRKDPSA VQEYVVVEWRE LHPGGDTQVP LNWLRSRPYN	480
V SALISENIK SYICYEIRVY ALSGDQGGCS SILGNSHKHA PLSPGHINAI TEEKGSILIS	540
WNSIPVQEQM GCLHYRIW KERDSNSQPQ LCEIPYRVSQ NSHPINSLQP RVTYVLWMTA	600
LTAAGESSHG NEREFCLOQGE ANWMAFVAPS ICIAIIMVGI FSTHYFQQKR RHSCPWTGS	659
 SEQ ID NO: 107	moltype = AA length = 230
FEATURE Location/Qualifiers	
source 1..230	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 107	
XQKGEQGTVA CTWERGRDTH LYTEYTLQLS GPKNLWTWQKR CKDIYCDYLD FGINLTPESP	60
ESNFTAKVTA VNSLGSSSSL PSTFTFLDIV RPLPPWDIRI KFQKASVSR C TLYWRDEGLV	120
LLNRLRLRYRPS NSRLWNMVNV TKAAGRHDLL DLKPFTYEYF QISSKLHL YK GSWSWDSES	180
RAQTPEEEPT GMULDVWYMKR HIDYSRQQIS LFWKVSFKRQ LKTQGNKTEG	230
 SEQ ID NO: 108	moltype = AA length = 635
FEATURE Location/Qualifiers	
source 1..635	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 108	
MAHTFRGCSL AFMFIITWLL IKAKIDACKR GDVTVKPSHV ILLGSTVNIT CSLKPRQGCF	60
HYSSRRNKLIL YKFDRRINFH HGHSLSNSQVT GLPLGTTLFV CKLACINSDE IQICGAEIFV	120
GAVAPEQPQNL SCIQKGEQGT VACTWERGRD THLYTEYTLQ LSGPKNLWTWQ KQCKDIYCDY	180
LDFGINLTPE SPESNFTAKV TAVNSLGSSS SLPSTFTFLD IVRPLPPWDI RIKFQKASVS	240
RCTLYWRDEG LVLLNRLRYR PSNSRLWNMV NVTKAKGRHD LLDLKPFTEY EFQISSKLHL	300
YKGWSWDWSE SLRAQTPEEE PTGMLDVWYM KRHIDYSRQQ ISLFWKNLNV SEARGKILHY	360
QVTLQELTGG KAMTNQNTGH TSWTIVIPRT GNWAVAVSAA NSKGSSLPTR INIMNLCEAG	420
LLAPRQVSAN SEGMDNILVT WQPPRKDPSA VQEYVVVEWRE LHPGGDTQVP LNWLRSRPYN	480
V SALISENIK SYICYEIRVY ALSGDQGGCS SILGNSHKHA PLSPGHINAI TEEKGSILIS	540
WNSIPVQEQM GCLHYRIW KERDSNSQPQ LCEIPYRVSQ NSHPINSLQP RVTYVLWMTA	600
LTAAGESSHG NEREFCLOQGE DTAALGQAPD RLAHA	635
 SEQ ID NO: 109	moltype = AA length = 776
FEATURE Location/Qualifiers	

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source          1..776
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 109
MAHTFRGCSL AFMFIITWLL IKAKIDACKR GDVTVKPSHV ILLGSTVNIT CSLKPRQGCF 60
HYSRRNKLIL YKFDRINFFH HGHSLSNSQVT GLPLGTTLFV CKLACINSDE IQICGAEIFV 120
GVAPEQPQNL SCIQKGEQGT VACTWERGRD THLYTEYTLQ LSGPKNLWTQ KQCKDIYCDY 180
LDFGINLTPE SPESNFTAKV TAVNSLGSSS SLPSTFTPLD IVRPLPPWDI RIKFQKASVS 240
RCTLYWRDEG LVLLNRLRYR PSNSRLWNMV NVTKAKGRHD LLDLKPFTEY EFQISSKLHL 300
YKGWSWDSE SLRAQTPEER PTGMLDWWMX KRHHIDYSRQQ ISLFWKNLSV SEARGKILHY 360
QVTLQELTGG KAMTNQITGH TSWTIVIPRT GNWAVAVSA NSKGSSLPTR INIMNLCEAG 420
LILAPRQVSAN SEGMDNILVW WQPPRKDPDA VQEYVVEWRE LHPGGDTQVP LNWLRSRPYN 480
VSALISEIYP RVSQNSHPIN SLQPRVTYVL WMTALTAAGE SSHGNEREF C LQGKANWMAF 540
VAPSICIAII MVGIFSTTHYF QOKVFPVLLAA LRQWCSREI PDPANSTCAK KYPIAEKTQ 600
LPLDRLLIDW PTPEDPEPLV ISEVLHQVTP VFRHPPPCSNU PQREKGIOGH QASEKDMMS 660
ASSPPPPRQL QAESRLVLDL YKVLESRSQD PKPENPACPW TVLPAGDLPT HDGYLPSNID 720
DLPSSHEAPLA DSLEELEPQH ISLSVFSSS LHPLTFSCGD KLTLQDKMR CDSLML 776

SEQ ID NO: 110      moltype = AA length = 370
FEATURE
source          1..370
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 110
MLPRLLLAALW LAGTRGGGLL ALLANQCRFV TGLRVRRQAQ IAQLYGRQLYS ESSRRVLLGR 60
LWRRRLHGRPG HASALMAALA GVFVWDEERI QEELQRSIN EMKRLEEMSN MFQSSGVQHH 120
PPEPKAQTEG NEDSEGKEQR WEMVMDKKHF KLWRRPITGP HLYQYRWFGT YTDVTPRQFF 180
NVQLDTEYRK KWDALVIKLE VIERDVVSGS EVLHWVTHFP YPMYSRDYVVY VRRYSVDQEN 240
NMMVLVSRAV EHPSVPESPE FVRVRSYESQ MViRPHKSFD ENGFDFYLTY SDNPQTVFPR 300
YCVSWMVSSG MPDFLEKLHM ATLAKANMEI KVKDYISAKP LEMSSEAKAT SQSSERKNEG 360
SCGPARIEYA 370

SEQ ID NO: 111      moltype = AA length = 154
FEATURE
source          1..154
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 111
MVKAKIVIN GWLFPAACLG CLSESFFMVK GAALFLQQGS SPQGQRSLQH PHKHAGDLPQ 60
HLQVMINLLR CEDRIKLA VR LESAWADRVY YMVVVYSSGR QDTEENILLG VDFSSKESKS 120
CTIGMVLRLW SDTKIHLDGD GGFSVSTAGR MHIF 154

SEQ ID NO: 112      moltype = AA length = 37
FEATURE
source          1..37
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 112
MALVTLQRSP TPSAASSSSAS NSELEAGSEE DRKLNL 37

SEQ ID NO: 113      moltype = AA length = 147
FEATURE
source          1..147
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 113
MAGNSILLAA VSILSACQQS YFALQVGKAR LKYKVTPPAV TGSPEFERVF RAQQNCVEFY 60
PIFIITLWMA GWYFNQVFAT CLGLVYIYGR HLYFWGYSEA AKKRITGFL SLGILALLTL 120
LGALGIANSF LDEYLDLNIA KKLRQF 147

SEQ ID NO: 114      moltype = AA length = 147
FEATURE
source          1..147
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 114
MAGNSILLAA VSILSACQQS YFALQVGKAR LKYKVTPPAV TGSPEFERVF RAQQNCVEFY 60
PIFIITLWMA GWYFNQVFAT CLGLVYIYGR HLYFWGYSEA AKKRITGFL SLGILALLTL 120
LGALGIANSF LDEYLDLNIA KKLRQF 147

SEQ ID NO: 115      moltype = AA length = 77
FEATURE
source          1..77
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 115

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MAGNSILLAA VSILSACQQS YFALQVGKAR LKYKVTPPAV TGSPEFERVF RAHFCYLSGS GVHIWPSPIL LGIFRSC	60 77
SEQ ID NO: 116 FEATURE source SEQUENCE:	moltype = AA length = 147 Location/Qualifiers 1..147 mol_type = protein organism = Homo sapiens
MAGNSILLAA VSILSACQQS YFALQVGKAR LKYKVTPPAV TGSPEFERVF RAQQNCVEFY PIFIITLWMA GWFNFNQVFAT CLGLVVIYGR HLYFWGYSEA AKKRITGFRL SLGILALLTL LGALGIANSF LDEYLDLNIA KKLRRQF	60 120 147
SEQ ID NO: 117 FEATURE source SEQUENCE:	moltype = AA length = 110 Location/Qualifiers 1..110 mol_type = protein organism = Homo sapiens
MFKSPLKVPA LIQCLGMYDS SLAAKYLLHS LVPGSAVYSS GSERHLTYIQ KIFRMEIFGC FALTELSHGNS NTKAIRTTAH YDPATEEFII HSPDFFEAAKF WVGNMGKTAT	60 110
SEQ ID NO: 118 FEATURE source SEQUENCE:	moltype = AA length = 121 Location/Qualifiers 1..121 mol_type = protein organism = Homo sapiens
XGHQNVPFNH ISVGTNRKRC LEDSEDFGVK KARTEAQSLD SAVPLTNGDT EDDADKMHD REFAVVTGGS GQFPVSCNNN PMVEDTKQQE SGSGVPKEIE IYTVSAMQTP CRCRNQYAYY F	60 120 121
SEQ ID NO: 119 FEATURE source SEQUENCE:	moltype = AA length = 37 Location/Qualifiers 1..37 mol_type = protein organism = Homo sapiens
MGVQVETISP GDGRTFPKRG QTCVVHYTGG DCILVNE	37
SEQ ID NO: 120 FEATURE source SEQUENCE:	moltype = AA length = 129 Location/Qualifiers 1..129 mol_type = protein organism = Homo sapiens
MGVQVETISP GDGRTFPKRG QTCVVHYTGM LEDGKKFDSS RDRNPKFKM LGKQE VIRGW EEGVAQVCSL ICFVLLSSIY LLYFFIGGIF IRPKNKKSEK SHPHAI PSDQ YPHKKLLL FLVLWFKHI	60 120 129
SEQ ID NO: 121 FEATURE source SEQUENCE:	moltype = AA length = 97 Location/Qualifiers 1..97 mol_type = protein organism = Homo sapiens
MGVQVETISP GDGRTFPKRG QTCVVHYTDE CGSESQTDYI SRLCLWCHWA PRHHPTTCHS RLRCGASKTG MTGMASSLSS LFLLDLPWRDL VPPDMCT	60 97
SEQ ID NO: 122 FEATURE source SEQUENCE:	moltype = AA length = 276 Location/Qualifiers 1..276 mol_type = protein organism = Homo sapiens
MVP PASWPHP PGPFL LLLTLL LGLTEVAGEEL ELQMIQPEKL LLVTVGKTAT LHCTVTSLLP VGPVLFWRGV GPGRELIYNQ KEGHFPRVTT VSDLTKRNNM DFSIRISSIT PADVGTYYCV KFRKGSPENV EFKSGPGTEM ALGAKPSAPV VLGAARTPP EHTVSFTCES HGFSPRDITL KWFKNGNELS DFQTNVDPTG QSVAYSIRST ARVVLDPWDV RSQVICEVAH VTLQGDPLRG TANLSEAIRG PASSLTALL IAVLLGPIYV PWKQKT	60 120 180 240 276
SEQ ID NO: 123 FEATURE source SEQUENCE:	moltype = AA length = 387 Location/Qualifiers 1..387 mol_type = protein organism = Homo sapiens

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SEQUENCE: 123
 MWPVPAWPHP PGPFLLLTLL LGLTEVAGEE ELQMIQPEKL LLVTVGKTAT LHCTVTSLLP 60
 VGPVLWFRGV GPGRELIYNQ KEGHFPRVTT VSDLTKRNNM DFSIRISSIT PADVGTYYCV 120
 KFRKGSPENV EFKSGPGTEM ALGAKPSAPV VLGPAARTTP EHTVSFTCES HGFSPRDITL 180
 KWFKNNGNELS DFQTNVDPDG QSVAYSIRST ARVVLDPWDV RSQVICEVAH VTLQGDPLRG 240
 TANLSEAIRV PPTLEVTQQP MRVGNQVNVT COVRKFYQOS LQLTWSENGN VCQRETASTL 300
 TENKDGTYNW TSWFLVNISD QKDDVVLTQV VKHDGQLAVS KRLALEVTVH QKDQSSDATP 360
 GPASSLTALL IAVLLGPIY VPWKQKT 387

SEQ ID NO: 124 moltype = AA length = 170
 FEATURE Location/Qualifiers
 source 1..170
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 124
 MWPVPAWPHP PGPFLLLTLL LGLTEVAGEE ELQMIQPEKL LLVTVGKTAT LHCTVTSLLP 60
 VGPVLWFRGV GPGRELIYNQ KEGHFPRVTT VSDLTKRNNM DFSIRISSIT PADVGTYYCV 120
 KFRKGSPENV EFKSGPGTEM ALGGPASSLT ALLIAVLLG PIYVPWKQKT 170

SEQ ID NO: 125 moltype = AA length = 354
 FEATURE Location/Qualifiers
 source 1..354
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 125
 MIQPEKLLLV TVGKTATLHC TVTSLLPVGP VLWFRGVGPG RELIYNQKEG HFPRVTTVSD 60
 LTKRNNMDFS IRISSITPAD VGTYYCVKFR KGSPENVEFK SGPGTEMALG AKPSAPVVLG 120
 PAARTTPEHT VSFTCESHGFGF SPRDITLKWF KNGNELSDFO TNVDPTGQSV AYSIRSTARV 180
 VLDPWDVRSQ VICEVAHVTL QGDPLRGTAN LSEAIRVPPT LEVTQQPMRV GNQVNVTQCV 240
 RKPYPPQLSQL TWSENGNVCQ RETASTLTEN KDGTYNWTSW FLVNISDQRD DVVLTCQVKH 300
 DGQLAVSKRL ALEVTVHQKD QSSDATPGPA SSLTALLLIA VLLGPIYVWP KQKT 354

SEQ ID NO: 126 moltype = AA length = 276
 FEATURE Location/Qualifiers
 source 1..276
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 126
 MWPVPAWPHP PGPFLLLTLL LGLTEVAGEE ELQMIQPEKL LLVTVGKTAT LHCTVTSLLP 60
 VGPVLWFRGV GPGRELIYNQ KEGHFPRVTT VSDLTKRNNM DFSIRISSIT PADVGTYYCV 120
 KFRKGSPENV EFKSGPGTEM ALGAKPSAPV VLGPAARTTP EHTVSFTCES HGFSPRDITL 180
 KWFKNNGNELS DFQTNVDPDG QSVAYSIRST ARVVLDPWDV RSQVICEVAH VTLQGDPLRG 240
 TANLSEAIRG PASSLTALLL IAVLLGPIYV PWKQKT 276

SEQ ID NO: 127 moltype = AA length = 556
 FEATURE Location/Qualifiers
 source 1..556
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 127
 MHGSLEALLF LPQVTLSLAH AHLICSNAQL EMCVFPHRFL GDLTTEGINK PGFYKGPGAGS 60
 QVTLSSLGNQ TRVLLEEQAR HLLNEQEHAAT MAYYLDEYRG GSVSVEALVM ALFKLLNTHA 120
 KFSLLSEVRG TISPQDLERF DHVLVRREIE SMKARQPPGP GAGDTYSMVS YSDTGSTG 180
 HGTSTTVSSA RNTLDLEETG EAVQGNINAL PDVSVDDVRS TSQGLSSFKP LPRPPPLAQG 240
 NDPLPLGQPRK LGREDLQPPS SMPSCSGTFV SAPQNRSPPA GTAPTPGTTSS AQDLPSSPIY 300
 ASVSPANPSS KRPLDAHLAL VNQHPIGFPF RVQSPPHLKS PSAEATVAGG CLLPPSPSGH 360
 PJDQTGTONQHF VMVEVHRPDS EPDVNEVRAL PQTRTASTLS QLSDSGQTLS EDSGVDAGEA 420
 EASAPGRGRQ SVSTKSRRSK ELPRNERPTD GANKPPGLLE PTSTLVRVKK SAATLGIAIE 480
 GGANTROQLP RIVTIQRGGS AHNCGQLKVG HVILEVNGLT LRGKEHREAA RIIAEAFKTK 540
 DRDYIDFLVT EFNVML 556

SEQ ID NO: 128 moltype = AA length = 180
 FEATURE Location/Qualifiers
 source 1..180
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 128
 MSVLRPLDKL PGLNTATILL VGTEDALLQQ LADSMLKEDC ASELKVHLAK SLPLPSSVNR 60
 PRIDLIVFFF NLHSKYSLQN TEESLRHVDA SFPLGKVCFI ATGAGRESHC SIHRHTVVKL 120
 AHTYQSPLLY CDLEVEGFRA TMAQRLVRVL QICAGHVPVG SALNLLSLLR SSEGPSLEDL 180

SEQ ID NO: 129 moltype = AA length = 146
 FEATURE Location/Qualifiers
 source 1..146
 mol_type = protein
 organism = Homo sapiens

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SEQUENCE: 129
 MKEDCASEL KVHLAKSLPL PSSVNRPRID LIVFVVNLHS KYSLQNTees LRHVDASFFL 60
 GKVCFLATGA GRESHCSIHR HTVVKLAHTY QSPLLYCDLE VEGFRATMAQ RLVRVLQICA 120
 GHVPGVSLN LLSLLRSSEG PSLEDL 146

SEQ ID NO: 130 moltype = AA length = 125
 FEATURE Location/Qualifiers
 source 1..125
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 130
 MKEDCASEL KVHLAKSLPL PSSVNRPRID LIVFVVNLHS KYRIREARTS AFSVVKFCSL 60
 VCFLTLAWPP QSPEHRGVPA PCGCQLLGE GVFPCHRWA GEPLQHSPA RGEAGPHLSK 120
 PPALL 125

SEQ ID NO: 131 moltype = AA length = 73
 FEATURE Location/Qualifiers
 source 1..73
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 131
 MKEDCASEL KVHLAKSLPL PSSVNRPRID LIVFVVNLHS KYSLQNTees LRHVDASFFL 60
 GKVCFLATGG GRL 73

SEQ ID NO: 132 moltype = AA length = 107
 FEATURE Location/Qualifiers
 source 1..107
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 132
 MSVLRPLDKL PGLNTATILL VGTEDALLQQ LADSMLKEDC ASELKVLAK SLPLPSSVNR 60
 PRIDLIVFVV NLHSKYSLQN TEESLRHVDA SFFLGKVCFL ATGGGRL 107

SEQ ID NO: 133 moltype = AA length = 166
 FEATURE Location/Qualifiers
 source 1..166
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 133
 MRIPALNAYM KSLLSLPVVW LMDEDVRIFF YQSPYDSEQV PQALRRRLRPR TRKVKSVPQ 60
 GNSVDRMAAP RAEALFDFTG NSKLELNPKA GDVIFLLSRI NWDLEGTVR GATGIFPLSF 120
 VKILKDFPPEE DDPTNWLRCY YYEDTISTIK SVAWEGGACP AFLPLS 166

SEQ ID NO: 134 moltype = AA length = 889
 FEATURE Location/Qualifiers
 source 1..889
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 134
 MVLAQGLLSSM ALLALCWERS LAGAEETIPL QTLRCYNDYT SHITCRWADT QDAQLVNVT 60
 LIRRVNEDLL EPVSCDLSD MPWSACPHPR CVPRRCVIPC QSFVVTDVDY FSFQPDRLPG 120
 TRLTVTLTQH VQPPEPRDLQ ISTDQDHFL TWSVALGSPQ SHWLSPGDLE FEVVKRLQD 180
 SWEDAAILLS NTSQATLGPE HLMPSTTYVA RVTRTRLAPGS RLSGRPSKWS PEVCWDSQPG 240
 DEAQPNQLEC FFDGAAVLSC SWEVRKEVAS SVSFGLFYKP SPDAGEEECS PVLREGLGSL 300
 HTRRHCOIPV PDPATHQGYI VSVQPRRAEK HIKSSVNIQM APPSLNVTKS GDSYSLRWET 360
 MKMRYEHIDH TFEIQYRKDT ATWKDSKTET LQNAHSMALP ALEPSTRYWA RVRVRTSRTG 420
 YNGIWSEHSE ARSWDTESTVL PMWVLALIVI FLTIAVLLLA RFCGIYCYRL RRKEEKIPN 480
 PSKSHLFQNG SAEWPNGSM SAFTSGSPPH QGPWGSRFP EGVFPVGFG DSEVSPLTIE 540
 DPKHVCDDPS GPDTTPAASP LPTEQPPSPQ PGPPAASHTP EKQASSFDNFN GPYLGPHSR 600
 SLPDILGQPE PQQEGGSQKS PPPGSLEYLC PLAQQAMPGQ AVEVERRPSQ 660
 GAAGSPSLES CGGPAPPALG PRVGGQDQKD SPVAIPMSG DTEDPGVASG YVSSADLVFT 720
 PNSGASSVSL VPSLGLPSDQ TPSLCPGLAS GPPGAPGPVK SGFEGYVELP PIEGRSPRSP 780
 RNNPVPPEAK SPVLPNGERP ADVSPTSPQ EGGLLVLQOQV DYCFLPGLGP GPLSLRSKPS 840
 SPGPGPPEIKN LDQAFQVKKP PGQAVPQV PV IQLFKALVVMSVGPPV 889

SEQ ID NO: 135 moltype = AA length = 897
 FEATURE Location/Qualifiers
 source 1..897
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 135
 MVLAQGLLSSM ALLALCWERS LAGAEETIPL QTLRCYNDYT SHITCRWADT QDAQLVNVT 60
 LIRRVNEDLL EPVSCDLSD MPWSACPHPR CVPRRCVIPC QSFVVTDVDY FSFQPDRLPG 120
 TRLTVTLTQH VQPPEPRDLQ ISTDQDHFL TWSVALGSPQ SHWLSPGDLE FEVVKRLQD 180
 SWEDAAILLS NTSQATLGPE HLMPSTTYVA RVTRTRLAPGS RLSGRPSKWS PEVCWDSQPG 240
 DEAQPNQLEC FFDGAAVLSC SWEVRKEVAS SVSFGLFYKP SPDAGEEECS PVLREGLGSL 300

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HTRHHCQIPV PDPATHGQYI VSVQPRRAEK HIKSSVNQHM APPSLNVTKD GDSYSLRWET	360
MKMRYEHDH TFEIQYRKDT ATWKDSKTBT LQNAHSMALP ALEPSTRYWA RVRVRTSRTG	420
YNGIWSEWSE ARSWDTESVL PMWVLALIVI FLTIAVLLAL RFCGIYGYRL RRKWEEKIPN	480
PSKSHLFQNG SAELWPMSGM SAFTSGSPPH QGPWGSRPE LEGVFVPGFG DSEVSPLTIE	540
DPKHVCDPPS GDPDTTPAASD LPTEQPPSPQ PGPPAASHTP EKQASSDFN GPYLGPPHSR	600
SLPDILQPE PPQEGGSQKS PPPGSLEYLC LPAGGQVOLV PLAQAMGPQQ AVEVERRPSQ	660
GAAGSPSLES GGGPAPPALG PRVGGQDQKD SPVAIPMSGG DTEDPGVASG YVSSADLVFT	720
PNSGASSVSL VPSLGLPDSQ TPSCLPGLAS GPPGAPGPVK SGFEGYVELP PIEGRSPRSP	780
RNNNPVPPEAK SPVLPNGERP ADVSPTSPQP EGLLVLQQVG DYCFPLGLGP GPLSLRSKPS	840
SPGPGPEIKN LDQAFQVKKP PGQAVPQPVV IQLFKALKQK DYLSLPPWEV NKPGEVC	897
 SEQ ID NO: 136 moltype = AA length = 903	
FEATURE Location/Qualifiers	
source 1..903	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 136	
MVLAQGLLSSM ALLALCWERS LAGAEETIPL QTLRCYNDYT SHITCRWADT QDAQLRVNVT	60
LIRRVNEDLL EPVSCDLSD MPWSACPHPR CVPRRCVIPC QSFFVTDVDY FSFQPDRLG	120
TRLTVTLTQH VQPPEPRDLQ ISTQDHFL TWSVALGSPQ SHWLSPGDLE FEVYVKRQLQD	180
SWEDAAILLS NTSQATLGPE HLMPSSYVA RVRTRLAPGS RLSPRPSKWS PEVCWDSQPG	240
DEAQPNLLEC FFDGAAVLSC SWEVRKEVAS SVSFGLFYKP SPDAGSAVLL REEECSPVLR	300
EGLGSLHTRH HCQIPVDPDA THGQYIVSVQ PRRAEKHIKS SVNIQMAPPS LNVTKDGDSY	360
SIRWETMKMR YEHDHTFET QYRKDTATWK DSKTETLQNA HSMALPALEP STRYWARVRV	420
RTSRTGYNGI WSEWSEARSW DTESVLPWMW LALIVIFLTI AVLLALRFCG IYGYRLRKW	480
EKIEPNPSKS HLFQNQGSAEL WPPGMSMAFT SGSPPHQGPW GSRFPELEGV FPVGPGDSEV	540
SPLITIEDPKH VCDPPSPGDT TPAASDLPTE QPFSPQPGPP AASHTPEKQA SSFDFNGPYL	600
GPPHSRSLPD ILGQPEPPQG GGSQKSPPPG SLEYLCLPAG GOVQLVPLAQ AMGPQOAVEV	660
ERRPSQAGG SPSLESGGGP APPALGPVRVQ GQDQKDSPVA IPMSSGDTED PGVASGGYSS	720
ADLVFTPNSG ASSVSLVPSL GLPSDQTPSL CPGLASGPVG APGPVKSGFE GYVELPPIEG	780
RSRSPRNNP VPPEAKSPVLP NPGERPADVS PTSPQPEGGLL VLQQVGDYCF LPGLGPGPLS	840
LRSKPPSPGP GPEIKNLDQA FQVKKPPGQA VPQVPVIQLF KALKQQDYL S LPPWEVINKPG	900
EVC	903
 SEQ ID NO: 137 moltype = AA length = 229	
FEATURE Location/Qualifiers	
source 1..229	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 137	
MPWSACPHPR CVPRRCVIPC QSFFVTDVDY FSFQPDRLG TRLTVTLTQH VQPPEPRDLQ	60
ISTQDHFL TWSVALGSPQ SHWLSPGDLE FEVYVKRQLQD SWEDAAILLS NTSQATLGPE	120
HLMPSSYVA RVRTRLAPGS RLSPRPSKWS PEVCWDSQPG DEAQPNLLEC FFDGAAVLSC	180
SWEVRKEVAS SVSFGLFYKP SPDAGEEECS PVLREGLGSL HTRHHCQIP	229
 SEQ ID NO: 138 moltype = AA length = 144	
FEATURE Location/Qualifiers	
source 1..144	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 138	
MAFTFAACFY MLALLTAAL IFFAIWHIIA FDELKTDYKN PIDQCNTLNP LVLPEYLIHA	60
FFCVMFLCAA EWLTGLLNMP LLAYHIWRYM SRPVMSGPGL YDPTTIMNAD ILAYCQKEGW	120
CKLAFYLLAF FYYLYGMIYV LVSS	144
 SEQ ID NO: 139 moltype = AA length = 96	
FEATURE Location/Qualifiers	
source 1..96	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 139	
MAFTFAACFY MLALLTAAL IFFAIWHIIA FDELKTDYKN PIDQCNTLNP LVLPEYLIHA	60
FFCVMFLCAA EWLTGLLNMP LLAYHIWSMI YVLVSS	96
 SEQ ID NO: 140 moltype = AA length = 121	
FEATURE Location/Qualifiers	
source 1..121	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 140	
MAFTFAACFY MLALLTAAL IFFAIWHLVL PEYLIHACF VMFLCAAEWL TLGLNMPLLA	60
YHIWRYMSRP VMSGPGLYDP TTIMNADILA YCQKEGWCKL AFYLLAFFYY LYGMIVLVS	120
S	121
 SEQ ID NO: 141 moltype = AA length = 33	
FEATURE Location/Qualifiers	

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source          1..33
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 141
MAFTFAACFY MLALLLTAAL IFFAIWHDKE EFG                         33

SEQ ID NO: 142      moltype = AA  length = 136
FEATURE
source          1..136
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 142
MAFTFAACFY MLALLLTAAL IFFAIWIIIA FDELKTDYKN PIDQCNTLNP LVLPEYLIHA 60
FFCVMFLCAA EWLTGLNMP LLAYHIWRYM SRPVMSGPGL YDPTTIMNAD ILAYCQKEGW 120
CKLAFYLLAF FYLYLG                                         136

SEQ ID NO: 143      moltype = AA  length = 53
FEATURE
source          1..53
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 143
MAFTFAACFY MLALLLTAAL IFFAIWIIIA FDELKTDYKN PIDQCNTLNP VYE             53

SEQ ID NO: 144      moltype = AA  length = 160
FEATURE
source          1..160
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 144
MAFTFAACFY MLALLLTAAL IFFAIWIIIA FDELKTDYKN PIDQCNTLNP TVEVKKKIKR 60
VKAALKLVLP EYLIHAFFCV MFLCAAEWLT LGLNMPPLLAY HIWRYMSRPV MSGPGLYDPT 120
TIMNADILAY CQKEGWCCKLA FYLLAFFYYL YGMIYVLVSS                                         160

SEQ ID NO: 145      moltype = AA  length = 435
FEATURE
source          1..435
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 145
MAAPLVLVVL VAVTVRAALF RSSLAEFISE RVEVVSPPLS WKRVVEGLSL LDLGVSPYSG 60
AVFHETPLII YLFHFLIDYA ELVFMITDAL TAIALYFAIQ DFNKVVFKKQ KLLLELDQYA 120
PDVAELIRTP MEMRYIPLKV ALFVLLNPYT ILSCVAKSTC AINNTLIAFF ILTTIKGSAF 180
LSAIFLALAT YQSLYPLTLF VPGLLYLLQR QYIPVKMKS AFWIFSWEYA MMVGSLVVI 240
ICLSFFLSS WDFIPAVYGF ILSVPDLTPN IGLFWYFFAE CVFQINVFFY 300
TIPLAIKLKE HPIFFMFQI AVIAIFKSYP TVGDVALYMA FFPVWNHLYR FLRNIFVLT 360
IIIVCSLLFP VLWHLWIYAG SANSNFFYAI TLTFNVGQIL LISDYFYAFL RREYYLTHGL 420
YLTAKGTEA MLVLK                                         435

SEQ ID NO: 146      moltype = AA  length = 415
FEATURE
source          1..415
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 146
MAAPLVLVVL VAVTVRAALF RSSLAEFISE RVEVVSPPLS WKRVVEGLSL LDLGVSPYSG 60
AVFHEITDAL TAIALYFAIQ DFNKVVFKKQ KLLLELDQYA PDVAELIRTP MEMRYIPLKV 120
ALFYLLNPYT ILSCVAKSTC AINNTLIAFF ILTTIKGSAF LSAIFLALAT YQSLYPLTLF 180
VPGLLYLLQR QYIPVKMKS AFWIFSWEYA MMVGSLVVI ICLSFLLSS WDFIPAVYGF 240
ILSVPDLTNP IGLFWYFFAE MFEHFSLFFV CVFQINVFFY TIPLAIKLKE HPIFFMFQI 300
AVIAIFKSYP TVGDVALYMA FFPVWNHLYR FLRNIFVLT 360
SANSNFFYAI TLTFNVGQIL LISDYFYAFL RREYYLTHGL YLTAKGTEA MLVLK                                         415

SEQ ID NO: 147      moltype = AA  length = 170
FEATURE
source          1..170
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 147
VSVPTHLVCP RTPLSPPAAV HTCENEESQL LDLFLGVCHD INVFFYTIPL AIKLKEHPIF 60
FMPIQIAVIA IFKSYPVTGD VALYMAFFPV WNHLYRFRLRN IFVLTICIIIV CSLLFPVLWH 120
LWYIAGSANS NFFYAITLTF NVGQILLISD YFYAFLRREY YLTHGLYLT 170

SEQ ID NO: 148      moltype = AA  length = 336
FEATURE
source          1..336
               mol_type = protein
               organism = Homo sapiens

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mol_type = protein
organism = Homo sapiens

SEQUENCE: 148
MARRRSQRVC ASGPSMLNSA RGAPELLRT ATNAEVSAAG AGATGSEELP PGDRGCRNGG 60
GRGPAATTSS TGAVGAEHG EDSLRSRKDP EPGRMDHHQ GTGRYQVLLN EEDNSESSAI 120
EQPPTSNPAP QIVQAASSAP ALETDSPPPP YSSITVEVPT TSDTEVYGEF YPVPPPYSAV 180
TSLPTYDEAE KAKAAAMAAA AAETSQRIQE EECPPRDDFS DADQLRVGND GIFMLAFM 240
FIFNWLGFCL SFCITNTIAG RYGAICGFL SLIKWILIVR PSDYFTGYFN GQYWLWWIFL 300
VLGLLFFFRG FVNLYLKVRNM SESMAAHRT RYFFLL 336

SEQ ID NO: 149      moltype = AA length = 222
FEATURE           Location/Qualifiers
source            1..222
mol_type = protein
organism = Homo sapiens

SEQUENCE: 149
MDHHQPGTGR YQVLLNEEDN SESSAIEQPP TSNPAPQIVQ AASSAPALET DSSPPPYSSI 60
TVEVPTTSDT EVYGEFPVP PPYSVATSLP TYDEAEKAKA AAMAAAAAET SQRIQEECP 120
PRDDFSADQ LRGNDGIFM LAFFTGRYGA ICGFGLSLIK WILIVRFSDY FTGYFNGQYW 180
LWWIFLVGL LLFFRGFVNLY LKVRNMSESM AAAHRTRYFF LL 222

SEQ ID NO: 150      moltype = AA length = 336
FEATURE           Location/Qualifiers
source            1..336
mol_type = protein
organism = Homo sapiens

SEQUENCE: 150
MARRRSQRVC ASGPSMLNSA RGAPELLRT ATNAEVSAAG AGATGSEELP PGDRGCRNGG 60
GRGPAATTSS TGAVGAEHG EDSLRSRKDP EPGRMDHHQ GTGRYQVLLN EEDNSESSAI 120
EQPPTSNPAP QIVQAASSAP ALETDSPPPP YSSITVEVPT TSDTEVYGEF YPVPPPYSAV 180
TSLPTYDEAE KAKAAAMAAA AAETSQRIQE EECPPRDDFS DADQLRVGND GIFMLAFM 240
FIFNWLGFCL SFCITNTIAG RYGAICGFL SLIKWILIVR PSDYFTGYFN GQYWLWWIFL 300
VLGLLFFFRG FVNLYLKVRNM SESMAAHRT RYFFLL 336

SEQ ID NO: 151      moltype = AA length = 242
FEATURE           Location/Qualifiers
source            1..242
mol_type = protein
organism = Homo sapiens

SEQUENCE: 151
MDHHQPGTGR YQVLLNEEDN SESSAIEQPP TSNPAPQIVQ AASSAPALET DSSPPPYSSI 60
TVEVPTTSDT EVYGEFPVP PPYSVATSLP TYDEAEKAKA AAMAAAAAET SQRIQEECP 120
PRDDFSADQ LRGNDGIFM LAFFMAFIFN WLGFCLSFCL TNTIAGRYGA ICGFGLSLIK 180
WILIVRFSDY FTGYFNGQYW LWWIFLVGL LLFFRGFVNLY LKVRNMSESM AAAHRTRYFF 240
LL 242

SEQ ID NO: 152      moltype = AA length = 325
FEATURE           Location/Qualifiers
source            1..325
mol_type = protein
organism = Homo sapiens

SEQUENCE: 152
MDMWTLALLIQLALLPSLAD GATPALRFA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFYFTGVQD INDKRQETF EDVFSDRSLR KVPWYVLAGN HDHGNVSAQ 120
IAYSKISKRW NFPSPFYRLH FKIPOTNVSV AIPMLDTVTL CGNSDDFLSQ QPERPRDVKL 180
ARTQLSWLKK QLAAAREDYV LVAGHYPVWS IAEHGPTHCL VKQLRPLLAT YGVTAYLCGH 240
DHNLQYLQDE NGVGYVLSGA GNFMDFPSKRH QRKVPNGYLR FHYGTEDSLG GFAYVEISSK 300
EMTVTYIEAS GKSLFKTRLP RRARP 325

SEQ ID NO: 153      moltype = AA length = 325
FEATURE           Location/Qualifiers
source            1..325
mol_type = protein
organism = Homo sapiens

SEQUENCE: 153
MDMWTLALLIQLALLPSLAD GATPALRFA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFYFTGVQD INDKRQETF EDVFSDRSLR KVPWYVLAGN HDHGNVSAQ 120
IAYSKISKRW NFPSPFYRLH FKIPOTNVSV AIPMLDTVTL CGNSDDFLSQ QPERPRDVKL 180
ARTQLSWLKK QLAAAREDYV LVAGHYPVWS IAEHGPTHCL VKQLRPLLAT YGVTAYLCGH 240
DHNLQYLQDE NGVGYVLSGA GNFMDFPSKRH QRKVPNGYLR FHYGTEDSLG GFAYVEISSK 300
EMTVTYIEAS GKSLFKTRLP RRARP 325

SEQ ID NO: 154      moltype = AA length = 325
FEATURE           Location/Qualifiers
source            1..325
mol_type = protein

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SEQUENCE: 154          organism = Homo sapiens
MDMWTLALL QALLPLSLAD GATPALRFVA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFYFTGVQD INDKRFQETF EDVFSDRSLR KVPWYVLAGN HDHGNVSAQ 120
IAYS KISKRW NFPSPFYRLH FKIPQTNVSV AIFMLDTVTL CGNSDDFLSQ QPERPRDVKL 180
ARTQLSLWKK QLAAAREDYV LVAGHYPVWS IAEHGPTHCL VKQLRPLLAT YGVTAYLCGH 240
DHNLQYLQDE NGVGYVLSGA GNFMDFPSKRH QRKVPNGYLR PHYGTEDSLG GFAYVEISSK 300
EMTVTYIEAS GKSLFKTRLP RRARP 325

SEQ ID NO: 155          moltype = AA length = 74
FEATURE
source
1..74
mol_type = protein
organism = Homo sapiens

SEQUENCE: 155          moltype = AA length = 74
MDMWTLALL QALLPLSLAD GATPALRFVA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFY 74

SEQ ID NO: 156          moltype = AA length = 59
FEATURE
source
1..59
mol_type = protein
organism = Homo sapiens

SEQUENCE: 156          moltype = AA length = 59
MDMWTLALL QALLPLSLGI SWTPQSGTSA RSPTAICAST MGLKTHWVAL PMWRSAPKR 59

SEQ ID NO: 157          moltype = AA length = 124
FEATURE
source
1..124
mol_type = protein
organism = Homo sapiens

SEQUENCE: 157          moltype = AA length = 124
MDMWTLALL QALLPLSLAD GATPALRFVA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFYFTGVQD INDKRFQETF EDVFSDRSLR KVPWYVLAGN HDHGNVSAQ 120
IAYS 124

SEQ ID NO: 158          moltype = AA length = 52
FEATURE
source
1..52
mol_type = protein
organism = Homo sapiens

SEQUENCE: 158          moltype = AA length = 52
MDMWTLALL QALLPLSLAD GATPALRFVA VGDWGGVPNA PFHTAREMAN AK 52

SEQ ID NO: 159          moltype = AA length = 325
FEATURE
source
1..325
mol_type = protein
organism = Homo sapiens

SEQUENCE: 159          moltype = AA length = 325
MDMWTLALL QALLPLSLAD GATPALRFVA VGDWGGVPNA PFHTAREMAN AKEIARTVQI 60
LGADFILSLG DNFYFTGVQD INDKRFQETF EDVFSDRSLR KVPWYVLAGN HDHGNVSAQ 120
IAYS KISKRW NFPSPFYRLH FKIPQTNVSV AIFMLDTVTL CGNSDDFLSQ QPERPRDVKL 180
ARTQLSLWKK QLAAAREDYV LVAGHYPVWS IAEHGPTHCL VKQLRPLLAT YGVTAYLCGH 240
DHNLQYLQDE NGVGYVLSGA GNFMDFPSKRH QRKVPNGYLR PHYGTEDSLG GFAYVEISSK 300
EMTVTYIEAS GKSLFKTRLP RRARP 325

SEQ ID NO: 160          moltype = AA length = 119
FEATURE
source
1..119
mol_type = protein
organism = Homo sapiens

SEQUENCE: 160          moltype = AA length = 119
MPSDFISLLS ADDLESPKS LYSRDSLKLH PSQNFHRAGL LEESVYDLLP KELQLPPSRE 60
TSVASMSQTS GGEAGSPPP A VVAAGIPEMF ILCILMCMIL RPKKGFASEA GSVCIKNDL 119

SEQ ID NO: 161          moltype = AA length = 150
FEATURE
source
1..150
mol_type = protein
organism = Homo sapiens

SEQUENCE: 161          moltype = AA length = 150
MSGSMATAEA SGSDGKGQEV ETSVTYYRLE EVAKRNSLKE LWLVIHGRVY DVTRFLNEHP 60
GGEEVVLLEQA GVDASESFED VGHSSDAREM LKQYYIGDIH PSDLKPESGS KDP SKNDTCK 120
SCWAYWILPI IGA VLLGFLY RYYTSESKSS 150

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SEQ ID NO: 162	moltype = AA length = 146
FEATURE	Location/Qualifiers
source	1..146
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 162	
MATAEASGSD GKGQEVEETSV TYYRLEEVAK RNSLKELWLV IHGRVYDVTR FLNEHPGSEE	60
VILLEQAGVDA SESFEDVGHS SDAREMLKQY YIGDIHPSDL KPESGSKDPS KNDTCKSCWA	120
YWILPIIGAV LLGFLYRYYT SESKSS	146
SEQ ID NO: 163	moltype = AA length = 64
FEATURE	Location/Qualifiers
source	1..64
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 163	
KRNSLKELWL VIHGRVYDVTR RFLNEDPSKN DTCKSCWAYW ILPIIGAVLL GFLYRYYTSE	60
SKSS	64
SEQ ID NO: 164	moltype = AA length = 317
FEATURE	Location/Qualifiers
source	1..317
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 164	
MTSRTRVTWP SPPRPLPVPA AAAAVAFGAKG TDPAEARSSR GIEEAGPRAH GRAGREPERR	60
RSRQQRGGGL QARRSTLLKT CARARATAPG AMKMVAPWTR FYSNSCCLCC HVRTGTILLG	120
VWYLIINAVV LLLLSALAD PDQYNFSSSE LGGDFEFMDD ANMCIAIAIS LLMILICAMA	180
TYGAYKQRAA WIIPFFCYQI FDFALNMLVA ITVLIYPNSI QEYIRQLPPN FPYRDDVMSV	240
NPICLVLIL LFISIILTFK GYLISCVWNC YRYINGRNSS DVLVYVTSND TTVLLPPYDD	300
ATVNGAAKEP PPPYVSA	317
SEQ ID NO: 165	moltype = AA length = 152
FEATURE	Location/Qualifiers
source	1..152
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 165	
MKVMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL	60
GGDFEFMDDA KILFNLSADM CIAIAISLMM ILICAMATYG AYKQRAAWII PFFCYQIFDF	120
ALNMLVAITV LIYPNSIQEY IRQLPPNFY RD	152
SEQ ID NO: 166	moltype = AA length = 226
FEATURE	Location/Qualifiers
source	1..226
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 166	
MKVMVAPWTRF YSNSCCLCCH VRTGTILLGV WYLIINAVVL LILLSALADP DQYNFSSSEL	60
GGDFEFMDDA NMCIACIAISL LMILICAMAT YGAYKQRAAW IIIPFFCYQIF DFALNMLVAI	120
TWVLIYPNSIQ EYIRQLPPNF PYRDDVMSVN PTCLVLILLL FISIILTFKG YLISCVWNCY	180
RYINGRNSSD VLVYVTSNDT TVLLPPYDDA TVNGAAKEP PPPYVSA	226
SEQ ID NO: 167	moltype = AA length = 317
FEATURE	Location/Qualifiers
source	1..317
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 167	
MTSRTRVTWP SPPRPLPVPA AAAAVAFGAKG TDPAEARSSR GIEEAGPRAH GRAGREPERR	60
RSRQQRGGGL QARRSTLLKT CARARATAPG AMKMVAPWTR FYSNSCCLCC HVRTGTILLG	120
VWYLIINAVV LLLLSALAD PDQYNFSSSE LGGDFEFMDD ANMCIAIAIS LLMILICAMA	180
TYGAYKQRAA WIIPFFCYQI FDFALNMLVA ITVLIYPNSI QEYIRQLPPN FPYRDDVMSV	240
NPICLVLIL LFISIILTFK GYLISCVWNC YRYINGRNSS DVLVYVTSND TTVLLPPYDD	300
ATVNGAAKEP PPPYVSA	317
SEQ ID NO: 168	moltype = AA length = 177
FEATURE	Location/Qualifiers
source	1..177
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 168	
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GKDGKQYESV LMVSIDQLLD SMKEIGSNCL	60
NNEFNFFKRH ICDANKEGMF LFRAARKLRQ FLKMNSTGDF DLHLLKVSEG TTILLNCTGQ	120
VKGRKPAALG EAQPTKSLEE NKSLKEQKKL NDLCFLKRLL QEIKTCWNKI LMGTKEH	177

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SEQ ID NO: 169      moltype = AA length = 115
FEATURE          Location/Qualifiers
source           1..115
mol_type = protein
organism = Homo sapiens
SEQUENCE: 169
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GKDGKQYESV LMVSIDQLLD SMKEIGSNCL 60
NNEFNFFKRH ICDANKEENK SLKEQKKLND LCFLKRLLQE IKTCWNKILM GTKEH      115

SEQ ID NO: 170      moltype = AA length = 71
FEATURE          Location/Qualifiers
source           1..71
mol_type = protein
organism = Homo sapiens
SEQUENCE: 170
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GKDGKQYESV LMVSIDQLLN QPYKKKEKRT 60
ERKQQSAMSN N                               71

SEQ ID NO: 171      moltype = AA length = 37
FEATURE          Location/Qualifiers
source           1..37
mol_type = protein
organism = Homo sapiens
SEQUENCE: 171
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GQHERNW                                37

SEQ ID NO: 172      moltype = AA length = 133
FEATURE          Location/Qualifiers
source           1..133
mol_type = protein
organism = Homo sapiens
SEQUENCE: 172
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GKDGKQYESV LMVSIDQLLD SMKEIGSNCL 60
NNEFNFFKRH ICDANKVKGR KPAALGEAQF TKSLEENKSL KEQKKLNDLC FLKRLLQEIK 120
TCWNKILMGT KEH                               133

SEQ ID NO: 173      moltype = AA length = 37
FEATURE          Location/Qualifiers
source           1..37
mol_type = protein
organism = Homo sapiens
SEQUENCE: 173
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GQHERNW                                37

SEQ ID NO: 174      moltype = AA length = 159
FEATURE          Location/Qualifiers
source           1..159
mol_type = protein
organism = Homo sapiens
SEQUENCE: 174
MFHVSFRYIF GLPPLILVLL PVASSDCDIE GKDGKQYESV LMVSIDQLLD SMKEIGSNCL 60
NNEFNFFKRH ICDANKEGMF LFRAARKLRQ FLKMNSTGDF DLHLLKVSEG TTILLNCTGQ 120
EENKSLKEQK KLNDLCFLKR LLQEIKTCWN KILMGTKEH      159

SEQ ID NO: 175      moltype = AA length = 229
FEATURE          Location/Qualifiers
source           1..229
mol_type = protein
organism = Homo sapiens
SEQUENCE: 175
MTQOLLLALV LWASCPPCSG RKGPPAALTL PRVQCRASRY PIAVDCSWTL PPAPNSTSPV 60
SFIATYRLGM AARGHSWPCL QQPTSTSCT ITDVQLFSMA PYVLNVTAVH PWGSSSSFVP 120
FITEHIKPQ PPEGVRLSPL AERQLQVQWE PPGSWPFFEI FSLKYWIRYK RQGAARFHHRV 180
GPIEATSFIL RAVRPRARYY VQVAQQDLTD YGELSDWSLP ATATMSLGK      229

SEQ ID NO: 176      moltype = AA length = 130
FEATURE          Location/Qualifiers
source           1..130
mol_type = protein
organism = Homo sapiens
SEQUENCE: 176
XMLENWRTRTS LEKQEQQPHED PERKGSLSNL MDFVKKTGIC ASKWEWGTTH NFLYKHGGIR 60
DKIMSSRKHL HLVDAGLAIN TPFPLVLPPT REVHLILSFD FSAGDPFEHP RSATSNELLC 120
MSVSSAVKLG                                         130

SEQ ID NO: 177      moltype = AA length = 36

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FEATURE	Location/Qualifiers
source	1..36
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 177	
MTRPRPRLR LECNGMISAH WHLHLLSSSD SPPSAS	36
SEQ ID NO: 178	moltype = AA length = 47
FEATURE	Location/Qualifiers
source	1..47
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 178	
MKEQGLLDAV TYLAGVSGST WAISSLYTND GDMEALEDL KHRFTRQ	47
SEQ ID NO: 179	moltype = AA length = 43
FEATURE	Location/Qualifiers
source	1..43
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 179	
MTRPRPRLR VSLLLPRLEC NGMISAHWHL HLLSSSDSPP SAS	43
SEQ ID NO: 180	moltype = AA length = 194
FEATURE	Location/Qualifiers
source	1..194
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 180	
AAAPPAEQAP RAKGRPRRSP ESHRRSSPE RRSPGSPVCR ADAKKSQQVR TSSTIRRTSS	60
LDTITGPYLT GQWPRDPHVH YPSCMKDKAT QTPSCWAEEG AEKRSHQRSA SWGSADQLKE	120
QIAKLRQQLQ RSKQSSRHSK EKDROSPHLG NHITISHQTA TGSSRWTYQM VEELHFLIT	180
GAVVLAALTL RLLL	194
SEQ ID NO: 181	moltype = AA length = 312
FEATURE	Location/Qualifiers
source	1..312
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 181	
MLRAPGCLLR TSVAPAAAALA AALLSSLARC SLLEPRDPVA SSLSPYFGTK TRYEDVNPVL	60
LSGPEAPWRD PELLEGTCPT VQLVALIRHG TRYPTVKQIR KLRQLHGLLQ ARGSRDGAS	120
STGSRDLGAA LADWPWLWYAD WMDGQLVEKG RQDMRQLALAR LASLFPALFS RENYGRRLI	180
TSSKHRCMDS SAAFLQGLWQ HYHPGLPPPD VADMEFGPPT VNDKLMRFDFD HCEKFLTEVE	240
KNATALYHVE AFKTGPEMQN ILKKVAAATLQ VPVNNDLNADL SQFLLQSSSS LVMQRLFH	300
FLSWATSKTR NP	312
SEQ ID NO: 182	moltype = AA length = 487
FEATURE	Location/Qualifiers
source	1..487
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 182	
MLRAPGCLLR TSVAPAAAALA AALLSSLARC SLLEPRDPVA SSLSPYFGTK TRYEDVNPVL	60
LSGPEAPWRD PELLEGTCPT VQLVALIRHG TRYPTVKQIR KLRQLHGLLQ ARGSRDGAS	120
STGSRDLGAA LADWPWLWYAD WMDGQLVEKG RQDMRQLALAR LASLFPALFS RENYGRRLI	180
TSSKHRCMDS SAAFLQGLWQ HYHPGLPPPD VADMEFGPPT VNDKLMRFDFD HCEKFLTEVE	240
KNATALYHVE AFKTGPEMQN ILKKVAAATLQ VPVNNDLNADL IQVAFFTCSF DLAIKGVKSP	300
WCDVFDIDDA KVLEYLNDLQ QYWKRGYGYT INSRSSCTLF QDIFQHLDKA VEQKQRSQPI	360
SSPVILQFGH AETLLPLLSL MGYFKDKEPL TAYNYKKQMH RKFRSGLIVP YASNLIIVLY	420
HCENAKTPKE QFRVQMLLNE KVLPLAYSQE TVSFYEDLKN HYKDILQSCQ TSEECELARA	480
NSTSDEL	487
SEQ ID NO: 183	moltype = AA length = 286
FEATURE	Location/Qualifiers
source	1..286
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 183	
MCLFQLCGLV RYMEFGPPTV NDKLMRFFDH CEKFLTEVEK NATALYHVEA FKTGPEMQNI	60
LKKVAAATLQV PVNDLNADLI QVAFFTCSD LAIKGVKSPW CDVFDIDDAK VLEYLNDLQ	120
YWKRGGYTYI NSRSSCTLFQ DIFQHLDKAV EQKQRSQPIS SPVILQFGHA ETLLPLLSLM	180
GYPFKDKEPLT AYNYKKQMH RKFSGLIVP ASNLIIVLYH CENAKTPKEQ FRVQMLLNEK	240
VLPPLAYSQET VSFYEDLKNH YKDILQSCQT SEECELARAN STSDEL	286
SEQ ID NO: 184	moltype = AA length = 207

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FEATURE	Location/Qualifiers
source	1..207
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 184	
MASFPPRVNE KEIVPLFLLL VRLRTIGELL APAAPFDKKG GRENWTVAFKA PDGSYFAWSQ	60
GHRTVKLVPW SQCLQNPLLH GTKNTNSSL LRLPRQNSDG GQKNKPREGHI IDCGDIVWSL	120
AFGSSVPEKQ SRCVNIEWHR FRFGQDQLLL ATGLNNNGRIK IWDVYTGKLL LNLDHTEVV	180
RDLTFAPDGS LILVSASRDK TLRVWDL	207
SEQ ID NO: 185	moltype = AA length = 74
FEATURE	Location/Qualifiers
source	1..74
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 185	
MASFPPRVNE KEIVRLRTIG ELLAPAAPFD KKCGRENWTV AFAPDGSYFA WSQGHRTVKL	60
VPWSQCLQNL KTPP	74
SEQ ID NO: 186	moltype = AA length = 54
FEATURE	Location/Qualifiers
source	1..54
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 186	
MASFPPRVNE KEIGNMMKVL RGHQNWWVYSC AFSPDSSMLC SVGASKAVVA AILV	54
SEQ ID NO: 187	moltype = AA length = 78
FEATURE	Location/Qualifiers
source	1..78
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 187	
MASFPPRVNE KEIAPAAPFD KKCGRENWTV AFAPDGSYFA WSQGHRTVKL VPWSQCLQNF	60
LLHGTKNVTN SSSLRLPR	78
SEQ ID NO: 188	moltype = AA length = 276
FEATURE	Location/Qualifiers
source	1..276
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 188	
MAGPAALSAA AAAALAAALL LLRREDPGPG AGPSMAETEA LSKLREDFRM QNKSVFILGA	60
SGETGRVLLK EILEQGLFSK VTLLIGRRKLT FDEEAYKVNQ QEVDVFEKLD DYASAFQGHD	120
VGCCCLGTTA GKAGAGFGVR VDRDYVLSKA ELAKAGGCKH FNLLSSKGAD KSSNPLLYLVQ	180
KGEVEAKVEE LKFDRYSVFR PGVLLCDRQE SRPGEWLVRK FFGSLPDSWA GHHSVPPVTV	240
VRAMLNNSVNR PRDKQMLELLE NKAIHDLGKA HGSLKP	276
SEQ ID NO: 189	moltype = AA length = 133
FEATURE	Location/Qualifiers
source	1..133
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 189	
MAETEALSKL REDFRMQNKS VFILGASGET GRVLLKEILE QGLFSKVTLI GRRKLTDFDEE	60
AYKNVNQEDEV DFEKLDDYAS AFQGHDVGFC CLGTTRGKAG AVRKAYALFP FCWPVISRIL	120
FLLTLFLCAC CNA	133
SEQ ID NO: 190	moltype = AA length = 133
FEATURE	Location/Qualifiers
source	1..133
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 190	
MAETEALSKL REDFRMQNKS VFILGASGET GRVLLKEILE QGLFSKVTLI GRRKLTDFDEE	60
AYKNVNQEDEV DFEKLDDYAS AFQGHDVGFC CLGTTRGKAG AVRKAYALFP FCWPVISRIL	120
FLLTLFLCAC CNA	133
SEQ ID NO: 191	moltype = AA length = 133
FEATURE	Location/Qualifiers
source	1..133
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 191	
MAETEALSKL REDFRMQNKS VFILGASGET GRVLLKEILE QGLFSKVTLI GRRKLTDFDEE	60
AYKNVNQEDEV DFEKLDDYAS AFQGHDVGFC CLGTTRGKAG AVRKAYALFP FCWPVISRIL	120

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FLLTLFLCAC CNA	133
SEQ ID NO: 192	moltype = AA length = 463
FEATURE	Location/Qualifiers
source	1..463
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 192	
MGAGPSLLA ALLLLSGDG AVRCDTPANC TYLDLLGTWV FQVGSSGSQR DVNCVMGPQ	60
EKKVVVYLQK LDTAYDDLGN SGHFTIIYNQ GFEIVLNDYK WFAFFKYKEE GSKVITYCNE	120
TMTGWHDVL GRNWACFTGK KVGTASENVY VNIAHLKNSQ EKYSNRLYKY DHNFVKAINA	180
IQKSWTATTY MEYETLTGLD MIRRSGGHSR KIPRPKPAPL TAEIQQKILH LPTSWDWRNV	240
HGINFVSPVR NQASCSCYS FASGMLEAR IRILTNNSQT PILSPQEVS CSQYAQGCEG	300
GFPYIAGKQ AQDFGLVEEA CFPYTGTDSP CKMKEDCFRY YSSEYHYVGG FYGGCNEALM	360
KLELVHHGPM AVAFEVYDDF LHYKKGIYHH TGLRDPFNPF ELTNHAVLV GYGTDSASGM	420
DYWIVKNSWG TGWGGENGYFR IRRGTDCAI ESTAVAAATPI PKL	463
SEQ ID NO: 193	moltype = AA length = 137
FEATURE	Location/Qualifiers
source	1..137
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 193	
MGAGPSLLA ALLLLSGDG AVRCDTPANC TYLDLLGTWV FQVGSSGSQR DVNCVMGPQ	60
EKKVVVYLQK LDTAYDDLGN SGHFTIIYNQ GFEIVLNDYK WFAFFKDVTD FISHLFMQLG	120
TVGIYDLPHL RNKLVIK	137
SEQ ID NO: 194	moltype = AA length = 245
FEATURE	Location/Qualifiers
source	1..245
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 194	
XVVDSPPLARS ARLPGPQEKK VVYVLQKLDT AYDDLGNNSGH FTIIYNQGFE IVLNDYKWFA	60
FFKYKEEGSK VTTYCNETMT GWVHDVLGRN WACFTGKVKG TASENVYVNI AHLKNSQEKY	120
SNRLYKDHN FVKAINAIQK SWTATTYMEY ETLTLGDMIR RSGGHSRKIP RPKPAPLTAE	180
IQQKILHLPT SWDWRNVHGI NFVSPVRNQA SCGSCSYSFAS MGMLEARIRI LTNNSQTPIL	240
SPQEVE	245
SEQ ID NO: 195	moltype = AA length = 36
FEATURE	Location/Qualifiers
source	1..36
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 195	
XDVTDFISHL FMQLGTVGIY DLPHLRNKLA MNRRWG	36
SEQ ID NO: 196	moltype = AA length = 141
FEATURE	Location/Qualifiers
source	1..141
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 196	
MGAGPSLLA ALLLLSGDG AVRCDTPANC TYLDLLGTWV FQVGSSGSQR DVNCVMGPQ	60
EKKVVVYLQK LDTAYDDLGN SGHFTIIYNQ GFEIVLNDYK WFAFFKDVTD FISHLFMQLG	120
TVGIYDLPHL RNKLAMNRRW G	141
SEQ ID NO: 197	moltype = AA length = 431
FEATURE	Location/Qualifiers
source	1..431
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 197	
MSSVCDMSFL QKSCITMVHF CGLLTLHREP VPLKSISVSV NIYEFVAGVS ATLNYYENEK	60
VPLEAFFVFP MDEDSAVYSF EALVDGKKIV AELQDKMKAR TNYEKAISQG HQ AFLLEGDS	120
SSRDVFSCNV CNLQPGSKAA VTLKYVQELP LEADGALRFV LP AVLNPRYQ FSGSSKDSC	180
NVKTPIVPVE DLPYTLSTMVA TIDSQHGIKEK VQSNCPPLST EYLGEDKTSQ QVSLAAGHKF	240
DRDVELLIIYY NEVHTPSVVL EMGMPNMKPG HLMGDPSAMV SFYPNIPEDQ PSNTCGEFIF	300
LMDRSGSMQS PMSSQDTSQL RIQAKEYTLI LLLLKSLPIGC YFNIYGFSSS YEACFPESVK	360
YTQQTMEAL GRVKLQMADL GGTEILAPLQ NIYRGPSIPG HPLQLFVFTD GEVTDTSVI	420
KEVRINRQKH R	431
SEQ ID NO: 198	moltype = AA length = 786
FEATURE	Location/Qualifiers
source	1..786
	mol_type = protein

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SEQUENCE: 198 MVHFCGGLTL HREPVLKSI SVSVNIYEFV AGVSATLNYE NEEKVPLEAF FVFPMDDESA 60 VYSFEALVDG KKIVAEQLDK MKARTNYEKA ISQGHQAFLL EGDSSSRDVF SCNVGNLQPG 120 SKAAVTLYKVY QELPLEADGA LRFVLPAVLN PRYQFSGSSK DSCLNVKTP1 VPVEDLPYTL 180 SMVATIDSQH GIEKVQSNCP LSPTEYLGED KTSAQVSLAA GHKFDRDVEL LIYYNEVHTP 240 SVVLEMGMNPN MKPGHLMGDP SAMVSFYPNI PEDQPSNTCG EFIFLMDRSG SMQSPMSSQD 300 TSQLRIQAQK ETLILLKLKSL PIGCYFNIYG FGSSYEACFP ESVKYTQQT MEEALGRVKLM 360 QADLGGEIL APLQNIYRGP SIPGHPLQLF VFTDGEVTDT FSVIKEVRIN RQKHRCFSFG 420 IGEGTSTSLI KGIAARASGGT SEFITGKDRM QSKALRTLKR SLQPVVEDVS LSWHLPPGLS 480 AKMLSPEQTV IFRGQRLISY AQLTRGMPAA ETTGEVCLKY TLQGKTFEDK VTFPLQPKPD 540 VNLTIHRLAA KSLLQTKDMG LRETPASDKK DALNLSLESG VISSFTAFIA INKELNKPVQ 600 GPLAHRDVPR PILLGASAPL KIKCQSGFRK ALHSDRPPSA SQPRGELMCY KAKTFQMDDY 660 SLCGLISHKD QHSPGFGENH LVQLIYHQNA NGSWDLNEDL AKILGMSLEE IMAAQPAELV 720 DSSGWATIL A WIWLHSNGKD LKCEWELLER KAVAWMRAHA GSTMPVVKA AITFLKSSVD 780 PAIFAF 786	organism = Homo sapiens
SEQ ID NO: 199 FEATURE moltype = AA length = 786 source Location/Qualifiers 1..786 mol_type = protein organism = Homo sapiens	
SEQUENCE: 199 MVHFCGGLTL HREPVLKSI SVSVNIYEFV AGVSATLNYE NEEKVPLEAF FVFPMDDESA 60 VYSFEALVDG KKIVAEQLDK MKARTNYEKA ISQGHQAFLL EGDSSSRDVF SCNVGNLQPG 120 SKAAVTLYKVY QELPLEADGA LRFVLPAVLN PRYQFSGSSK DSCLNVKTP1 VPVEDLPYTL 180 SMVATIDSQH GIEKVQSNCP LSPTEYLGED KTSAQVSLAA GHKFDRDVEL LIYYNEVHTP 240 SVVLEMGMNPN MKPGHLMGDP SAMVSFYPNI PEDQPSNTCG EFIFLMDRSG SMQSPMSSQD 300 TSQLRIQAQK ETLILLKLKSL PIGCYFNIYG FGSSYEACFP ESVKYTQQT MEEALGRVKLM 360 QADLGGEIL APLQNIYRGP SIPGHPLQLF VFTDGEVTDT FSVIKEVRIN RQKHRCFSFG 420 IGEGTSTSLI KGIAARASGGT SEFITGKDRM QSKALRTLKR SLQPVVEDVS LSWHLPPGLS 480 AKMLSPEQTV IFRGQRLISY AQLTRGMPAA ETTGEVCLKY TLQGKTFEDK VTFPLQPKPD 540 VNLTIHRLAA KSLLQTKDMG LRETPASDKK DALNLSLESG VISSFTAFIA INKELNKPVQ 600 GPLAHRDVPR PILLGASAPL KIKCQSGFRK ALHSDRPPSA SQPRGELMCY KAKTFQMDDY 660 SLCGLISHKD QHSPGFGENH LVQLIYHQNA NGSWDLNEDL AKILGMSLEE IMAAQPAELV 720 DSSGWATIL A WIWLHSNGKD LKCEWELLER KAVAWMRAHA GSTMPVVKA AITFLKSSVD 780 PAIFAF 786	
SEQ ID NO: 200 FEATURE moltype = AA length = 327 source Location/Qualifiers 1..327 mol_type = protein organism = Homo sapiens	
SEQUENCE: 200 MLSLCICGTA ITSQYLAERY KVNTPMQLSF INYCLLFLII TVMLAFRSGS DNLLVILKRK 60 WWKYIILLGLA DVEANYVIVR AYQYTTLTSV QLLDCFGIPV LMALSWFILH ARYRVIFHIA 120 VAVCLLGVGT MVGADILLAGR EDNNGSDVLI GDILVLLGAS LYAISNVCEE YIVKKLSRQE 180 FLGMVGLFGT IISGIQLLIV EYKDIASILFVA DWKIALLFVA FALCMFCFLS FMPLVIKVTS 240 ATSVNLGLT ADLYSLFVGL FLFGYKFSGL YILSFTVIMV GFILYCSTPT RTAEPAESSV 300 PPVTSIGIDN LGLKLEENLQ ETHSAVL 327	
SEQ ID NO: 201 FEATURE moltype = AA length = 357 source Location/Qualifiers 1..357 mol_type = protein organism = Homo sapiens	
SEQUENCE: 201 MEADSPAGPG APEPLAEGAA AEFSSLRRI KGKLFTWNIL KTIALGQMLS LCICGTAITS 60 QYLAERYKVN TPMLQSFINY CLLFLIYTVM LAFRSGSDNL LVILKRWKWK YILLGLADVE 120 ANYVIVRAYQ YTTLTSVQLL DCFGIPVLM A SWFILHARY RVIHFIHAVAV CLLGVGTMVG 180 ADILAGREDN SGSDVLLIGDI LVLLGASLYA ISNVCEEYIV KKLSRQEFLG MVGLFGTIIS 240 GIQLLIVEYK DIASIHWWDWK IALLFVAFAL CMFCFLYSFMP LVIKVTSA TS VNLGILTADL 300 YSLFVGLFLF GYKDSTSCPS LSSWWGLSCT APPLLARPSR LKAACLQSPA LGLTTWG 357	
SEQ ID NO: 202 FEATURE moltype = AA length = 374 source Location/Qualifiers 1..374 mol_type = protein organism = Homo sapiens	
SEQUENCE: 202 MEADSPAGPG APEPLAEGAA AEFSSLRRI KGKLFTWNIL KTIALGQMLS LCICGTAITS 60 QYLAERYKVN TPMLQSFINY CLLFLIYTVM LAFRSGSDNL LVILKRWKWK YILLGLADVE 120 ANYVIVRAYQ YTTLTSVQLL DCFGIPVLM A SWFILHARY RVIHFIHAVAV CLLGVGTMVG 180 ADILAGREDN SGSDVLLIGDI LVLLGASLYA ISNVCEEYIV KKLSRQEFLG MVGLFGTIIS 240 GIQLLIVEYK DIASIHWWDWK IALLFVAFAL CMFCFLYSFMP LVIKVTSA TS VNLGILTADL 300 YSLFVGLFLF GYKFSGLYIL SFTVIMVGF LYCSTPTRTA EPAESSVPPV TSIGIDNLGL 360	

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KLEENLQETH SAVL	374
SEQ ID NO: 203	moltype = AA length = 265
FEATURE	Location/Qualifiers
source	1..265
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 203	
MEADSPAGPG APEPLAEGAA AEFSSLRRI KGKLFTWNIL KTIALGQMLS LCICGTAITS	60
QYLAERYKVN TPMLQSFINY CLLFLIYTVM LAPRSGSDNL LVIKRKWWK YILLGLADVE	120
ANVVIVRAYQ TTLLTSVQLL DCFGIPVLM A LSWFILHARY RVIHFIHAVAV CLLGVGTMVG	180
ADILAGREDN SGSDVLLIGDI LVLLGASLYA ISNVCEEYIV KKLSRQEFLG MVGLPGTIIS	240
GIQLPAVRGI CPVYVLPVQL HAIGD	265
SEQ ID NO: 204	moltype = AA length = 49
FEATURE	Location/Qualifiers
source	1..49
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 204	
MEAMAASTSL PDPGDFDRNV PRICGVCGDR ATGFHFNAMT CEGCKGFFR	49
SEQ ID NO: 205	moltype = AA length = 1093
FEATURE	Location/Qualifiers
source	1..1093
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 205	
MSQPGIPASG GAPASLQAQN GAALASGSPY TNGPVQNALL SSQESVSQGY NFQLPGSYPH	60
PIPAKTLNPV SGQSNYGGSQ GSGQTLNRPV VASNPVPTSL HSGPAPRMPM PASQNPATT	120
MPSSSFLPVA NLPPPLNWQY NYPSTSASQTN HCPRASSQPT VSGNTSLTTN HQYVSSGYP	180
LQNSFIKSGP SVPPLVNPL PTTFQPGAPH GPPPAGGGPP VRALTPLTSS YRDVPQPLFN	240
SAVNQEGITS NTNNGSMVHV SSYDEIEGGG LLATPQLTNK NPKMSRSVGY SYPSLPPGYQ	300
NTTPPGATGV PPSSLNYPNG PQAFQTQPLG ANHLTTSMSG LSLQPEGLRV VNLLQERNML	360
PSTPLKPPVP NLHEDIQKLN CNPPELFRCTL TSIPQTQALL NKAKLPLGLL LHPFKDLVQL	420
PVVTSSITVR CRSCRTYINP FVFSLDQRWR KCNLCYRVND VPEEEFLYNPL TRVYGEPHRR	480
PEVQNATIEF MAPSEYMLRP PQPPVYLFVF DVSHNAVETG YLNSVCQSSL DNLLLLPGNT	540
RTKIGFITFD STIHFYGLQE SLSQPQMLIV SDIEDVFIPM PENLLVNLNE SKELVQDLLK	600
TLPQMFTKTL ETQSQALGPAL QAAFPVMSPT GGRMSVFTQ LPTLGVGALK PREEPNHRSS	660
AKDIHMTPST DFYKKLALDC SGQQVQYSDLA SLGCISRYSA GSVYYYYPSYH	720
HQHNPVQVQK LQKELQRYLT RKIGFEAVMR IRCTKGLSIH TFHGNFFVRS TDLLSLPNVN	780
PDAGYAVQMS VEESLTDTQL VSFQSALLYT SSKGERRIRV HTLCLPVVST LNDVFLGADV	840
QASIGLLANM AVDRSMTASL SDARDALVNA VIDSL SAYRS SVLSNQOPGL MVPFSLRLFP	900
LFVLLALLKQK SFQGTGNARL DERIFAMCV KNQPLVYLM TTHPSLYRVD NLSDEGALNI	960
SDRTIPQPPQI LQLSVKEKLSR DGAFLMDAGS VLMLWVGKNC TQNFLSQLVLG VQNYASIPQP	1020
MTDLPEDLTP ESARIIAFIS WLREQRPFFF ILYVIRDESP MKANFLQNMI EDRTESALSY	1080
YEFLLLHIQQQQ VNK	1093
SEQ ID NO: 206	moltype = AA length = 398
FEATURE	Location/Qualifiers
source	1..398
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 206	
MRLRYVLLVMG VSAFTLQPAAS HTGAARSRCF RGRHYKREFR LEGEPVALRC PQVPYWLWAS	60
VSPRINLWTWH KNDTSARTVPG EEEETRNMWAQD GALWLLPALQ EDSTGYVCTT RNASYCDKMS	120
IELRVVENTD AFLPFISYPQ ILTLLSTSGVL VCPDLSEPTR DKTDVKIQWY KDSLLDDKD	180
EKFLSVRGTT HLLVHDVALE DAGYYRCVLT FAHEGQQYNI TRSIELRIKK KKEETIPVII	240
SPLKTISASL GSRLTIPCKV FLGTGTPLTT MLWWTANDTH IESAYPGGRV TEGPRQEYSE	300
NNENYIEVPL IFDPVTREDL HMDFKCVVHN TLSFQTLRTT VKEASSTFSW GIVLAPLSA	360
FLVLGGIWMH RRCKHRTGKA DGLTBLWPHH QDFQSYPK	398
SEQ ID NO: 207	moltype = AA length = 398
FEATURE	Location/Qualifiers
source	1..398
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 207	
MRLRYVLLVMG VSAFTLQPAAS HTGAARSRCF RGRHYKREFR LEGEPVALRC PQVPYWLWAS	60
VSPRINLWTWH KNDTSARTVPG EEEETRNMWAQD GALWLLPALQ EDSTGYVCTT RNASYCDKMS	120
IELRVVENTD AFLPFISYPQ ILTLLSTSGVL VCPDLSEPTR DKTDVKIQWY KDSLLDDKD	180
EKFLSVRGTT HLLVHDVALE DAGYYRCVLT FAHEGQQYNI TRSIELRIKK KKEETIPVII	240
SPLKTISASL GSRLTIPCKV FLGTGTPLTT MLWWTANDTH IESAYPGGRV TEGPRQEYSE	300
NNENYIEVPL IFDPVTREDL HMDFKCVVHN TLSFQTLRTT VKEASSTFSW GIVLAPLSA	360
FLVLGGIWMH RRCKHRTGKA DGLTBLWPHH QDFQSYPK	398

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SEQ ID NO: 208	moltype = AA length = 296
FEATURE	Location/Qualifiers
source	1..296
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 208	
MRLRYLVLMG VSAFTLQPA A HTGAARSCR RGRHYKREFR LEGEPVALRC PQVPYWLWAS	60
VSPRINLWTW KND SARTVPG EEE TRMWA QD GALWLLPALQ EDS GTVCTT RNASYCDKMS	120
I ELRVFENTD AFLPFISYPQ ILT LSTSGVL VCPDLSEFTR DKTDVKIQWY KDSLLLKDKN	180
EKFLSVRGTT HLLVHDVALE DAGYYRCVLT FAHEGQQYNI TRSIELRIKK KKEETIPVII	240
SPLKTISASL GSRLTIPCKV FLGTGTPLTT MLWWTANDTH IESAYPGGRV TEGPRQ	296
SEQ ID NO: 209	moltype = AA length = 229
FEATURE	Location/Qualifiers
source	1..229
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 209	
MRLRYLVLMG VSAFTLQPA A HTGAARSCR RGRHYKREFR LEGEPVALRC PQVPYWLWAS	60
VSPRINLWTW KND SARTVPG EEE TRMWA QD GALWLLPALQ EDS GTVCTT RNASYCDKMS	120
I ELRVFENTD AFLPFISYPQ ILT LSTSGVL VCPDLSEFTR DKTDVKIQWY KDSLLLKDKN	180
EKFLSVRGTT HLLVHDVALE DAGYYRCVLT FAHEGQQYNI TRSIELRIK	229
SEQ ID NO: 210	moltype = AA length = 447
FEATURE	Location/Qualifiers
source	1..447
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 210	
MKVLLRLICF I ALLISSL EA DKCKERE EKI ILVSSANEID VRPCPLNPNE HKGTITWYKD	60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL	120
CYNAQAIFKQ KLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKP LL ND NIHFSGVKDR	180
LIVMNVAEKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE NKPTRPVI VS PANETMEVDL	240
GSQLQLICNV TGQLSDIAYW KWNGSVIDED DPVLGEDYYS VENPANKRRS TLITVLNISE	300
I ESRFYKHPF TCFAKNTHGI DAAYIQLIYP VTNFQKHMI G ICVTLTVIIV CSVFIYKIFK	360
IDIVLWYRDS CYDFLPIKAS DGKTYDAYIL YPKTVGE GST SDCDIFVF KV LPEVLEKQCG	420
YKLFIYGRDD YVGEGMCVME QSKGLL	447
SEQ ID NO: 211	moltype = AA length = 447
FEATURE	Location/Qualifiers
source	1..447
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 211	
MKVLLRLICF I ALLISSL EA DKCKERE EKI ILVSSANEID VRPCPLNPNE HKGTITWYKD	60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL	120
CYNAQAIFKQ KLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKP LL ND NIHFSGVKDR	180
LIVMNVAEKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE NKPTRPVI VS PANETMEVDL	240
GSQLQLICNV TGQLSDIAYW KWNGSVIDED DPVLGEDYYS VENPANKRRS TLITVLNISE	300
I ESRFYKHPF TCFAKNTHGI DAAYIQLIYP VTNFQKHMI G ICVTLTVIIV CSVFIYKIFK	360
IDIVLWYRDS CYDFLPIKAS DGKTYDAYIL YPKTVGE GST SDCDIFVF KV LPEVLEKQCG	420
YKLFIYGRDD YVGEGMCVME QSKGLL	447
SEQ ID NO: 212	moltype = AA length = 173
FEATURE	Location/Qualifiers
source	1..173
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 212	
MKVLLRLICF I ALLISSL EA DKCKERE EKI ILVSSANEID VRPCPLNPNE HKGTITWYKD	60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL	120
CYNAQAIFKQ KLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKVA VSRVWA TAL	173
SEQ ID NO: 213	moltype = AA length = 538
FEATURE	Location/Qualifiers
source	1..538
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 213	
MKVLLRLICF I ALLISSL EA DKCKERE EKI ILVSSANEID VRPCPLNPNE HKGTITWYKD	60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL	120
CYNAQAIFKQ KLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKP LL ND NIHFSGVKDR	180
LIVMNVAEKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE NKPTRPVI VS PANETMEVDL	240
GSQLQLICNV TGQLSDIAYW KWNGSVIDED DPVLGEDYYS VENPANKRRS TLITVLNISE	300
I ESRFYKHPF TCFAKNTHGI DAAYIQLIYP VTNFQKHMI G ICVTLTVIIV CSVFIYKIFK	360
IDIVLWYRDS CYDFLPIKVL PEVLEKQCGY KLFIYGRDDY VGEDIVEVIN ENVKKSRLI	420

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IILVRETSGF SWLGGSSSEQ IAMYNALVQD GIKVVLLELE KIQDYEKMPE SIKFIKQKHG 480	AKWSGDFTQ GPQSAKTRFW KNVRYHMPVQ RRSPSSKHQL LSPATKEKLQ REAHVPLG 538
<hr/>	
SEQ ID NO: 214	moltype = AA length = 569
FEATURE	Location/Qualifiers
source	1..569
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 214	
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60	DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL 120
CYNAQAIFQK QLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKPPLLD NIHFSGVKDR 180	LIVMNVAEKKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE NKPTRPVIWS PANETMEVDL 240
GSIQIQLICNV TGQLSDIAYW KWNGSVIDED DPVLGEDYYS VENPANKRRS TLITVLNISE 300	IESRFYKHPF TCFAKNTHGI DAAYIQLIYP VTNFQKHMIG ICVTLTVIIV CSVFIYKIFK 360
IDIVLWYRDS CYDFLPIKAS DGKTYDAYIL YPKTVGEGST SDCDIFVFVKG LPEVLEKQCG 420	YKLFIYGRDD YVGEDIVEVI NENVKKSRLI IIILVRETSG FSWLGGSSSEE QIAMYNALVQ 480
DGIKVVLLEL EKIQDYEKMP ESIKFIKQKH GAIRWSDFT QGPQSAKTRF WKNVRYHMPV 540	QRSPSSKHQL LLSPATKEKL QREAHVPLG 569
<hr/>	
SEQ ID NO: 215	moltype = AA length = 119
FEATURE	Location/Qualifiers
source	1..119
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 215	
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60	DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN ANLYFLTIYT LVESKIGSS 119
<hr/>	
SEQ ID NO: 216	moltype = AA length = 124
FEATURE	Location/Qualifiers
source	1..124
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 216	
XKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD DSKTPVSTEQ ASRIHQHKEK 60	LWFVPAKVED SGHYYCVETE DLCALIWSFL KMKIMSYLNY SGIRIANLYF LTIYTLVESK 120
IGSS	
	124
<hr/>	
SEQ ID NO: 217	moltype = AA length = 447
FEATURE	Location/Qualifiers
source	1..447
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 217	
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60	DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL 120
CYNAQAIFQK QLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKPPLLD NIHFSGVKDR 180	LIVMNVAEKKH RGNYTCHASY TYLGKQYPIT RVIEFITLEE NKPTRPVIWS PANETMEVDL 240
GSIQIQLICNV TGQLSDIAYW KWNGSVIDED DPVLGEDYYS VENPANKRRS TLITVLNISE 300	IESRFYKHPF TCFAKNTHGI DAAYIQLIYP VTNFQKHMIG ICVTLTVIIV CSVFIYKIFK 360
IDIVLWYRDS CYDFLPIKAS DGKTYDAYIL YPKTVGEGST SDCDIFVFVKG LPEVLEKQCG 420	YKLFIYGRDD YVGEGMVCME QSKGLL 447
<hr/>	
SEQ ID NO: 218	moltype = AA length = 298
FEATURE	Location/Qualifiers
source	1..298
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 218	
MEFKKNENNE LPKLOWYKDC KPPLLDNIHF SGVKDRLLIV NVAEKHRGNY TCHASYTYLG 60	KQYPITRVE FITLEENKPT RPVIVSPAN EMEVDLGSQI QLICNTGQL SDIAYWKNG 120
SVIDEDEDPVL GEDYYSVENP ANKRSTSLIT VLNISETIERS FYKHPFTCFA KNTHGIDAAY 180	IQLIYPVTNF QKHMIGICVT LTVIIVCSVF IYKIFKIDIV LWYRDSCYDF LPIKASDGKT 240
YDAYIYLIPK VGEGSTSDC IFVFKVLPEV LEKQCGYKLF IYGRDDYVGE DIVEVINE 298	
<hr/>	
SEQ ID NO: 219	moltype = AA length = 182
FEATURE	Location/Qualifiers
source	1..182
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 219	
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60	DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFVENEPNL 120
CYNAQAIFQK QLPVAGDGGL VCPYMEFFKN ENNELPKLQW YKDCKPPLLD NIHFSGVKDR 180	LI 182

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SEQ ID NO: 220      moltype = AA  length = 114
FEATURE          Location/Qualifiers
source           1..114
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 220
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLRIKIS AKFV       114

SEQ ID NO: 221      moltype = AA  length = 106
FEATURE          Location/Qualifiers
source           1..106
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 221
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60
DSKTPVSTEQ ASRIHQHKEK LWFVPAKVED SGHYYCVVRN SSYCLR                   106

SEQ ID NO: 222      moltype = AA  length = 80
FEATURE          Location/Qualifiers
source           1..80
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 222
MKVLLRLICF IALLISSLEA DKCKEREeki ILVSSANEID VRPCPLNPNE HKGTITWYKD 60
DSKTPVSTEQ ASRIHQHKEK                                         80

SEQ ID NO: 223      moltype = AA  length = 575
FEATURE          Location/Qualifiers
source           1..575
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 223
MWSLLLCGLS IALPLSVTAD GCKDIFMKNE ILSASQPFAF NCTFPPIITSG EVSVTWYKNS 60
SKIPVSKIIQ SRIHQDETWE LFLPMEWGS GVYQCVIKGR DSCHRIVHNL TVFEKHWCDT 120
SIGGLPNLSD EYKQILHLGK DDSLTCHLF PKSCVLGPIK WYKDCNEIKG ERFTVLETRL 180
LVSNVSAEDR CNYACQAILT HSGKQYEVLN GITVSITERA GYGGSVPKII YPKNHSIEVQ 240
LGTTLIVDCN VTDTKDNTNL RCWRVNNTLV DDYYDESKRI REGVETHVSF REHNLYTVNI 300
TFLEVVKMEDY GLPFMCHAGV STAYIILQLP APDPFRAYLIG GLIALVAVAV SVVYIYNIFK 360
IDIVLWYRSA FHSTETIVDG KLYDAYVLYP KPHKESQRHA VDALVLNILP EVLERQCGYK 420
LFFIGRDEFQ GQA VANVIDE NVKLCCRRLIV IVVPESLGFV LLKNLSEEQI AVYSALIQDG 480
MKVILITELEK IEDYTVMPES IQYIKQKHGA IRWHGDFTEQ SQCMKTKFWK TVRYHMPPR 540
CRPFPPVQLL QHTPCYRTAG PELGSRRKKC TLTTG                         575

SEQ ID NO: 224      moltype = AA  length = 172
FEATURE          Location/Qualifiers
source           1..172
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 224
MWSLLLCGLS IALPLSVTAD GCKDIFMKNE ILSASQPFAF NCTFPPIITSG EVSVTWYKNS 60
SKIPVSKIIQ SRIHQDETWE LFLPMEWGS GVYQCVIKGR DSCHRIVHNL TVFEKHWCDT 120
SIGGLPNLSD EYKQILHLGK DDSLTCHLF PKSCVLGPIK WYKDCNEIKG ER             172

SEQ ID NO: 225      moltype = AA  length = 457
FEATURE          Location/Qualifiers
source           1..457
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 225
MTGLVSLSYF PLSTRSCALQ SCSPVGCGP CCSAGCPSPF HCLSQQDCNE IKGERFTVLE 60
TRLLVSVNSA EDRGNYACQA ILTHSGKQYE VLNGITVSIK RAGYGGSVPK IIYPKNHSIE 120
VQLGTTLIVD CNVTDTKDNTNL NRCLWRVNNTV LVDDYYDESKR RIREGVETHV SFREHNLYTV 180
NITFLEVVKME DYGLPPMCHA GVSTAYIILQ LPAPDFRAYLIG IGGLIALVAV AVSVVYIYNI 240
FKIDIVLWYR SAFHSTETIV DGKLYDAYVLY PPKPHKESQR HA VDALVLNI LPEVLERQCG 300
YKLFIFGRDE FPGQAVANVI DENVKLCRRLIV IVIVVPESLGFV FGLLKNLSEE QIAVYSALIQ 360
DGMKVILLIEL EKIEDYTVMP ESIQYIKQKH GAIRWHGDFT EQSQCMKTKF WKTVRYHMPP 420
RRCRPFPPVQ LLQHTPCYRT AGPELGSRRK KCTLTG                         457

SEQ ID NO: 226      moltype = AA  length = 556
FEATURE          Location/Qualifiers
source           1..556
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 226

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MGFWILAILT	ILMYSTAAKF	SKQSWGLENE	ALIVRCPRQG	KPSYTVWDWYY	SQTNKSIP	TQ
ERNRVFASGQ	LLKFLPAAVA	DSGIYTCIVR	SPTFNRTGYA	NVTIYKKQSD	CNVPDYL	MY
TVSGSEKNSK	IYCPTIDLYN	WTAPLEWFKN	CQALQGSRYR	AHKSFV	IDN	VMTEDAGD
CKFIHNENGA	NYSVTATRSF	TVKDEQGFSL	FPVIGAPAQN	EIKEVEIG	KNA	LCACFG
KGTQFLAABL	WQLNGTKITD	FGEPRIQQEE	GQNQSF	SNGL	ACLD	MVLRIA
YDCLALNLHG	LRRHTVRLSR	KNPDIHHSIY	CIIAVCSVFL	MLINVLV	IIL	KMF
WRDIAKPYKT	RNDGKLYDAY	VVYPRNYKSS	TDGASRVEHF	VHQILPDVLE	NKC	GYTLCIY
GRDMLPGEDV	VIAVETNIRK	SRRHIFILTP	QITHNKEFAY	EQEVALH	CA	L
EMEALSELDM	LQAELQDSL	QHLMKVQGTI	KWREDHIA	NIK RSLNSKF	WKH	VRYQMPVPSK
IPRKASSLTP	LAAQKQ					
						556

SEQ ID NO:	227	moltype = AA	length = 328			
FEATURE		Location/Qualifiers				
source		1..328				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	227					
MGFWILAILT	ILMYSTAAKF	SKQSWGLENE	ALIVRCPRQG	KPSYTVWDWYY	SQTNKSIP	TQ
ERNRVFASGQ	LLKFLPAAVA	DSGIYTCIVR	SPTFNRTGYA	NVTIYKKQSD	CNVPDYL	MY
TVSGSEKNSK	IYCPTIDLYN	WTAPLEWFKN	CQALQGSRYR	AHKSFV	IDN	VMTEDAGD
CKFIHNENGA	NYSVTATRSF	TVKDEQGFSL	FPVIGAPAQN	EIKEVEIG	KNA	LCACFG
KGTQFLAABL	WQLNGTKITD	FGEPRIQQEE	GQNQSF	SNGL	ACLD	MVLRIA
YDCLALNLHG	LRRHTVRLSR	KNPSKECF				
						328

SEQ ID NO:	228	moltype = AA	length = 211			
FEATURE		Location/Qualifiers				
source		1..211				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	228					
MYSTVSGSEK	NSKIYCP	TID LYNWTAPLEW	FKNCQALQGS	RYRAHK	SFLV	IDNVMTEDAG
DYCKFIHNE	NGANYSVTAT	RSFTVKDEQG	FSLFPVIGAP	AQNEIKE	VEI G	GKNA
CPFGKGTQFLA	AVLWQLNGTK	ITDFGEPIQ	QEEGQNQSFS	NGLAC	DMVL RIADV	KEEDL
LLQYDCLALN	LHGLRRHTVR	LSRKNP	SKEC F			211

SEQ ID NO:	229	moltype = AA	length = 314			
FEATURE		Location/Qualifiers				
source		1..314				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	229					
MGFWILAILT	ILMYSTAAKF	SKQSWGLENE	ALIVRCPRQG	KPSYTVWDWYY	SQTNKSIP	TQ
ERNRVFASGQ	LLKFLPAAVA	DSGIYTCIVR	SPTFNRTGYA	NVTIYKKQSD	CNVPDYL	MY
TVSGSEKNSK	IYCPTIDLYN	WTAPLEWFKN	CQALQGSRYR	AHKSFV	IDN	VMTEDAGD
CKFIHNENGA	NYSVTATRSF	TVKDEQGFSL	FPVIGAPAQN	EIKEVEIG	TQ FLAAVL	WQLN
GTKITDFGEP	RIQQEEGQNQ	SFSNGLACLD	MVLRIADVKE	EDLLQYDCL	ALNLHGLRRH	F
TVRLSRKNPS	KECF					314

SEQ ID NO:	230	moltype = AA	length = 259			
FEATURE		Location/Qualifiers				
source		1..259				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	230					
MGFWILAILT	ILMYSTAAKF	SKQSWGLENE	ALIVRCPRQG	KPSYTVWDWYY	SQTNKSIP	TQ
ERNRVFASGQ	LLKFLPAAVA	DSGIYTCIVR	SPTFNRTGYA	NVTIYKKQSD	CNVPDYL	MY
TVSGSEKNSK	IYCPTIDLYN	WTAPLEWFKN	CQALQGSRYR	AHKSFV	IDN	VMTEDAGD
CKFIHNENGA	NYSVTATRSF	TVKDEQGFSL	FPVIGAPAQN	EIKEVEIG	TQ KLKKSLIF	SN F
CCRVVFNLCL	QYFQHHQWP					259

SEQ ID NO:	231	moltype = AA	length = 38			
FEATURE		Location/Qualifiers				
source		1..38				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	231					
MGFWILAILT	ILMYSTAAKF	SKQSWGLENE	ALIVRCPR			38

SEQ ID NO:	232	moltype = AA	length = 425			
FEATURE		Location/Qualifiers				
source		1..425				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	232					
MVKALLRLV	SAVNRRRMKL	LLGIALLAYV	ASVWGNFVN	M SFLLNRSI	QE NGELKIES	SKI
EEMVEPLREK	IRDLEKSFTQ	KYPPVKFLSE	KDRKRILITG	GAGFVGSHLT	D KLMMDGHEV	120

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TVVDNFFTGR	KRNVEHWIGH	ENFELINHDV	VEPLYIEVDQ	IYHLASPASP	PNYMPNPIKT	180	
LKTNTIGLN	MLGLAKRVG	RLLL	LASTSEV	YDPEVHPOS	EDYWGHNPI	GPRACYDEGK	240
RVAETMCYAY	MKQEGVEVRV	ARIFNTFGPR	MHMNDGRVVS	NFLQALQGE	PLTVYGSGSQ	300	
TRAFQYVSDL	VNGLVALMNS	NVSSPVNLGN	PEEH TILEFA	QLIKNLVGSG	SEIQLSEAQ	360	
DDPQKRKPDI	KKAKMLLGWE	PVVPLEEGLN	KAIHYFRKEL	EYQANNQYIP	KPKPARIKKG	420	
RTRHS						425	

SEQ ID NO: 233	moltype = AA	length = 420
FEATURE	Location/Qualifiers	
source	1..420	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 233						
MVKALLRLV	SAVNRRRMKL	LLGIALLAYV	ASVWGNFVN	RSIQENGELK	IESKIEEMVE	60
PLREKIRDLE	KSFTQKYPPV	KFLSEKDRKR	ILITGGAGFV	GSHLTDKLM	DGHEVTVDN	120
FFTGRKRNRVE	HWHIGHENFEL	INHDVVEPLY	IEVDQIYHLA	SPASPPNMYM	NPIKTLKTNT	180
IGTLMNLGLA	KRKGARLLA	STSEVYGDPE	VHPQSEDYWG	HVNPIGPAC	YDEGKRAET	240
MCAYAMKQEG	VEVVRARIFN	TFGPRMHMD	GRVVSNFILQ	ALQGEPLTVY	GSGSOTRAFO	300
YVSDLVNGLV	ALMNSNVSSP	VNLGNPEEHT	ILEFAQLIKN	LVGSGSEIQF	LSEAQDDPQK	360
RKPDIIKAKL	MLGWEPPVPL	EEGLNKAIHY	FRKELEYQAN	NQYIPKPKPA	RIKKGRTRHS	420

SEQ ID NO: 234	moltype = AA	length = 171
FEATURE	Location/Qualifiers	
source	1..171	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 234								
MVKALLRLV	SAVNRRRMKL	LLGIALLAYV	AWLA	KRKGAR	LLL	LASTSEVY	GDPEVHPQSE	60
DWGHVNPIG	PRACYDEGKR	VAETMCYAYM	KQEGVEVRV	A	RIFNTFGPRM	HMN	NDGRVVS	120
FILQALQGEP	LTVYGSQ	RAFQYVSDLV	NGLVALMNSN	V	VSSPVNLVSA	P	171	

SEQ ID NO: 235	moltype = AA	length = 190
FEATURE	Location/Qualifiers	
source	1..190	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 235							
MVEPLREKIR	DLEKSFTQKY	PPVKFLSEKD	RKRILITGG	GFVGSHLT	DK	LMMDGHEVTV	60
VDNFFTGRKR	NVEHWIGHEN	FELINHDVVE	PLYIEVDQIY	HLASPAS	PN	YMYNPIKTLK	120
TNTIGTLNML	GLAKRKGARL	LLASTSEVY	G DPEVHPQSE	YWG	HVNPIGP	RACYDEGKRV	180
ATMCYAYMK							190

SEQ ID NO: 236	moltype = AA	length = 210
FEATURE	Location/Qualifiers	
source	1..210	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 236							
MAVKVQTTKR	GDPHELRNIF	LQYASTEVDG	ERYMTPEDFV	QRYLGLYNDP	NSNPKIVQL	60	
AGVADQTKDG	LISYQEFLAF	ESVLCAPDSM	FIVAFQLFDK	SGNGEVT	FGG	VLWPHRWYSS	120
SFQAHSWNRH	GGSLGESECQP	RSEKMSKKFL	DRLLFIII	LSLTGIVNLSDC	ILGITGRSIL	180	
TTQNSRSFSR	SCNWNMQDKP	LHSKTKAKVA				210	

SEQ ID NO: 237	moltype = AA	length = 870
FEATURE	Location/Qualifiers	
source	1..870	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 237							
MGVKKKKEMQ	VAALTICHQD	LETLKSFADV	EGKNLASLLL	HCVQLTDGVS	QIHYIKQIVP	60	
LLEKADKNGM	CDPTIQSCLD	ILAGIYLSLS	LNPLKKVLA	SSLNSLPDFF	LPEAMHRFTS	120	
RLQEELNTTD	LYSYRKVTDN	ISSCMENFNL	GRASVNNLLK	NVLHFLQKSL	IEILEENRKC	180	
AGNHIIQTQL	MNDLLVGIRV	SMMLVQKVQD	FQGNLWKTSD	SPIWQNMCG	LSIFTKVLSD	240	
DDLQTVQST	SGLAILFLF	TMFPLSEKIP	HLISSVLLRS	VDCTSVEWE	MSSCRSLCCG	300	
DISQSAVLFL	CQGTTLAMLDW	QNQSMGRSGE	ALLLDTAHLV	FTLSSQIKEP	TLEMFLSRIL	360	
ASWTNSAIQV	LESSPSLTD	SLNGNSSIVG	RLEEVYVTHW	EHPLDALRHQ	TKIMPKNLQ	420	
MHRLTVEGAD	FVPDPFFVEL	TESLRLWEH	IKGKYTCLGC	LVECIGVEHI	LAIDKTIPSQ	480	
ILEVMGDQSL	VPYASDLLET	MFRNHKSHLK	SQTAESSWI	QWHE	TWSPL	540	
QKSYVIDYYL	PKLLSYSPES	LQYMVKILQ	SIDAKTGQEQ	SFP	SLGSCNS	RGALGALMAC	600
LRIARAHGHL	QSATDTWENL	VSDARIKQGL	IHQHCQVRID	TLGLL	CESNR	STEIVSMEEM	660
QWIQFFITYN	LNSQSPGVRQ	QICSLKKLF	CRIQESSQVL	YKLEQSKSKR	EPENE	LTQKQ	720
PSVSLQQYKN	FMSSICNSLF	EALFPGSSYS	TRFSAL	TI	LG	GKCLIMLGEV	780
IFVFFQNLILI	LHFALFEVSV	LLPFFEVS	PYN	NSCLYIMK	FASKGQKRKK	LSPFSLIIIC	840
QPQSIIFMDY	AYYGKSSYY	LTNLFVA	VLR				870

SEQ ID NO: 238	moltype = AA	length = 906
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FEATURE	Location/Qualifiers
source	1..906
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 238	
MICQKFCVVL LHWEFIYVIT AFNLNSYIPTP WRFKLSCMPP NSTYDYFLLP AGLSKNTSNS	60
NGHYETAVEP KFNSSGTHFS NLSKTTFHCC FRSEQDRNCS LCADNIEGKT FVSTVNSLVF	120
QQIDANWNIQ CWLKGDLKLF ICYVESLFKN LFRNYNYKVH LLYVLPEVLE DSPLVPQKGS	180
FQMVHCNCV HECCECLVPV PTAKLNDTLL MCLKITSGGV IFQSPLMSVQ PINMVKPDP	240
LGLHMEITDD GNLKISWSSP PLVFPPLQYQ VKYSENSTTV IREADKIVSA TSLLVDSILP	300
GSSYEVQVRG KRLDGPGIWS DWSTPRVFTT QDVIYFPPKI LTSVGSNSVF HCIYKKENKI	360
VPSKEIVWWM NLAEKIPQSQ YDVVDSDHVK VTFPNLNNETK PRGKFTYDAV YCCNEHECHH	420
RYAELYVIDV NINISCETDG YLTAKMTCRWS TSTIQSLAES TLQLRYHRS	480
PISEPKDCYL QSDGFYECIF QPIFLLSGYT MWIRINHSLG SLDSPPTCVL PDSVVKPLPP	540
SSVKAETIN IGLLKISWEK PVFPENNQLF QIRYGLSGKE VQWKMYEVYD AKSKSVSLPV	600
PDLCAVYAVQ VRCKRLDGLG YWSNWSNPAY TVVMDIKVPM RGPEFWRIIN GDTMKKEKNV	660
TLLWKPLMKN DSQLCSVQRVY INHHHTSCNGT WSEDVGHNHTK FTFLWTEQAH TVTVLAINSI	720
GASVANFNLT FSWPMSKVNI VQSL SAYPLN SSCVIVSWIL SPSDYKLMYF IIIEWKNLNED	780
GEIKWLRSS SVKKYYIHDH FIPIEKYQFS LYPIFMEGVG KPPIINSFTQ DDIEKHQSDA	840
GLYVIVPVII SSSILLGTL LISHQRMKKL FWEDVPNPKN CSWAQGLNFQ KKMPGTKE	900
GGGWLT	906
SEQ ID NO: 239	moltype = AA length = 1165
FEATURE	Location/Qualifiers
source	1..1165
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 239	
MICQKFCVVL LHWEFIYVIT AFNLNSYIPTP WRFKLSCMPP NSTYDYFLLP AGLSKNTSNS	60
NGHYETAVEP KFNSSGTHFS NLSKTTFHCC FRSEQDRNCS LCADNIEGKT FVSTVNSLVF	120
QQIDANWNIQ CWLKGDLKLF ICYVESLFKN LFRNYNYKVH LLYVLPEVLE DSPLVPQKGS	180
FQMVHCNCV HECCECLVPV PTAKLNDTLL MCLKITSGGV IFQSPLMSVQ PINMVKPDP	240
LGLHMEITDD GNLKISWSSP PLVFPPLQYQ VKYSENSTTV IREADKIVSA TSLLVDSILP	300
GSSYEVQVRG KRLDGPGIWS DWSTPRVFTT QDVIYFPPKI LTSVGSNSVF HCIYKKENKI	360
VPSKEIVWWM NLAEKIPQSQ YDVVDSDHVK VTFPNLNNETK PRGKFTYDAV YCCNEHECHH	420
RYAELYVIDV NINISCETDG YLTAKMTCRWS TSTIQSLAES TLQLRYHRS	480
PISEPKDCYL QSDGFYECIF QPIFLLSGYT MWIRINHSLG SLDSPPTCVL PDSVVKPLPP	540
SSVKAETIN IGLLKISWEK PVFPENNQLF QIRYGLSGKE VQWKMYEVYD AKSKSVSLPV	600
PDLCAVYAVQ VRCKRLDGLG YWSNWSNPAY TVVMDIKVPM RGPEFWRIIN GDTMKKEKNV	660
TLLWKPLMKN DSQLCSVQRVY INHHHTSCNGT WSEDVGHNHTK FTFLWTEQAH TVTVLAINSI	720
GASVANFNLT FSWPMSKVNI VQSL SAYPLN SSCVIVSWIL SPSDYKLMYF IIIEWKNLNED	780
GEIKWLRSS SVKKYYIHDH FIPIEKYQFS LYPIFMEGVG KPPIINSFTQ DDIEKHQSDA	840
GLYVIVPVII SSSILLGTL LISHQRMKKL FWEDVPNPKN CSWAQGLNFQ KPETFEHLFI	900
KHTASVTCGP LLLEPETISE DISVTDWSKN KDEMMPPTTVV SLLSTTDLEK GSVCISDQFN	960
SVNFSSEAEGT EVTYEDESQV QPFVKYATLI SNSKPSSETGE EQGLINNSVT KCFSSKNSP	1020
KDSFSNSSSWE IEAQAFFILS DQHPNIISPH LTFSEGLDEL LKLEGNFPEE NNDKKSIIY	1080
GVTSIKRRES GVLLTDSRSV SCPFPAPCLF TDIRVLQDSC SHFVENNINL GTSSKTFAS	1140
YMPQFQTST QTHKIMENKM CDLTV	1165
SEQ ID NO: 240	moltype = AA length = 906
FEATURE	Location/Qualifiers
source	1..906
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 240	
MICQKFCVVL LHWEFIYVIT AFNLNSYIPTP WRFKLSCMPP NSTYDYFLLP AGLSKNTSNS	60
NGHYETAVEP KFNSSGTHFS NLSKTTFHCC FRSEQDRNCS LCADNIEGKT FVSTVNSLVF	120
QQIDANWNIQ CWLKGDLKLF ICYVESLFKN LFRNYNYKVH LLYVLPEVLE DSPLVPQKGS	180
FQMVHCNCV HECCECLVPV PTAKLNDTLL MCLKITSGGV IFQSPLMSVQ PINMVKPDP	240
LGLHMEITDD GNLKISWSSP PLVFPPLQYQ VKYSENSTTV IREADKIVSA TSLLVDSILP	300
GSSYEVQVRG KRLDGPGIWS DWSTPRVFTT QDVIYFPPKI LTSVGSNSVF HCIYKKENKI	360
VPSKEIVWWM NLAEKIPQSQ YDVVDSDHVK VTFPNLNNETK PRGKFTYDAV YCCNEHECHH	420
RYAELYVIDV NINISCETDG YLTAKMTCRWS TSTIQSLAES TLQLRYHRS	480
PISEPKDCYL QSDGFYECIF QPIFLLSGYT MWIRINHSLG SLDSPPTCVL PDSVVKPLPP	540
SSVKAETIN IGLLKISWEK PVFPENNQLF QIRYGLSGKE VQWKMYEVYD AKSKSVSLPV	600
PDLCAVYAVQ VRCKRLDGLG YWSNWSNPAY TVVMDIKVPM RGPEFWRIIN GDTMKKEKNV	660
TLLWKPLMKN DSQLCSVQRVY INHHHTSCNGT WSEDVGHNHTK FTFLWTEQAH TVTVLAINSI	720
GASVANFNLT FSWPMSKVNI VQSL SAYPLN SSCVIVSWIL SPSDYKLMYF IIIEWKNLNED	780
GEIKWLRSS SVKKYYIHDH FIPIEKYQFS LYPIFMEGVG KPPIINSFTQ DDIEKHQSDA	840
GLYVIVPVII SSSILLGTL LISHQRMKKL FWEDVPNPKN CSWAQGLNFQ KKMPGTKE	900
GGGWLT	906
SEQ ID NO: 241	moltype = AA length = 958
FEATURE	Location/Qualifiers
source	1..958
	mol_type = protein

-continued

organism = Homo sapiens

SEQUENCE: 241

MICQKFCVVL	LHWEFIYVIT	AFNLSYTIP	WRFKLSCMPP	NSTYDYFLLP	AGLSKNTSNS	60
NGHYETAVEP	KFNSSGTHFS	NLSKTFHCC	FRSEQDRNCS	LCADNIEGKT	FVSTVNSL VF	120
QQIDANWNIQ	CWLKGDLKLF	ICYVESLFKN	LFRNYNYKVH	LLYVLPEVLE	DSPLVPQKGS	180
FQMVHCNC SV	HECCECLVPV	PTAKLNDTLL	MCLKITSGGV	IFQSPLMSVQ	PINMVKPDP	240
LGLHMEITDD	GNLKISWSSP	PLVFPPLQYQ	VKYSENSTTV	IREADKIVSA	TSLLVDSILP	300
GSSYEVQVRG	KRLDGP GIWS	DWSTPRVFTT	QDVYFPPKI	LTSVGSNVSF	HCIYKKENKI	360
VPSKEIVWWM	NLAEKIPQS Q	YDVVS DHVSK	VTFFNLNETK	PRGKFTYDAV	YCCNEHECHH	420
RYAELYVIDV	NINISCETDG	YLTKMTCRWS	TSTIQSLAES	TLQLRYHRSS	LYCSDIPS IH	480
PISEPKDCY	QSDGFYECIF	QPIFLLSGYT	MWIRINHSLG	SLDSPPTC VL	PDSVVKPLP	540
SSVKAETIN	IGLLKISWEK	PVFPENN LQF	QIRYGLSGKE	VQWKMYEVYD	AKSKSVSLPV	600
PDLCAVYAVQ	VRCKRDLGLG	YWSNWSNPAY	TVVMDIKVPM	RGPEFWRI IN	GDTMKKEKNV	660
TLLWKPLMKN	DSLCSVQR YV	INHHHTSCNGT	WSE DVG NH	FTFLWTEQAH	TVTVLAINSI	720
GASVANFNL T	FSWPMSKVNI	VQSL SAYPLN	SSCVIVSWIL	SPSDYKLMYF	II EWKNLNED	780
GEIKWLRSS	SVKKYYIHHD	FIPIEKYQFS	LYPIFMEGV G	KPKIINSFTQ	DDIEKHQS DA	840
GLYVIVPVI	SSSILLGTL	LISHQRMKK L	FWEDVPNPKN	CSWAQGLNFQ	KMLEGSMFVK	900
SHHHSLSI ST	QGHKHCGRPQ	GPLHRKTRDL	CSLVYLLTP	PLLSYDPAKS	PSVRNTQE	958

SEQ ID NO: 242 moltype = AA length = 896

FEATURE Location/Qualifiers

source 1..896

mol_type = protein

organism = Homo sapiens

SEQUENCE: 242

MICQKFCVVL	LHWEFIYVIT	AFNLSYTIP	WRFKLSCMPP	NSTYDYFLLP	AGLSKNTSNS	60
NGHYETAVEP	KFNSSGTHFS	NLSKTFHCC	FRSEQDRNCS	LCADNIEGKT	FVSTVNSL VF	120
QQIDANWNIQ	CWLKGDLKLF	ICYVESLFKN	LFRNYNYKVH	LLYVLPEVLE	DSPLVPQKGS	180
FQMVHCNC SV	HECCECLVPV	PTAKLNDTLL	MCLKITSGGV	IFQSPLMSVQ	PINMVKPDP	240
LGLHMEITDD	GNLKISWSSP	PLVFPPLQYQ	VKYSENSTTV	IREADKIVSA	TSLLVDSILP	300
GSSYEVQVRG	KRLDGP GIWS	DWSTPRVFTT	QDVYFPPKI	LTSVGSNVSF	HCIYKKENKI	360
VPSKEIVWWM	NLAEKIPQS Q	YDVVS DHVSK	VTFFNLNETK	PRGKFTYDAV	YCCNEHECHH	420
RYAELYVIDV	NINISCETDG	YLTKMTCRWS	TSTIQSLAES	TLQLRYHRSS	LYCSDIPS IH	480
PISEPKDCY	QSDGFYECIF	QPIFLLSGYT	MWIRINHSLG	SLDSPPTC VL	PDSVVKPLP	540
SSVKAETIN	IGLLKISWEK	PVFPENN LQF	QIRYGLSGKE	VQWKMYEVYD	AKSKSVSLPV	600
PDLCAVYAVQ	VRCKRDLGLG	YWSNWSNPAY	TVVMDIKVPM	RGPEFWRI IN	GDTMKKEKNV	660
TLLWKPLMKN	DSLCSVQR YV	INHHHTSCNGT	WSE DVG NH	FTFLWTEQAH	TVTVLAINSI	720
GASVANFNL T	FSWPMSKVNI	VQSL SAYPLN	SSCVIVSWIL	SPSDYKLMYF	II EWKNLNED	780
GEIKWLRSS	SVKKYYIHHD	FIPIEKYQFS	LYPIFMEGV G	KPKIINSFTQ	DDIEKHQS DA	840
GLYVIVPVI	SSSILLGTL	LISHQRMKK L	FWEDVPNPKN	CSWAQGLNFQ	KRTDIL	896

SEQ ID NO: 243 moltype = AA length = 232

FEATURE Location/Qualifiers

source 1..232

mol_type = protein

organism = Homo sapiens

SEQUENCE: 243

MPPTTVVS LL	STTDLEKG SV	CISDQFNSVN	FSEAEGT EVT	YEDESQRQPF	VKYATLISNS	60
KPSETGEEQ Q	LINSSVT KCF	SSKN SPLKDS	FSN SSWIEIA	QAFFILSDQH	PNIISPHLTF	120
SEGLDELLKL	EGNFPEEN ND	KKSI YYLGVT	SIKKRESGV L	LTD KSRVSCP	FPAPCLFTDI	180
RVLQDSCSHF	VENNIN LGTS	SKKTFAS YMP	QFQTCSTQTH	KIMENKMC DL	TV	232

SEQ ID NO: 244 moltype = AA length = 896

FEATURE Location/Qualifiers

source 1..896

mol_type = protein

organism = Homo sapiens

SEQUENCE: 244

MICQKFCVVL	LHWEFIYVIT	AFNLSYTIP	WRFKLSCMPP	NSTYDYFLLP	AGLSKNTSNS	60
NGHYETAVEP	KFNSSGTHFS	NLSKTFHCC	FRSEQDRNCS	LCADNIEGKT	FVSTVNSL VF	120
QQIDANWNIQ	CWLKGDLKLF	ICYVESLFKN	LFRNYNYKVH	LLYVLPEVLE	DSPLVPQKGS	180
FQMVHCNC SV	HECCECLVPV	PTAKLNDTLL	MCLKITSGGV	IFQSPLMSVQ	PINMVKPDP	240
LGLHMEITDD	GNLKISWSSP	PLVFPPLQYQ	VKYSENSTTV	IREADKIVSA	TSLLVDSILP	300
GSSYEVQVRG	KRLDGP GIWS	DWSTPRVFTT	QDVYFPPKI	LTSVGSNVSF	HCIYKKENKI	360
VPSKEIVWWM	NLAEKIPQS Q	YDVVS DHVSK	VTFFNLNETK	PRGKFTYDAV	YCCNEHECHH	420
RYAELYVIDV	NINISCETDG	YLTKMTCRWS	TSTIQSLAES	TLQLRYHRSS	LYCSDIPS IH	480
PISEPKDCY	QSDGFYECIF	QPIFLLSGYT	MWIRINHSLG	SLDSPPTC VL	PDSVVKPLP	540
SSVKAETIN	IGLLKISWEK	PVFPENN LQF	QIRYGLSGKE	VQWKMYEVYD	AKSKSVSLPV	600
PDLCAVYAVQ	VRCKRDLGLG	YWSNWSNPAY	TVVMDIKVPM	RGPEFWRI IN	GDTMKKEKNV	660
TLLWKPLMKN	DLS CSVQR YV	INHHHTSCNGT	WSE DVG NH	FTFLWTEQAH	TVTVLAINSI	720
GASVANFNL T	FSWPMSKVNI	VQSL SAYPLN	SSCVIVSWIL	SPSDYKLMYF	II EWKNLNED	780
GEIKWLRSS	SVKKYYIHHD	FIPIEKYQFS	LYPIFMEGV G	KPKIINSFTQ	DDIEKHQS DA	840
GLYVIVPVI	SSSILLGTL	LISHQRMKK L	FWEDVPNPKN	CSWAQGLNFQ	KRTDIL	896

SEQ ID NO: 245 moltype = AA length = 214

FEATURE Location/Qualifiers

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source          1..214
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 245
MGLRDWLRTV CCCCCGCECLE ERALPEKEPL VSDNNPYSSF GATLVRDDEK NLWSMPHDVS 60
HTEADDDRTL YNLIVIRNQQ AKDSEEWQKL NYDIHTLRQV RREVNRWRKC ILEDLGFQKE 120
ADSLLSVTKL STISDSKNTR KAREMLLKLA EETNIFPTSW ELSERYLFVV DRLIALDAAE 180
EFFKLARRTY PKKPGVPCLA DGQKELHYLP FPSP                           214

SEQ ID NO: 246      moltype = AA length = 214
FEATURE          Location/Qualifiers
source           1..214
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 246
MGLRDWLRTV CCCCCGCECLE ERALPEKEPL VSDNNPYSSF GATLVRDDEK NLWSMPHDVS 60
HTEADDDRTL YNLIVIRNQQ AKDSEEWQKL NYDIHTLRQV RREVNRWRKC ILEDLGFQKE 120
ADSLLSVTKL STISDSKNTR KAREMLLKLA EETNIFPTSW ELSERYLFVV DRLIALDAAE 180
EFFKLARRTY PKKPGVPCLA DGQKELHYLP FPSP                           214

SEQ ID NO: 247      moltype = AA length = 526
FEATURE          Location/Qualifiers
source           1..526
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 247
MVNEGPQEE SDDTPVPESA LQADPSVSVH PSVSVHPVS INPSVSVHPS SSAHPSALAQ 60
PSGLAHPSSS GPEDLSVIKV SRRRWAVVLV FSCYSMCNSF QWIQYGSINN IFMHFYGVSA 120
FAIDWLSMCY MLTYIPLL PVAWLLEKPG RTIALTGSAL NCLGAWVKLG SLKPHLFPV 180
VVGQLICSV A QVFILGMPSR IASVWFGANE VSTACSVAVF GNQLGIAIGF LVPPVLVPNI 240
EDRDELAYHI MFYIIGGV ATLLLILV PFKEPKPKYP SRAQSLSYAL TSPDASYLGS 300
IAFLFKNLNF VLLVITYGLN AGAFYALSTL LNRMVVIWHYP GEEVNAGRIG LTIVIAGMLG 360
AVISGIWLD SKTYKETTLV VYIMTLVGMV VYFTFLNLGH LWVVFITAGT MGFFMTGYLP 420
LGPEFAVELT YPESEGIISSG LLNISAQVFG IIPTISQGQI IDNYGTKPGN IFLCVFLTLG 480
AALTAFIKAD LRRQKANKET LENKLQEEEE ESNTSKVPTA VSEDHL                           526

SEQ ID NO: 248      moltype = AA length = 321
FEATURE          Location/Qualifiers
source           1..321
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 248
MSADNSSTIC VCRSRVQELG IAIGFLPPV LPVNIEDRDE LAYHISIMFY IIGGVATLLL 60
ILVIIIVFKEK PKYPPSRAQS LSYALTSPDA SYLGSIARLF KNLFVLLVI TYGLNAGAFY 120
ALSTLLNRMV IWHYPGEENV AGRILTIVI AGMLGAVISG IWLDRSKTYK ETTLVYYIMT 180
LVGMVVYTFT LNGLGHLWVVF ITAGTMGFFM TGYLPLGFEE AVELTYPESE GISSGLLNIS 240
AQVFGIIFTI SQGQIIDNYG TKPGNIFLCV FTLGALTA FIKADLRRQK ANKETLENKL 300
QEEEEEESNTS KVPTAVSEDH L                           321

SEQ ID NO: 249      moltype = AA length = 203
FEATURE          Location/Qualifiers
source           1..203
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 249
MFYIIGGVAT LLLLILVIIGL NAGAFYALST LLNRMVVIWHY PGEEVNAGRIG GLTIVIAGML 60
GAVISGIWLD RSCTYKETTLV VVYIMTLVGM VVYTFITLNLG HLWVVFITAG TMGFFMTGYL 120
PLGFEFAVEL TYPESEGISS GLLNISAQVFG GIIFTISQGQ IIDNYGTKPG NIFLCVFLTL 180
GAALTAFIKA DLRRQKANKE TLE                           203

SEQ ID NO: 250      moltype = AA length = 133
FEATURE          Location/Qualifiers
source           1..133
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 250
MFYIIGGVAT LLLLILVIIVF KEKPKYPPSR AQSLSYALTS PDASYLGSIA RLFKNLNFL 60
LVITYGLNAG AFYALSTLLN RMVIWHYPGE EVNAGRIGLT IVIAGMLGAV ISGIWLDRSK 120
TYKNLCHPNC LIQ                           133

SEQ ID NO: 251      moltype = AA length = 203
FEATURE          Location/Qualifiers
source           1..203
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 251

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MSPYGISSLG NGLSKWLSLN AGAFYALSTL LNRMVIWHYP GEEVNAGRIG LTIVIAGMLG	60
AVISGIWLDK SKTYKETTLV VYIMTLVGMV VYFTLNLGH LWVVFITAGT MGFFMTGYLP	120
LGFEFAVELT YPESEGIISSG LLNISAQVFG IIIFTISQGQI IDNYGTPGN IFLCVFLTLG	180
ALTAFIKAD LRRQKANKET LEN	203
SEQ ID NO: 252 moltype = AA length = 241	
FEATURE Location/Qualifiers	
source 1..241	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 252	
MCPCDLHPSKY VQPPLSSSS PLKGGQEAFS PLGLNAGAFY ALSTLLNRMV IWHYPGEEVN	60
AGRIGLTIVI AGMLGAVISG IWLDRSKTYK ETTLVVYIMT LVGMVVYTFT LNLGHLWWVF	120
ITAGTMGFM TGYPLPLGFEF AVELTYPESE GISSLNLNIS AQVFGIIFTI SQGQIIDNYG	180
TKPGNIFLCV FTLGAALTA FIKADLRRQK ANKETLENKL QEEEEESNTS KVPTAVSEDH	240
L	241
SEQ ID NO: 253 moltype = AA length = 88	
FEATURE Location/Qualifiers	
source 1..88	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 253	
MFYIIGGVAT LLLILVIIIVF KEKPKYPPSR AQSLSYALT PDASYLGSIA RLFKNLNFVL	60
LVITYGLNAG AFYALSTLLN RMVIWHYP	88
SEQ ID NO: 254 moltype = AA length = 93	
FEATURE Location/Qualifiers	
source 1..93	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 254	
MFYIIGGVAT LLLILVIIIVF KEKPKYPPSR AQSLSYALT PDASYLGSIA RLFKNLNFVL	60
LVITYETPRG GGGEQHQSA HCCVRGSSLR GRW	93
SEQ ID NO: 255 moltype = AA length = 102	
FEATURE Location/Qualifiers	
source 1..102	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 255	
MTLRCLEPSG NGGEGRTRSQW GTAGSAAEPS PQAARLAKAL RELGQTGREP IGRDAGCRER	60
LPKEAARKRG RGGKQRIRWK YVPCFQGTAE STLAGSWVLG NA	102
SEQ ID NO: 256 moltype = AA length = 46	
FEATURE Location/Qualifiers	
source 1..46	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 256	
XAPSLQHLCR LTINKCTGAI WGLPLPTRLK DYLEEYKQPQ AVFYPG	46
SEQ ID NO: 257 moltype = AA length = 341	
FEATURE Location/Qualifiers	
source 1..341	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 257	
MNIVVEFFVV TFKVLWAFVL AAARWLVRPK EKSVAGQVCL ITGAGSGLGR LFALEFARRR	60
ALLVLWDINT QSNEETAGMV RHIYLDEAA DAAAALQAGNG EEEILPHCNL QVFTYTCDVG	120
KRENVYLTAE RVRKEVGEVS VLVNNAGVRVS GHHLLECPDE LIERTMMVNC HAHFWTTKAF	180
LPTMLEINHG HIVTVASSLG LFSTAGVEDY CASKFGVVG FHESLSHELKA AEKDGIKTTL	240
VCPYLVDTGM PRGCIRKEI EPFLPPLKPD YCVKQAMKAI LTDQPMICTP RLMYIVTFMK	300
SILPFEAVVC MYRFLGADKC MYPFIAQRKQ ATNNNEAKNG I	341
SEQ ID NO: 258 moltype = AA length = 176	
FEATURE Location/Qualifiers	
source 1..176	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 258	
MMVNCHAFW TTKAFLPTML EINHGHVITV ASSLGLFSTA GVEDYCASKF GVVGPHESLS	60
HELKAAEKDG IKTTLVCYPL VDTGMFRGCR IRKEIEPPLP PLKPDYCVKQ AMKAILTDQP	120
MICTPRLMYI VTFMKSILPF EAVVCMYRFL GADKCMYPFI AQRKQATNNN EAKNGI	176
SEQ ID NO: 259 moltype = AA length = 62	

-continued

FEATURE	Location/Qualifiers
source	1..62
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 259	
MMVNCHAHFW TTKAFLPTML EINHGHIVTV ASSLGLFSTA GVEDYCASKF GVVGPHESLS	60
HE	62
SEQ ID NO: 260	moltype = AA length = 382
FEATURE	Location/Qualifiers
source	1..382
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 260	
MRSHFLQWL ATSRNQDQIT NIFSGFAGLL AILLVVAVFC ILWNWNKRKK RQVPPYLRTV	60
MPLLTLQPTR QRAKNIYDIL PWRQEDLGRH ESRSMRIFST ESLLSRNSES PEHVPSQAGN	120
AFQEHTAHIH ATEYAVGIYD NAMVPQMCN LTPSAHCINV RASRDCASIS SEDSHDVNV	180
PTAAEIAETL ASTKSPSRLN FVLPLSTQKLE FTEERDECGG DAGDCTSLYS PGAEDSDSLS	240
NGEGSSQISN DYVNMTQLDL SAIQERQLWV AFQCCRDYEN VPAADPSGSQ QQAEKDVPSS	300
NIGHVEDKTD DPGTHVQCVR RTFLASGDYA DFQPFQTQSED SQMKHREEMS NEDSSDYENV	360
LTAKLGGRDS EQGPGTQLLP DE	382
SEQ ID NO: 261	moltype = AA length = 398
FEATURE	Location/Qualifiers
source	1..398
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 261	
MDGVTPTLST IRGRTLESST LHVTPRSLDR NKDQITNIFS GFAGLLAILL VVAVFCILWN	60
WNKRKKRQVP YLRVTVMPPL TLPQTRQRAK NIYDILPWRQ EDLGRHESRS MRIFSTESLL	120
SRNSESPEHV PSQAGNAFQE HTAHIQEST AVGIYDNAMV PQMCGNLTPS AHCIINVRAZR	180
DCASISSEDS HDYVNVPTEA EIAETLASTK SPSPRNLFVLP STQKLEFTEE RDEGCGDAGD	240
CTSLYSPGAE DSDSLSNGEQ SSQISNDYVN MTGLDLSAIQ ERQLWVAFQC CRDYENVPAA	300
DPSGSQQQAE KDVPSSNIGH VEDKTDDPGT HVQCVKRTFL ASGDYADFQP FTQSEDSQMK	360
HREEMSNEWS SDYENVLTAK LGGRDSEQGP GTQLLPDE	398
SEQ ID NO: 262	moltype = AA length = 48
FEATURE	Location/Qualifiers
source	1..48
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 262	
MEAATETEAAA AALEVLAEEVA GILEPVGLQE EAELPAKILV EFVVVCTR	48
SEQ ID NO: 263	moltype = AA length = 439
FEATURE	Location/Qualifiers
source	1..439
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 263	
MRRAALRLCA LGKGQLTPGR GLTQGPQNPQ KQGIFHIHEV RDKLREIVGA STNWRDHVK	60
MEERKLLHSF LAKSQDGLPP RRMKDSYIEV LLPLGSEPEL REKYLTQNT VRFGRILEDL	120
DSLGVLCYMH NHIHSAKMS PLISIVTALVD KIDMCKKSLS PEQDIKFSGH VSWVGKTSME	180
VKMQMFQLHG DEFCPVLDAT FVMVARDSEN KGPAFVNPLI PESPEEEELF RQGELNKGR	240
IAFSSTSLLK MAPSABERTT IHEMFLSTLD PKTISFRSRV LPSNAWMEN SKLKSLEICH	300
PQERNIFNRII FGFGFLMRKAY ELAWATACSF GGSRPFVVAV DDIMFQKPVE VGSLFLSSQ	360
VCFCTQNYYIQ VRVHSEVASL QEKOHTTTNV FHPTFMSEKE VPLVFPKTYG ESMLYLDGQR	420
HFNSMSGPAT LRKDYLVEP	439
SEQ ID NO: 264	moltype = AA length = 448
FEATURE	Location/Qualifiers
source	1..448
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 264	
MRRAALRLCA LGKGQLTPGR GLTQGPQNPQ KQGIFHIHEA CSSIIVHNVR DKLREIVGAS	60
TNWRDHVKAM EERKLLHSFL AKSDQDGLPP RMKDSYIEV LPLGSEPEL REKYLTQNTV	120
RFGRILEDLD SLGVLCYMH NHIHSAKMSP LSIVTALVDK IDMCKKSLSPE EQDIKFSGHV	180
SVWGKTSMEV KMQMFOQLHGDF EFCPVLDATF VMVARDSENK GPAFVNPLIP ESPEEEELFR	240
QGELNKGRRI AFSSTSLLKM APSAEERTTI HEMFLSTLDP KTISFRSRVL PSNAWMENS	300
KLKSLEICH PQRNIFNRII GGFLMRKAYE LAWATACSF GGSRPFVVAV DIMFQKPVEV	360
GSLLFLSSQV CFTQNYYIQV RVHSEVASLQ EKQHTTTNVF HFTFMSEKEV PLVFPKTYGE	420
SMLYLDGQRH FNSMSGPATL RKDYLVEP	448
SEQ ID NO: 265	moltype = AA length = 46
FEATURE	Location/Qualifiers

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source          1..46
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 265
MRAALRLCA LGKGQLTPGR GLTQGPQNPK KQGIFHIHEG KHGVSV           46

SEQ ID NO: 266      moltype = AA  length = 663
FEATURE
source          1..663
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 266
MSARLPVLSP PRWPRLLLLS LLLLGAAPGP RRSGAFYLPG LAPVNFCDEE KKSDECKAEI 60
ELFVNRLDSV ESVLPYEYTA FDFCQASEGK RPSENLGQVL FGERIEPSPY KFTFNKKETC 120
KLVCTKTYHT EKAEDKQKLE FLKKMSLNY QHHWIVDNMP VTVCYDVEDG QRFCNPGFPI 180
GCYITDKGHA KDACVISSDF HERDTFYIHN HVDIKIYHV VETGSMGARL VAAKLEPKSF 240
KHTHIDKPDC SGPPMDISNK ASGEKIAYT YSVSFEEDK IRWASRWYI LESMPHTKIQ 300
WFSIMNSLVI VLFLSGMVAM IMLRDLHBDI ARYNQMDSTF DAQEERFGWKL VHGDIFRPPR 360
KGMLLSVFLG SGTQILIMTF VTLFFACLGF LSPANRGALM TCAVVLWVLL GTPAGYVAAR 420
FYKSFGGEKW KTNVLLTSL CPGIVFADFF IMNLILWGGG SSAAIIFPGTL VAILALWFCI 480
SVPLTFIGAY FGFKKNAIEH PVRTNQIPRQ IPEQSFTKLP LPGIIMGGIL PFGCIFIQLF 540
FILENSIWSHQ MYMFGLFL VFIIILVITCS EATILLCYFH LCAEDYHWQW RSFLTSGFTA 600
VYFLIYAVHY FFSKLQITGT ASTILYFGYT MIMVLIFLFL TGTGIFFACF WFVTKIYSVV 660
KVD                                663

SEQ ID NO: 267      moltype = AA  length = 390
FEATURE
source          1..390
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 267
MGQRLSGGRS CLDVPGRLLP QPPPPPPPVR RKLALLFAML CVWLHYMFLYS CAGSCAAPP 60
LLLLGSRSRA AHDPPALATA PDGTPPRLPF RAPPATPLAS GKEMAEAGAAS PEEQSPEVPD 120
SPSPISFFS GSGSKQLPQA IIIGVKKGGT RALLEFLRVH PDVRAVGAEP HFFDRSYDKG 180
LAWYRDLMPR TLDGQITMEK TPSYFVTREA PARISAMSKD TKLIVVVRDP VTRAISDYTQ 240
TLSKRDPDIPT FESLTFKNRT AGLIDTSWSA IQIGIYAKHL EHWRHRHPIR QMLFVSGERL 300
ISDPAGEGLR VQDFLGLKRI ITDKHFYFNK TKGFPCLKKA EGSSRPHCCLG KTKGRTHPEI 360
DREVVRRLRE FYRPFNLKFY QMTGHDFGWD                                390

SEQ ID NO: 268      moltype = AA  length = 390
FEATURE
source          1..390
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 268
MGQRLSGGRS CLDVPGRLLP QPPPPPPPVR RKLALLFAML CVWLHYMFLYS CAGSCAAPP 60
LLLLGSRSRA AHDPPALATA PDGTPPRLPF RAPPATPLAS GKEMAEAGAAS PEEQSPEVPD 120
SPSPISFFS GSGSKQLPQA IIIGVKKGGT RALLEFLRVH PDVRAVGAEP HFFDRSYDKG 180
LAWYRDLMPR TLDGQITMEK TPSYFVTREA PARISAMSKD TKLIVVVRDP VTRAISDYTQ 240
TLSKRDPDIPT FESLTFKNRT AGLIDTSWSA IQIGIYAKHL EHWRHRHPIR QMLFVSGERL 300
ISDPAGEGLR VQDFLGLKRI ITDKHFYFNK TKGFPCLKKA EGSSRPHCCLG KTKGRTHPEI 360
DREVVRRLRE FYRPFNLKFY QMTGHDFGWD                                390

SEQ ID NO: 269      moltype = AA  length = 649
FEATURE
source          1..649
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 269
MSSFGAGKTK EVIFSVEDGS VKMFLRGRPV PMMPIDELAP TYSLDTRSEL PSCRALKLEWV 60
YGYRGRDCRA NLYLLPTGEI VYFVASVAVL YSVEEQRORH YLGHNNDDIKC LAIHPDMVTI 120
ATGQVAGTTK EGKPLPPHVR IWDSVSLSTL HVLGLGVFDR AVCCVGFSKS NGGNLLCAVD 180
ESNDHMLLSWV DWAKETKVVD VKCSNEAFLV ATFHPTDPTV LITCGKSHIY FWTLEGGSL 240
KRQGLFEKHE KPKYVLCVTF LEGGDDVVTGD SGGNLYWNGK GGNRITQAVL GAHDGGVFGL 300
CALRDGTLVS GGGRDRRVVL WGSYDSLQVE VEVPEDFGPV RTVAEGHGDYI LYVGTRNSI 360
LQGSVHTGFS LLVQGHVEEL WGLATHPSRA QFVTCGQDKL VHLWSSDSHQ PLWSRIIEDP 420
ARSAGFHPSG SVLAGVTVG RWLDDTEH DLVAIHTDGN EQISVVSFSP DGAYLAVGSH 480
DNLVYVYTVD QGGRKVSRIG KCSGHSSFIT HLDWAQDSSC FVTNSGDYEI LYWDPATCKQ 540
ITSADAVRNW EWATATCVLG FGVRGIWSEG ADGTDINAVA RSHDGKLLAS ADDFGKVHLF 600
SYPCCQPRAL SHKYGGHSSH VTNVAFLWDD SMALTTGGKD TSVLQWRV 649

SEQ ID NO: 270      moltype = AA  length = 145
FEATURE
source          1..145
               mol_type = protein
               organism = Homo sapiens

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SEQUENCE: 270
 MSSFGAGKTK EVIFSVAWPS TQIWSPSPRD RWREPLRKGS RCRPTCAGT QFPSPPYTCW 60
 AWGCLTEPCA VVASPNLMEA TCCVQWMNPM ITCSRCGTGP RRPRWWMSSA PMRLYWWPPS 120
 TPRTPLCLSP AGNLTSTSGP WRGAA 145

SEQ ID NO: 271 moltype = AA length = 76
 FEATURE Location/Qualifiers
 source 1..76
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 271 XGRKVSRLGK CSGHSSFITH LDWAQDSSCF VTNSGDYEIL YLEMGFHHLG QAGLELLTSG 60
 DPARCCGSCC LLGLQT 76

SEQ ID NO: 272 moltype = AA length = 225
 FEATURE Location/Qualifiers
 source 1..225
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 272 MFLRGRPVPM MIPDEALPTY SLDTRSELPS CRLKLEWVY YRGRDCRANL YLLPTGEIVY 60
 FVASVAVLYS VEEQRQRHYL GHNDDIKCLA IHEDMVITIAT GQVAGTTKEG KPLPPHVRW 120
 DSVSLSTLHV LGLGVFDRAV CCVGFSKSNG GNLLCAVDES NDHMLSVDW AKETKVVDVK 180
 CSNEAVLVAT PHPTDPTVLI TCGKSHIYFW TLEGGSLSKR QGLFE 225

SEQ ID NO: 273 moltype = AA length = 850
 FEATURE Location/Qualifiers
 source 1..850
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 273 MIERALLWQ REAGPGWGDR ARAGTGGAGG GCGGAMAERG PAFCGLYDTS SLLRYCNDDN 60
 LSGTSGMEVD DRVSALEQRL QLQEDELAVL KAALADALRR LRACEEQGAA LRARGTPKGR 120
 APPRLGTTAS VCQLLKGLPT RTPLNQSGPP RRVGGYATSP SSPKKREATSG RSSVRRYLSP 180
 ERLASVRRED PRSRRTTSSSS NCSAKKEGKT KEVIFSVEDG SVKMFLRGRP VPMMIPDELA 240
 PTYSLDTRSE LPSCRKLWV YGYGRDRCR ANLYLLPTGE IVYFVASVAV LYSVEEQRQR 300
 HYLGHNDDIK CLAIHPDMVT IATGQVAGTT KEGKPLPPHV RIWDSVSLST LHVLGLGVFD 360
 RAVCCVGFSK SNGGNLLCAV DESNDHMLSV WDWAKETKVV DVKCSNEAVL VATFHPTDPT 420
 VLIITCGKSHI YFTWTLEGGSK SKRQGLFEKH EKPKYVLCVT FLEGDDVVVTG DSGGNLYVWG 480
 KGGNRITQAV LGAHDGVFGV LCALRDGTLV SGGRDRRNVW LWGSDYSKLQ EVEVPEDDFGP 540
 VRTVAEGHGD TLYVGTTRNS ILQGSVHTGF SLLVQGHVVE LWGLATHPSR AQFVTCGQDK 600
 LVHLWSSDSH QPLWSRIIED PARSAQFHPG GSVLAvgTVT GRWLLDTET HDLVAIHTDG 660
 NEQISVVSFS PDGAYLAVGS HDNLVYVYTV DQGGRKVSRL GKCSGHSSFI THLDWAQDSS 720
 CFVTNSGDYE ILYWDPATCK QITSADAVRN MEWATATCVL GFVFGIWE GADGTDINAV 780
 ARSHDGKLLA SADDFGKVHL FSYPCCQPRA LSHKYGGHSS HVTNVAFLWD DSMALTTGGK 840
 DTSVLQWRVV 850

SEQ ID NO: 274 moltype = AA length = 73
 FEATURE Location/Qualifiers
 source 1..73
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 274 XHQPLWSRII EDPARSAGFH PSGSVLAVGT VTGRWLLLDT ETHDLVAIHT DGNEQISVVS 60
 FSPGPQFYH PPG 73

SEQ ID NO: 275 moltype = AA length = 121
 FEATURE Location/Qualifiers
 source 1..121
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 275 XLCAVDESND HMLSVWDWAK ETKVVDVKVP EDPGPVRTVA EGHGDTLYVG TTRNSILQGS 60
 VHTGFSLLVQ GHVEELWGLA THPSRAQFVT CGQDKLHWL SSDSHQPLWS RIIEDPARSA 120
 G 121

SEQ ID NO: 276 moltype = AA length = 427
 FEATURE Location/Qualifiers
 source 1..427
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 276 MSSFGAGKTK EVIFSVAWPS PMMIPDELAP TYSLDTRSEL PSCRKLWV 60
 YGYGRDRDRA NLYLLPTGEI VYFVASVAVL YSVEEQRQRH YLGHNDDIKC LAIHPDMDTI 120
 ATGQVAGTTK EGKPLPPHVR IWDSVSLSTL HVLGLGVFDRAVCCVGFSKS NGGNLLCAVD 180
 ESNDHMLSVW DWAKETKVV DWAQKSHIYFW TLEGGSLSKR QGLFE 240

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KRQGLFEKHE	KPKYVLCVTF	LEGGDVVTGD	SGGNLYVWGK	GGNRITQAVAL	GAHDGGVFGL	300
CALRDGTLVS	GGGRDRRVVL	WGSDYSKLQE	VEVPEDFGPV	RTVAEGHGD	T LYVGTRNSI	360
LQGSVHTGFS	LLVQGHVEEL	WGLATHPSRA	QFVTCQDKL	VHLWSSDSHQ	PLWSRIIEMA	420
AAGHGDP						427

SEQ ID NO: 277	moltype = AA length = 773
FEATURE	Location/Qualifiers
source	1..773
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 277						
MSSFGAGKTK EVIFSVEDGS	VKMFLRGRPV PMMIPDELAP	TYSLDTRSEL PSCRKLKLEWV	60			
YGYRGRDCRA	NLYLLPTGEI	YVFVASVAVL YSVEEQRQRH	YLGHNDDIKC LAIHPDMVTI	120		
ATCQVAGTTK	EGKPLPSPHVR	IWDSDYSLSTL HVLGLGVDFR	AVCCVGFSKS NGGNLLCAVD	180		
ESNDHMLSVW	LLVQGHVEEL	WGLATHPSRA QFVTCQDKL	VHLWSSDSHQ PLWSRIIEMA	240		
KRQGLFEKHE	KPKYVLCVTF	LEGGDVVTGD	SGGNLYVWGK GGNRITQAVAL	GAHDGGVFGL	300	
CALRDGTLVS	GGGRDRRVVL	WGSDYSKLQE	VEVPEDFGPV	RTVAEGHGD	T LYVGTRNSI	360
LQGSVHTGFS	LLVQGHVEEL	WGLATHPSRA	QFVTCQDKL	VHLWSSDSHQ	PLWSRIIEMA	420
ARSAGFHPSG	SVLAVGTVTG	RWLLDDTETH DLVAIHTDGN	EQISVVSFP DGAYLAVGSH	480		
DNLVYVYTVD	QGGRKVSRLG	KCSGHSSFIT HLDWAQDSSC	FVTNSGDYEI LYWDPATCKQ	540		
ITSADAVRN	EWATATCVLG	FGVFGIWSEG ADGTDINAVA	RSHDGKLLAS ADDFGKVHLF	600		
SYPCCQPRVL	GKWPSSAAEAA	LSSGIRVLF RLVASLGPW KNVPRKECWK	SAGDSPRDP	660		
PPRPQGHQSQPS	FPSSGPWETA	VCKFYRQGRW REVRVFASWA PPCIPIHSQWL	WFPSSSEPQFL	720		
WELELSLETG	NRLPPCPFCP	RLAMASCPLR MVPWGRPILC	GFLHSAHPSI NCP	773		

SEQ ID NO: 278	moltype = AA length = 98
FEATURE	Location/Qualifiers
source	1..98
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 278			
MFLRGRPVPM MIPDELAPTY	SLDTRSELPS CRLKLEWVY	YRGRDCRANL YLLPTGEIVY	60
UVASVAVLYS	VEEQRQRHYL	GHNDIHKCLA IHPDMVTI	98

SEQ ID NO: 279	moltype = AA length = 111
FEATURE	Location/Qualifiers
source	1..111
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 279				
MFLRGRPVPM MIPDELAPTY	SLDTRSELPS CRLKLEWVY	YRGRDCRANL YLLPTGEIVY	60	
UVASVAVLYS	VEEQRQRHYL	GHNDIHKCLA IHPDMVTIAT	GQVAGTTKEG K	111

SEQ ID NO: 280	moltype = AA length = 51
FEATURE	Location/Qualifiers
source	1..51
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 280				
WTLEGGSLSK RQGLFEKHEK	P KPKYVLCVTF	LEGGDVVTGD	GGNLYVWGKG P	51

SEQ ID NO: 281	moltype = AA length = 148
FEATURE	Location/Qualifiers
source	1..148
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 281				
MFLRGRPVPM MIPDELAPTY	SLDTRSELPS CRLKLEWVY	YRGRDCRANL YLLPTGEIVY	60	
UVASVAVLYS	VEEQRQRHYL	GHNDIHKCLA IHPDMVTIAT	GQVAGTTKEG KPLPPHVRIW	120
DSVSLSTLHV	LGLGVFDRAV	CCVGF	SKS	148

SEQ ID NO: 282	moltype = AA length = 91
FEATURE	Location/Qualifiers
source	1..91
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 282				
PLPHVRIWD SVSLSTLHV	GLGVFDRAVC	CVGFSKSNGG	NLLCAVDESN DHMLSVWDWA	60
KETKVVVDVKA	GVQWHNLGSL	QPPPPRFQRF	S	91

SEQ ID NO: 283	moltype = AA length = 133
FEATURE	Location/Qualifiers
source	1..133
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 283	
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MFLRGRPVPM MIPDELAPTY SLDTRSELPs CRLKLEWVYg YRGRDCRANL YLLPTGEIVY	60
FVASVAVLYs VEEQRQRHyl GHNDDIKCLA IHPDMDVTIAT QGVAGTTKEG KPLPPHVRIW	120
DSVSLSTLHV LGL	133
 SEQ ID NO: 284 moltype = AA length = 252	
FEATURE Location/Qualifiers	
source 1..252	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 284	
MKMKLfqTIC RQLRSSKFsv EsaALVAFST SSySCGRKKK VNPyEEVDQe KYSNLVQSVL	60
SSRGVAQTPG SVEEDALLCG PVSKHKLpNQ GEDRRVPQNW FPIFNPERSD KPNASDPSPV	120
LKIPLQRNVI PSVTRVLQQT MTKQQVFLL E RWKQRMILEL GEDGFKEYTS SSMWLNCGL	180
QRWITCPPTF HGCRALFPVL DQVASSTRRI YGKEKEPEYS ETRIFRIGSK LLFGNIQHLL	240
TVWEHILLFT PV	252
 SEQ ID NO: 285 moltype = AA length = 264	
FEATURE Location/Qualifiers	
source 1..264	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 285	
MKMKLfqTIC RQLRSSKFsv EsaALVAFST SSySCGRKKK VNPyEEVDQe KYSNLVQSVL	60
SSRGVAQTPG SVEEDALLCG PVSKHKLpNQ DVELQGKRHF EALESILSPQ ETLKERDENL	120
LKSGYIESVQ HILKDVSGrVr ALESAVQHET LNYIGLLDCV AEYQGKLCVI DWKTSEKPKP	180
FIQSTFDNPL QVVAYMGAMN HDTNYSFQVQ CGLIVVAYKD GSPAHPHFMD AELCSQYWTk	240
WLLRLEEYTe KKKNQNIQKP EYSE	264
 SEQ ID NO: 286 moltype = AA length = 344	
FEATURE Location/Qualifiers	
source 1..344	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 286	
MKMKLfqTIC RQLRSSKFsv EsaALVAFST SSySCGRKKK VNPyEEVDQe KYSNLVQSVL	60
SSRGVAQTPG SVEEDALLCG PVSKHKLpNQ GEDRRVPQNW FPIFNPERSD KPNASDPSPV	120
LKIPLQRNVI PSVTRVLQQT MTKQQVFLL E RWKQRMILEL GEDGFKEYTS NVFLQGKRHF	180
EALESILSPQ ETLKERDENL LKSGYIESVQ HILKDVSGrVr ALESAVQHET LNYIGLLDCV	240
AEYQGKLCVI DWKTSEKPKP FIQSTFDNPL QVVAYMGAMN HDTNYSFQVQ CGLIVVAYKD	300
GSPAHPHFMD AELCSQYWTk WLLRLEEYTe KKKNQNIQKP EYSE	344
 SEQ ID NO: 287 moltype = AA length = 355	
FEATURE Location/Qualifiers	
source 1..355	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 287	
MGPGRCLLTA LLLLALAPPp EASQYCGRL E YWNPDNKCCS SCLQRFGPPP CPDYEFRENC	60
GLNDHGDFVT PPFRKCSSGQ CNPDGAELCS PCGGGAVPT PAAGGGRTPW RCRERPVAK	120
GHCPLTPGNP GAPSSQERSS PASSIAWRTP EPVPQQAWPn FLPLVVLVLL LTLaVIAILL	180
FILLWHLCWP KEKADPYPYP GLVCGVPNT TPSSSHLSSP GALETGDTWK EASLPLLRS	240
ELSSLASLWP SRLLDELEVl EELIVLLDPE PGPGGGMahG TTRHLAARYG LPAAWSTFAY	300
SLRPSRSPLR ALIEMVARE PSASLGQLGT HLAQLGRADA LRVLSKLGSs GVCWA	355
 SEQ ID NO: 288 moltype = AA length = 132	
FEATURE Location/Qualifiers	
source 1..132	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 288	
MGPGRCLLTA LLLLALAPPp EASQYCGRL E YWNPDNKCCS SCLQRFGPPP CPDYEFRENC	60
GLNDHGDFVT PPFRKCSSGQ CNPDGAELCS PCGGGAVPT PAAGGGRTPW RCRAEGPCQG	120
ALPPHTWKPR RP	132
 SEQ ID NO: 289 moltype = AA length = 187	
FEATURE Location/Qualifiers	
source 1..187	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 289	
MGPGRCLLTA LLLLALAPPp EASQYCGRL E YWNPDNKCCS SCLQRFGPPP CGALETGDT	60
WKEASLLPLL SRELSSLASQ PLsRLLDELE VLEELIVLLD PEPGPGGGMA HGTTTRHLAAR	120
YGLPAAWSTF AYSLRPSRSP LRALIEMVVA REPSASLGQL GTHLAQLGRA DALRVLSKL	180
SSGVCWA	187
 SEQ ID NO: 290 moltype = AA length = 138	

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FEATURE	Location/Qualifiers
source	1..138
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 290	
MGPGRCLLTA LLLLALAPPP	EASQYCGRL EWNPDNKCCS SCLQRFGPPP CPDYEFRENC 60
GLNDHGFVT PPFRKCSSQG	CNPDGELCS PCGGGAVPTP PAAGGGRTPW RCRERPVPAK 120
GHCPLTPGNP GAPSSQER	
	138
SEQ ID NO: 291	moltype = AA length = 74
FEATURE	Location/Qualifiers
source	1..74
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 291	
XNGLNDHGD FVTPPFRKCS	SGQCNPDGAE LCSPCGGGAV TPTPAAGGR TPWRCREAPW 60
RQGTHGRRPH YFHS	
	74
SEQ ID NO: 292	moltype = AA length = 355
FEATURE	Location/Qualifiers
source	1..355
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 292	
MGPGRCLLTA LLLLALAPPP	EASQYCGRL EWNPDNKCCS SCLQRFGPPP CPDYEFRENC 60
GLNDHGFVT PPFRKCSSQG	CNPDGELCS PCGGGAVPTP PAAGGGRTPW RCRERPVPAK 120
GHCPLTPGNP GAPSSQERSS	CAIICAWRTP EPVPOQAWPN FLPLVVLVLL LTAVIAILL 180
FILLWHLCWP KEKADPYYP	GLVCGVPTNTPSSSHLSSP GALETGDTWK EASLLPLLSR 240
ELSSLASQPL SRLLDELEVL	EELIVLLDPE PGPGGGMAHG TTRHLAARYG LPAAWSTFAY 300
SLRPSRSPLR ALIEMVARE	PSASLGQLGT HLAQLGRADA LRVLSKLGSS GVCWA 355
SEQ ID NO: 293	moltype = AA length = 60
FEATURE	Location/Qualifiers
source	1..60
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 293	
XGRLEYWNPD NKCCSSCLQR	FGPPPCPGEN PRPSLAWAEL AEAGPCQGAL PPHTWKPRRP 60
SEQ ID NO: 294	moltype = AA length = 167
FEATURE	Location/Qualifiers
source	1..167
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 294	
MGPGRCLLTA LLLLALAPPP	EASQYCGRL EWNPDNKCCS SCLQRFGPPP CPELSSLASQ 60
PLSRLLDELE VLEELIVLDD	PEPGPGGMA HGTRHLAAR YGLPAAWSTF AYSLRPSRSP 120
LRLALIEMVVA REPSASLGQL	GTHLAQLGRA DALRVLSKLQ SSGVCWA
	167
SEQ ID NO: 295	moltype = AA length = 1742
FEATURE	Location/Qualifiers
source	1..1742
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 295	
MAVAELYTQY NRVWIPDPEE	VWKSAEIAKD YRGDKVLR LLEDGTELDY SVNPESLPLL 60
RNPDLIVGEN DLTALSYLHE	PAVLHNLIRI FABESKLIITY SGIIILVAMNP YKQLPIYGDA 120
IIHAYSGQNM GDMDPHIFAV	AEEAYKQMAR NNRNQSIIVS GESGAGKTVS ARYAMRYFAT 180
VSKSGSNAHV EDKVVLASNPI	TEAVGNAKTT RNDNSSRPKY YTEISFDEQN QIIGANMSTY 240
LLEKSRVVFQ YOLCASAQQS	EFKHLKLGSA EEFNYTRMGG NTVIEGVNDR 300
AEMVETOKTF TLLGFKEFDQ	MDVFKILAI LHLGNVQITA VGNERSSVE DDSHLKVFCE 360
LLGLESGRVA QWLCSRKIVT	SSETVVKPMT RPQAVNARDL LAKKIYAHF DFIVERINQA 420
LQFSGKQHTF IGVLIDIYGF	TDFDVSFEOF CINYANEKLO QOFNMHVFKL EQEEYMKEDI 480
PWTLDIDFYDN QPVIDLIEAK	MGILELLDDE CLLPHGTDEN WLQKLYNNFV NRNPFLFEKPR 540
MSNTTSFVIQH YDMVVEILRA	GDLEKNRDTV KFHLCANFF QENPTPPSPF 600
GSMITVKSQK QVIKPNSKHF	RTTVGSKFRS SLYLLMETLN ATPHVVRCI KPNDEKLKPFE 660
FDSKRIVQQL RACGVLETIR	ISAQSYPSRW TYIEFYSRYG ILMTKQELSF SDKKEVCKVV 720
LHRLIQDSNQ YQFGKTKIFF	RAGQVAYLEK LRLDKLRLQSC VMVQKHMRGW LQRKKFLRER 780
RAALIIQOYF RGQQTVRKA	TAVALKEAWA AIIIQKHCRG YLVRSLYQLI RMATITMQAY 840
SRGFLARRRY RKMLEEHKAV	ILOQKYARAWL ARRRFQSIRR FVULNIQLTYR VQRLQKLED 900
QNKENHGLVE KLTSALALRA	GDVEKIQKLE AELEKAATHR RNYEEKGKRY RDAVEEKLAK 960
LQKHINSELET QKEQIQLKLQ	EKTEELKEKM DNLTQQLFDV VQKEERQML LEKSFEKLTQ 1020
DYEKQIQLSK EEIKALKDEK	MQLQHVLVEGE HVTSDFGLKAE VARLSKQVKT ISEFEKEIEL 1080
LOAQKIDVEK HVQSQKREMR	EKMSEITKQL LESYDIEDVR SRLSVEDLEH LNEDGELWFA 1140
YEGLKKATRV LESHFQSQKD	CYEKEIEALN FKVVHLSQEI NHLQKLFREE NDINESIRHE 1200
VTRLTSNMM IPDFKQOISE	LEKQKQDLEI RLNEQAEKMK GKLEELSNQL HRSQEEEGTQ 1260

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RKALEAQNEI	HTKEKEKLID	KIQEMQEASD	HLKKQFETES	EVKCNFRQEA	SRLTLENRDL	1320
EELDLMKDRV	IKKLQDQVKT	LSKTIGKAND	VHSSGPKEY	LGMLQYKRED	EAKLJQNLLIL	1380
DLKPRGVVVN	MIPGLPAHIL	FMCVRYADSL	N DANMLKSJM	NSTINGIKQV	VKEHLEDFEM	1440
LSFWLSNTCH	FLNCLQYSG	EEEFMKHNSP	QQNKNCLNNF	DLSEYRQILS	DVAIRIYHQF	1500
IIIMEKNIQP	IIVPGMLEYE	SLQGISGLKP	TGFRKRSSSI	DDTDGYTMITS	VLQQLSYFYT	1560
TMCQNGLDPE	LVRQAVKQLF	FLIGAVTLNS	LFLRKDMCSC	RKGMQIRCNI	SYLEEWLSDK	1620
NLQNSLAKET	LEPLSQAAWL	LQVKTTDSD	AKEIYERCTS	LSAVQIIL	NSYTPIDDDE	1680
KRVTPSFVRK	VQALLNSRED	SSQLMLDTKY	LFQVTFPPPTP	SPHALEMHQI	PSSFKLGFLN	1740
RL						1742

SEQ ID NO: 296	moltype = AA	length = 612				
FEATURE	Location/Qualifiers					
source	1..612					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 296						
MAAAGRGPSS	WALFSPPLAG	LALLGVGPVP	ARALHNVTAE	LFGAEAWGTL	AAFGDLNSDK	60
QTDLFVLRER	NDLIVFLADQ	NAPYFKPKVK	VSFKNHSALI	TSVVPGDYDG	DSQMDVLLTY	120
LPKNYAKSEL	GAVIFWGQNQ	TLDPNNMNTIL	NRTFQDEPLI	MDFNGDLIPD	IFGIFTNESNQ	180
PQILLGGNLN	WHPALTTSE	MRIPHSHAFI	DLTEDFTADL	FLTTLNATT	TFQFEIWEWNL	240
DGNFSVSTIL	EKPQNMMVVG	QSAFADFDDG	GHMDHLLPGC	EDKNCQKSTI	YLVRSGMKQW	300
VPVLQDFSNK	CTLWGFVPFV	DEQQPTEIPI	PITLHIGDYN	MDGYPDALVI	LKNNTSGSNQQ	360
AFLLENVPCN	NASCEEARM	FKVYWELETDL	NQIKDAMVAT	FFDIYEDGIL	DIVVLSKGYT	420
KNDFAITHLK	NNFEDAYFV	KVIVLSGLC	NDCPRKITPF	GVNQPGPYIM	YTTVDANGYL	480
KNGSAGQLSQ	SAHLALQLPY	NVGLGLRSAN	FLDHLYVGIP	RPSGEKSIRK	QEWTAIIPNS	540
QLIVIPYPHN	VPRSWSAKLY	LTPSNIVLLT	AIALIGVCVF	ILAIIGILHW	QEKKADDREK	600
RQEAHRFHFD	AM					612

SEQ ID NO: 297	moltype = AA	length = 464				
FEATURE	Location/Qualifiers					
source	1..464					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 297						
MDVLLTYLPK	NYAKSELGAV	IFWGQNQTL	PNNMTILNRT	FQDEPLIMDF	NGDLIPDIFG	60
ITNESNQPQI	LLGGNLSWHP	ALTTTISKMRI	PHSHAFIDL	EDFTADLFLT	TLNATTSTFQ	120
FEIWEENLDG	FSVSTILEKP	QNMMVGQSA	FADFDGDGHM	DHLLPGCEDK	NCQKSTIYLV	180
RSGMKQWV	LQDFESNKGT	WGFVPFVDEQ	QPTEIPIPIT	LHIGDYNMDG	YPDALVILKN	240
TSGSNQQAFL	LENVPCNNAS	CEEAMPKV	YWELETDLNQI	KDAMVATFFD	IYEDGILDIV	300
VLSKGYTKND	FAIHTLKNNF	EADAYFVVI	VLSGLCSNDC	PRKITPFGVN	QPGPYIMYTT	360
VDANGYLKNG	SAGQLSQSAH	LALQLPYNVL	GLGRSANFLD	HLYVGIPRPS	GEKSIRKQEW	420
TAIIPNSQLI	VIPYPHNVPR	SSHRCLCFH	GNNWHTFLAG	KESR		464

SEQ ID NO: 298	moltype = AA	length = 74				
FEATURE	Location/Qualifiers					
source	1..74					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 298						
MDVLLTYLPK	NYAKSELGAV	IFWGQNQTL	PNNMTILNRT	FQDEPLIMDF	NGDLIPDIFG	60
ITNESNQPQI	LLGG					74

SEQ ID NO: 299	moltype = AA	length = 178				
FEATURE	Location/Qualifiers					
source	1..178					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 299						
VLSKGYTKND	FAIHTLKNNF	EADAYFVVI	VLSGLCSNDC	PRKITPFGVN	QPGPYIMYTT	60
VDANGYLKNG	SGRSANFLDH	LYVGIPRPSG	EKSIRKQEW	AIIPNSQLIV	IPYPHNVPRS	120
WSAKLYLTPS	NIVLTLAIAL	IGVCVFILEAI	IGILHWQEKK	ADDREKRQEA	HRFHFDAM	178

SEQ ID NO: 300	moltype = AA	length = 113				
FEATURE	Location/Qualifiers					
source	1..113					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 300						
XKPKVKVSFK	NHSALITSVV	PGDYDGDSQM	DVLLTYLPKN	YAKSELGAVI	FWGQNQTLDP	60
NNMTILNRTF	QDEPLIMDFN	GDLIPDIFGI	TNESNQPQIL	LGGHTTLNAP	HLF	113

SEQ ID NO: 301	moltype = AA	length = 431
FEATURE	Location/Qualifiers	
source	1..431	
	mol_type = protein	
	organism = Homo sapiens	

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SEQUENCE: 301
 MAEITNIRPS PDVSPVVAGL IGASVLVVCV SVTVFVWSCC HQQAEEKQKN PPYKFIHMLK 60
 GISIYYPETLS NKKKIIKVRR DKDGPGREGG RRNLLVDAAE AGLLSRDKDP RGPSSGSCID 120
 QLPIKMDYGE ELRSPITSLT PGESKTTSPS SPEEDVMLGS LTFSVDYNFP KKALVVTIQE 180
 AHGLPVMDDQ TQGSDPYIKM TILPDKRHRV KTRVLRKTLID PVFDETFTFY GIPYSQLQDL 240
 VLIHFLVLSFD RFSRDDVIGE VMVPLAGVDP STGKVQLTRD IIKRNIQKCI SRGELQVSL 300
 YQPVAQRMTV VVLKARHLPK MDITGLSGNP YVKVNYYGR KRIAKKKTHV KKCTLNPIFN 360
 ESIPIYDPTD LLPDISIEFL VIDFDRTTKN EVVGRRLILGA HSVTASGAEH WREVCESPRK 420
 PVAKWHLSE Y 431

SEQ ID NO: 302 moltype = AA length = 513
 FEATURE Location/Qualifiers
 source 1..513
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 302
 MSSKPEPKDV HQLNGTGPSA SPCCSDGPGR EPLAGTSEFL GPDGAGVEVV IESRANAKGV 60
 REEDALLENG SQSNESDDVS TDRGPAPPSP LKBTSFSIGL QVLFPFLLAG FGTVAAGMVL 120
 DIVQHWEVFQ KVTEVFLVPL ALLGLKGNNL MTLASRLSTAS ANIGHMDTPK ELWRMITGNM 180
 ALIQVQATVV CGFLASIAAVV FGWIPEGHFS IPHAFRLSTAS SVATAFIASL VLGMIMIGVI 240
 IGSRKIGINP DNVATPIAS LGDLITLALL SGISWGGLYLE LNHWRYIYPL VCAFFVALLP 300
 VVWVLARRSP ATREVLYSGW EPVIIAMAIS SVGGLILDKT VSDPNFAGMA VFTPVINGVG 360
 GNLVAVQASR ISTFLHMNGM PGENSEQAPR RCPSPCCTTFV SPDVNSRSAR VLFLVVPGH 420
 LVPFLYTISCM QGGHTTLI FIIYFMTAA LQVLILLYIA DWMVHWMWGR GLDPDNFSIP 480
 YLTALGDLG TGLLALSFH LWLIGDRDTD VGD 513

SEQ ID NO: 303 moltype = AA length = 1226
 FEATURE Location/Qualifiers
 source 1..1226
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 303
 MDRERKTIN QQQEDEMEIY GYNLRSRWKLA IVSLGVICSG GFLLLLLYWM PEWRVKATCV 60
 RAAIKDCEVV LLRTTDEFKM WFCAKIRVLS LETYPVSSPK SMSNKLSNMG AVCLIENPTE 120
 ENRHRISKYS QTESQQIRYF THHSVKYFWN DTIHNFDFLK GLDEGVSCSTS IYEKHSAGLT 180
 KGMHAYRKLL YGVNEIAVKV PSVFKL LIKE VLNPFYIFQFL FSIVILWSTDE YYYYALAIIV 240
 MSIVSIVSSL YSIRKQYVML HDVMATHSTV RVSVCRVNEE IEEIFSTDVL PGDMVVIPLN 300
 GTIMPCDAVL INGTCIVNES MLTGESVPVT KTNLPNPSVD VKGIGDELYN PETHKRHTLF 360
 CGTTVIQTRF YTGEVLKAIV VRTGFSTSKG QLVRSLIYPP PTDFKLYRDA YLFLLCLVAV 420
 AGIGFIYII NSILNEVQVG VVIESLDII TITVPPALPA AMTAGIVYAQ RRLKKIGIFC 480
 ISPQRINICG QLNLVCFDKT GTLTEDGLDL WG1QRVENAR FLSPEENVCN EMLVKSQFVA 540
 CMATCHSLTK IEGVLSGDPL DLKMFEAIGW ILEEATEEET ALHNRMIMPTV VRPPKQLP 600
 STPAGNQEME LFELPATYET GIVRQPFPS ALQRMSSVAR VLGDRKMDAY MKGAPEAIA 660
 LCKPETVQPV DQNVLEDFTK QGFRVIALAH RKLESKLTWH KVQNISRDAI ENNMDFMGLI 720
 IMQNKLQET PAVLEDLHK NIRTVMVTGD SMLTAVSVAR DCGMILPQDK VIIABALPPK 780
 DGKVAKINWH YADSLTQCASH PSAIDPPEAIP VKLVHDSLED LQMTRYHFAM NGKSFSVILE 840
 HQDQLVPKLM LHGTVPARMA PDQKTQLIEA LQNVDYFVGM CGDGANDCGA LKRAHGGISL 900
 SELEASVASP FTSKTPSISC VPNIIREGRA ALITSFVCVK PMALYSIIQY FSVTLLYSIL 960
 SNLGDFQFLF IDLAIIILVVV FTMSLNPWAK ELVAQRPPSG LISGALLFSV LSQIIICIGF 1020
 QSLGFFWVKQ QPWYEVWHPK SDACNTTGSG FWNSSHVDNE TELDEHNIQN YENTTVFFIS 1080
 SFQYLIVAI AFSKGKPFRQF CYKNYVVFVS VIFLYIFILF IMLYPVASVD QVLQIVCVPY 1140
 QWRVTMLIIV LVNAFVSITV EESVDRWGKC CLPWALGCRK KTPKAKYMYL AQELLVDPREW 1200
 PPKPQTTEA KALVKEENGSC QIITIT 1226

SEQ ID NO: 304 moltype = AA length = 162
 FEATURE Location/Qualifiers
 source 1..162
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 304
 XPPRQPCYKN YFFVFSVIFL YIFILFIMLY PVASVDQVLI IVCVPYQWRV TMLIIVLVNA 60
 FVSITVENFF LDMVLWKVVF NRDQKQGEYRF STTQPPQESV DRWGKCLPW ALGCRKTPK 120
 AKMYLAQEL LVDPEWPPKP QTTTEAKALV KENGSCQIIT IT 162

SEQ ID NO: 305 moltype = AA length = 1226
 FEATURE Location/Qualifiers
 source 1..1226
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 305
 MDRERKTIN QQQEDEMEIY GYNLRSRWKLA IVSLGVICSG GFLLLLLYWM PEWRVKATCV 60
 RAAIKDCEVV LLRTTDEFKM WFCAKIRVLS LETYPVSSPK SMSNKLSNMG AVCLIENPTE 120
 ENRHRISKYS QTESQQIRYF THHSVKYFWN DTIHNFDFLK GLDEGVSCSTS IYEKHSAGLT 180
 KGMHAYRKLL YGVNEIAVKV PSVFKL LIKE VLNPFYIFQFL FSIVILWSTDE YYYYALAIIV 240
 MSIVSIVSSL YSIRKQYVML HDVMATHSTV RVSVCRVNEE IEEIFSTDVL PGDMVVIPLN 300
 GTIMPCDAVL INGTCIVNES MLTGESVPVT KTNLPNPSVD VKGIGDELYN PETHKRHTLF 360

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CGTTVIQTRF YTGEVKAIV VRTGFSTSKG QLVRSLYPK PTDFKLYRDA YLFLLCLVAV	420
AGIGFIYTII NSILNEVQVG VIIIESTDII TITVPPALPA AMTAGIVYAQ RRLKKIGIFC	480
ISPQRINICG QLNLVCFDKT GTLTEGDLW WGIQRVENAR FLSPEENVCN EMLVKSQFVA	540
CMATCHSLTK IEGVLSGDPL DLKMFPEAIGW ILEEATEBET ALHNRMPTV VRPPQLLP	600
STPAGNQEME LFELPATYEI GIVRQFPFSS ALQRMSVVAR VLGDRKMDAY MKGAPEAIAG	660
LCKPETVPVD FQNVLLEDFTK QGFRVIALAH RKLESKLTH KVQNI SRDAI ENNMDFMGLI	720
IMQNKLKQET PAVLEDLHK NIRTVMVTGD SMLTAWSVAR DCGMILPQDK VIIAEALPPK	780
DGKVAKINWH YADSLTQCASH PSAIDPEAIP VKLVHDSLED LQMTRYHFAM NGKSFVILE	840
HFQDLPVKLM LHGTVFARMA PDQKTQLIEA LQNVDFVGM CGDGANDCGA LKRAHGGISL	900
SELEASVASP PTSKTPSIC VPNLIREGRA ALITSFCVFK FMALYSIIQF FSVTLLYSIL	960
SNLGDFQFLF DLAILLVVV FTMSLNPWK ELVAQRPPSG LISGALLFSV LSQIIICIGF	1020
QLSLGFFWVKQ QPWYEVWHPK SDACNTTGSG FWNSSHVDNE TELDEHNQN YENTTWFIS	1080
SFQYLIVIAIA FSKGKPFRQP CYKNYFFVFS VIFLYIFILF IMLYPVASVD QVLQIVCPY	1140
QWRVTMLIIV LVNAFVSITV EESVDRWGKC CLPWALGCRK KTPKAKYMYL AQELLVDPEW	1200
PPKPQTTEA KALVKENGSC QIITIT	1226
SEQ ID NO: 306 moltype = AA length = 47	
FEATURE Location/Qualifiers	
source 1..47	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 306 MDREERKTIN QGQEDEMEIY GYNLSRWKLA IVSLGVICSG GFLLLLL	47
SEQ ID NO: 307 moltype = AA length = 103	
FEATURE Location/Qualifiers	
source 1..103	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 307 MDREERKTIN QGQEDEMEIY GYNLSRWKLA IVSLGVICSG GFLLLLLYWM PEWRVKATCV	60
RAAIKDCEVV LLRTTDEFKM WFCAKIRVLS LETYPVSSPK SMS	103
SEQ ID NO: 308 moltype = AA length = 701	
FEATURE Location/Qualifiers	
source 1..701	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 308 ISEIEEIFST DLVPGDVMVI PLNGTIMPCD AVLINGTCIV NESMLTGESV PVTKTNLPNP	60
SVDVKGIGDE LYNPETHKRH TLFCGTTVIQ TRFYTGELVK AIVVRTGFST SKGQLVRSIL	120
YKPKTDKFY RDAYLFLCL VAVAGIGFIY TIINSILNEV QVGVIIIESL DIITITVPPA	180
LPAMTAGIV YAQRRLKKIG IFCPSQRIN ICQQLNLVCF DKTGTLTEDG LDLWGIQRVE	240
NARFLSPEEN VCNEMLVKSQ FVACMATCHS LTKIEGVLSG DPLDLKMFEA IGWILEEATE	300
EETALHNRM PTVVVRPKQL LPESTPAGNC EMBLFELPAT YEIGIVRQFP FSSALQRMSV	360
VARVLGDRKM DAYMKGAPEA IAGLCKPETV PVDFQNVLED FTKQGFRVIA LAHRKLESKL	420
TWHKVQNISR DAIENNMDFM GLIIMQNKLK QETPAVLEDL HKANIRTVMV TGDSMLTAVS	480
VARDCGMILP DQKVIIAEAL PPKDGKVAKI NWHYADSLTQ CSHPSAIDPE AIPVKLVHDS	540
LEDLQMTRYH FAMNGKSFV ILEHFQDLVP KLMLHGTVFA RMAPDQKSQL IEALQNVDF	600
VGMCGDGAN CGALKRAHGG ISLSELEASV ASPFTSKTPS ISCVPNLIRE GRAALITSFC	660
ELALFSIVTY SLHDHFIISIL ISNMLVLFSS DFHNCAFYSL V	701
SEQ ID NO: 309 moltype = AA length = 976	
FEATURE Location/Qualifiers	
source 1..976	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 309 MGENEDKEQA QAGQVFENFV QASTCKGTLQ AFNILTRHLD LDPLDHRNFV SKLKSKVTTW	60
KAKALWYKLD KRGSHKEYKR GKSCTNTKLD IVGGGPCLGR TAIELAYLGA KVVVVEKRDS	120
FSRNNVHLHW PFTIHDLRGL GAKFYGKPC AGSIDHHSIR QLQLILFKVA LMLGVEIHVN	180
VEFVKVLEPP EDQENQKIGW RAEFLPTDHS LSEFEFDVII GADGRRNTLE GFRRKEFRGK	240
LAIAITANFI NRNSTAAEKV EEISGVAFIF NQKPFQDLKE ETGIDLLENIV YYKDCHTYFV	300
MTAKKQSLLD KGVIIDNYID TEMLLCAENV NQDNLLSYAR EAADFATNYQ LPSLDFAMNH	360
YQQPDVAMFD FTCMYASENA ALVRERQAHQ LLVALVGDSN LEPEFWPMGTG CARGFLAAFD	420
TAWMVKSWNQ GTPPLELLAE RESLYRLLPQ TTPEENINKNF EQYTLDPGTR YPNLNHSFCR	480
PHQVKHLYIT KELEYHPLER LGSVRRSVMN SRKESDIRPS KLLTWCQQQT EGYQHVNVTD	540
LTTSWRSGLA LCAIIHRFRP ELINPDSLNE DDAVENNGLA FDVAEREFGI PPVTTGKEMA	600
SAQEPDKLSM VMYLSKFYEL FRGTPLRPVD SWRKNYGENA DLSLAKSSIS NNYLNLTFFPR	660
KRTPRVDGQT GENDMNKRR KGFTNLDEPS NFSSRSILGSN QECGSSKEGG NQNKVKSMAN	720
QLLAKKEEST RNPSLMKQEK KSPSGFHFP SHLRTVHPQE SMRKSFLNL GGSDTCYFCK	780
KRVYVMERLS AEGHFFHREC FRCSICATTI RLAAYTFDCD EGKFYCKPHF IHCKTNQQR	840
KRRAELKQQR EEEATWQEQE APRRDPTES SCAVAAIGL EGSPPGISTS FFRKVLGWP	900
RILPRDLCNWM QGLLQAAGLH IRDNAYNYCY MYELLSLGIP LLWAFSEVLA AMYRESEGSL	960
ESICNWVLRC FPVKLR	976

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SEQ ID NO: 310	moltype = AA length = 633
FEATURE	Location/Qualifiers
source	1..633
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 310	
MAAAAAAAATT AACSSGSAGT DAAGASGLQQ PPPQPQPQPA AAAPAQPPE PPRKPRMDPR	60
RRAAALSLFLT NISLDGRLPP QDAEWGGEE GGAAKPGAGG ACGARTFSL LAAABRGCGI	120
ALAAPGTPAA GLAAGSGPCL PQPSSLPPPLI PGGHATVSGP GVARGFASPL GAGRASGEQW	180
QPPrPAPLAA CAQLQLLDGS GAAGQEELEEE DDAFISVQVP AAAFLGSGTP GSGSGSRGRGL	240
NSFTQGILPI ASRPTTSQNY CSLEQPCQGG STSAFEQLQR SRRRLISQRS SLETLEDIEE	300
NAPLRRCTRL SGSPRPKNFK KIHFIKNMRQ HDTRNGRIVL ISGRRSFCSTI FSVLVYRDST	360
QVGDLLKDDGQ RQSTGAVSLK EIIGLEGVEL GADGKTVSYT QFLLPTNAFG ARRNTIDSTS	420
SFSQFRNLSH RSLSIGRASG TGQSLDTGSD LGDFMDYDPN LLDDPQWPCG KHKRVLIFPS	480
YMTTVIDYVK PSDLKDMNE TFKEKFPHIK LTLSKIRSLK REMRKLAQED CGLEEPTVAM	540
AFVYFEKLAL KGKLNKQNRE LCAGACVLLA AKIGSDLKKH EVKHLIDKLE EKFRLNRREL	
IAFEFPVLVA LEFALHLPEH EVMPHYRRRLV QSS	633
SEQ ID NO: 311	moltype = AA length = 38
FEATURE	Location/Qualifiers
source	1..38
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 311	
MRQHDTRNGR IVLISGRRSF CSIFSVPYR DSTQVGQQ	38
SEQ ID NO: 312	moltype = AA length = 301
FEATURE	Location/Qualifiers
source	1..301
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 312	
MFSHLPLFDCV LLLLLLLLTR SSEVEYRAEV GQNAYLPCFY TPAAPGNLVP VCWGKGACPV	60
FECKGNVVLRT DERDVNYWTS RYWLNGDFRK GDVSLTIEVN TLADSGIYCC RIQIPGIMND	120
EKFNLKLVIK PAKVTPAPTR QRDFTAAFPF MLTTRGHGPB ETQTLGSLPD INLTQISTLA	180
NELRDSRLAN DLRDGATIR IGYIGAGIC AGLALALIFG ALIFKWYSHS KEKIQNLSLI	240
SLANLPPSGL ANAVAEGIRS EENIYTIE VYEVEEPNEY YCYVSSRQQP SQPLGCRFAM	300
P	301
SEQ ID NO: 313	moltype = AA length = 273
FEATURE	Location/Qualifiers
source	1..273
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 313	
MFSHLPLFDCV LLLLLLLLTR SSEVEYRAEV GQNAYLPCFY TPAAPGNLVP VCWGKGACPV	60
FECKGNVVLRT DERDVNYWTS RYWLNGDFRK GDVSLTIEVN TLADSGIYCC RIQIPGIMND	120
EKFNLKLVIK PAETQTLGSL PDINLTQIST LANELRDSRL ANDLRDSGAT IRIGIYIGAG	180
ICAGLALALI PGALIFKWYS HSKEKIQNLIS LISLANLPPS GLANAVAEGI RSEENIYTIE	240
ENVYEVEEPNN EYYCYVSSRQ QPSQPLGCRF AMP	273
SEQ ID NO: 314	moltype = AA length = 116
FEATURE	Location/Qualifiers
source	1..116
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 314	
MQLSFWSHCR CFCMFISIPLL MCRVRDQICD CPECTLQENP FFSQPGAPIL QCMLGCCFSRA	60
YPTPLRSKKT MLVQKNVTSE STCCVAKSYN RVTVMGGPKV ENHTACHCST CYYHKS	116
SEQ ID NO: 315	moltype = AA length = 147
FEATURE	Location/Qualifiers
source	1..147
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 315	
MDYYRKYAAI FLVTLSVFLH VLHSAPDVQE TGFFHVAQAA LKLLSSSNPP TKASQSARIT	60
DCPECTLQEN PFFSQPGAPI LQCMGCCFSR AYPTPLRSK TMLVQKNVTS ESTCCVAKSY	120
NRVTVMGGFK VENHTACHCS TCYYHKS	147
SEQ ID NO: 316	moltype = AA length = 62
FEATURE	Location/Qualifiers
source	1..62
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 316	

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MDYYRKYAAI	FLVTLCSVFLH	VLHSAPDVQD	CPECTLQENP	FFSQPGAPIL	QCMGCCFSRA	60
YP						62
SEQ ID NO: 317			moltype = AA	length = 116		
FEATURE			Location/Qualifiers			
source			1..116			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 317						
MDYYRKYAAI	FLVTLCSVFLH	VLHSAPDVQD	CPECTLQENP	FFSQPGAPIL	QCMGCCFSRA	60
YPTPLRSKKT	MLVQKNVTSE	STCCVAKSYN	RVTVMGGFKV	ENHTACHCST	CYYHKS	116
SEQ ID NO: 318			moltype = AA	length = 101		
FEATURE			Location/Qualifiers			
source			1..101			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 318						
MDYYRKYAAI	FLVTLCSVFLH	VLHSAPDVQD	CPECTLQENP	FFSQPGAPIL	QCMGCCFSRA	60
YPTPLRSKKT	MLVQKNVTSE	STCCVAKSYN	RVRTSRSPEA	F		101
SEQ ID NO: 319			moltype = AA	length = 316		
FEATURE			Location/Qualifiers			
source			1..316			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 319						
MTQGKLTSVAN	KAPGTEGQQQ	VHGEKKEAPA	VPSAPPSSYEE	ATSGEGMKAG	AFPPAPTA	60
LHPSWAYVDP	SSSSYDNGF	PTGDHELPFTT	FSWDDQKVRR	VFVRKVYTIL	LIQLLVTLAV	120
VALFTFCDPV	KDYVQANPGW	YWASYAVFFA	TYLTLACCSG	PRRHFPWNLI	LLTVETLSMA	180
YLTMGLSSYY	NTTSVLLCLG	ITALVCLS	VFSFQTKFDF	TSCQGVLFV	LMTLFFSGLI	240
LAILLPFQYV	PWLHAVYAA	GAGVPTLFLA	LDTQLLMGNR	RHSLSPPEYI	FGALNIYLDI	300
IYIFTFFLQL	E					316
SEQ ID NO: 320			moltype = AA	length = 111		
FEATURE			Location/Qualifiers			
source			1..111			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 320						
MKAGAFPPP	TAVPLHPSWA	YVDPSSSSY	DNGFPTGDHE	LFTTFSWDDQ	KVRRVFVRKV	60
YTILLIQLLV	TLAVVALFTF	CDPVKDYVQA	NPGWYWASYA	VFFATYLT	LA	111
SEQ ID NO: 321			moltype = AA	length = 208		
FEATURE			Location/Qualifiers			
source			1..208			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 321						
MTQGKLSVAN	KAPGTEGQQQ	VHGEKKEAPA	VPSAPPSSYEE	ATSGEGMKAG	AFPPAPTA	60
LHPSWAYVDP	SSSSYDNGF	PTGDHELPFTT	FSWDDQKVRR	VFVRKNPSHP	QVYTILLIQL	120
LVTLAVALF	TFCDPVDYV	QANPGWYWAS	YAVFFATYLT	LACCSGPRRH	FPWNLLILTV	180
FTLMSMAYLTG	MLSSSTSPPA	RACSSCFS				208
SEQ ID NO: 322			moltype = AA	length = 248		
FEATURE			Location/Qualifiers			
source			1..248			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 322						
MTQGKLSVAN	KAPGTEGQQQ	VHGEKKEAPA	VPSAPPSSYEE	ATSGEGMKAG	AFPPAPTA	60
LHPSWAYVDP	SSSSYDNGF	PTGDHELPFTT	FSWDDQKVRR	VFVRKVYTIL	LIQLLVTLAV	120
VALFTFCDPV	KDYVQANPGW	YWASYAVFFA	TYLTLACCSG	PRRHFPWNLI	LLTVETLSMA	180
YLTMGLSSYY	NTTSVLLCLG	ITALVCLS	VFSFQTKFDF	TSCQGVLFV	LMTLFFSGLI	240
LAILLPFQ						248
SEQ ID NO: 323			moltype = AA	length = 270		
FEATURE			Location/Qualifiers			
source			1..270			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 323						
MKAGAFPPP	TAVPLHPSWA	YVDPSSSSY	DNGFPTGDHE	LFTTFSWDDQ	KVRRVFVRKV	60
YTILLIQLLV	TLAVVALFTF	CDPVKDYVQA	NPGWYWASYA	VFFATYLT	LA	120
WNLILLTVFT	LSMAYLTGML	SSYYNTTSVL	LCLGITALVC	LSVTVF	SQFQT	180
LFVLLMTLFF	SGLLAILLLP	FQYVPWLHAV	YAALGAGVFT	LFLALDTQ	LLMGNRHSLSP	240

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EEYIFGALNI YLDIYIIFTF FLQLFGTNRE	270
 SEQ ID NO: 324	moltype = AA length = 266
FEATURE	Location/Qualifiers
source	1..266
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 324	
MVYTSHYKSP GRRPLKTHPT VTYWRVNEGS SSSYDNGFP T GDHELPFTFS WDDQKVRRVF 60	
VRKVYNTILLI QLLVTLAVVA LFTFCDPVKD YVQANPGWYW ASYAVFFATY LTLACCSGPR 120	
RHPPWNLLIL TVFTLSMAYL TGMLSSYYNT TSVLLCLGIT ALVCLSVTVF SFQTKFDFTS 180	
CQGVLFVLLM TLFFSGLILA ILLPFQYWPW LHAVYALGA GVFTLFLALD TQLLMGNRRH 240	
SLSPPEEYIFG ALNIYLDIIY IFTFFL 266	
 SEQ ID NO: 325	moltype = AA length = 145
FEATURE	Location/Qualifiers
source	1..145
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 325	
XYVQANPGWY WASYAVFFAT YLTACCSGP RRHFPWNLIL LTVFTLSMAY LTGMLSSYYN 60	
TTSVLLCLGI TALVCLSVTV FSFQTKFDFT SCQGVLFVLL MTLFFSGLIL AILLPFQYFL 120	
ALDTQLLMGN RRHSLSPPEY IFGAL 145	
 SEQ ID NO: 326	moltype = AA length = 695
FEATURE	Location/Qualifiers
source	1..695
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 326	
XEGGQGPRGL GTVPWLRLDP GSENHMPWE PAGEKPSCSH SQKAFHMEPA QKPCFTTDMV 60	
TWALLCISAE TVRGEAPSQP RGIPHRSPVS VDDLWLEKTQ RKKLQKQAHV ERRLHIGAVH 120	
KDGVCKWRKT IITSPESLNL PRRSHPLSQS APTGLNHMGW PEHTPGTAMP DGALDTAVCA 180	
DEVGSEEDLY DDLHSSHHY SHPGGGGEQL AINEELISDG5 VVCAEALWDH VTMDQELGF 240	
KAGDVIEVM ATNRREWWGR VADGEGWPPA SFVRLRVNQD EPADDAPLA GNSGAEDGGA 300	
EAQSSKDQMR TNVINEILST ERDYIKHLRD ICEGYVRQCR KRADMFSEQ LRTIFGNIED 360	
IYRCQKAFVK ALEQRFNREK PHLSELGACF LEHQADFQIY SEYCNHHPNA CVELSRLTKL 420	
SKVYVFFEAC RLLQKMDIS LDGFLLTPVQ KICKYPLQLA ELLKYTHPQH RDFKDVEAAL 480	
HAMKNUQLI NERKRRLENI DKIAQWQSSI EDWEGEDLLV RSSELIYSGE LTRVTQPQAK 540	
SQORMFFLFD HQLIYCKKDL RLRRDVLYYKG RLMDGLEV DLEDGKDRDL HVSIKNAFRL 600	
HRGATGDSHL LCTRKEEQKQ RWLKAFARER EQVQLDQETG FSITELQRKQ AMLNASKQQV 660	
TGPKGRRTA APPPRLPGPY PADIIPFSEP QSQAS 695	
 SEQ ID NO: 327	moltype = AA length = 573
FEATURE	Location/Qualifiers
source	1..573
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 327	
MTNSKGRSIT DKTSGGPSSG GGFVDWTLRL NTIQSDKFLN LLLSMVPVIY QKNQEDRHKK 60	
ANGIWQDGLS TAVQTSNRS EQHMEYHSFS EQSFHANNHG ASSSCSQYD DYANYNYCDG 120	
RETSETTAML QDEDISSDGD EDAIVEVTPL LPKESSGIMA LQILVPFLA GFGTWSAGMV 180	
LDIVQHWEVF RKVTEVFILV PALLGLKGNL EMTLASRLST AVNIGKMDSP IEKWNLIGN 240	
LALKQVQATV VGFLAAVAAI ILGWIPEGKY YLDHSILLCS SSVATAFIAS LLQGIIMVG 300	
IVGSKKTGIN PDNVATPIA SFGLDLITAI LAWISQGLYS CLETYYYISP LVGVFPLALT 360	
PIWIIIAAKH PATRTVLHSG WEPVITAMV SSIGGLILIDT TVSDPNLVGI VVYTPVINGI 420	
GGNLVAIQAS RISTYLHLHS IPGELPDEPK GCYYPFRFFF GPGVNNSKAQ VLLLLVIPH 480	
LIFLYTIHLM KSGHTSLII FIVVYLGAV LQVFTLLWIA DWMVHHFWRK GKDPDSFSIP 540	
YLATALDLLG TALLALSFHF LWLIGDRDGD VGD 573	
 SEQ ID NO: 328	moltype = AA length = 149
FEATURE	Location/Qualifiers
source	1..149
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 328	
XDDYANYNYC DGRETSETTA MLQDEDISSD GDEDAIVEVT PKLPKESSGI MALQILVPFL 60	
LAGFGTVSAG MVLDIVQVNI GKMDSPIEKW NLIIGNLALK QVQATVVGFL AAVAAIILGW 120	
IPEGKYYLDH SILLCSSVA TAFIASLLQ 149	
 SEQ ID NO: 329	moltype = AA length = 68
FEATURE	Location/Qualifiers
source	1..68
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 329	

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XLKALKGYIK HEARKGNENQ DSSTSKRRTL CGFYSHQPTT LARPVLWPCK SEYLGSEGVT QALCYLCSS	60 68
 SEQ ID NO: 330 moltype = AA length = 76 FEATURE Location/Qualifiers source 1..76 mol_type = protein organism = Homo sapiens	
SEQUENCE: 330 M1IPSLEELD SLKYSIDLQNL AKSGLRLANL RATKLLKALK GYIKHEARKG NENQFHSCCP GWSAMTRSRSL TATSTS	60 76
 SEQ ID NO: 331 moltype = AA length = 748 FEATURE Location/Qualifiers source 1..748 mol_type = protein organism = Homo sapiens	
SEQUENCE: 331 MVLLRVLILL LSWAAGMGGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRACK RAVSHEDQFL RLDFHAHGRH PNLRMKRDTS LFSDEFKVET SNKVLDYDTS HIYTGHIFYGE EGFSFHSVSI DGRFEGFIQT RGGTFYVEPA ERYIKDRTLP FHSVIYHEDD INYPHKYGPQ GGCADHSVFE RMRKYQMTGV EEVTOIPQEE HAANGPELLR KKRRTTSAEKN TCQLYIQTDH LFFKYVGTR AVIAQISSHV KAIDTIYQTT DFSGIRNISF MVKRIRINTT DEKDPTNPFRFPNIGVEKF LELNSEQNHD DYCLAYVFTD RDFDDGVGLL AWVGAPSGSS GGICEKSKEYL SDGKKKSLNT GIITVQNYGS HVPPKVSHIT FAHEVGHNFSPHDSGTECT PGESKNLGQK ENGNYIMYAR ATSGFDKLNNN KPSLCSIRNI SQVLEKKRNN CFVESGQPICNMGVEQGEE CDCGYSQCK DECFCFDANQP EGRKCKLKGPK QCSPSQGPC CTAQCAFKSK SEKCRDDSDC AREGICNGFT ALCPASDPKP NFTDCNRHTQ VCINGQACAGS ICEKYGLEEC TCASSDGKDD KELCHVCCK KMDPSTCAST GSVQNSRHFS GRTITLQPGS PCNDFRGYCD VFMRCRLVDA DGPLARLKKA IFSPELYENI AEWIVAHWWA VLLMGIALIM LMAGFIKICS VHTPSSNPKL PPPKPLPGTL KRRRPPQPIQ QPQRQRPRES YQMGHMRR	748
 SEQ ID NO: 332 moltype = AA length = 58 FEATURE Location/Qualifiers source 1..58 mol_type = protein organism = Homo sapiens	
SEQUENCE: 332 XEEGSFSHGS VIDGRFEGFI QTRGGTFYVE PAERYIKDRT LPFHSVIYHE DDISEGLN	58
 SEQ ID NO: 333 moltype = AA length = 71 FEATURE Location/Qualifiers source 1..71 mol_type = protein organism = Homo sapiens	
SEQUENCE: 333 MVLLRVLILL LSWAAGMGDR DFDDGVGLA WVGAPSGSSG GICEKSKEYL DVPTMGKLHS KEKPIKSSSP N	60 71
 SEQ ID NO: 334 moltype = AA length = 125 FEATURE Location/Qualifiers source 1..125 mol_type = protein organism = Homo sapiens	
SEQUENCE: 334 MVLLRVLILL LSWAAGMGGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRACK RAVSHEDQFL RLDFHAHGRH PNLRMKRDTS LFSDEFKVET SNKVLDYDTS HIYTGHIFYDY PHKYGPQGGC ADHSV	60 120 125
 SEQ ID NO: 335 moltype = AA length = 59 FEATURE Location/Qualifiers source 1..59 mol_type = protein organism = Homo sapiens	
SEQUENCE: 335 MVLLRVLILL LSWAAGMGAP ARWRIPKSSP PPRPAAQTRG KLCCLQLGSC IVLYPARRS	59
 SEQ ID NO: 336 moltype = AA length = 115 FEATURE Location/Qualifiers source 1..115 mol_type = protein organism = Homo sapiens	
SEQUENCE: 336 MVLLRVLILL LSWAAGMGGQ YGNPLNKYIR HYEGLSYNVD SLHQKHQRACK RAVSHEDQFL RLDFHAHGRD GVLPCCPGWS QTPGLKRSTC LSLPQCWDYR CEPSPMISVF DYPHK	60 115

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SEQ ID NO: 337	moltype = AA length = 148
FEATURE	Location/Qualifiers
source	1..148
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 337	
MVLLRVLILL LSWAAGMGDR DFDDGVGLA WVGAPSGSSG GICEKSKLYS DGKKKSLNTG	60
IITVQNYGSH VPPKVSHITF AHEVGHNFGS PHDSGTECTP GESKNLGQKE NGNYIMYARA	120
TSGDKLNNNK FSLCSIRNIS QVLEKKRN	148
SEQ ID NO: 338	moltype = AA length = 38
FEATURE	Location/Qualifiers
source	1..38
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 338	
MVLLRVLILL LSWAAGMGVP TMGKLHSKEK PIKSSSPN	38
SEQ ID NO: 339	moltype = AA length = 452
FEATURE	Location/Qualifiers
source	1..452
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 339	
MTLVSGWLLY GWIIAVQTKT KKTTLAKPNIR NVVVVDGVRT PFLLSGTSYK DLMPHDLARA	60
ALTGLLHRTS VPKEVVDYI FGTVIQEVKT SNVAREAALG AGFSDKTPAH TVTMACISAN	120
QAMTTGVLGI ASGQCDVIVA GGVELMSDVP IRHSRKRMKFL MLDLNKAKSM QRQLSLISKF	180
RFNFLAFLP AVSEFSTSET MGHSADRLAA AFAVSRLEQD EYALRSHSLA KKAQDEGLLS	240
DVVPFKVPGK DTVTKDNGIR PSSLEQMAKL KPAFIKPYGT VTAANNSFLT DGASAMLIIMA	300
EKCALAMGYK FKAYLRFDMY VSQDPKDQLL LGPTYATPKV LEKAGLTMDN IDAEFPHEAF	360
SGQILANFKA MDSDWFAENY MGRKTKVGLP PLEKFNNWGG SLSLGHPFGA TGCRLVMAAA	420
NRLRKEGGQY GLVAACAAGG QGHAMIVEAY PK	452
SEQ ID NO: 340	moltype = AA length = 260
FEATURE	Location/Qualifiers
source	1..260
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 340	
MARPHPWVLC VLGTLVGLSA TPAPKSCPER HYWAQGKLCC QCMEPGTFLV KDCDQHRKAA	60
QCDCPCIPGVs FSPDHHTRPH CESCRHCNSG LLVRNCTITA NAECACRNW QCRDKECTEC	120
DPLPNPSLTA RSSQALSPHP QPTHLPLYVS EMLARTAGHM QTLADFRQLP ARTLSTHWPP	180
QRSLCSSDFI RILVIFSGMF LVFTLAGALF LHQRKKYRSN KGESPVPEAE PCHYSCPREE	240
EGSTIPIQED YRKPEPACSP	260
SEQ ID NO: 341	moltype = AA length = 819
FEATURE	Location/Qualifiers
source	1..819
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 341	
MWGLVRLLLA WLGGWGCMGR LAAPARAWAG SREHPGPALL RTRRSWVWNQ FFVIEEYAGP	60
EPVLIGKLHS DVDRGEGRTK YLLTGEAGT VFVIDEATGN IHVTKSNDRE EKAQYVLLAQ	120
AVDRASNRL EPPSEFIICKV QDINDNPPIF PLGPYHATVP EMSNVGTSVI QVTAHDADDP	180
SYGNSAKLVY TVLDGLPFFS VDPQTGVVTE AIPNMMDRETQ EEFLVVIQAK DMGGHMGGLS	240
GSTTVTVTLS DVNDNPSPKFP QSYLQFSVVE TAGPGTLVGR LRAQDPDLDG NALMAYSILD	300
GEGSEAFSIS TDLQGRDGLL TVRKPLDFES QRYSYFRVEA TNTLIDPAYL RRGPFKDVAS	360
VRVAVQDAPE PPAFTQAAYH LTVPENKAPG TLVGQISAAD LDSPASPIRY SILPHSDPER	420
CFSIQPEEGT IHTAAPLDRE ARAWHNLNTV ATELGWSWGP ERGWVPLLVA EWSAPAAPPQ	480
RSPVGSAGVI PQDSSAQASR VQVAIQLDE NDNPQQLAEP YDTFVCDSSA PGQLIQVIRA	540
LDRDEVGNSS HVSFQGPLR DANFTVQDNR DGSASLLPS RPAPPRHAPY LVPVIELWDWG	600
QPALSSTATV TVSVRCQPD GSVASCWPEA HLSAAGLSTG ALLAIITCVG ALLALVVLFV	660
ALRRQKQEAL MVLEEEVDRE NIITYDDEGG GEEDTEAPDI TALQNPDGAA PPAPGPARR	720
DVLPRARVSR QPRPPGADV AQLLALRLRE ADEDPGVPPY DSVQVYGYEG RGSSCGSLSS	780
LGSGSEAGGA PGPAEPLDDW GPLFRTLAEL YGAKEPPAP	819
SEQ ID NO: 342	moltype = AA length = 819
FEATURE	Location/Qualifiers
source	1..819
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 342	
MWGLVRLLLA WLGGWGCMGR LAAPARAWAG SREHPGPALL RTRRSWVWNQ FFVIEEYAGP	60
EPVLIGKLHS DVDRGEGRTK YLLTGEAGT VFVIDEATGN IHVTKSNDRE EKAQYVLLAQ	120
AVDRASNRL EPPSEFIICKV QDINDNPPIF PLGPYHATVP EMSNVGTSVI QVTAHDADDP	180
SYGNSAKLVY TVLDGLPFFS VDPQTGVVTE AIPNMMDRETQ EEFLVVIQAK DMGGHMGGLS	240

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GSTTVTVTLS	DVNDNPKFP	QSLYQFSVVE	TAGPGTLVGR	LRAQDPDLGD	NALMAYSILD	300
GEGSEAFSIS	TDLQGRDGLL	TVRKPLDFES	QRYSYSFRVEA	TNTLIDPAYL	RRGPFKDVAS	360
VRVAVQDAPE	PPAFTQAAYH	LTVPENKAPG	TLVGQISAAD	LDSPASPIRY	SILPHSDPER	420
CFSIQPEEGT	IHTAAPLDRE	ARAWHNLTVL	ATELGWSWGP	ERGWVPLLVA	EWSAPAAPPQ	480
RSPVGSAVGI	PQDSSAQASR	VQVAIQLDE	NDNAPQLAEP	YDTFVCDCAA	PQQLIQVIRA	540
LDRDEVGNSS	HVSFGQPLGP	DANPTVQDNR	DGSASLLLP	RPAPPKRHAPY	LVPIELWDWG	600
QPALSSTATV	TVSVCRQPD	GSVASCWPEA	HLSAAGLSTG	ALLAIITCVG	ALLALVVLFV	660
ALLRRKQEAL	MVLEEDDVRE	NIITYDDDEGG	GEEDTEAEPDI	TALQNPDGAA	PPAPGPARR	720
DVLPRARVR	QPRPPGPADV	AQLLALRLRE	ADEDPGVPPY	DSVQVYGYEG	RGSSCGSLSS	780
LGSGSEAGGA	PGPAEPLDDW	GPLFRTLAE	YGAKEPPAP			819

SEQ ID NO: 343	moltype = AA	length = 781				
FEATURE	Location/Qualifiers					
source	1..781					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 343						
MWGLVRLLLA	WLGGWGCMBR	LAAPARAWAG	SREHPGPALL	RTRRSWWWNQ	FFVIEEYAGP	60
EPVLIGKLHS	DVDRGEGRTK	YLLTGEAGT	VVFVIDEATGN	IHVTKSLDRE	EKAQYVLLAQ	120
AVDRASNRPL	EPPSEFIKV	QDINDNPPIF	PLGPYHATVP	EMSNVGTSVI	QVTAHDADDP	180
SYGNSAKLVY	TVLDGLPFFS	VDPQTGVVRT	AIPNMDRETQ	EEFLVVIQAK	DMGGHMGGGLS	240
GSTTVTVTLS	DVNDNPKFP	QSLYQFSVVE	TAGPGTLVGR	LRAQDPDLGD	NALMAYSILD	300
GEGSEAFSIS	TDLQGRDGLL	TVRKPLDFES	QRYSYSFRVEA	TNTLIDPAYL	RRGPFKDVAS	360
VRVAVQDAPE	PPAFTQAAYH	LTVPENKAPG	TLVGQISAAD	LDSPASPIRY	SILPHSDPER	420
CFSIQPEEGT	IHTAAPLDRE	ARAWHNLTVL	ATELDSSAQ	SRVQVIAQTL	DENDNAPQLA	480
EYDVTFCDS	AAPGQLIQVI	RALDRDEVGN	SSHVSFQGPL	GPDANFTVQD	NRDGSAALL	540
PSRPAPPVRA	PYLVPIELWD	WGQPALSSTA	TVTVSVCRQ	PDGSVASCWP	EAHLSAAGLS	600
TGALLAIITC	VGALLALVVL	FVALRRQKQE	ALMVLEEDDV	RENIITYDDE	GGGEEDTEAF	660
DITALQNPDG	AAPPAPGPPA	RRDVLPRARV	SQPRPPGPA	DVAQLLALRL	READEDPGVP	720
PYDSVQVYGY	EGRGSSCGSL	SSLGSGSEAG	GAPGPAEPLD	DWGPLFRTLA	ELYAKEPPA	780
P						781

SEQ ID NO: 344	moltype = AA	length = 781				
FEATURE	Location/Qualifiers					
source	1..781					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 344						
MWGLVRLLLA	WLGGWGCMBR	LAAPARAWAG	SREHPGPALL	RTRRSWWWNQ	FFVIEEYAGP	60
EPVLIGKLHS	DVDRGEGRTK	YLLTGEAGT	VVFVIDEATGN	IHVTKSLDRE	EKAQYVLLAQ	120
AVDRASNRPL	EPPSEFIKV	QDINDNPPIF	PLGPYHATVP	EMSNVGTSVI	QVTAHDADDP	180
SYGNSAKLVY	TVLDGLPFFS	VDPQTGVVRT	AIPNMDRETQ	EEFLVVIQAK	DMGGHMGGGLS	240
GSTTVTVTLS	DVNDNPKFP	QSLYQFSVVE	TAGPGTLVGR	LRAQDPDLGD	NALMAYSILD	300
GEGSEAFSIS	TDLQGRDGLL	TVRKPLDFES	QRYSYSFRVEA	TNTLIDPAYL	RRGPFKDVAS	360
VRVAVQDAPE	PPAFTQAAYH	LTVPENKAPG	TLVGQISAAD	LDSPASPIRY	SILPHSDPER	420
CFSIQPEEGT	IHTAAPLDRE	ARAWHNLTVL	ATELDSSAQ	SRVQVIAQTL	DENDNAPQLA	480
EYDVTFCDS	AAPGQLIQVI	RALDRDEVGN	SSHVSFQGPL	GPDANFTVQD	NRDGSAALL	540
PSRPAPPVRA	PYLVPIELWD	WGQPALSSTA	TVTVSVCRQ	PDGSVASCWP	EAHLSAAGLS	600
TGALLAIITC	VGALLALVVL	FVALRRQKQE	ALMVLEEDDV	RENIITYDDE	GGGEEDTEAF	660
DITALQNPDG	AAPPAPGPPA	RRDVLPRARV	SQPRPPGPA	DVAQLLALRL	READEDPGVP	720
PYDSVQVYGY	EGRGSSCGSL	SSLGSGSEAG	GAPGPAEPLD	DWGPLFRTLA	ELYAKEPPA	780
P						781

SEQ ID NO: 345	moltype = AA	length = 314				
FEATURE	Location/Qualifiers					
source	1..314					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 345						
MWGLVRLLLA	WLGGWGCMBR	LAAPARAWAG	SREHPGPALL	RTRRSWWWNQ	FFVIEEYAGP	60
EPVLIGKLHS	DVDRGEGRTK	YLLTGEAGT	VVFVIDEATGN	IHVTKSLDRE	EKAQYVLLAQ	120
AVDRASNRPL	EPPSEFIKKI	ITCVGALLAL	VVLFVALRQQ	KQEALMVLEE	EDVRENITY	180
DDEGGGEEDT	EAFDITALQN	PDGAAPPAG	PPARRDVLP	ARVSROPRPP	GPADVAQLLA	240
LRLREADEDP	GVPPYDSVQV	YGYEGRGSSC	GSLSSLGSGS	EAGGAPGPAE	PLDDWGPLFR	300
TLAELYAKE	PPAP					314

SEQ ID NO: 346	moltype = AA	length = 45				
FEATURE	Location/Qualifiers					
source	1..45					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 346						
MFRAAAPPQQL	RRARRGFPM	PRLVSNSCPQ	VIHLPRPPKV	LELQA		45
SEQ ID NO: 347	moltype = AA	length = 45				
FEATURE	Location/Qualifiers					

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source          1..45
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 347
MFRAAAPPQL RRARRGFPMI PRLVSNSCPQ VIHLPRPPKV LELQA        45

SEQ ID NO: 348      moltype = AA  length = 46
FEATURE
source          1..46
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 348
MNEAKVKETL RRCGASGDEC GRLQYALTCL RKVTGLGGEH KEDSSW        46

SEQ ID NO: 349      moltype = AA  length = 248
FEATURE
source          1..248
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 349
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EGWDSPICTE GVVSVSWGEn TVMSCNISNA 60
FSHVNIKLRA HGQESAIFNE VAPGYFSRDG WQLQVQGGVA QLVKGARDS HAGLYMWHLV 120
GHQRNNRQVT LEVSGAEQPS APDTGFWPVP AVVTAVFILL VALVMFAWYR CRCSQQRREK 180
KFFLLEPQMK VAALRAGAQQ GLSRASAAELW TPDSEPTPRP LalVFKPSPL GALELLSPQP 240
LFPYAADP          248

SEQ ID NO: 350      moltype = AA  length = 149
FEATURE
source          1..149
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 350
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EGWDSPICTE GVVSVSWGEn TVMSCNISNA 60
FSHVNIKLRA HGQESAIFNE VAPGYFSRDG WQLQVQGGVA QLVKGARDS HAGLYMWHLV 120
GHQRNNRQVT LEVSGAAVPS NAGRSSSS 149

SEQ ID NO: 351      moltype = AA  length = 178
FEATURE
source          1..178
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 351
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EGWDSPICTE GVVSVSWGEn TVMSCNISNA 60
FSHVNIKLRA HGQESAIFNE VAPGYFSRDG WQLQVQGGVA QLVKGARDS HAGLYMWHLV 120
GHQRNNRQVT LEVSGAEQPS APDTGFWPVP AVVTAVFILL VALVMFAWYR CRCSQQRREK 178

SEQ ID NO: 352      moltype = AA  length = 43
FEATURE
source          1..43
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 352
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EAACPRAGER HLQ          43

SEQ ID NO: 353      moltype = AA  length = 44
FEATURE
source          1..44
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 353
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EGWDSPICTE GVVS          44

SEQ ID NO: 354      moltype = AA  length = 85
FEATURE
source          1..85
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 354
MQTCPLAFPG HVSQALGTLL FLAASLSAQN EGWDSPICTE GVVSVSWGEn TVMSCNISNA 60
FSHVNIKLRA HGQESAIFNE VAPGY          85

SEQ ID NO: 355      moltype = AA  length = 170
FEATURE
source          1..170
               mol_type = protein
               organism = Homo sapiens

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SEQUENCE: 355
 MQTCPLAFTP HVSQALGTLL FLAASLSAQN EGWDSPICTE GVSVSWGEN TVMSCNISNA 60
 FSHVNIKLR A HQQESAFNE VAPGYFSRDG WQLQVQGGVA QLVIKGARDS HAGLYMWHLV 120
 GHQRNNRQVT LEVSEPRGLK DRASAQLLG P GTSRGAEPOS APDTGFWPV 170

SEQ ID NO: 356 moltype = AA length = 147
 FEATURE Location/Qualifiers
 source 1..147
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 356
 MQTCPLAFTP HVSQALGTLL FLAASLSAQN EGWDSPICTE GVSVSWGEN TVMSCNISNA 60
 FSHVNIKLR A HQQESAFNE VAPGYFSRDG WQLQVQGGVA QLVIKGARDS HAGLYMWHLV 120
 GHQRNNRQVT LEVSEPRGLK DRASAQLLG P 147

SEQ ID NO: 357 moltype = AA length = 165
 FEATURE Location/Qualifiers
 source 1..165
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 357
 MDAPRRDMEL LSNSLAAyah IRANPESFGL YFVLGVCPGL LLTLCLLVIS ISWAPRPRPR 60
 GPAQRDRDPRS STLEPEDDE DEEDTVTRLG PDDTLPGPTEL SAEPDGPLNV NVFTSAEEL 120
 RAQRLEERER ILREIWRGQ PDLLGTGTLG PSPTATGTLG RMHYY 165

SEQ ID NO: 358 moltype = AA length = 639
 FEATURE Location/Qualifiers
 source 1..639
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 358
 MNLEKLSKPE LLTFLSILEG ELEARDLVIE ALKAQHRDTF IEERYGKYNI SDPLMALQRD 60
 FETLKEKNNDG EKQPVCTNPL SILKVVMKQC KNMQERMLSQ LAAAESRHK VILDLEERQ 120
 RHAQDTAEGD DVTYMLEKER ERLTQQLEFE KSQVKKFKE QKKLSSQLEE ERSRKQLSS 180
 MLVLECKKAT NKAEEEGQKA GELSLKLEKE KSRVSKLEEE LAAERKRGLQ TEAQVEKQLS 240
 EFDIEREQLR AKLNREENRT KTLKEEMESL KKIVKDLEAS HOHSSPNEQL KKPVTVSKGT 300
 ATEPLMLMSV FCQTESFPAA RTHGSNIAKM TNTGLPGPAT PAYSYAKTNG HCDPEIQTTR 360
 ELTAGNNVEN QVPPREKSVLA LAQEKPVENG GCPVGIETPV PMPSPLSSSG SSLSPSSTAS 420
 SSSLTSSPCSS PVLTKRLLGS SASSPGYQSS YQVGINQRFH AARHKFQSQA DQDQQASGLQ 480
 SPPSRDLSPPT LIDNSAAKQL ARNTVQVL RFTSQQQPIK PVSPNSSPFG TDYRNLANTA 540
 NPGDGTSHSP TPGKVSSPLS PLSPGIKSPT I PRAERGNPP PIPPKKPGLT PSPSATPLT 600
 KTHSQAAASLT TAEDLASSCS SNTVVANGKD VELLPLTSS 639

SEQ ID NO: 359 moltype = AA length = 271
 FEATURE Location/Qualifiers
 source 1..271
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 359
 MNLEKLSKPE LLTFLSILEG ELEARDLVIE ALKAQHRDTF IEERYGKYNI SDPLMALQRD 60
 FETLKEKNNDG EKQPVCTNPL SILKVVMKQC KNMQERMLSQ LAAAESRHK VILDLEERQ 120
 RHAQDTAEGD DVTYMLEKER ERLTQQLEFE KSQVKKFKE QKKLSSQLEE ERSRKQLSS 180
 MLVLECKKAT NKAEEEGQKA GELSLKLEKE KSRVSKLEEE LAAERKRGLQ TEAQVEKQLS 240
 EFDIEREQLR AKLNREENRT KTLKEEMESL K 271

SEQ ID NO: 360 moltype = AA length = 396
 FEATURE Location/Qualifiers
 source 1..396
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 360
 MSATDRMGPV AVPGLRLALL LLLLVLGTPKS GVQGQEGLDF PEYDGVRVI NVNAKNYKNV 60
 FKKYEVLLALL YHEPPEDDKA SQRFQEMEEL ILELAAQVLE DKGVGFGLVD SEKDAAVAKK 120
 LGLTEVDSMY VFKGDEVIEY DGEFSADTV EFLLDVLEDV VELIEGEREL QAFENIEDEI 180
 KLIGYFKSKD SEHYKAFEDA EEEFHYPYIPF FATFDISKVAK KLTLKLNEID FYEAFMEEPV 240
 TIPDKPNSEE EIVNFVEEHRR RSTLRKLKE SMYETWEDMM DGIHIVAFAE EADPDGFEST 300
 ETLKAVAQDN TENPDLSIIW IDPDDFPILL PYWEKTFDID LSAPQIGVNV VTDADSVME 360
 MDDEEDLPSA EEELEDWLEDV LEGEINTEDD DDDDDDD 396

SEQ ID NO: 361 moltype = AA length = 188
 FEATURE Location/Qualifiers
 source 1..188
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 361
 MDVNIAPLRA WDDFFPGSDR FARPDFRDIS KWNNRVVSNL LYYQTNYLVV AAMMISIVGF 60

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LSPFNAMILGG	IVVVLVFTGF	VWAHNKDVL	RRMKKRYPTT	FVMVMLASY	FLISMFGGVM	120
VFVFGITFPL	LLMFIHASLR	LRNLKNKLEN	KMEIGIGLKR	PMGIVLDALE	QQEEGINRLT	180
DYISKVKE						188
 SEQ ID NO: 362						
FEATURE	moltype = AA	length = 88				
source	Location/Qualifiers					
	1..88					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 362						
MDVNIAPLRA	WDDFFPGSDR	FARPDFRDIS	KWNNRVVSNL	LYYQTNYLVV	AAMMISIVGF	60
LSPFNPIVS	EVSRVFMKSN	GKWITRFL				88
 SEQ ID NO: 363						
FEATURE	moltype = AA	length = 93				
source	Location/Qualifiers					
	1..93					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 363						
MDVNIAPLRA	WDDFFPGSDR	FARPDFRDIS	KWNNRVVSNL	LYYQTNYLVV	AAMMISIVGL	60
ECNGVISAHC	NLHLLSSSDS	PASASQVAGI	TGF			93
 SEQ ID NO: 364						
FEATURE	moltype = AA	length = 59				
source	Location/Qualifiers					
	1..59					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 364						
MDVNIAPLRA	WDDFFPGSDR	FARPDFRDIS	KWNNRVVSNL	LYYQTNYLVV	AAMMISIVG	59
 SEQ ID NO: 365						
FEATURE	moltype = AA	length = 357				
source	Location/Qualifiers					
	1..357					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 365						
MEKYVAAML	SAAGDALGYY	NGKWEFLQDG	EKIHRQLAQL	GGLDALDVGR	WRVSDDTVMH	60
LATAEALVEA	GKAPKLTLQY	YLLAKHYQDC	MEDMDGRAPG	GASVHNAMQL	KPGKPNGWRI	120
PFNSHEGGCG	AAMRAMCIGL	RFPHHSQLDT	LIQVSIESGR	MTHHHPTGYL	GALASALFTA	180
YAVNSRPLQ	WGKGLMELLNP	EAKKYIVQSG	YFVEENLQHW	SYFQTKWENY	LKLRGILDGE	240
SAPTFPESFG	VKERDQFYTS	LSYSGWGGSS	GHDAPMIAYD	AVLAAGDSWK	ELAHRAFFHG	300
GDSDSTAAIA	GCWWGVMYGF	KGVSPSNYEK	LEYRNRLleet	ARALYSLGSK	EDTVISL	357
 SEQ ID NO: 366						
FEATURE	moltype = AA	length = 357				
source	Location/Qualifiers					
	1..357					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 366						
MEKYVAAML	SAAGDALGYY	NGKWEFLQDG	EKIHRQLAQL	GGLDALDVGR	WRVSDDTVMH	60
LATAEALVEA	GKAPKLTLQY	YLLAKHYQDC	MEDMDGRAPG	GASVHNAMQL	KPGKPNGWRI	120
PFNSHEGGCG	AAMRAMCIGL	RFPHHSQLDT	LIQVSIESGR	MTHHHPTGYL	GALASALFTA	180
YAVNSRPLQ	WGKGLMELLNP	EAKKYIVQSG	YFVEENLQHW	SYFQTKWENY	LKLRGILDGE	240
SAPTFPESFG	VKERDQFYTS	LSYSGWGGSS	GHDAPMIAYD	AVLAAGDSWK	ELAHRAFFHG	300
GDSDSTAAIA	GCWWGVMYGF	KGVSPSNYEK	LEYRNRLleet	ARALYSLGSK	EDTVISL	357
 SEQ ID NO: 367						
FEATURE	moltype = AA	length = 357				
source	Location/Qualifiers					
	1..357					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 367						
MEKYVAAML	SAAGDALGYY	NGKWEFLQDG	EKIHRQLAQL	GGLDALDVGR	WRVSDDTVMH	60
LATAEALVEA	GKAPKLTLQY	YLLAKHYQDC	MEDMDGRAPG	GASVHNAMQL	KPGKPNGWRI	120
PFNSHEGGCG	AAMRAMCIGL	RFPHHSQLDT	LIQVSIESGR	MTHHHPTGYL	GALASALFTA	180
YAVNSRPLQ	WGKGLMELLNP	EAKKYIVQSG	YFVEENLQHW	SYFQTKWENY	LKLRGILDGE	240
SAPTFPESFG	VKERDQFYTS	LSYSGWGGSS	GHDAPMIAYD	AVLAAGDSWK	ELAHRAFFHG	300
GDSDSTAAIA	GCWWGVMYGF	KGVSPSNYEK	LEYRNRLleet	ARALYSLGSK	EDTVISL	357
 SEQ ID NO: 368						
FEATURE	moltype = AA	length = 357				
source	Location/Qualifiers					
	1..357					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 368						
MEKYVAAML	SAAGDALGYY	NGKWEFLQDG	EKIHRQLAQL	GGLDALDVGR	WRVSDDTVMH	60

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LATAEALVEA	GKAPKLTQLY	YLLAKHYQDC	MEDMDGRAPG	GASVHNAMQL	KPGKPNGWRI	120
PFNSHEGGCG	AAMRAMCIGL	RFPHHSQLDT	LIQVSIESGR	MTHHHPTGYL	GALASALFTA	180
YAVNSRPPHQ	WGKGLMELL	EAKKYIVQSG	YFVEENLQHW	SYFQTKWENY	LKLRGILDGE	240
SAPTFPESFG	VKERDQFYTS	LSYSGWGSSS	GHDAPMTIAYD	AVLAAGDSWK	ELAHRFFHG	300
GDSDSTAIA	GCWWGVMYGF	KGVSPSNYEK	LEYNRLEET	ARALYSLGSK	EDTVISL	357
 SEQ ID NO: 369			moltype = AA	length = 125		
FEATURE			Location/Qualifiers			
source			1..125			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 369						
MEKYVAAMVL	SAAGDALGYY	NGKWEFLQDG	EKIHRQLAQL	GGLDALDVGR	WRVSDDTVMH	60
LATAEALVEA	GKAPKLTQLY	YLLAKHYQDC	MEDMDGRAPG	GASVHNAMQL	KPGKPNGWRI	120
PFNSH						125
 SEQ ID NO: 370			moltype = AA	length = 974		
FEATURE			Location/Qualifiers			
source			1..974			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 370						
MAGRVPSSLV	LLVFPSCL	FRSPLSVFKR	FKEETTRPFN	ECLGTTRPVV	PIDSSDFALD	60
IRMPGVTPKQ	SDTYFCMSMR	IPVDEEAFVI	DFKPRASMDT	VHHMLLFGCN	MPSSTGSYWF	120
CDEGTCTDKA	NILYAWARNA	PPTRLPKVG	FRVGETGSK	YFVLQVHYGD	ISAFRDNNKD	180
CSGVSVLHLTR	LPQPLIAGMY	LMMSVDTVIP	AGEKVVNSDI	SCHYKNYPMH	VFAYRVHTHH	240
LGKVVSGYRV	RNGQWTLIGR	QSPQLPQAFY	PVGHPVDVFS	GDLLAACRVF	TGEGRTEATH	300
IGGTSSDEM	NLYIMYMEA	KHAWSFMTCT	QNVPADMFR	IPPEANIPIP	VKSDMVMMHE	360
HKETEYDKD	IPLLQQPKRE	EEEVLDQGDF	YSLLSKLLGE	REDVVHVHKY	NPTEKAES	420
DIVAEIANVV	QKKDLGRSDA	REGAEHERGN	A1LVRDR1HK	FHRLVSTLRP	PESRVFSLQQ	480
PPPGEGTWEP	EHTGDFHMEE	ALDWPGVYLL	PGQVSGVALD	PKNNLVIFHR	GDHWDGNSF	540
DSKFVYQQIG	LGPIERDTIL	VIDPNNAAVL	QSSGKNLFLY	PHGLSIDKDG	NYWVTDVALH	600
QVKLDPNNK	EGPVVLILGRS	MQPQSDQNHF	CQPTDVAWDP	GTGAIYVSDG	YCNSRIVQFS	660
PSGKFITQWG	EESSGSPLP	GQFTVPHSLA	LVPLLQQLCV	ADRENRIQC	FKTDTKEFVR	720
EIKHSSFGRN	VFAISYIPGL	GDQEPVQGFV	MNFSNGEIID	IFKPVRKHFD	780	
MPHDIVASED	GTVYIGDAHT	NTVWKFTLTE	KLEHRSVKKA	GIEVQEIKGA	EAVVETKMN	840
KPTSSELQKM	QEKKQKLIKEP	GSGVPVVLIT	TLLVIPVVL	LAIAIFIRWK	KSRAFGADSE	900
HKLETSSGRV	LGRFRKGSG	GLNLGNFFAS	RKGYSRKCFD	RLSTEGSDQE	KEDDGSESEE	960
EYSAPLPA	PSSS					974
 SEQ ID NO: 371			moltype = AA	length = 175		
FEATURE			Location/Qualifiers			
source			1..175			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 371						
MAGRVPSSLV	LLVFPSCL	FRSPLSVFKR	FKEETTRPFN	ECLGTTRPVV	PIDSSDFALD	60
IRMPGVTPKQ	LTSLEPAWI	LSITCYFLDA	ICLHPLEVTG	FVMKEPVQIK	PIFCMPGREM	120
LPLPGSPKVL	DSELEERLEV	NTLYYRYTMG	ILVLLEIITR	TVLVCPTYSH	VCHSL	175
 SEQ ID NO: 372			moltype = AA	length = 887		
FEATURE			Location/Qualifiers			
source			1..887			
			mol_type = protein			
			organism = Homo sapiens			
SEQUENCE: 372						
MAGRVPSSLV	LLVFPSCL	FRSPLSVFKR	FKEETTRPFN	ECLGTTRPVV	PIDSSDFALD	60
IRMPGVTPKQ	SDTYFCMSMR	IPVDEEAFVI	DFKPRASMDT	VHHMLLFGCN	MPSSTGSYWF	120
CDEGTCTDKA	NILYAWARNA	PPTRLPKVG	FRVGETGSK	YFVLQVHYGD	ISAFRDNNKD	180
CSGVSVLHLTR	LPQPLIAGMY	LMMSVDTVIP	AGEKVVNSDI	SCHYKNYPMH	VFAYRVHTHH	240
LGKVVSGYRV	RNGQWTLIGR	QSPQLPQAFY	PVGHPVDVFS	GDLLAACRVF	TGEGRTEATH	300
IGGTSSDEM	NLYIMYMEA	KHAWSFMTCT	QNVPADMFR	IPPEANIPIP	VKSDMVMMHE	360
HKETEYDKD	IPLLQQPKRE	EEEVLDQGDF	YSLLSKLLGE	REDVVHVHKY	NPTEKAES	420
DIVAEIANVV	QKKDLGRSDA	REGAEHERGN	A1LVRDR1HK	FHRLVSTLRP	PESRVFSLQQ	480
PPPGEGTWEP	EHTGDFHMEE	ALDWPGVYLL	PGQVSGVALD	PKNNLVIFHR	GDHWDGNSF	540
DSKFVYQQIG	LGPIERDTIL	VIDPNNAAVL	QSSGKNLFLY	PHGLSIDKDG	NYWVTDVALH	600
QVKLDPNNK	EGPVVLILGRS	MQPQSDQNHF	CQPTDVAWDP	GTGAIYVSDG	YCNSRIVQFS	660
PSGKFITQWG	EESSGSPLP	GQFTVPHSLA	LVPLLQQLCV	ADRENRIQC	FKTDTKEFVR	720
EIKHSSFGRN	VFAISYIPGL	GDQEPVQGFV	MNFSNGEIID	IFKPVRKHFD	780	
MPHDIVASED	GTVYIGDAHT	NTVWKFTLTE	KLEHRSVKKA	GIEVQEIKGA	GSGGLNLGNF	840
FAEKRGYSRK	GFDRRLSTEGS	SEEYYSAPL	ALAPSSS			887
 SEQ ID NO: 373			moltype = AA	length = 866		
FEATURE			Location/Qualifiers			
source			1..866			
			mol_type = protein			

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SEQUENCE: 373	organism = Homo sapiens
MAGRVPSSLLV LLVFPSCLAFRSPLSVFKR FKETTRPFSN ECLGTTTRPVV PIDSSDFALD	60
IRMPGVTPKQ SDTYFCMSMR IPVDEEAFVI DFKPRASMDT VHHMLLFGCN MPSSTGSYWF	120
CDEGTCTDKA NILYAWARNA PPTRLPKGVG FRVGGETGSK YFVLQVHYGD ISAFRDNNKD	180
CSGVSLHLTR LPQPLIAGMY LMMSVDTVIP AGEKVVNSDI SCHYKNYPMH VFAYRVHTHH	240
LGKVVSGYRV RNGQWTLIGR QSPQLPQAFY PVGHPVDVSF GDLLAARCVF TGEGRTEATH	300
IGGTSSDEMC NLYIMYMEA KHAWSFMTCT QNVAPDMFR IPPEANIPIP VKSDMVMH	360
HHKETEYDK IPLLQOPKRE EEEVLDQDFH MEEALDWPGV YLLPGQVSGV ALDPKNNLVI	420
FHRGDHWDG NSFDISKFVYQ QIGLQPIED TILVIDPNNA AVLQSSGKNL FYLPHGLSID	480
KDGNYWNTDV ALHQVKLDP NNKEGPVIL GRSMQPGSDQ NHFCQPTDVA VDPGTGAIYV	540
SDGYCNSRIV QFSPSGKFIQ QWGEESSGSS PLPGQFTVPH SLALVPLLGQ LCVADRENGR	600
IQCFCFTDTKE FVREIKHSSF GRNVFAISYI PGLLFAVNKG PHFGDQEPMQ GFVMNFSNGE	660
IIDIFPKVRK HFDMPHDIVA SEDGTVYIGD AHNTNTVWKFT LTEKLEHRSV KKAGIEVQEI	720
KEAEAVVETK MENKPTTSEL QMKMEQKQLI KEPGSGVPVV LITLLVIPV VVLLAIAIFI	780
RWKKSRAFGD SEHKLETSSG RVLGRFRKGK SGGLNLGNFF ASRKGYSRKG FDRLSTEGSD	840
QEKEEDDGSES EEEYSAPLPA LAPSSS	866
 SEQ ID NO: 374	moltype = AA length = 973
FEATURE Location/Qualifiers	
source 1..973	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 374	
MAGRVPSSLLV LLVFPSCLAFRSPLSVFKR FKETTRPFSN ECLGTTTRPVV PIDSSDFALD	60
IRMPGVTPKQ SDTYFCMSMR IPVDEEAFVI DFKPRASMDT VHHMLLFGCN MPSSTGSYWF	120
CDEGTCTDKA NILYAWARNA PPTRLPKGVG FRVGGETGSK YFVLQVHYGD ISAFRDNNKD	180
CSGVSLHLTR LPQPLIAGMY LMMSVDTVIP AGEKVVNSDI SCHYKNYPMH VFAYRVHTHH	240
LGKVVSGYRV RNGQWTLIGR QSPQLPQAFY PVGHPVDVSF GDLLAARCVF TGEGRTEATH	300
IGGTSSDEMC NLYIMYMEA KHAWSFMTCT QNVAPDMFR IPPEANIPIP VKSDMVMH	360
HHKETEYDK IPLLQOPKRE EEEVLDQDFH YSLLSKLLGE REDVHVVKY NPTEKAES	420
DIVAEIANVV QKQDGLGRSDA REGAEHERGN AILVRDRIHK FHRLVSTLRP PESRVSLSQQ	480
PPPGEGTWEP EHTGDFHME ALDWPGVYLL PGQVSGVALD PKNNLVIFHR GHVWDGNSF	540
DSKFVYQQIG LGPIEEDTIL VIDPNNAAVL QSSGKNLFLY PHGLSIDKDG NYWVTDVALH	600
QVFKLDPNNK EGTVLILGRS MQPGSDQNHF CQPTDVAVDP GTGAIYVSDG YCNSRIVQFS	660
PSGKFITQWG EESSGGSSPLP GQFTVPHSLA LVPLLGQLCV ADRENRIQCF KFTDTKEFVR	720
EIKHSSFGRN VFAISYIPGL LFAVNGKPHF GDQEPVQGFV MNFSNGEIID IFKPVRKHFD	780
MPHDIVASED GTVYIGDAHT NTWKFTLTLK LEHRSVKKA GIEVQEIKEA EAVVETKMEM	840
KPTSSELQKM QEKEQKLIKEP GSGVPVVLIT TLLVIPVVL LAIAIFIRWK KSRAFGDSEH	900
KLETSSGRVL GRFRGKGSGG LNGLNFFASR KGYSRKGFDR LSTEGSDQEK EDDGSESEE	960
YSAPLPA LAPSSS	973
 SEQ ID NO: 375	moltype = AA length = 905
FEATURE Location/Qualifiers	
source 1..905	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 375	
MAGRVPSSLLV LLVFPSCLAFRSPLSVFKR FKETTRPFSN ECLGTTTRPVV PIDSSDFALD	60
IRMPGVTPKQ SDTYFCMSMR IPVDEEAFVI DFKPRASMDT VHHMLLFGCN MPSSTGSYWF	120
CDEGTCTDKA NILYAWARNA PPTRLPKGVG FRVGGETGSK YFVLQVHYGD ISAFRDNNKD	180
CSGVSLHLTR LPQPLIAGMY LMMSVDTVIP AGEKVVNSDI SCHYKNYPMH VFAYRVHTHH	240
LGKVVSGYRV RNGQWTLIGR QSPQLPQAFY PVGHPVDVSF GDLLAARCVF TGEGRTEATH	300
IGGTSSDEMC NLYIMYMEA KHAWSFMTCT QNVAPDMFR IPPEANIPIP VKSDMVMH	360
HHKETEYDK IPLLQOPKRE EEEVLDQDFH YSLLSKLLGE REDVHVVKY NPTEKAES	420
DIVAEIANVV QKQDGLGRSDA REGAEHERGN AILVRDRIHK FHRLVSTLRP PESRVSLSQQ	480
PPPGEGTWEP EHTGDFHME ALDWPGVYLL PGQVSGVALD PKNNLVIFHR GHVWDGNSF	540
DSKFVYQQIG LGPIEEDTIL VIDPNNAAVL QSSGKNLFLY PHGLSIDKDG NYWVTDVALH	600
QVFKLDPNNK EGTVLILGRS MQPGSDQNHF CQPTDVAVDP GTGAIYVSDG YCNSRIVQFS	660
PSGKFITQWG EESSGGSSPLP GQFTVPHSLA LVPLLGQLCV ADRENRIQCF KFTDTKEFVR	720
EIKHSSFGRN VFAISYIPGL LFAVNGKPHF GDQEPVQGFV MNFSNGEIID IFKPVRKHFD	780
MPHDIVASED GTVYIGDAHT NTWKFTLTLK LEHRSVKKA GIEVQEIKDS EHKL	840
VLRFRKGKGS GGGLNLGNFFA SRKGYSRKGF DRLSTEGSDQ EKEEDDGSESE EYYSAPLPA	900
APSSS	905
 SEQ ID NO: 376	moltype = AA length = 250
FEATURE Location/Qualifiers	
source 1..250	
mol_type = protein	
organism = Homo sapiens	
SEQUENCE: 376	
XRIQCFKTD KEVREIKHS SFGRNVFAIS YIPGLLFAVN GKPHFGDQEP VQGFVMNFSN	60
GEIIDIFPKV RKFDMPHDI VASEDGTYI GDAHTNTVWK FTLTEKLEHR SVKKAGIEVQ	120
EIKEAEAVVE TKMENKPTSS ELQKMQEKQK LIKEPGSGVP VVLITLLVI PVVVLLAIAI	180
FIRWKKSRAG GGKGSGGLNL GNFFASRKGY SRKGFDRLST EGSDQEKEDD GSESEEYSA	240
PLPALAPSSS	250

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SEQ ID NO: 377      moltype = AA  length = 29
FEATURE          Location/Qualifiers
source           1..29
mol_type = protein
organism = Homo sapiens
SEQUENCE: 377
MAGRVPSSLV LLVFPSSCLA FRSPSLSVFK          29

SEQ ID NO: 378      moltype = AA  length = 28
FEATURE          Location/Qualifiers
source           1..28
mol_type = protein
organism = Homo sapiens
SEQUENCE: 378
MAGRVPSSLV LLVFPSSCLA FRSPSLSVF          28

SEQ ID NO: 379      moltype = AA  length = 53
FEATURE          Location/Qualifiers
source           1..53
mol_type = protein
organism = Homo sapiens
SEQUENCE: 379
MAGRVPSSLV LLVFPSSCLA FRSPSLSVFKR FKETTRPPFSN ECLGTTTRPVV PID          53

SEQ ID NO: 380      moltype = AA  length = 42
FEATURE          Location/Qualifiers
source           1..42
mol_type = protein
organism = Homo sapiens
SEQUENCE: 380
MAGRVPSSLV LLVFPSSCLA FRSPSLSVFKR FKETTRPPFSN EC          42

SEQ ID NO: 381      moltype = AA  length = 68
FEATURE          Location/Qualifiers
source           1..68
mol_type = protein
organism = Homo sapiens
SEQUENCE: 381
MAGRVPSSLV LLVFPSSCLA FRSPSLSVFKR FKETTRPPFSN ECLGTTTRPVV PIDSSDFALD IRMPGVTP          60
68

SEQ ID NO: 382      moltype = AA  length = 25
FEATURE          Location/Qualifiers
source           1..25
mol_type = protein
organism = Homo sapiens
SEQUENCE: 382
MAGRVPSSLV LLVFPSSCLA FRSPSL          25

SEQ ID NO: 383      moltype = AA  length = 691
FEATURE          Location/Qualifiers
source           1..691
mol_type = protein
organism = Homo sapiens
SEQUENCE: 383
MMRNHRIASS LCGDQVFSKK KKKKKKNNMA AKEKLEAVLN VALRVPSIML LDVLYRWDSV 60
SFFQQIQRSS LSNNPLFQYK YLALNMHYVG YILSVVLLTL PRQHLVQLYL YFLTALLLYA 120
GHQISRDYVR SELEFAVEGY MYLEPLSMNR FTALIGOLV VCTLCSCVMK TKQIWLFSAH 180
MLPLLARLCL VPLETEIVIN KFAMIFTGLE VLYFLGSNLL VPYNLAKSAY RELVQVVEVY 240
GILLALGMSLW NQLVVVPVLFM VFVLVLFALQ IYSYFSTRDQ PASRERLLFL FLTSAECCS 300
TPYSLLGLVF TVSFVALGVL TLCKFYLQGY RAFMNDPAMN RGMTEGVTL ILAVQTGLIE 360
LQVVHRAFLL SIILFIVVAS ILQSMLEIAD PIVLALGASR DKSLWKHFRA VSLCLFLLVF 420
PAYMAMYICQ FFHMDFWLLI IISSSILTSQ QVLGTLFIYV LFMVEEFRKE PVENMDDVIY 480
YVNGTYRLLF PLVALCVVAY GVSETIFGEW TVMGSMIIIFK HSYYNVNLRA QLGWKSFLLR 540
RDAVNKIKSL PIATKBQLEK HNDICAICYQ DMKSAVITPC SHFFFAGCLK KWLYVQETCP 600
LCHCHLKNSS QLPGLGTEPV LQPHAGAEQN VMFQEGETEPP GQEHTPGTRI QEGSRDNNEY 660
IARRPDNQEG AFDPKEYPHS AKDEAHPVES A 691

SEQ ID NO: 384      moltype = AA  length = 663
FEATURE          Location/Qualifiers
source           1..663
mol_type = protein
organism = Homo sapiens
SEQUENCE: 384
MAAKEKLEAV LNVALRVPSI MLLDVLYRWD VSSFFQQIQR SSLSNPLFQ YKYLALNMHY 60

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VGYILSVVLL TLPRQHLVQL YLYFLTALLL YAGHQISRDY VRSELEFAYE GPMYLEPLSM	120
NRFTTALIGQ LVVCTLCSCV MKTKQIWLFS AHMLPILLAR CLVPLETIVI INKFAMIFTG	180
LEVLYFLGSN LLVPYNLAKS AYRELVQVVE VYGLLALGMS LWNQLVVPVL FMVFWLVLF	240
LQIYSYFSTR DQPASRERLL FLFLTSIAEC CSTPYSSLGL VFTVSFVALG VLTLCKFYLQ	300
GYRAFMNDPA MNRGMTEGVT LLILAVQTGL IELQVHRAF LLSIILFIVV ASILQSMLEI	360
ADPIVLALGA SRDKSLWKHF RAVSLCLFLL VFPPAYMAYMI CQFFHMDFWL LIIISSSILT	420
SLQVLGTLFI YVLFMVEEFR KEPVENMDDV IYYVNGTYRL LEFLVALCVV AYGSETIFG	480
EWTVMGSMII FIHSYYNVWL RAQLGWKSFL LRRDAVNKIK SLPIATKEQL EKHNDICAIC	540
YQDMKSAVIT PCSHFFHAGC LKKWLYVQET CPLCHCHLKN SSQLPGLGTE PVLQPHAGAE	600
QNVMFQEGETE PPGQEHTPGT RIQEGRDNN EYIARRPDNQ EGAFDPKEYP HSAKDEAHPV	660
ESA	663

SEQ ID NO: 385 moltype = AA length = 693
 FEATURE Location/Qualifiers
 source 1..693
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 385
 MHRDRISPNS PPTWSLQVFS KKKKKKKNN MAAKEKLEAV LNVALRVPSI MLLDVLYRWD 60
 VSSFFQQIQR SSLSNNPLFQ YKYLALNMHY VGYILSVVLL TLPRQHLVQL YLYFLTALLL 120
 YAGHQISRDY VRSELEFAYE GPMYLEPLSM NRFTTALIGQ LVVCTLCSCV MKTKQIWLFS 180
 AHMLPILLAR CLVPLETIVI INKFAMIFTG LEVLYFLGSN LLVPYNLAKS AYRELVQVVE 240
 VYGLLALGMS LWNQLVVPVL FMVFWLVLF AYRELVQVVE DQPASRERLL FLFLTSIAEC 300
 CSTPYSSLGL VFTVSFVALG VLTLCKFYLQ GYRAFMNDPA MNRGMTEGVT LLILAVQTGL 360
 IELQVHRAF LLSIILFIVV ASILQSMLEI ADPIVLALGA SRDKSLWKHF RAVSLCLFLL 420
 VFPPAYMAYMI CQFFHMDFWL LIIISSSILT SLQVLGTLFI YVLFMVEEFR KEPVENMDDV 480
 IYYVNGTYRL LEFLVALCVV AYGSETIFG EWTVMGSMII FIHSYYNVWL RAQLGWKSFL 540
 LRRDAVNKIK SLPIATKEQL EKHNDICAIC YQDMKSAVIT PCSHFFHAGC LKKWLYVQET 600
 CPLCHCHLKN SSQLPGLGTE PVLQPHAGAE QNVMFQEGETE PPGQEHTPGT RIQEGRDNN 660
 EYIARRPDNQ EGAFDPKEYP HSAKDEAHPV ESA 693

SEQ ID NO: 386 moltype = AA length = 663
 FEATURE Location/Qualifiers
 source 1..663
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 386
 MAAKEKLEAV LNVALRVPSI MLLDVLYRWD VSSFFQQIQR SSLSNNPLFQ YKYLALNMHY 60
 VGYILSVVLL TLPRQHLVQL YLYFLTALLL YAGHQISRDY VRSELEFAYE GPMYLEPLSM 120
 NRFTTALIGQ LVVCTLCSCV MKTKQIWLFS AHMLPILLAR CLVPLETIVI INKFAMIFTG 180
 LEVLYFLGSN LLVPYNLAKS AYRELVQVVE VYGLLALGMS LWNQLVVPVL FMVFWLVLF 240
 LQIYSYFSTR DQPASRERLL FLFLTSIAEC CSTPYSSLGL VFTVSFVALG VLTLCKFYLQ 300
 GYRAFMNDPA MNRGMTEGVT LLILAVQTGL IELQVHRAF LLSIILFIVV ASILQSMLEI 360
 ADPIVLALGA SRDKSLWKHF RAVSLCLFLL VFPPAYMAYMI CQFFHMDFWL LIIISSSILT 420
 SLQVLGTLFI YVLFMVEEFR KEPVENMDDV IYYVNGTYRL LEFLVALCVV AYGSETIFG 480
 EWTVMGSMII FIHSYYNVWL RAQLGWKSFL LRRDAVNKIK SLPIATKEQL EKHNDICAIC 540
 YQDMKSAVIT PCSHFFHAGC LKKWLYVQET CPLCHCHLKN SSQLPGLGTE PVLQPHAGAE 600
 QNVMFQEGETE PPGQEHTPGT RIQEGRDNN EYIARRPDNQ EGAFDPKEYP HSAKDEAHPV 660
 ESA 663

SEQ ID NO: 387 moltype = AA length = 677
 FEATURE Location/Qualifiers
 source 1..677
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 387
 MVESKKKKK KKNNMAAKEK LEAVLNVALR VPSIMLLDV YRWDVSSFFQ QIQRSSLNSN 60
 PLFQYKYLAL NMHYVGYILS VVLLTLPQH LVQLYLYFLT ALLYAGHQI SRDYVRSELE 120
 FAYEGPMYLE PLSMNRFTA LIGLQVCTL CSCVMKTKQI WLFSAHMLPL LARLCLVPLE 180
 TIVIINKFAM 1IFTGLEVLYF LGNSLWVPYH LAKSAYRELV QVVEVYGLLA LGMSLWNQLV 240
 VPVLFMFWL VLFLAQIYS FSTRDQPASR ERLLFLFLTS IAECCTPYS LLGLVFTVSF 300
 VALGVLTCK FYLQGYRAFM NDPAMNRGMT EGVTLLILAV QTGLIELQVV HRAFLLSIL 360
 FIVVASILQS MLEIADPIV ALGASRDKSL WKHFRAVSLC LFLVVFPAYM AYMICQFHM 420
 DFWLILIIS SILTSQVLG TLFYIYVLFMV EEFRKEPVEN MDDVIYVNG TYRLLEFLVA 480
 LCVVAYGVSE TIFGEWVVMG SIIIFIHSYV NVWLRAQLGW KSFLRRAV NKİKLSPİAT 540
 KEQLEKHNDI CAICYQDMKS AVITPCSHF HAGCLKKWLY VQETCPLCHC HLKNNSQLPG 600
 LGTEPVLPQH AGAEQNVMFQ EGTEPPGQEH TPGTRIQEGS RDNNEYIARR PDNQECAFDP 660
 KEYPHSAKDE AHPVESA 677

SEQ ID NO: 388 moltype = AA length = 680
 FEATURE Location/Qualifiers
 source 1..680
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 388
 MAEVVFSKKK KKKKKNNMAA KEKLEAVLNV ALRVPSIMLL DVLYRWDVSS FFQQIQRSSL 60

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SNNPLFQYKY	LALNMHYVGY	ILSVVLLTP	RQHLVQLYLY	FLTALLYAG	HQISRVDYVRS	120
ELEFAYECPM	YLEPILSMNRR	TTALIGQLVV	CTLCSCVMKT	KQIWLFSAHM	LPLLARLCLV	180
PLETIVIINK	FAMIFTGLEV	LYFLGSNLVV	PYNLAKSAYR	ELVQVVEVYVG	LLALGMSLWN	240
QLVVPVLFMV	FWLVLFALQI	YSYFSTRDQP	ASRERLFLF	LTSIAECST	PYSLLGLVFT	300
VSFVALGVLT	LCKFYLQGYR	AFMNDPAMNR	GMTEGVTLII	LAVQTGLIEL	QVVRHRAFLLS	360
IILFIVVASI	LQSMLEIADP	IVLALGASRD	KSLWKHFRAV	SLCLFLVFP	AYMAYMICQF	420
FHMDFWLLII	ISSSILTSLO	VLGTLFIYVL	FMVEEFRKEP	VENMDDVIYY	VNGTYRLLEF	480
LVALCVVAYG	VSETIFGEWT	VMGSMIIIFIH	SYNNVWLRAQ	LGWKSFLRR	DAVNKIKSLP	540
IATKEQLEKH	NDICAICYQD	MKSADVTPCS	HFFHAGCLKK	WLYVQETCPL	CHCHLKNSSQ	600
LGPGTPEPVL	QPHAGAEQN	MFQEGTEPPG	QEHTPGTRIQ	EGSRDNNEYI	ARRPDNQEGA	660
DPKEYPHSA	KDEAHPVESA					680

SEQ ID NO: 389	moltype = AA	length = 663				
FEATURE	Location/Qualifiers					
source	1..663					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 389						
MAAKEKLEAV	LNVALRVPSI	MLLDVLYRW	VSSFFQQIQR	SSLSNNNPLFQ	YKYLALNMHY	60
VGYILSVULL	TLPQRHLVQL	YLYFLTALLL	YAGHQISRDY	VRSELEFAYE	GPMYLEPLSM	120
NRFTTALIGQ	LVVTCLCSCV	MKTQIWLFS	AHMLPLLARL	CLVPLETIVI	INKFAMIFTG	180
LEVLYFLGSN	LLVPYNNLAKS	AYRELVQVVE	VYGLLALGMS	LWNQLVPPVL	FMVFWLVLFA	240
LQIYSYFSTR	DQPASRERLL	FLFLTSIAEC	CSTPYSLLGL	VFTVSFVALG	VTLCKFYLQ	300
GYRAFMNDPA	MNRGMTEGVT	LLILAVQATGL	IELQVHVRAF	LLSIIILFIVV	ASIQSMLI	360
ADPIVLALGA	SRDKSLWKHF	RAVSLCLFL	VFPAYMAYMI	CQFFFHMDFWL	LIIISSSILT	420
SIQVLGTLFI	YVLFMVEEFR	KEPVENMDV	IYVNVNTYRL	LEFLVALCVV	AYGVSETIFG	480
EWTVMGSMII	PIHSYYNWL	RAQLGWKSFL	LRRDAVNKKI	SPLIATKEQL	EKHNDICAIC	540
YQDMKSAVIT	PCSHFFHAGC	LKKWLWYQET	CPLCHCHLKN	SSQLPGLGTE	PVLQPHAGAE	600
QNVMFQEGTE	PPGQEHTPGT	RIQEGSRDNN	EYIARRPDNQ	EGAFDPKEYP	HSAKDEAHPV	660
ESA						663

SEQ ID NO: 390	moltype = AA	length = 185				
FEATURE	Location/Qualifiers					
source	1..185					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 390						
MAGRPRWRD	QLLFMSIIVL	VIVVICLMFY	ALLWEAGNL	DLPNLRIGFY	NFCLWNEDTS	60
TLQCHQFPEL	EALGVPRVGL	GLARLGVYGS	LVLTLFAPQP	LLLAQCNSDE	RAWRLAVGFL	120
AVSSVLLAGG	LGLFLSYVWK	WVRSLSPGPG	FLALGSAQAL	LILLIAMI	AVRAERAES	180
KLESC						185

SEQ ID NO: 391	moltype = AA	length = 486				
FEATURE	Location/Qualifiers					
source	1..486					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 391						
MKGRRRRRRE	YCKFALLLVL	YTLLVLLVPS	VLDGGRDGDK	GAEHCPGLQR	SLGVWSLEAA	60
AAGEREQGAE	ARAAEEGGAN	QSPRFPNSL	GAVGEAVSRE	KQHIYVHATW	RTGSSFLGEL	120
FNQHDPVFY	YPEMWHLWQA	LYPGDAESLQ	GALRDMRLSL	FRCDFSVURL	YAPPGDPAAR	180
APDTANLTTA	ALFRWRTNKV	ICSPPLCPGA	PRARAEVGLV	EDTACERSCP	PVAIRALEAE	240
CRKYPVWVK	DVRLLDLGV	VPLLDRPGLN	LKVQQLFRDP	RAVHNRSRJKS	RQGLLRESIQ	300
VLRTRQRGDR	FHRVLLAHGV	GARPGGQSRA	LPAAPRADF	LTGAEVICE	AWLRDILLFAR	360
GAPAWLRRY	LRLRYEDLVR	QPRQLRLLL	RFSGLRALAA	LDAFALNMT	GAAYGADRPF	420
HLSARDAREA	VHAWRERLSR	EQVRQVEAAC	APAMRLLAYP	RSGEEGDAEQ	PREGETPLEM	480
DADGAT						486

SEQ ID NO: 392	moltype = AA	length = 494				
FEATURE	Location/Qualifiers					
source	1..494					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 392						
MLTSKGQGFL	HGGCLCLWLCV	FTPFFKGCVG	CATEERLPHK	LFSHYNQFIR	PVENVSMPVT	60
VHFEVAITQL	ANVDEVNQIM	ETNLWLRHIW	NDYKLWRDPM	EYDGIETLRV	PADKIWKPD	120
VLYNNNAVDF	QVEGKTKALL	KYNGMITWTP	PAIFKSSCPM	DITFFPFDHQ	NCSLKFGSWT	180
YDKAEIDLII	IGSKVDMNDF	WENSEWEIID	ASGYKHDIKY	NCCEEIYTDI	TYSFYIRRLP	240
MFYTINLIIP	CLFISFLTVL	VFYLPSCDGE	KVTLICISVLL	SLTVFLLVIT	ETIPSTSLVV	300
PLVGEYLLFT	MIFVTLISIVV	TVFVLNIHYR	TPTTHTMPRW	VKTVFLKLLP	QVLLMRWPLD	360
KTRGTGSDAV	PRGLLARRPAK	GKLASHGEPR	HLKECFCHCK	SNELATSKRR	LSHQPLQWVV	420
ENSEHSPPEV	DVINSVQFIA	ENMKSHNETK	EVEDDWKYVA	MVDRVFLWV	IIICVFGTA	480
GLFLQPLLLGN	TGKS					494

SEQ ID NO: 393	moltype = AA	length = 111
FEATURE	Location/Qualifiers	

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source          1..111
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 393
METNLWLRHI WNDYKLRWDP MEYDGIETLR VPADKIWKPD IVLYNNNAVGD FQVEGKTKAL 60
LKYNGMITWT PPAIFKSSCP MDITFFPFDH QNCSLKFGSW TYDKAEIDL I           111

SEQ ID NO: 394      moltype = AA  length = 479
FEATURE          Location/Qualifiers
source           1..479
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 394
MLTSKGCGFLL HGGGLCLWLKV FTPPFKGCVG CATEERLFLHK LFSHYNQFIR PVENVSDPVT 60
VHFEEV рАІQL ANVIWNDYKL RWDPMEYDG1 ETLRVPADKI WKPDIVLYNN AVGDFQVEGK 120
TKALLKYNGM ITWTPPAIFK SSCPMIDTF PFDHQNCNSLK FGSWTDYKAE IDLIIIGSKV 180
DMNDFWENSE WEIIDASGYK HDIKYNCCEE IYTDITYSFY IRLPLMFYTI NLIIPCLFIS 240
FILTVLVFYL P DSCGEKVTL С ISVLLSLTVP LLVITETIPS TSLVVLVGE YLLFTMIFVT 300
LSIVVTVPTTH TMPRVLKTVF LKLLPQVLLM RWPLDKTRGT GSDAVPRGLA 360
RRPAKGLAS HGEPRHLKEC FHCKHSNELA TSKRRLSHQW LQWVENSEH SPEVEDVINS 420
VQFIAENMKS HNETKEVEDD WKYVAMWDR VFLWVFIIIVC VFGTAGLFLQ PLLGNTGKS 479

SEQ ID NO: 395      moltype = AA  length = 1337
FEATURE          Location/Qualifiers
source           1..1337
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 395
MKPAAREARL PPRSPGLRWA LPPLLLLRL GQILCAGGTP SPIPDPSVAT VATGENGITQ 60
ISSTAESFHK QNGTGTPOVE TNTSEDESS GANDSLRTPE QGSNGTDGAS QKTPSSTGPS 120
PVFDIKAVSI SPTNVLTWK SNDTAASEYK YVVKHKMENE KTITVHVQWP CNITGLRPAT 180
SYVFSITPGI GNETWGDPRV IKVITEPIV SDLRVALTGV RKAALSWNSG NGTASCRLVLL 240
ESIGSHEELT QDSRLQVNIS GLKPGVQYNI NPYLLQSNKT KGDPLGTEGG LDASNTERSR 300
AGSPTAPVHD ESLVGPVDPS SGQSQSRDTEV LLVGLEPGTR YNATVYSQAA NGTEQOPQAI 360
EFRTNAIQVF DTVAVNISAT SLTLIWKVSD NESSSNYTYK IHVAGETDSS NLNVSEPRAV 420
IPGLRSSTFY NITVCPVLDG IEGTPGFLQV HTPPPVPSDF RVTVVSTTEI GLAWNSHDAE 480
SFQMHHITQEG AGNSRVEITT NQSIIIGGLF PGTKYCFEIV PKGPNTEGA SRTVCNRTVP 540
SAVFDIHVVY VITTEMWLDW KSPDGASEYV YHLVIESKHG SNHTSTYDKA ITLQCLIPGT 600
LYNITISFHK DHVWGDPNST AQYTPRSPNS NIDVSTNTTA ATLSWQNDD ASPTYSYCLL 660
IEKAGNNSNA TQVVTNDIGT DATVTELI P SSYTVEIPAQ VGDGIKSLEP GRKSFCTDPA 720
SMASFDCEVV PKEPALVWK TCPPGANAGF ELEVSSGAWN NATHLESCSS ENGTEYRTEV 780
TYLFNFSTSYN ISITTVSCGK MAAPTRNTCT TGITDPPPDD GSPNITSVSH NSVKVFKSGF 840
EASHGPIKAY AVILITGEAG HPSADVLKYT YEDFKKGASD TYVTYLI RTE EKGRSQSLSE 900
VLYKEIDVGN ESTLGYYNG KLEPLGCVN CAVGFTNTF HPQNKGLIDG AESYVFSFRY 960
SDAVSLPQDP CVICGAVFGC IFGALVIVTV GGPFWRKRR DAKANNEVSF SQIKPKKSKL 1020
IRVENFEAYF KKQQADSNCG FAEYYEDLKL VGISQPKYAA ELAENRGKNR YNNVLPYDIS 1080
RVKLSVQTHS TDDYINANYM PGYHKKDFI ATQGPLPNTL KDFWWRMVWEK NVYAIIMLTK 1140
CVBQGRTKCE EYWPSKQAQD YGDTIVAMTS EIVLPEWTIR DFTVKNIQTS ESHPLRQPHF 1200
TSWPDHGVPD TTDLLINFYR LVRDYMKQSP PESPILVHCS AGVGRGTGFI AIDRLIYQIE 1260
NENTVDVYGI VYDLRMHRPL MVQTEDQYVF LNQCVL DIVR SQKDSKVLDI YQNTTAMTIY 1320
ENLAPVTTFG KTNGYIA                                         1337

SEQ ID NO: 396      moltype = AA  length = 539
FEATURE          Location/Qualifiers
source           1..539
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 396
MKPAAREARL PPRSPGLRWA LPPLLLLRL GQILCAGGTP SPIPDPSVAT VATGENGITO 60
ISSTAESFHK QNGTGTPOVE TNTSEDESS GANDSLRTPE QGSNGTDGAS QKTPSSTGPS 120
PVFDIKAVSI SPTNVLTWK SNDTAASEYK YVVKHKMENE KTITVHVQWP CNITGLRPAT 180
SYVFSITPGI GNETWGDPRV IKVITEPIV SDLRVALTGV RKAALSWNSG NGTASCRLVLL 240
ESIGSHEELT QDSRLQVNIS GLKPGVQYNI NPYLLQSNKT KGDPLGTEGG LDASNTERSR 300
AGSPTAPVHD ESLVGPVDPS SGQSQSRDTEV LLVGLEPGTR YNATVYSQAA NGTEQOPQAI 360
EFRTNAIQVF DTVAVNISAT SLTLIWKVSD NESSSNYTYK IHVAGETDSS NLNVSEPRAV 420
IPGLRSSTFY NITVCPVLDG IEGTPGFLQV HTPPPVPSDF RVTVVSTTEI GLAWNSHDAE 480
SFQMHHITQEG AGNSRVEITT NQSIIIGGLF PGTKYCFEIV PKGPNTEGA SRTVCNRTG 539

SEQ ID NO: 397      moltype = AA  length = 147
FEATURE          Location/Qualifiers
source           1..147
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 397
MKPAAREARL PPRSPGLRWA LPPLLLLRL GQILCAGGTP SPIPDPSVAT VATGENGITO 60
ISSTAESFHK QNGTGTPOVE TNTSEDESS GANDSLRTPE QGSNGTDGAS QKTPSSTEPI 120

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PVSDLRVALT GVRKAALSW S NGNGTAS	147
SEQ ID NO: 398	moltype = AA length = 120
FEATURE	Location/Qualifiers
source	1..120
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 398	
MKPAAREARL PPRSPGLRWA LPLLLLLRL QOILCAGGRP SPVFDIKAVS ISPTNVILTW 60	
KSNNTAASEY KYVVVKHMKEN EKTITVVHQW WCNITGLRPA TSYVFSITPG IGNETWGDP 120	
SEQ ID NO: 399	moltype = AA length = 1338
FEATURE	Location/Qualifiers
source	1..1338
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 399	
MKPAAREARL PPRSPGLRWA LPLLLLLRL QOILCAGGTP SPIPDPSVAT VATGENGITQ 60	
ISSTAESFH K QNGTGTQVE TNTSEDESS GANDSLRTPE QGSNGTDGAS QKTPSSTGPS 120	
PVFDIKA VSI SPTNVILTWK SNDTAASEYK YVVKHKMENE KTITVVHQPW CNITGLRPAT 180	
SYVFSITPGI GNETWGDP RV IKVITEPIPV SDLRVALTGV RKAALSWNSG NGTASCRLVLL 240	
ESIGSHEELT QDSRLQVNIS GLKPGVQYNI NPYLLQSNKT KGDPGLTEGG LDASNTERSR 300	
AGSPTAPVH ESLVGPVDP S QQSQSRDTEV LLVGLEPGTR YNATVYSQAA NGTEQPQAI 360	
EFRFTNAIQVF DVTAVNISAT SLTLIWKVSD NESSSNYTYK IHVAGETDSS NLNVSEPRAV 420	
IPGLRSSTFY NITVCPVLGD IEGTPGFLQV HTPPVPSDF RVTVVSTTEI GLAWSSHDAE 480	
SFQMHHITQEG AGNSRVEIT NQSIIIGGLF PGTKYCPEIV PKGPNTEGA SRTVCNRTVP 540	
SAVFDIHVVY VTTTEMWLW KSPDGASEYV YHLVIESKGH SNHTSTYDKA ITLQGLIPGT 600	
LYNITISPEV DHVWGDPNST AQYTRPSNV S NIDVSTNTTA ATLSWQNFD ASPTYSYCLL 660	
IEKAGNNSNA TQVVT DIGIT DATVTELIPG SSYTVEFAQ VGDGIKSLEP GRKSFC TDPA 720	
SMASFDCEVV PKEPALVWK TCPGPAGNAGF ELEVSSGAWN NATHLES CSS ENGTEYRTEV 780	
TYLNFSTSYN ISITTVSCG MAAPIRNTCT TGITDPPPPD GSPNITSVSH NSVKVKFSGF 840	
EASHGPIKAY AVILTTGEAG HPSADVLKY T YEDFKKGASD TYVTYLIRTE EKGRSQSLSE 900	
VILKEYIDVGN ESTTLGYYNG KLEPLGSYRA CVAGFTNITF HPQNKG LI DG AESVVSFSRY 960	
SDAVSLPDPD CVICGAVFGC IFGLAVLIVTV GGFIFWRKRR KDAKNNEV SF SQIKSLKRSK 1020	
LIRVENPEAY FKKQQADNSNC GFEEYEDLK LVGISQPKYA AELAENRGKN RYNNVLPYDI 1080	
SRVKLVSQTH STDDYINANY MPGYSK KDP IATQGPLPNT LKDFWRMVWE KNVYAIIMLT 1140	
KCVEQGRTKC BEYWP SKQAO DYGDITVAMT SEI VLPWE TI RDFTVKNIQT SESHPLRQPH 1200	
FTSWPDHGPV DTTDLLINFR YLVRDYM KQS PPESPILVHC SAGVGR GTF IAIDRLIYQI 1260	
ENENTVDVYQ IVYDLMRHRP LMVQTEDQYV FLNQCVLDIV RSQKDSKVDL IYQNTTAMTI 1320	
YENLAPVTTF GKTNGYIA 1338	
SEQ ID NO: 400	moltype = AA length = 1342
FEATURE	Location/Qualifiers
source	1..1342
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 400	
MKPAAREARL PPRSPGLRWA LPLLLLLRL QOILCAGGTP SPIPDPSVAT VATGENGITQ 60	
ISSTAESFH K QNGTGTQVE TNTSEDESS GANDSLRTPE QGSNGTDGAS QKTPSSTGPS 120	
PVFDIKA VSI SPTNVILTWK SNDTAASEYK YVVKHKMENE KTITVVHQPW CNITGLRPAT 180	
SYVFSITPGI GNETWGDP RV IKVITEPIPV SDLRVALTGV RKAALSWNSG NGTASCRLVLL 240	
ESIGSHEELT QDSRLQVNIS GLKPGVQYNI NPYLLQSNKT KGDPGLTEGG LDASNTERSR 300	
AGSPTAPVH ESLVGPVDP S QQSQSRDTEV LLVGLEPGTR YNATVYSQAA NGTEQPQAI 360	
EFRFTNAIQVF DVTAVNISAT SLTLIWKVSD NESSSNYTYK IHVAGETDSS NLNVSEPRAV 420	
IPGLRSSTFY NITVCPVLGD IEGTPGFLQV HTPPVPSDF RVTVVSTTEI GLAWSSHDAE 480	
SFQMHHITQEG AGNSRVEIT NQSIIIGGLF PGTKYCPEIV PKGPNTEGA SRTVCNRTVP 540	
SAVFDIHVVY VTTTEMWLW KSPDGASEYV YHLVIESKGH SNHTSTYDKA ITLQGLIPGT 600	
LYNITISPEV DHVWGDPNST AQYTRPSNV S NIDVSTNTTA ATLSWQNFD ASPTYSYCLL 660	
IEKAGNNSNA TQVVT DIGIT DATVTELIPG SSYTVEFAQ VGDGIKSLEP GRKSFC TDPA 720	
SMASFDCEVV PKEPALVWK TCPGPAGNAGF ELEVSSGAWN NATHLES CSS ENGTEYRTEV 780	
TYLNFSTSYN ISITTVSCG MAAPIRNTCT TGITDPPPPD GSPNITSVSH NSVKVKFSGF 840	
EASHGPIKAY AVILTTGEAG HPSADVLKY T YEDFKKGASD TYVTYLIRTE EKGRSQSLSE 900	
VILKEYIDVGN ESTTLGYYNG KLEPLGSYRC LLRACVAGFT NITFHPO NKG LIDGAESYVS 960	
FSRYSDAVSL PQDPGVICGA VF GCFVGALV I VT VGGFIFW RKKRKDAKNN EVSF SQIKSL 1020	
KRSKLIRVEN FEAYFKKQQA DSNCGFAEY EDLKLVVGISQ PKYAAELAEN RGKNRYNNVL 1080	
PYDISRKVLS QVTHSTDDYI NAN YMPGYHS KKDFIATQGP LPNTLKD FWR MVWEKNVYAI 1140	
IMLTKCVEQG RTKCEEWPS KQADYGDIT VAMTSEIVLP EWTIRDFTVK NIQTSESHPL 1200	
RQPHFTSWPD HGVPDTT DLL INF RYLVDRY MKQSPPEPSI LVHCSAGVGR TGT FIAIDRL 1260	
IYQIENENTV DVY GIVYDLR MHRPLMVQTE DQYVFLNQCV LDIVRSQKDS KV DLIYQNTT 1320	
AMTIYENLAP VTTFGKTN YIA 1342	
SEQ ID NO: 401	moltype = AA length = 858
FEATURE	Location/Qualifiers
source	1..858
	mol_type = protein
	organism = Homo sapiens

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SEQUENCE: 401
 MLIQTKDLIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
 KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARQNI VNATANLGQS VTLVCDAEFG 240
 PEPTMSWTKD GEQIEQEEDD EKYIFSDSSS QLTIKKVVDKN DAEAYCIAE NKAGEQDATI 300
 HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKASWTRPE 360
 KQETLDGHMV VRSHARVSSL TLKSIQYTDA GEYICTASNT IGGDSQSMLY EVQYAPKLQG 420
 PVAVYTWEGN QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS 480
 ENDFGNYNCCT AVNRIGQESL EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI 540
 LYKAEWRAV GEEVWHSKWY DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISAA 600
 SEFKTQPVQG EPSAKPLEGQ MGEDGNSIKV NLIKQDDGGS PIRHYLVRYR ALSSEWKPEI 660
 RLPGSDHVM LKSLDWNAEY EVYVVAENQQ GKSAAHFVFR RTSAQPTAIP ANGSPSGLS 720
 TGAIVGLILV IFVULLVVVD ITCYFLNKGCG LFMCIAVNLC GKAGPGAKGK DMEEGKAIFS 780
 KDESKEPIVE VRTEEERTPN HDGGKHTEPN ETTPLTEPEK GPVEAKPECQ ETETKPAPE 840
 VKTVPNDATQ TKENESKA 858

SEQ ID NO: 402 moltype = AA length = 725
 FEATURE Location/Qualifiers
 source 1..725
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 402
 MLIQTKDLIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
 KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARQNI VNATANLGQS VTLVCDAEFG 240
 PEPTMSWTKD GEQIEQEEDD EKYIFSDSSS QLTIKKVVDKN DAEAYCIAE NKAGEQDATI 300
 HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKATLDGHMV 360
 VRSHARVSSL TLKSIQYTDA GEYICTASNT IGGDSQSMLY EVQYAPKLQG PVAVYTWEGN 420
 QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS ENDFGNYNCCT 480
 AVNRIGQESL EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LYKAEWRAV 540
 GEEVWHSKWY DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISAA SEFKTQPVRE 600
 PSAPKLEGQMGEDGNSIKVNLIKQDDGGSPIRHYLVRYRALSSEWKPEIRLPSGSDHVML 660
 KSLDWNAEYE VYVVAENQQG KSAAHFVFR TSAQPTAIPA TLGGNSASYTFVSSLFSAVT 720
 LLLL 725

SEQ ID NO: 403 moltype = AA length = 84
 FEATURE Location/Qualifiers
 source 1..84
 mol_type = protein
 organism = Homo sapiens
 SEQUENCE: 403 XQDDGGSPIR HYLVRYRALS SEWKPEIRLP SGSDHVMLKS LDWNAEYEVY VVAENQQGKS 60
 KAAHFVFRS AQPTAIPVTL LLLL 84

SEQ ID NO: 404 moltype = AA length = 305
 FEATURE Location/Qualifiers
 source 1..305
 mol_type = protein
 organism = Homo sapiens
 SEQUENCE: 404 YNTPSASYLE VTPDSENDGF NYNCTAVNRI GOESLEFILV QADTPSSPSI DVVEPYSSSTA 60
 QVQFDEPEAT GGVPILKKA EWRAVGEVW HSKWYDAKEA SMEGIVTIHG LKPETTYAVR 120
 LAALNKGGLG EISAASEFKT QPVHSPPPAA SASSSTPVPL SPPDTTWPLP ALATTEPARE 180
 PSAPKLEGQMGEDGNSIKVNLIKQDDGGSPIRHYLVRYRALSSEWKPEIRLPSGSDHVML 240
 KSLDWNAEYE VYVVAENQQG KSAAHFVFR TSAQPTAIPA TLGGNSASYTFVSSLFSAVT 300
 LLLL 305

SEQ ID NO: 405 moltype = AA length = 468
 FEATURE Location/Qualifiers
 source 1..468
 mol_type = protein
 organism = Homo sapiens
 SEQUENCE: 405 XSGSDHVMLK SLWDWNAEYEV YVVAENQQGK SKAAHFVFR SAQPTAIPAN GSPTSGLSTG 60
 AIVGILIVIF VLLVVVDIT CYFLNKCGLF MCIAVNLCGK AGPGAKGKDM EEGKAASKD 120
 ESKEPIVEVR TEEERTPNHD GGKHTEPNET TPLTEPELPA DTTATVEDML PSVTTVTNS 180
 DTITETFATA QNSPTSETTT LTSSIAPPAT ATPDSNSVPA QGATPSKGPS ASAPSPAPAS 240
 APKVPLVDSL SDPTSTPAA SNLSSVLAN QGAVLSPSAP AGVGEASKAP PASKPTPAPV 300
 PTPTGAASPL AAAAAPATEA PQAKQEAPST KGPDPEPTQP GAAKSPAEEA TALASPKEA 360
 ASVSTTNPSQ GEDFKMDEGN FKTPDIDLAK DVFAALGSPA PAAGASGQAP ELAPSTADSS 420
 VSPAPAKTEK GPVEAKPECQ ETETKPAPE VKTVPNDATQ TKENESKA 468

SEQ ID NO: 406 moltype = AA length = 372
 FEATURE Location/Qualifiers

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source          1..372
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 406
XTPSSPSIDQ VEPYSSTAQV QFDEPEATGG VPILKYKAESW RAVGEEVVHWS KWDYDAKEASM 60
EGIVTIVGLK PETTYAVRLA ALNGKGLGEI SAASEFKTQP VHSPPPPASA SSSTPVPLSP 120
PDKGEPSAPK LEGQMGEDGN SIKVNLIKQD DGGSPIRHYL VRYRALSEW KPEIRLPGS 180
DHVMLKSLDW NAEYEVYVVA ENQQGKSAA HFVERTSQAQP TAIPANGSPT SGLSTGAIVG 240
ILIVIFVLLL VVVDITCYFL NKCGLFMCIA VNLCGKAGPG AKGKDMEEGK AAFSKDESKE 300
PIVEVRTEEE RTPNHDDGGKH TEPNETTPLT EPEKGVPREAK PECQETETKTP APAEVKTVPN 360
DATQTKENES KA                                372

SEQ ID NO: 407      moltype = AA  length = 364
FEATURE           Location/Qualifiers
source            1..364
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 407
MLQTKDLIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFLL CQVAGDAKDK DISWFSPNGE 60
KLTPNQRIS VVWNNDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARONI VNATANLGQS VTLVCDAEFG 240
PEPTMSWTKD GEQIEQEEEDD EKYIIFSDSS QLTIKVVDKN DEAEYICIAE NKAGEQDATI 300
HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPIPSIT WRTSTRNISS EEKASWTRPE 360
KQEV

SEQ ID NO: 408      moltype = AA  length = 848
FEATURE           Location/Qualifiers
source            1..848
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 408
MLQTKDLIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFLL CQVAGDAKDK DISWFSPNGE 60
KLTPNQRIS VVWNNDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARONI VNATANLGQS VTLVCDAEFG 240
PEPTMSWTKD GEQIEQEEEDD EKYIIFSDSS QLTIKVVDKN DEAEYICIAE NKAGEQDATI 300
HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPIPSIT WRTSTRNISS EEKASWTRPE 360
VRSHARVSSL TLKSIQYTDA GEYICTASNT IGQDSQSMYL EVQYAPKLQG PVAVYTWEGR 420
QVNITCEVFA YPSATISWFR DGQLLPSSNY SNKIYNTPS ASYLEVTPDS ENDFGNYNCT 480
AVNRIGQESL EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LKYKAEWRRAV 540
GEEVWHSKWY DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISA SEFKTQPVQG 600
EPSAPKLEQG MGEDGNSIKV NLIKQDDGGS PIRHYLVRYY ALSSEWKPEI RLPGSDHVHM 660
LKSLDWNAEY EVYVVAENQQ GKSAAHFVFR RTSAQPTAIP ANGSPTSGLS TGAIVGILIV 720
IFVLLVVVD ITCYFLNKCG LFMCIAVNLC GAKPGAKGD MEEGKAAFS KDEKEPIIVE 780
VRTEEERTPN HDGGKHTEPN ETPLTEPEK GPVEAKPECQ ETETKPAPEE VKTPNDAEQ 840
TENESKA                                848

SEQ ID NO: 409      moltype = AA  length = 165
FEATURE           Location/Qualifiers
source            1..165
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 409
EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LKYKAEWRRAV GEEVWHSKWY 60
DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISA SEFKTQPVHS PPPPASASSS 120
TPVPLSPPD TWPPLPALATT EPAKNIAQNH CCNMFQAGLH NALMK                165

SEQ ID NO: 410      moltype = AA  length = 357
FEATURE           Location/Qualifiers
source            1..357
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 410
XFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LKYKAEWRRAV GEEVWHSKWY 60
DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISA SEFKTQPVRE PSAPKLEGQM 120
GEDGNSIKVN LIKQDDGGSP IRHYLVRYYA LSSEWKPEIR LPSGSDHVML KSLDWNAEYE 180
VYVVAENQQ GKSAAHFVFR TSAQPTAIP ANGSPTSGLS TGAIVGILIVI FVLLVVVDI 240
TCYFLNKCG LFMCIAVNLC GAKPGAKGD MEEGKAAFSK DESKEPIIVE RTEEERTPNH 300
DGGKHTEPNE TTPLTEPEKG PVEAKPECQE TETKPAPEE VKTPNDAEQ TENESKA    357

SEQ ID NO: 411      moltype = AA  length = 133
FEATURE           Location/Qualifiers
source            1..133
               mol_type = protein
               organism = Homo sapiens

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SEQUENCE: 411				
MLQTKDLIWT LFFLGLTAAKP KITYVENOTA MELEEQVTLT CEASGDPIPS ITWRTSTRNI	60			
SSEEKTLGDH MVVRSHARVS SLTLKSIQYT DAGEYICTAS NTIGQDSQSM YLEVQYAPKL	120			
QGPVAVYTWE GNQ	133			
SEQ ID NO: 412	moltype = AA length = 858			
FEATURE	Location/Qualifiers			
source	1..858			
	mol_type = protein			
	organism = Homo sapiens			
SEQUENCE: 412				
MLQTKDLIWT LFFLGLTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE	60			
KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF	120			
KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK	180			
KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARQNI VNATANLGQS VTLVCDAEFG	240			
PEPTMSWKD GEQIEQEEEDD EKYIIFSDDSS QLTIKKVVDK DEAEYICIAE NKAGEQDATI	300			
HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKASWTRPE	360			
KQETLTDGHMV VRSHARVSSL TLKSIQYTDA GEYICTASNT IGQDSQSMLY EVQYAPKLQG	420			
PVAVYTWEGRN QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS	480			
ENDFCNYNCT AVNRIGQESL EFILVQADTP SSPSIDQVFP YSSTAQVQFD EPEATGGVPI	540			
LKYKAERWRAV GEEVWHSKWY DAKEASMIGI VTIVGLKPET TYAVRLAALN GKGLGEISAA	600			
SEPKTQPVPG EPSAPKLEGQ MGEDGNSIKV NLIKQDDGGS PIRHYLVRYR ALSSEWKPEI	660			
RLPSGSDHVM LKSLDWNAEY EVYVVAENQQ GKSAAHFVFR RTSAQPTAIP ANGSPSGLS	720			
TGAIVGILIV IFVLLLVVVD ITCYFLNKCG LFMCIAVNLCKAGPGAKGK DMEEGKAAFS	780			
KDESKEPIVE VRTEEEERTPN HDGGKHTEPN ETTPLTEPEK GPVEAKPECQ ETETKPAPE	840			
VKTVPNDATQ TKENESKA	858			
SEQ ID NO: 413	moltype = AA length = 884			
FEATURE	Location/Qualifiers			
source	1..884			
	mol_type = protein			
	organism = Homo sapiens			
SEQUENCE: 413				
MLQTKDLIWT LFFLGLTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE	60			
KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF	120			
KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK	180			
KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARQNI VNATANLGQS VTLVCDAEFG	240			
PEPTMSWKD GEQIEQEEEDD EKYIIFSDDSS QLTIKKVVDK DEAEYICIAE NKAGEQDATI	300			
HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKASWTRPE	360			
KQEVHAPWNW QVGRQKGQAG SAGFPGSHEQ LDGHMVRSH ARVSSLTLKS IQYTDAGEYI	420			
CTASNTIQGD SQSMSMLEVQY APKLQGPVAV YTWEGRNQVNT TCEVFAYPSA TISWFRDGQL	480			
LPSSNNYSNIK IYNTPSASYL EVTPDSENDF GNYNCTAVMR IQQESLEFIL VQADTPSSPS	540			
IDQVEPYST AQVQFDEPEA TGGVPILKQY AEWRAVEGEEV WHSKWYDAKE ASMEGIVTIV	600			
GLKPETTYAV RLAALNGKGL GEISAASEFK TQPVGEPSA PKLEGQMGED GNSIKVNLK	660			
QDDGGSPPIRHL VLVRYRALSS EWKPEIRLPS GSDHVMLKSL DWNAEYEVVV VAENQGKSK	720			
AAHFVFRNTSA QPTAIPANGS PTSGLSTGAI VGILIVIFVL LLVVVDITCY FLNKGFLFMC	780			
IAVNLCGKAG PGAKGKDMEE GKAFAFSKDES KEPIVEVRTE EERTPNHDGG KHTEPNETTP	840			
LTEPEKGPGVE AKPECQETET KPAPAEVKTV PNDATQTKEN ESKA	884			
SEQ ID NO: 414	moltype = AA length = 848			
FEATURE	Location/Qualifiers			
source	1..848			
	mol_type = protein			
	organism = Homo sapiens			
SEQUENCE: 414				
MLQTKDLIWT LFFLGLTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE	60			
KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF	120			
KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK	180			
KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQARQNI VNATANLGQS VTLVCDAEFG	240			
PEPTMSWKD GEQIEQEEEDD EKYIIFSDDSS QLTIKKVVDK DEAEYICIAE NKAGEQDATI	300			
HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKTLGDHMV	360			
VRSHARVSSL TLKSIQYTDA GEYICTASNT IGQDSQSMLY EVQYAPKLQG PVAVYTWEGR	420			
QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS ENDFCNYNCT	480			
AVNRIGQESL EFILVQADTP SSPSIDQVFP YSSTAQVQFD EPEATGGVPI LKYKAERWRAV	540			
GEEVWHSKWY DAKEASMIGI VTIVGLKPET TYAVRLAALN GKGLGEISAA SEFKTQPVPG	600			
EPSAPKLEGQ MGEDGNSIKV NLIKQDDGGS PIRHYLVRYR ALSSEWKPEI RLPSGSDHVM	660			
LKSLDWNAEY EVYVVAENQQ GKSAAHFVFR RTSAQPTAIP ANGSPSGLS TGAIVGILIV	720			
IFVLLLVVVD ITCYFLNKCG LFMCIAVNLCKAGPGAKGK DMEEGKAAFS KDESKEPIVE	780			
VRTEEEERTPN HDGGKHTEPN ETTPLTEPEK GPVEAKPECQ ETETKPAPE VKTVPNDATQ	840			
TKENESKA	848			
SEQ ID NO: 415	moltype = AA length = 884			
FEATURE	Location/Qualifiers			
source	1..884			
	mol_type = protein			
	organism = Homo sapiens			

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SEQUENCE: 415
 MLQTKDLDIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
 KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQRONI VNATANLGQS VTLVCDAEFG 240
 PEPTMSWTKD GEQIEQEEDD EKYIFSDSSS QLTICKVDKN DEAEYICIAE NKAGEQDATI 300
 HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKASWTRPE 360
 KQEVHAPWNW QVGRQKGQAC SAGFPGSHEI LDGHMVVRSH ARVSSLTLKS IQYTDAGEYI 420
 CTASNTIGQD SQSMYLEVQY APKLQGPVAV YTWEQNQVN1 TCEVFAYPSA TISWFRDGQL 480
 LPSSNYSNIK IYNTTPSASYL EVTPDSENDF GNYNCTAVNR IGGESLEFIL VQADTPSSPS 540
 IDQVEPYNSIKAQVQFDEPEA TCGVPILKYK AEWRAVGEEV WHSKWYDAKE ASMEGIVTIV 600
 GLKPETTYAV RLAALNGKGL GEISAASEFK TQPVQGEPSA PKLEGQMGED GNSIKVNLIK 660
 QDDGGSPIRH YLVRYRALSS EWKPEIRLPS GSDHVMLKSL DWNAEYEVVY VAENQQGKSK 720
 AZAHFVFRRTSA QPTAIPANGS PTSGLSTGAI VGILIVIFP LLVVDITCY FLNKCGLFMC 780
 IAVNLCGKAG PGAKGKDMEE GKAFAFSKDES KEPIVEVRTE EERTPNHDGG KHTEPNETTP 840
 LTREPEKGPKVE AKPECQETET KPAPEVKTV PNDATQTKEN ESKA 884

SEQ ID NO: 416 moltype = AA length = 136
 FEATURE Location/Qualifiers
 source 1..136
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 416
 MLQTKDLDIWT LFFLGTAGEP SAPKLEGQMG EDGNSIKVN1 IKQDDGGSPI RHYLVRYRAL 60
 SSEWKPEIRL PSGSDHVMLK SLDWNAEYEV YVVAENQQK SKAAHVFVFT SAQPTAIPAN 120
 GSPTSGLSTG AIVGIL 136

SEQ ID NO: 417 moltype = AA length = 726
 FEATURE Location/Qualifiers
 source 1..726
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 417
 MLQTKDLDIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
 KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQRONI VNATANLGQS VTLVCDAEFG 240
 PEPTMSWTKD GEQIEQEEDD EKYIFSDSSS QLTICKVDKN DEAEYICIAE NKAGEQDATI 300
 HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKTLGDGHMV 360
 VRSHARVSSL TLKSIQYDTA GEYICTASNTT IGGDSQSMLY EVQYAPKLQG PVAVYTWEGRN 420
 QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS ENDFGNYNCT 480
 AVNRIGQESL EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LKYKAERWRAV 540
 GEEVWHSKWY DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISAA SEFKTQPVQG 600
 EPSAPKLEGQ MGEDGNSIKV NLIKQDDGGS PIRHYLVRYR ALSSEWKPEI RLPGSDHVM 660
 LKSLDWNAEY EVYVVAENQQ GKSAAHVFV RTSAQPTAIP ATLGGNSASY TVFSLFLSAV 720
 TLLLLC 726

SEQ ID NO: 418 moltype = AA length = 761
 FEATURE Location/Qualifiers
 source 1..761
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 418
 MLQTKDLDIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180
 KTDEGTYRCE GRILARGEIN FKDIQVIVNV PPTIQRONI VNATANLGQS VTLVCDAEFG 240
 PEPTMSWTKD GEQIEQEEDD EKYIFSDSSS QLTICKVDKN DEAEYICIAE NKAGEQDATI 300
 HLKVFAKPKI TYVENQTAME LEEQVTLTCE ASGDPPIPSIT WRTSTRNISS EEKTLGDGHMV 360
 VRSHARVSSL TLKSIQYDTA GEYICTASNTT IGGDSQSMLY EVQYAPKLQG PVAVYTWEGRN 420
 QVNITCEVFA YPSATISWFR DGQLLPSSNY SNIKIYNTPS ASYLEVTPDS ENDFGNYNCT 480
 AVNRIGQESL EFILVQADTP SSPSIDQVEP YSSTAQVQFD EPEATGGVPI LKYKAERWRAV 540
 GEEVWHSKWY DAKEASMEGI VTIVGLKPET TYAVRLAALN GKGLGEISAA SEFKTQPVHS 600
 PPPPASASSS TPVPLSPPDT TWPLPLATL EPATGEPSAP KLEGQMGEDG NSIKVNLIKQ 660
 DDGGSPIRH LVRYRALSSE WKPEIRLPSG SDHVMLKSLD WNAEYEVVY AENQQGKSKA 720
 AHFVFRRTSAQ PTAIPATLGG NSASYTFVSL LFSAVTLLL C 761

SEQ ID NO: 419 moltype = AA length = 761
 FEATURE Location/Qualifiers
 source 1..761
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 419
 MLQTKDLDIWT LFFLGTAVSL QVDIVPSQGE ISVGESKFFL CQVAGDAKDK DISWFSPNGE 60
 KLTPNQQRIS VVWNDDSSST LTIYNANIDD AGIYKCVVTG EDGSESEATV NVKIFQKLMF 120
 KNAPTPQEFR EGEDAVIVCD VVSSLPPPTII WKHKGRDVIL KKDVRFIVLS NNYLQIRGIK 180

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KTDEGTYRCE	GRILARGEIN	FKDIQVIVNV	PPTIQARQNI	VNATANLGQS	VTLVCDAEGF	240
PEPTMSWTKD	GEQIQQEEDD	EKYIFSDSSS	QLTIKKVVDK	DEAEYICIAE	NKAGEQDATI	300
HLKVFAKPKI	TYVENQTAME	LEEQVTLTCE	ASGDPIPSIT	WRTSTRNISS	EEKTLGDGHMV	360
VRSHARVSSL	TLKSIIQYTDA	GEYICTASNT	IGODSQSMSYL	EVQYAPKLQG	PVAVYTWEGR	420
QVNITCEVFA	YPSATISWFR	DGQLLPSSNY	SNIKIYNTPS	ASYLEVTPDS	ENDFGNYNCT	480
AVNRIGQESL	EFLVQADTP	SSPSIDQVFP	YESTAAQVQFD	EPEATGGVPI	LKYKAERWRAV	540
GEEVWHHSWKY	DAKEASMEGI	VTIVGLKPET	TYAVRLLAALN	GKGLGEISAA	SEFKTQPVHS	600
PPPPASASSS	TPVPLSPPD	TWPLPALATT	EPAKGEPSAP	KLEGQMGEDG	NSIKVNLIKQ	660
DDGGSPIRHY	LVRYRALSSE	WKPEIRLPSG	SDHVMLKSLD	WNAEYEVYVV	AENQQGKSKA	720
AHFVFRRTSAQ	PTAIPATLGG	NSASYTFVSL	LFSAVTLLL C			761

SEQ ID NO: 420	moltype = AA	length = 88				
FEATURE	Location/Qualifiers					
source	1..88					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 420						
MSDILRELLC	VSEKAANIAR	ACRQQEALFQ	LLIEEKKEGE	KNKKFAVDFK	TLADVLVQEV	60
IKQNMMENKFP	GLEKNIFGEE	SNEFTNDW				88

SEQ ID NO: 421	moltype = AA	length = 190				
FEATURE	Location/Qualifiers					
source	1..190					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 421						
MSDILRELLC	VSEKAANIAR	ACRQQEALFQ	LLIEEKKEGE	KNKKFAVDFK	TLADVLVQEV	60
IKQNMMENKFP	GLEKNIFGEE	SNEFTNDW	KITLRLCSTE	EETAELLSKV	LNGNKVASEA	120
LARVVHQDVA	FTDPTLDSTE	INVPOQDILGI	WVDPIDSTYQ	YIKGSADIKS	NQGIFPCGLQ	180
CVTILIGVYD						190

SEQ ID NO: 422	moltype = AA	length = 30				
FEATURE	Location/Qualifiers					
source	1..30					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 422						
MSDILRELLC	VSEKAANIAR	ACRQQEALFQ				30

SEQ ID NO: 423	moltype = AA	length = 68				
FEATURE	Location/Qualifiers					
source	1..68					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 423						
MSDILRELLC	VSEKAANIAR	ACRQQEALFQ	LLIEEKKEGE	KNKKFAVDFK	TLADVLVQEV	60
IKQNMMENK						68

SEQ ID NO: 424	moltype = AA	length = 831				
FEATURE	Location/Qualifiers					
source	1..831					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 424						
MSKKGRSKGE	KPEMETDAVQ	MANEELRAKL	TSIQIEFOQE	KSKVGKLRER	LQEAKELEREQ	60
EQRRTAYIS	ELAKALKHEEK	TKELQALREG	LIRQHEQEAA	RTAKIKEGEL	QRLQATLNLV	120
RDGAADKVKT	ALLTEAREEA	RRAFDGERLR	LQOEILELKA	ARKQAEEALS	NCMQADKTKA	180
ADLRAAYQAH	QDEVHRIKRE	CERDIRRLMD	EIKGKDRVIL	ALEKELGVQA	GQTQKLLQK	240
EALDEQLVQV	KEAERHHSSE	KRELPPGIGD	MVELMGVQDQ	HMDERDVRFF	QLKTAELNSV	300
IRKLEDRLNTL	RSRTEVQLK	PLVEKNKRMN	KKNEDLQLQSI	QRMEEKIKNL		360
TRENVENMEK	LSAQASLKRH	TSLNDLSSLTR	DEQEIEFLRL	QVLEQOHVID	DLSLERERLL	420
RSKRHRGKSL	KPPKKHVVET	FFGFDEESVD	SETLSETS	YTDRTDRPAT	PEEDLDDATA	480
REBADLRFQ	LTRYQALQR	AYALLQEQVG	GTLDAEEREAR	TREQLQADLL	RCQAKIEDLE	540
KLLVEKGQDS	KWVEKQLL	RTNQDLLEKI	YRLEMEEENQL	KNEMQDAKDQ	NELLEFRVLE	600
LEERERRSPA	FNLQITTFPE	NHSSALQLPFC	HQEGVKDVNV	SELMKKLDIL	GDNGNLRNEE	660
QVAAIIQAGTV	LALCEKWLQK	IEGTEAALTQ	KMLDLEKEKD	LFSRQKGYLE	EELDYRKQAL	720
DQAYLKIQDL	EATLYTALQQ	EPGRRAGEAL	SEGQREDLQA	AVEKVRQRQIL	RQSREFDSQI	780
LRERMELLQQ	AQQRIRELED	KLEFQKRHLK	ELEEKFLFL	LFPSLAFILE	P	831

SEQ ID NO: 425	moltype = AA	length = 646				
FEATURE	Location/Qualifiers					
source	1..646					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 425						
MSKKGRSKGE	KPEMETDAVQ	MANEELRAKL	TSIQIEFOQE	KSKMDEIKGK	DRVILALEKE	60

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LGVQAGQTQK	LLLQKEALDE	QLVQVKEAER	HHSSPKRELP	PGIGDMVELM	GVQDQHMDER	120
DVRRFQLKIA	ELNSVIRKLE	DRNTLLADER	NELLKRSRET	EVQLKPLVEK	NKRMNKKNED	180
LLQSIQRMEE	KIKNLTRENV	EMKEKLSAQAA	SLKRHTSLLND	LSSLTRDEQEII	EFLRLQVLEQ	240
QHVIDDLSLK	HVETTFGFD	EESVDSETLS	ETSYNTDRTD	RTPATPEEDL	DDATAREAD	300
LRFCQLTREY	QALQRAYALL	QEQQGGTLDA	EREARTREQL	QADLLRCQAK	IEDLEKLVE	360
KGQDSKWKVEE	KQLLIRTNQD	LLEKIYRLEM	EEQNLKNEMQ	DAKDQNELLIE	FRVLELEERE	420
RRSPAFNLQI	TTFPENHSSA	QLQFCHQEGV	KDVNVSELMK	KLDILGDNGN	LRNEEQVAII	480
QAGTVLALCE	KWLQKIEGTE	AALTQKMLLDL	EKEKDLFSQL	KGYLEEEELDY	RKQALDQAYL	540
KIQDLEATLY	TALQQEPEGR	AGEALSEGQR	EDLQAAVEKV	RRQILRQSRE	FDSQILRERM	600
ELLQQAQQR	RELEDKLEFQ	KRHLKELEEK	FLFLFLFFSL	AFILWP		646
 SEQ ID NO: 426		moltype = AA	length = 66			
FEATURE		Location/Qualifiers				
source		1..66				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 426						
MAAIRKKLVI	VGDGACGKTC	LLIVFSKDQF	PEVYVPTVFE	NYIADIEVDG	KQTGSVTWAE	60
SLCLWV						66
 SEQ ID NO: 427		moltype = AA	length = 66			
FEATURE		Location/Qualifiers				
source		1..66				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 427						
MAAIRKKLVI	VGDGACGKTC	LLIVFSKDQF	PEVYVPTVFE	NYIADIEVDG	KQTGSVTWAE	60
SLCLWV						66
 SEQ ID NO: 428		moltype = AA	length = 66			
FEATURE		Location/Qualifiers				
source		1..66				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 428						
MAAIRKKLVI	VGDGACGKTC	LLIVFSKDQF	PEVYVPTVFE	NYIADIEVDG	KQTGSVTWAE	60
SLCLWV						66
 SEQ ID NO: 429		moltype = AA	length = 500			
FEATURE		Location/Qualifiers				
source		1..500				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 429						
MPPAVGGPVG	YTPPDGGWGW	AVVIGAFISI	GFSYAFPKSI	TVFFKEIEGI	FHATTSEVSW	60
ISSIMLAVMY	GGGPISSILV	NKYGSRIVMI	VGGCLSGCGL	IAASFNCNTVQ	QLYVCIGVIG	120
GLGLAFNLNP	ALTMIGKYFY	KRRLPLANGLA	MAGSPVFLCT	LAPLNQVFFG	IFGWRGSFLI	180
LGGLLLNCCV	AGALMRPIGP	KPTKAGKDKS	KASLEKAGKS	GVKKDLHDAN	TDLIGRHPKQ	240
EKRSVFQTIN	QFLDLTFLFT	RGFLLYLSGN	VIMFFGLFAP	LVFLSSYGKS	QHYSSEKSASF	300
LLSILAFVDM	VARPSMGLVA	NTKPIRPRIQ	YFFAASVAN	GVCHMLAPLS	TTYVGFCVYA	360
GFFGFAFGWL	SSVLFETLMD	LVGPORFSSA	VGLVTIVECC	PVLLGPPLLG	RLNDMYGDYK	420
TYYWACGVVL	IISGIIYLFIG	MGINYRLLAK	EOKANEQKKE	SKEEETSIDV	AGKPNEVTKA	480
AESPDQKTD	GGPKEEESPV					500
 SEQ ID NO: 430		moltype = AA	length = 215			
FEATURE		Location/Qualifiers				
source		1..215				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 430						
MPPAVGGPVG	YTPPDGGWGW	AVVIGAFISI	GFSYAFPKSI	TVFFKEIEGI	FHATTSEVSW	60
ISSIMLAVMY	GGGPISSILV	NKYGSRIVMI	VGGCLSGCGL	IAASFNCNTVQ	QLYVCIGVIG	120
GLGLAFNLNP	ALTMIGKYFY	KRRLPLANGLA	MAGSPVFLCT	LAPLNQVFFG	IFGWRGSFLI	180
LGGLLLNCCV	AGALMRPIGP	KPTKAGKDKS	KASLEKAGKS	GVKKDLHDAN	TDLIGRHPKQ	240
EKRSVFQTIN	QFLDLTFLFT	RGFLLYLSGN	VIMFFGLFAP	LVFLSSYGKS	QHYSSE	215
 SEQ ID NO: 431		moltype = AA	length = 296			
FEATURE		Location/Qualifiers				
source		1..296				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 431						
MPPAVGGPVG	YTPPDGGWGW	AVVIGAFISI	GFSYAFPKSI	TVFFKEIEGI	FHATTSEVSW	60
ISSIMLAVMY	GGGPISSILV	NKYGSRIVMI	VGGCLSGCGL	IAASFNCNTVQ	QLYVCIGVIG	120
GLGLAFNLNP	ALTMIGKYFY	KRRLPLANGLA	MAGSPVFLCT	LAPLNQVFFG	IFGWRGSFLI	180
LGGLLLNCCV	AGALMRPIGP	KPTKAGKDKS	KASLEKAGKS	GVKKDLHDAN	TDLIGRHPKQ	240
EKRSVFQTIN	QFLDLTFLFT	RGFLLYLSGN	VIMFFGLFAP	LVFLSSYGKS	QHYSSE	296

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SEQ ID NO: 432      moltype = AA length = 456
FEATURE          Location/Qualifiers
source           1..456
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 432
MPPAVGGPVG YTPPDGGWGW AVVIGAFISI GFSYAFPKSI TVFFKEIEGI FHATTSEVSW 60
ISSIMLAVMY GGGPISSILV NKYGSRIVMI VGGCLSGCGL IAASFNCNTVQ QLYVCIGVIG 120
GLGLAFLNLP ALTMIGKYFY KRRPLANGLA MAGSPVFLCT LAPLNQVFFG IFGWRGSFLI 180
LGGLLLNCCV AGALMRPIGP KPTKAGKDKS KASLEKACKS GVKKDLHDAN TDLIGRHPKQ 240
EKRSVFQTIN QFLDLTFLFTH RGFLLYLSGN VIMFFGLFAP LVFLSSYGKS QHYSSEKSASF 300
LLSILAFVDM VARPSMGLVA NTKPIRPRIQ YFFAASVAN GVCHMLAPLS TTYYVGFCVYA 360
GFFGFARFGWL SSVLFETLMD LVGPQRFSSA VGLVTIVECC PVLLGPPLLG RLNDMYGDYK 420
YTYYWACGVVL IISGIYLFIG MGINYRLLAK EQKANE 456
AESPDKDTE GGPKEEEESPV

SEQ ID NO: 433      moltype = AA length = 500
FEATURE          Location/Qualifiers
source           1..500
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 433
MPPAVGGPVG YTPPDGGWGW AVVIGAFISI GFSYAFPKSI TVFFKEIEGI FHATTSEVSW 60
ISSIMLAVMY GGGPISSILV NKYGSRIVMI VGGCLSGCGL IAASFNCNTVQ QLYVCIGVIG 120
GLGLAFLNLP ALTMIGKYFY KRRPLANGLA MAGSPVFLCT LAPLNQVFFG IFGWRGSFLI 180
LGGLLLNCCV AGALMRPIGP KPTKAGKDKS KASLEKACKS GVKKDLHDAN TDLIGRHPKQ 240
EKRSVFQTIN QFLDLTFLFTH RGFLLYLSGN VIMFFGLFAP LVFLSSYGKS QHYSSEKSASF 300
LLSILAFVDM VARPSMGLVA NTKPIRPRIQ YFFAASVAN GVCHMLAPLS TTYYVGFCVYA 360
GFFGFARFGWL SSVLFETLMD LVGPQRFSSA VGLVTIVECC PVLLGPPLLG RLNDMYGDYK 420
YTYYWACGVVL IISGIYLFIG MGINYRLLAK EQKANE 480
AESPDKDTE GGPKEEEESPV
500

SEQ ID NO: 434      moltype = AA length = 109
FEATURE          Location/Qualifiers
source           1..109
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 434
MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRFIIDR IQILPRNGNC 60
PRKEIIIWKK NKSIVCVDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP 109
109

SEQ ID NO: 435      moltype = AA length = 729
FEATURE          Location/Qualifiers
source           1..729
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 435
MDDLTLLDLL ECPVCPEKLD VTAKVLPCQH TFCKPCLQRV FKAHKELRCP ECRTPVFSNI 60
EALPANLLLV RLLDGVRSGQ SSGRGGSFRR PGTMTLQDGR KSRTNPRRLQ ASPFRLVPNV 120
RIHMDGVPR A KALCNYRGQN PGDLRFNKGD IILLRRQLDE NWYQGEINGI SGNFPASSVE 180
VIKQLPQPPI LCRALYNFDL RGKDSENQD CLTFLKDDII TVISRVDENW AEGKLGDKV 240
IFPILFVEPN LTARHLLNEKN KGRQSSRTKN LSLVSSSSRG NTSTLRRGPG SRRKVPQF 300
ITTAALNTLN R MVHSPSGRHNM VEISTPVLI SSNPSSVITQ P MEKADVPSSC VGQVSTYHPA 360
PVSPGHSTAV VSLPGSQQHL SANMFVALHS YSAHGPDELD LQKGEGVRL GKQCDGWL 420
VSLVTRGVGI FPNNYVPIIF RKTSSFPDSR SPGLYTTWTL STSSVSSQGS ISEGDPQR 480
PFKSVFVPTA IVNPVRSTAG PGTLQGQSLR KGRSSMRKNG SLQRPLQSGI PTLVVGLSLR 540
SPTMVLRPQQ PQFYQPQGIP SSPSAVVEM GSKPALTGEP ALTCISRGSE AWIHSAASSL 600
IMEDKEIPIK SEPLPKPPAS APPSILVKPE NSRNGIEKQV KVTRFQNYSP PPTKHYTSHP 660
TSGKPEOPAT LKASQPEAAS LGPEMTVLF A HRSGCHSGQQ TDLRRKSALG KATTLVSTAS 720
GTQTVFPSK 729

SEQ ID NO: 436      moltype = AA length = 729
FEATURE          Location/Qualifiers
source           1..729
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 436
MDDLTLLDLL ECPVCPEKLD VTAKVLPCQH TFCKPCLQRV FKAHKELRCP ECRTPVFSNI 60
EALPANLLLV RLLDGVRSGQ SSGRGGSFRR PGTMTLQDGR KSRTNPRRLQ ASPFRLVPNV 120
RIHMDGVPR A KALCNYRGQN PGDLRFNKGD IILLRRQLDE NWYQGEINGI SGNFPASSVE 180
VIKQLPQPPI LCRALYNFDL RGKDSENQD CLTFLKDDII TVISRVDENW AEGKLGDKV 240
IFPILFVEPN LTARHLLNEKN KGRQSSRTKN LSLVSSSSRG NTSTLRRGPG SRRKVPQF 300
ITTAALNTLN R MVHSPSGRHNM VEISTPVLI SSNPSSVITQ P MEKADVPSSC VGQVSTYHPA 360
PVSPGHSTAV VSLPGSQQHL SANMFVALHS YSAHGPDELD LQKGEGVRL GKQCDGWL 420
VSLVTRGVGI FPNNYVPIIF RKTSSFPDSR SPGLYTTWTL STSSVSSQGS ISEGDPQR 480
PFKSVFVPTA IVNPVRSTAG PGTLQGQSLR KGRSSMRKNG SLQRPLQSGI PTLVVGLSLR 540

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SSEQ ID NO: 437	moltype = AA length = 398
FEATURE	Location/Qualifiers
source	1..398
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 437	
MSGSSLPSAL ALSLLLVSWS LLPGPGAAQN AGFVKSPMSE TKLTGDAFEL YCDVVGSPPTP	60
EIQWWYAEVN RAESFRQLWD GARKRRTVTN TAYGSNGVSV LRITRLTLED SGTYECRASN	120
DPKRNDLRQN PSITWIRQAQ TISVLQKPRI VTSEEVIIRD SPVLPVTLCQ NLTSSSHTLT	180
YSWTKGVE LSATRKNASN MEYRINKPRA EDSGEYHCVY HFVSAPKANA TIEVKAAPDI	240
TGHKRSEENKN EGQDATMYCK SVGYPHPDWI WRKKENGMPM DIVNTSGRFF IINKENYTEL	300
NIVNLQITED PGEYECNATN AIGSASVVTV LRVRSHLAPL WPFLGILAEI IILVVIIVVY	360
EKRKRDPDEVP DDDEPAGPMK TNSTNNHKDK NLRQRNTN	398
SSEQ ID NO: 438	moltype = AA length = 282
FEATURE	Location/Qualifiers
source	1..282
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 438	
MSGSSLPSAL ALSLLLVSWS LLPGPGAAQN EPRIVTSEEV IIRDSPVLPV TLQCNLTSSS	60
HTLTYSWTK NGVELSATRK NASNMEYRIN KGRAEDSGEY HCIVYHFVSAP KANATIEVKA	120
APDITGHKRS ENKNEGQDAT MYCKSVGYPH PDWIWRKKEN GMPPMDIVNTS GRFFIINKEN	180
YTELNIVNLQ ITEDPGEYEC NATNAIGSAS VVTVLRVRSH LAPLWPFLGI LAEIIILVVI	240
IVVYEKRKRDP DEVPDDDEPA GPMKTNSTNN HKDKNLRQRNTN	282
SSEQ ID NO: 439	moltype = AA length = 278
FEATURE	Location/Qualifiers
source	1..278
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 439	
MSGSSLPSAL ALSLLLVSWS LLPGPGAAQN EPRIVTSEEV IIRDSPVLPV TLQCNLTSSS	60
HTLTYSWTK NGVELSATRK NASNMEYRIN KGRAEDSGEY HCIVYHFVSAP KANATIEVKA	120
APDITGHKRS ENKNEGQDAT MYCKSVGYPH PDWIWRKKEN GMPPMDIVNTS GRFFIINKEN	180
YTELNIVNLQ ITEDPGEYEC NATNAIGSAS VVTVLRVRSH LAPLWPFLGI LAEIIILVVI	240
IVVYEKRKRDP DEVPDDDEPA GPMKTNSTNN HKDKNLRQRNTN	278
SSEQ ID NO: 440	moltype = AA length = 394
FEATURE	Location/Qualifiers
source	1..394
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 440	
MSGSSLPSAL ALSLLLVSWS LLPGPGAAQN AGFVKSPMSE TKLTGDAFEL YCDVVGSPPTP	60
EIQWWYAEVN RAESFRQLWD GARKRRTVTN TAYGSNGVSV LRITRLTLED SGTYECRASN	120
DPKRNDLRQN PSITWIRQAQ TISVLQKPRI VTSEEVIIRD SPVLPVTLCQ NLTSSSHTLT	180
YSWTKGVE LSATRKNASN MEYRINKPRA EDSGEYHCVY HFVSAPKANA TIEVKAAPDI	240
TGHKRSEENKN EGQDATMYCK SVGYPHPDWI WRKKENGMPM DIVNTSGRFF IINKENYTEL	300
NIVNLQITED PGEYECNATN AIGSASVVTV LRVRSHLAPL WPFLGILAEI IILVVIIVVY	360
EKRKRDPDEVP DAGPMKTNSTNN NNHDKNLRQRNTN	394
SSEQ ID NO: 441	moltype = AA length = 184
FEATURE	Location/Qualifiers
source	1..184
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 441	
MSGSSLPSAL ALSLLLVSWS LLPGPGAAQN AAPDITGHKR SENKNEGQDA TMYCKSVGYP	60
HPDWIWRKKE NGMPMDIVNT SGRFFIINKE NYTELNIVNL QITEDPGEYE CNATNAIGSA	120
SVVTVLRVRSH LAPLWPFLG ILAEIIILVVI IVVYEKRKRDP DEVPDDDEPA AGPMKTNSTN	180
NHKD RNTN	184
SSEQ ID NO: 442	moltype = AA length = 518
FEATURE	Location/Qualifiers
source	1..518
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 442	
XRKWSRQFLL SFWCTVCSAH QGTIFLSLKI QFADQKQEFN KRPTKIGRRS LSRSISQSST	60
DSYSSAASYT DSSDDETSR DKQQKNSKGS SDPCVKNIQ AEFGRREIEI AEQEMPALMA	120

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LRKRAQGEKP	LAGAKIVGCT	HITAQTAVALM	ETLGALGAQC	RWAACNIYST	LNEVAALAE	180
SGFPVFAWK	ESEDDFWWC1	DRCVNVEGWQ	PNNMILDDGGD	LTHWIYKKYP	NMFKKIKGIV	240
EESVTGVHRL	YQLSKAGKLC	VPAMNVNDSV	TKQKFDNLYC	CRESILDGLK	RTTDMFFGGK	300
QVVVCYGEV	GKGCCAALKA	MGSIVYVTB1	DPICALQACM	DGFRLVKLINE	VIROQDIVIT	360
CTGNKNVVTR	EHLDRMKNSC	IVCNMGHSNT	EIDVASLRTP	ELTWERVRSQ	VDHVIWPDGK	420
RIVLLAEGRL	LNLSCSTVPT	FVLSITATTQ	ALALIELYNA	PEGRYKQDVY	LLPKKMDEYV	480
ASLHLPTFDA	HLTELTDEQA	KYLGPNKNGP	FKPNYYRY			518

SEQ ID NO: 443	moltype = AA	length = 386
FEATURE	Location/Qualifiers	
source	1..386	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 443						
MADSCRNLTY	VRGSVGPATS	TLMFVAGVVG	NGLALGILSA	RRPARPSAFA	VLVTGLAATD	60
LLGTSFLSPA	VVFVAYARNSS	LLGLARGGP	LCDAFAFAMT	FFGLASMLIL	FAMAVERCLA	120
LSHPYLYAQL	DGPRCARLAL	PAIYAFCVLF	CALPLLGLGQ	HQQYCPGSWC	FLRMRWAQPG	180
GAAFSLAYAG	LVALLVAAIF	LCNGSVTSL	CRMYRQQKRH	QGSLGPRPRT	GEDEVDHIL	240
LALMTVVMMAV	CSLPLTIRCFC	TQAVAPDSSS	EMGDLLAFRF	YAFNPILD PW	VFILFRKAVF	300
QRLKLWVCCCL	CLGPAHGDSQ	TPLSQLASGR	RDPRAPSAPV	GKEGSCVPLS	AWGEQVEPL	360
PPTQQSSGSA	VGTSSKAEAS	VACSLC				386

SEQ ID NO: 444	moltype = AA	length = 143
FEATURE	Location/Qualifiers	
source	1..143	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 444						
MTVVMAVCSL	PLTIRCFTQA	VAPDSSEMEG	DLLAFRFYAF	NPILD PWFI	LFRKAVFQRL	60
KLWVCCCLLG	PAHGSQTPL	SQLASGRDP	RAPSAPVGKE	GSCVPLSAWG	EGQVEPLPPT	120
QQSSGSAVGT	SSKAEASVAC	SLC				143

SEQ ID NO: 445	moltype = AA	length = 296
FEATURE	Location/Qualifiers	
source	1..296	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 445						
MADSCRNLTY	VRGSVGPATS	TLMFVAGVVG	NGLALGILSA	RRPARPSAFA	VLVTGLAATD	60
LLGTSFLSPA	VVFVAYARNSS	LLGLARGGP	LCDAFAFAMT	FFGLASMLIL	FAMAVERCLA	120
LSHPYLYAQL	DGPRCARLAL	PAIYAFCVLF	CALPLLGLGQ	HQQYCPGSWC	FLRMRWAQPG	180
GAAFSLAYAG	LVALLVAAIF	LCNGSVTSL	CRMYRQQKRH	QGSLGPRPRT	GEDEVDHIL	240
LALMTVVMMAV	CSLPLTHVER	PRQDRMRWL	PVIPALWEAE	AGGSFEVRSS	RPVWPT	296

SEQ ID NO: 446	moltype = AA	length = 115
FEATURE	Location/Qualifiers	
source	1..115	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 446						
MDGLLAFRFY	AFNPILD PWV	FILFRKAVFQ	RLKLWVCCCL	LGPAHGDSQT	PLSQLASGR	60
DPRAPSAPVG	KEGSCVPLSA	WGEQVEPLP	PTQQSSGSAV	GTSSKAEASV	ACSLC	115

SEQ ID NO: 447	moltype = AA	length = 174
FEATURE	Location/Qualifiers	
source	1..174	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 447						
MYRQQKRHOG	SLGPRPRTGE	DEVDHILL	LMTVVMAVCS	LPLTIRCFTQ	AVAPDSSSEM	60
GDLLAFRFYA	FNPILDPWVF	I	LKLWVCCCL	GPAHGDSQT	LSQLASRRD	120
PRAPSAPVGK	EGSCVPLSAW	GEGQVEPLP	TQQSSGSAV	TSSKAEASVA	CSC	174

SEQ ID NO: 448	moltype = AA	length = 454
FEATURE	Location/Qualifiers	
source	1..454	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 448						
MGENDPPAVE	APPFSFRSLFG	LDDLKISPVA	PDADAVAAQI	LSLLPLKFFP	IIVIGIIIALI	60
LALAIGLGIH	FDCCSKYCR	SSFKCIELIA	RCDGVSDCKD	GEDEYRCV	GGQNAVLQVF	120
TAASWKTMC	DDWKGHYANV	ACAQLGFP	S VSSDNLRVSS	LEGQFREEFV	SIDHLLPDK	180
VITALHHSYVV	REGCASGHVV	T	QGYSSRIVGG	NMSLLSQWPW	QASIQFQGYH	240
LCGGSVITPL	WIITAAHCYV	DLYLPKS	WTI QVGLVSLLDN	PAPSHLVEKI	VYHHSKYKPKR	300
LGNDIALMKL	AGPLTFNEMI	QPVCLPNSEE	NFPDGKVCWT	SGWGATEDGA	GDASPVLNHA	360
AVPLISNKIC	NHRDVYGGII	SPSMLCAGYL	TGGVDSCQGD	SGGPLVCQER	RLWKLVGATS	420

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FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT	454
SEQ ID NO: 449	moltype = AA length = 344
FEATURE	Location/Qualifiers
source	1..344
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 449	
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI	60
LAIAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF	120
TAASWKTMCSS DDWKGHYANV ACAQLGFPVS VSSDNLRVSS LEGQFREEFV SIDHLLPDK	180
VTELHHSVYVV REGCASGHVV TLQCTACGHR RGYSRIVGG NMSLLSQWPW QASLQFQGYH	240
LCCGSVITPL WIITAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR	300
LGNDIALMKL AGPLTFNGTS GSLCGSAALP LFQEDLQLLI EAFL	344
SEQ ID NO: 450	moltype = AA length = 451
FEATURE	Location/Qualifiers
source	1..451
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 450	
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDAVAAQILS LLPLKFPPII VIGIIALILA	60
LAIAIGLGIH FDCSGKYCRSS FKCIELIARC DGVSCKDGE DEYRCVRVGG QNAVLQVFTA	120
ASWKTMCSSD WKGHYANVAC AQLGFPSYVS SDNLRVSSLE QOFREEFVSI DHLLPDKVT	180
ALHHHSVYVRE GCASGHVVTL QCTACGHRRG YSSRIVGGNM SLLSQWPWA SLQFQGYHLC	240
GGSVITPLWI ITAAHCYVDL YLPKSWTI QV GLVSLLDNP A SHLVKEKIVY HSKYKPKRLG	300
NDIALMKLAG PLTFNEMIQP VCLPNSEENF PDGKVWCWTSG WGATEDGGDA SPVLNHAAPV	360
LISNPKICNHR DVYGGIISPS MLCAGYLGG VDSCQGDGGG PLVCQERRRW KLVGATSF	420
GCAEVNPKGV YTRVTSFLDW IHEQMERDLK T	451
SEQ ID NO: 451	moltype = AA length = 453
FEATURE	Location/Qualifiers
source	1..453
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 451	
MGENDPPAVE APFSFRSLFG LDDLKISPVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI	60
LAIAIGLGIH FDCSGKYRCR SSFKCIELPA RCDGVSDCKD GEDEYRCVRV GGQNAVLQVF	120
TAASWKTMCSS DDWKGHYANV ACAQLGFPVS VSSDNLRVSS LEGQFREEFV SIDHLLPDK	180
VTELHHSVYVV REGCASGHVV TLQCTACGHR RGYSRIVGG NMSLLSQWPW QASLQFQGYH	240
LCCGSVITPL WIITAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR	300
LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFDPDGKVWT SGWGATEDGG DASPVLNHA	360
VPLISNPKICN HRDVYGGIIS PSMICAGYL GGVDSQCQDS GPLVCQERR LWKLVGATSF	420
GIGCAEVNPK GVYTRVTSFL DWIHEQMERD LKT	453
SEQ ID NO: 452	moltype = AA length = 734
FEATURE	Location/Qualifiers
source	1..734
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 452	
MLLWLLLLL TPGREQSGVA PKAVLLLNP WSTAFKGEKV ALICSSISHS LAQGDTYWYH	60
DEKLLKIKHD KIQITEPGNY QCKTRGSSL DAVHVEFSPD WLILQALHPV FEGDNVILRC	120
QGKDNKNTHQ KVYYKDGKQL PNSYNLEKIT VNSVSRDN SK YHCTAYRKFY ILDIEVTSKP	180
LNIQVQELFL HPVLRASSST PIEGSPMTL CETQLSPQR DVQLQFSLFR DSQTLGLGWS	240
RSPRLQIPAM WTEDSGSYWC EVETVTHSIK KRSLRSQIRV QRVPVSNVNL EIRPTGGQLI	300
EGERNMVLICS VAQGSGTVTF SWHKEGRVRS LGRKTKRSLL AELHVLTVKE SDAGRYYCAA	360
DNVHSPILST WIRVTVRIPV SHPVLTFRAP RAHTVVGDL ELHCESLRGS PPILYRFYHE	420
DVTLGNSSAP SGGGASFNLN LTAEHSGNYS CDADNGLGAQ HSHGVSLLRTV VPVSPRVTL	480
RAPGAQAVVG DLLELHCESL RGSFPILYWF YHEDDTLGNM SAHSGGGASF NLSLTTEHSG	540
NYSCCEADNGL GAQHSKVVTL NVTGTSRNR GLTAAGITGL VLSILVLAIAA AALLHYARAR	600
RKPGGLSATG TSSHSPSECQ EPSSSRPSRI DPQEPTHSKP LAPMELEPMY SNVNPDSNP	660
IYSQIWSIQH TKENSANCPM MHQEHEELTV LYSELKKTHP DDSAGEASSR GRAHEEDEE	720
NYENVPRVLL ASDH	734
SEQ ID NO: 453	moltype = AA length = 742
FEATURE	Location/Qualifiers
source	1..742
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 453	
MLLWLLLLL TPGREQSGVA PKAVLLLNP WSTAFKGEKV ALICSSISHS LAQGDTYWYH	60
DEKLLKIKHD KIQITEPGNY QCKTRGSSL DAVHVEFSPD WLILQALHPV FEGDNVILRC	120
QGKDNKNTHQ KVYYKDGKQL PNSYNLEKIT VNSVSRDN SK YHCTAYRKFY ILDIEVTSKP	180
LNIQVQELFL HPVLRASSST PIEGSPMTL CETQLSPQR DVQLQFSLFR DSQTLGLGWS	240
RSPRLQIPAM WTEDSGSYWC EVETVTHSIK KRSLRSQIRV QRVPVSNVNL EIRPTGGQLI	300

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EGENMVLLICS	VAQGSGTVTF	SWHKEGRVRS	LGRKTQRSL	AELHVLT	VKE	SDAGRYYCAA	360
DNVHSPILST	WIRVTVRIPV	SHPVLTFRAP	RAHTVVGDLL	ELHCESLRGS	PPILYRFYHE	420	
DVTLGNS	SSGGASFNL	S	TAEHSGNYS	CDA	DNGLGAQ	HSHGVSLRVT	480
RAPGAQAVVG	DLELHCESL	RGSF	PILYWF	YHEDDTLGN	I SAHSGGGASF	NLSLTTEHSG	540
NYSCEADNGL	GAQHSKV	VTL	NVTGTSRNRT	GLTAAGITGL	VLSILVLA	AA ALLHYARAR	600
RKPGGLSATG	TSSHSPSECQ	E	PSRRPSRI	DPOEP	THSKP LAPMELEPMY	SNVNPGDSNP	660
IYSQIWSIQH	TKENSANCPM	MHQEHEELTV	LYSELKKTHP	DDSA	GEASSRGRAH	GRAHEEDE	720
NYENILNPRK	NKVQDP	PCLC	NT				742

SEQ ID NO: 454	moltype = AA	length = 639						
FEATURE	Location/Qualifiers							
source	1..639							
	mol_type = protein							
	organism = Homo sapiens							
SEQUENCE: 454								
MILWLLLLLTPGREQSGVA	PKAV	LLLNPP	WSTA	FKG	EVK ALICSSISHS	LAQGDTYWYH	60	
DEKLLKIKHD	KIQITEPGNY	QCKTRGSSL	DAV	HVEFSPD	WLILQALHPV	FE	GDNVILRC	120
QGKDNKNTHQ	KVYYKDGKQL	PNSY	NLEKIT	VNSVSRDN	SK YHCTAYRK	FY	ILDIEVTSKP	180
LNIQVQGPV	S	NVN	LEIRPT	GQ	QLGENM VLICSVAQ	G	TFSWHE GRVRS	240
QRSLLAELHV	LTVKESDAGR	YYCA	ADNVHS	PIL	STWIRT V	RIPVSHPVL	TFRAPRAHTV	300
VGDLLEHCE	SLRGSP	PILY	RFYHEDVTL	G	SSAPSGGG	SFN	LSLTAEH SGN	360
GLGAQHSHGV	SLRV	TPVPSR	PV	L	APG	QAVVGDL	LE HCESLRGS	420
TLGNISAHS	G	GASFN	S	TEHSGNYS	CE ADNGLGAQ	H KV	TLNVTG SRNRTGLTAA	480
GITGLVL	SIL	VLA	AAAALLH	YARARKP	GG	LSATGTSS	PSECQEP	540
THSKPLAPME	LEPMYSNVNP	GDSNPIYSQI	W	SIQHTKENS	ANCPMMHQEH	EELTV	LYSEL	600
KKTHPDDSA	EASSRGRAHE	EDDEENYENV	P	PRVLLASDH				639

SEQ ID NO: 455	moltype = AA	length = 734						
FEATURE	Location/Qualifiers							
source	1..734							
	mol_type = protein							
	organism = Homo sapiens							
SEQUENCE: 455								
MILWLLLLLTPGREQSGVA	PKAV	LLLNPP	WSTA	FKG	EVK ALICSSISHS	LAQGDTYWYH	60	
DEKLLKIKHD	KIQITEPGNY	QCKTRGSSL	DAV	HVEFSPD	WLILQALHPV	FE	GDNVILRC	120
QGKDNKNTHQ	KVYYKDGKQL	PNSY	NLEKIT	VNSVSRDN	SK YHCTAYRK	FY	ILDIEVTSKP	180
LNIQVQELFL	HPV	LRASS	ST	PIEGSP	M	CETQ	LSPQR DVQLQFSL	240
RSRPLQIPAM	WTEDSGSYWC	EVETV	THS	KRSLR	QIRV	Q	RPVVSNVNL EIRPTG	300
EGENMVLLICS	VAQGSGTV	TP	WHKEGRVRS	LGRKT	QRS	LSL	AGRYYCAA	360
DNVHSPILST	WIRV	TPRIPV	S	HPV	LTFRAP	AEL	HVLT	SDAGRYYCAA
DVTLGNS	SSGGASFNL	L	TAEHSGNYS	CDA	DNGLGAQ	HSHG	VSLR	420
RAPGAQAVVG	DLELHCESL	RGSF	PILYWF	YHEDDTLGN	I SAHSGGGASF	NLS	LTTEHSG	480
NYSCEADNGL	GAQHSKV	VTL	NVTGTSRN	GLTAAGITGL	VLSILVLA	AA ALLHYARAR	540	
RKPGGLSATG	TSSHSPSECQ	E	PSRRPSRI	DPOEP	THSKP LAPMELEPMY	SNVNPGDSNP	600	
IYSQIWSIQH	TKENSANCPM	MHQEHEELTV	LYSEL	KKTHP	DDSA	GEASSRGRAH	GRAHEEDE	660
NYENIPRVL	ASDH							720
								734

SEQ ID NO: 456	moltype = AA	length = 740						
FEATURE	Location/Qualifiers							
source	1..740							
	mol_type = protein							
	organism = Homo sapiens							
SEQUENCE: 456								
MILWLLLLLTPGREQSGVA	PKAV	LLLNPP	WSTA	FKG	EVK ALICSSISHS	LAQGDTYWYH	60	
DEKLLKIKHD	KIQITEPGNY	QCKTRGSSL	DAV	HVEFSPD	WLILQALHPV	FE	GDNVILRC	120
QGKDNKNTHQ	KVYYKDGKQL	PNSY	NLEKIT	VNSVSRDN	SK YHCTAYRK	FY	ILDIEVTSKP	180
LNIQVQELFL	HPV	LRASS	ST	PIEGSP	M	CETQ	LSPQR DVQLQFSL	240
RSRPLQIPAM	WTEDSGSYWC	EVETV	THS	KRSLR	QIRV	Q	RPVVSNVNL EIRPTG	300
EGENMVLLICS	VAQGSGTV	TP	WHKEGRVRS	LGRKT	QRS	LSL	AGRYYCAA	360
DNVHSPILST	WIRV	TPR	LL	SPSPV	SHP	L	TFRAPRAHT	420
YRFYHEDV	TLL	GTNS	APSGGG	AFN	LSL	A	HSGNYS	480
RPV	TLR	APG	AQAVVGDLL	LHC	ESLRG	SF	PILYWFYH DTLGN	540
TTEHSGNYS	EADNGLGAQH	SKV	UTLN	TSR	RTGL	I AGITGLVLSI	LVLAAAALL	600
HYARARRKPG	GLS	ATGTSS	SPSECQEP	SPS	SRPSR	IDPQ	PTHSKPLAPM ELEPMYSNVN	660
PGDSNPIYSQ	IWSIQHTKEN	SANCPMMHQE	HEELTV	LKK	THPDDSA	GEASSRGRAH	EADNGLGAQH	720
EEDDEENYEN	VPRVLLASDH							740

SEQ ID NO: 457	moltype = AA	length = 256						
FEATURE	Location/Qualifiers							
source	1..256							
	mol_type = protein							
	organism = Homo sapiens							
SEQUENCE: 457								
MILWLLLLLTPGREQSGVA	PKAV	LLLNPP	WSTA	FKG	EVK ALICSSISHS	LAQGDTYWYH	60	
DEKLLKIKHD	KIQITEPGNY	QCKTRGSSL	DAV	HVEFSPD	WLILQALHPV	FE	GDNVILRC	120
QGKDNKNTHQ	KVYYKDGKQL	PNSY	NLEKIT	VNSVSRDN	SK YHCTAYRK	FY	ILDIEVTSKP	180

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LNIQVQELFL HPVLRASSST PIEGSPMTLT CETQLSPQRP DVQLQFSLFR DSQTLGLGWS	240
RSRPLQIPAM WTEDSG	256
SEQ ID NO: 458	moltype = AA length = 234
FEATURE	Location/Qualifiers
source	1..234
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 458	
MAFLAGPRLL DWASSPPHLQ FNKFVLTGYR PASSGSGCLR SLFYLNELG NIYTHGSVLY	60
HIFMCHQGS AVYARLLALD MCGVCLVNTL GALPIIHCTL ACRPWLRPAAC LVGTVLSGV	120
AGWRALTAPS TSARLRAFGW QAAARLLVVG ARGVGLGSGA PGSLPCYLRM DALALLGGLV	180
NVARLPERWG PGRFDYWGNS HQIMHLLSVG SILQLHAGVV PDLLWAHHHA CPRD	234
SEQ ID NO: 459	moltype = AA length = 273
FEATURE	Location/Qualifiers
source	1..273
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 459	
MAFLAGPRLL DWASSPPHLQ FNKFVLTGYR PASSGSGCLR SLFYLNELG NIYTHGLALL	60
GFLVLVPMTM PWGQLGKDGW LGGTHCVACL APPAGSVLYH LFMCHQGSA VYARLLALDM	120
CGVCLVNTLG ALPIIHCTL A CRPWLRPAAL VGYTVLSGV A GWRLALTAPST SARLRAFGWQ	180
AAARLLVFGA RGVLGSGAP GSLPCYLRMD ALALLGGLVN VARLPERWGP GRFDYWGNSH	240
QIMHLLSVGS ILQLHAGVVP DLLWAHHAC PRD	273
SEQ ID NO: 460	moltype = AA length = 199
FEATURE	Location/Qualifiers
source	1..199
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 460	
MAFLAGPRLL DWASSPPHLQ FNKFVLTGYR PASSGSGCLR SLFYLNELG NIYTHGALPI	60
IHTCLACRPW LRPAALVGYT VLSGVAGWRA LTAPSTSARL RAFGWQAAR LLVFGARGVG	120
LGSGAPGSLP CYLRMDALAL LGGLVNVARL PERWGPGRDF YWGNSHQIMH LLSVGSILQL	180
HAGVVPDLLW AAHHACPRD	199
SEQ ID NO: 461	moltype = AA length = 206
FEATURE	Location/Qualifiers
source	1..206
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 461	
MTMPWGQLGK DGWLGGTHCV ACLAPPAGSV LYHLMCHQG GSAVYARLLA LDMCGVCLVN	60
TIGALPIIHC TLACRPWLRP AALVGYTVLS GVAGWRALTA PSTSARLRAF GWQAARLLV	120
FGARGVGLGS GAPGSLPCYL RMDALALLGG LVNVARLPER WGPGRFDYWG NSHQIMHLLS	180
VGSILQLHAG VVPDLLWAHH HACPRD	206
SEQ ID NO: 462	moltype = AA length = 206
FEATURE	Location/Qualifiers
source	1..206
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 462	
MTMPWGQLGK DGWLGGTHCV ACLAPPAGSV LYHLMCHQG GSAVYARLLA LDMCGVCLVN	60
TIGALPIIHC TLACRPWLRP AALVGYTVLS GVAGWRALTA PSTSARLRAF GWQAARLLV	120
FGARGVGLGS GAPGSLPCYL RMDALALLGG LVNVARLPER WGPGRFDYWG NSHQIMHLLS	180
VGSILQLHAG VVPDLLWAHH HACPRD	206
SEQ ID NO: 463	moltype = AA length = 208
FEATURE	Location/Qualifiers
source	1..208
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 463	
MGAQGAQESI KAMWRVPGTT RRPVTGESPG MHRPEAMLLL LTLALLGGPT WAGKMYGPGG	60
GYKFSTTEDY DHEITGLRVS VGLLLVKSVQ VKLGDSDVWK LGALGGNTQE VTLQPGEYIT	120
KVFVAFQAFL RGMVMTSKD RYFYFGKLKG QISSAYPSQE GQVLVGIYQQ YQLLGIKSIG	180
FEWNYPLEEP TTEPPVNLTY SANSPVGR	208
SEQ ID NO: 464	moltype = AA length = 95
FEATURE	Location/Qualifiers
source	1..95
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 464	

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SEQ ID NO: 465	moltype = AA length = 69	
FEATURE	Location/Qualifiers	
source	1..69	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 465		
XRAQGAQESIK AMWRVPGTTR RPVTGESPGM HRPEAMLLL TLALLGGPTW AGKMYGPGGG	60	
KYFSTTEDYD HEITGLRVSV GLLLVKRFLE GVIYE	95	
SEQ ID NO: 466	moltype = AA length = 178	
FEATURE	Location/Qualifiers	
source	1..178	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 466		
MHRPEAMLL LTLALLGGPT WAGKMYGPGG GKYFSTTEDY DHEITGLRV VGLLLKVSVQ	60	
VKLGDSDWDVK LGALGGNTQE VTLOPGEYIT KVPVAFQAFL RGMVMTSKD RYFYPGKLDG	120	
QISSAYPSQE GQVLVGIYQQ YQLLGIKSIG FEWNYPLEEP TTEPPVNLTY SANSPVGR	178	
SEQ ID NO: 467	moltype = AA length = 399	
FEATURE	Location/Qualifiers	
source	1..399	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 467		
MAELLRLSLQD SQLVARFQRR CGLFPAPDEG PRENGADPTE RAARVPGVEH LPAANGKGGE	60	
APANGLRRAA APEAYVQKYV VKNYFYYYYLF QFSAALGOEV FYITFLPFTW WNIDPYLSRR	120	
LIIIWVVLVMY IGQVAKDVLK WPRPSSPPVV KLEKRLLIAEY GMPSTHAMAA TAIATLLIS	180	
TMDRYQYFPV LGLVMAVVF S TLVCLSRLYT GMHTVLDVLG GVLITALLIV LTYPAWTFID	240	
CLDSASPLFP VCVIVVPPFFL CYNYPVSDYY SPTRADTTI LAAGAGVTIG FWINHFFQLV	300	
SKPAESLPVI QNIIPPLTYM LVLGLTKFAV GIVLILLVRQ LVQNLSQLVL YSWFKVVTRN	360	
KEARRRLEIE VPYKFVTVTS VGICATTFVPM MLHRFLGLP	399	
SEQ ID NO: 468	moltype = AA length = 128	
FEATURE	Location/Qualifiers	
source	1..128	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 468		
MDVYGTTKAI ELLDPTASRL PTPMPWDSL KAVPEPKCFG PKDLALPTGN LKATWHLCLR	60	
EHLPTLHTRR GVCHLSSRC QHPPCALRPH ILLQILCLAG LQRYGQVPCV PLADRGGSPC	120	
AGPSCSEG	128	
SEQ ID NO: 469	moltype = AA length = 104	
FEATURE	Location/Qualifiers	
source	1..104	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 469		
MDVYGTTKAI ELLDPTASRL PTPMPWDSL KAVPEPKATP GEECAICFYH AANTRLVPCG	60	
HTYFCRYCAW RVFSDTAKCP VCRWQIEAVA PAQGPPALRV EEGS	104	
SEQ ID NO: 470	moltype = AA length = 83	
FEATURE	Location/Qualifiers	
source	1..83	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 470		
MAPGCKIMKV MPSKFLCEFV LLQKDLGQLM ESRTYAYLCC PPRVSGCTPT LSPRPSRLIM	60	
LQMWIPLRNL YSQLWLKALW SLA	83	
SEQ ID NO: 471	moltype = AA length = 438	
FEATURE	Location/Qualifiers	
source	1..438	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 471		
MPCTCTWRNW RQWIRPLVAV IYLVSIVVAV PLCVWELQKL EVGIHTKAWF IAGIFLLTI	60	
PISLWVILQH LVHYTQPELQ KPIIRILWMV PIYSLDSWIA LKYPGIAIYV DTCRECYEAY	120	
VIYNFMGFLT NYLTNRYPNL VLILEAKDQQ KHFPPLCCCP PWAMGEVLLF RKLGVLQYT	180	
VVRPFATTIVA LICELLGIYD EGNFSFSNAW TYLVIINNMS QLFAMYCLL FYKVLKEELS	240	
PIQPVGKFLC VKLFFFVFSFW QAVVIALLVK VGVISEKHTW EWQTVEAVAT GLQDFIICIE	300	
MFLAAIAAHY TFSYKPYVQE AEEGSCFDSE LAMWDVSDIR DDISEQVRHV GRTVRGHPRK	360	

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KLFPEDQDQN EHTSLLSSSS QDAISIASSM PPSPMGHYQG FGHTVTPQTT PTTAKISDEI	420
LSDTIGEKKE PSDKSVDs	438
SEQ ID NO: 472	moltype = AA length = 72
FEATURE	Location/Qualifiers
source	1..72
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 472	
LGIFYDEGNFS FSNAWTYLVI INNMSQLFAM YCLLLFYKVL KEELSPIQPV GKFLCVKLVV	60
FVSFCIRGNG KL	72
SEQ ID NO: 473	moltype = AA length = 261
FEATURE	Location/Qualifiers
source	1..261
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 473	
MPCTCTWRNW RQWIRPLVAV IYLVSVIVAV PLCVWELQKL EVGIHTKAWF IAGIFLLLT	60
PISLWVILQH LVHYTQPELQ KPIIRILWMV PIYSLDSWIA LKYPGTAIYV DTCRCYEAY	120
VIYNFMGFLT NYLTNRYPNL VLILEAKDQQ KHFPLLCPPC PWAMGEVLLF RKCLGVLQYT	180
VVRPFTTIVA LICELLGIYD EGNFSFSNAW TYLVIINNMS QLFAMYCLLL FYKVLKEELS	240
PIQPVGKFLC VKLVVVFVSW P	261
SEQ ID NO: 474	moltype = AA length = 115
FEATURE	Location/Qualifiers
source	1..115
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 474	
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLEFTKDP CPLCDEAKEV LKPYENRFL	60
QEVNITLPEN SVWYERYKFD IPVFHNLNGQF LMMHRVNTSK LEKQLLKLEQ QSTGG	115
SEQ ID NO: 475	moltype = AA length = 55
FEATURE	Location/Qualifiers
source	1..55
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 475	
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLEFTKEF LSTRSLFACC HPCKM	55
SEQ ID NO: 476	moltype = AA length = 59
FEATURE	Location/Qualifiers
source	1..59
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 476	
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLEFTKDP CPLCDEAKEV LKPYENRVI	59
SEQ ID NO: 477	moltype = AA length = 138
FEATURE	Location/Qualifiers
source	1..138
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 477	
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLEFTKDP CPLCDEAKEV LKPYENRQPY	60
KDQKLPGTRR RRSPSSPSHP HMASQSGKRY NLTLNQVLSF DYDMGLDAPK TISSDCGAFY	120
CLRMFKSPDM TCCFYPKQ	138
SEQ ID NO: 478	moltype = AA length = 57
FEATURE	Location/Qualifiers
source	1..57
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 478	
KTTLPVLTTF TKDPCPLCDE AKEVLKPYEN RFLMMHRVNT SKLEKQLLKL EQQSTGG	57
SEQ ID NO: 479	moltype = AA length = 138
FEATURE	Location/Qualifiers
source	1..138
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 479	
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVLTLEFTKDP CPLCDEAKEV LKPYENRQPY	60
KDQKLPGTRR RRSPSSPSHP HMASQSGKRY NLTLNQVLSF DYDMGLDAPK TISSDCGAFY	120
CLRMFKSPDM TCCFYPKQ	138

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SEQ ID NO: 480      moltype = AA length = 89
FEATURE
source
1..89
mol_type = protein
organism = Homo sapiens
SEQUENCE: 480
MLWFQGNSMQ LARSSFGLFL RNCSASKTTL PVTLFLTKDP CPLCDEAKEV LKPYENRRST 60
SQSLGNNAIYR KKVLHSCCCP GGLNLFMKE 89

SEQ ID NO: 481      moltype = AA length = 215
FEATURE
source
1..215
mol_type = protein
organism = Homo sapiens
SEQUENCE: 481
MKDYDELLKY YELHETIGTG GFAVKVLACH ILTGEMVAIK IMDKNTLGSD LPRIKTEIEA 60
LNKLRHQHIC QLYHVLETAAN KIFMVLEENL LFDEYHKLKL IDFGCAKPK GNKDYHLQTC 120
CGSLAYAAPE LIQGKSYLGS EADVVWSMGIL LYVLMCGFLP FDDDNVMALY KKIMRGKYDV 180
PKWLSPSSIL LLQQMLQVDP KKRISMKNLL NHPWI 215

SEQ ID NO: 482      moltype = AA length = 580
FEATURE
source
1..580
mol_type = protein
organism = Homo sapiens
SEQUENCE: 482
MNMFNSNIMNY MKLLGQYCPG GELFDYIISQ DRLSEEEETRV VFRQIVSAVA YVHSQGYAHR 60
DLKPENLLFD EYHKLKLIDF GLCAKPKGNK DYHLQTCCGS LAYAAPELIQ GKSYLGSEAD 120
VWSMGILLYY LMCGFLPFDD DNVMALYKKI MRGKYDVPKW LSPSSILLLQ QMLQVDPKKR 180
ISMKNLNNHNP WIMQDYNYPV EWQSKNPFIH LDDDCVTELS VHHRNNRQTM EDLISLWQYD 240
HITATYLLLL AKKARGKPVR LRLSSFSCGQ ASATPFTDIK SNNWSLEDVT ASDKNYVAGL 300
IDYDWCEDDL STGAATPRTS QFTKYWTESN GVESKSLTPA LCRTPANKLK NKENVYTPKS 360
AVKNEEYFMF PEPKTPVNKN QHKREILTTP NRYTTPSKAR NQCLKETPIK IPVNSTGTDK 420
LMTGVISPER RCRSVELLDLN QAHMEETPKR KGAKVFGSLE RGLDKVITVL TRSKRKGSAR 480
DGPRRLKLHY NVTTTRLVNP DQLLNEIMSI LPKKHVDFVQ KYTLKCQTQ SDFGKVTMQF 540
ELEVVCQLQKP DVVGIRRQRL KGDAWVYKRL VEDILSSCKV 580

SEQ ID NO: 483      moltype = AA length = 520
FEATURE
source
1..520
mol_type = protein
organism = Homo sapiens
SEQUENCE: 483
MVLEENLLFD EYHKLKLIDF GLCAKPKGNK DYHLQTCCGS LAYAAPELIQ GKSYLGSEAD 60
VWSMGILLYY LMCGFLPFDD DNVMALYKKI MRGKYDVPKW LSPSSILLLQ QMLQVDPKKR 120
ISMKNLNNHNP WIMQDYNYPV EWQSKNPFIH LDDDCVTELS VHHRNNRQTM EDLISLWQYD 180
HITATYLLLL AKKARGKPVR LRLSSFSCGQ ASATPFTDIK SNNWSLEDVT ASDKNYVAGL 240
IDYDWCEDDL STGAATPRTS QFTKYWTESN GVESKSLTPA LCRTPANKLK NKENVYTPKS 300
AVKNEEYFMF PEPKTPVNKN QHKREILTTP NRYTTPSKAR NQCLKETPIK IPVNSTGTDK 360
LMTGVISPER RCRSVELLDLN QAHMEETPKR KGAKVFGSLE RGLDKVITVL TRSKRKGSAR 420
DGPRRLKLHY NVTTTRLVNP DQLLNEIMSI LPKKHVDFVQ KYTLKCQTQ SDFGKVTMQF 480
ELEVVCQLQKP DVVGIRRQRL KGDAWVYKRL VEDILSSCKV 520

SEQ ID NO: 484      moltype = AA length = 619
FEATURE
source
1..619
mol_type = protein
organism = Homo sapiens
SEQUENCE: 484
MNMFNSNIMNY MKLLGQSDLR RIKTEIEALK NLRHQHICOL YHVLETANKI FMVLEYCPGG 60
ELFDYIISQD RLSEEEETRVV FRQIVSAVAY VHSQGYAHRD LKPNELLFDE YHKLKLIDFG 120
LCAKPKGNKD YHLQTCCGSL AYAAPELIQ KSYLGSEADW WSMGILLYYL MCGFLPFDDD 180
NVMALYKKIM RGKYDVPKW SPSSILLLQO MLQVDPKKRI SMKNLNNHNPW IMQDYNYPVE 240
WQSKNPFIHL DDDCVTELSV HHRNNRQTMED DLISLWQYD LTATYLLLLA KKARGKPVR 300
RLLSFSCCGQA SATPFTDIKS NNWSLEDVTA SDKNYVAGLI DYDWCEEDLS TGAATPRTSQ 360
FTKYWTEESNG VESKSLTPAL CRTPANKLN KENVYTPSKA VKNEEYFMFP EPKTPVNKNQ 420
HKREILTPN RYTTPSKARN QCLKETPIKI PVNSTGTDKL MTGVVISPER CRSVELLDLNQ 480
AHMEETPKR GAKVFGSLER GLDKVITVLT RSKRKGSARD GPRRLKLHYN VTTTRLVNPD 540
QLLNEIMSIL PKKHVDFVQK GYTLKCQTQS DFGKVTMQFE LEVCQLQKPD VVGIRRQLK 600
GDAWVYKRLV EDILSSCKV 619

SEQ ID NO: 485      moltype = AA length = 129
FEATURE
source
1..129
mol_type = protein

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SEQUENCE: 485	organism = Homo sapiens
MVLEYCPGGE LFDYIISQDR LSEEETRVVF RQIVSAVAYV HSQGYAHSDL KPNLLFDEY	60
HKLKLIDFGL CAKPKGNKDY HLQTCGSLA YAAPELIQGK SYLGSEMFAGA WAYCYMFLCV	120
DFYHLMIMM	129
 SEQ ID NO: 486	moltype = AA length = 532
FEATURE	Location/Qualifiers
source	1..532
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 486	
MAPSFTARIQ LFLLRLALGFL IGLVGRAALV LGGPKFASKT PRPVTEPLLL LSGMQLAKLI	60
RQRKVKCIDV VQAYINRIKD VNPMINGIVK YRFEEAMKEA HADVDQKLAEK QEDEATLENK	120
WPFLGVPLTV KEAFQLQGMP NSSGLMNRRD AIAKTDATVV ALLKGAGAIP LGITNCSEL	180
MYWESSNKKIY GRSNNPYDLQ HIVGSSGGE GCTLAAACSV HIVGSSGGE IRMPAFFNGI	240
FGHKPSPGVV PNKGQFPLAV GAQELFLCTG PMCRYAEDLA PMLKVMAGPG IKRKLDTKV	300
HILKDLKFWHM EHDGGSFLMS KVDQDLIMTQ KKVVVHLETI LGASVQHVKL KKMKYSFQLW	360
IAMMSAKGH DKEPVKFVDL DLGDHGKVSP LWELIKWCIG LSVYTIPIG LALLEEKLRY	420
SNEKYQKPKA VEESLRKELV DMLGDDGVPFL YPSHPTVAPK HHVPLTRPFN FAYTGVFSAL	480
GLPVTQCPLG LNAKGLPLGI QVVAGPFNDH LTLAVAQYLE KTFGGWVCPG KF	532
 SEQ ID NO: 487	moltype = AA length = 563
FEATURE	Location/Qualifiers
source	1..563
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 487	
MGLQACLLGL FALILSGKCS YSPEPDQRRT LPPGWVSLGR ADPEEELSLT FALRQQNVER	60
LSELVQAVSD PSSPQYKGYL TLENADLVR PSPLTLHTVQ KWLLAAGAQK CHSVITQDFL	120
TCWLSIRQAE LLLPGAEFHH YVGGPTETHV AGMRDRSPSC SGSCCSVMSQ PCHMCIL	177
SLRQRPEPQV TGTGVLHLGV TPSVIRKRYN LTSQDVGSST SNNSQACAQF LEQYPHDSL	240
AQFMRLFGGN FAHQASVARV VGQQGRGRAG IEASLDVQYL MSAGANISTW VYSSPGRHEG	300
QEFPFLWML LSNESALPHV HTVSYGDED SLS SAYIQRV NTELMAAAR GLTLLFASGD	360
SGAGCWSVSG RHQFRPTFPV SSPYVTTVGG TSFQEPFLIT NEIVDYISGG GFSNVFPRPS	420
YQBEAVTKFL SSSPHLPPSS YFNASGRAYP DVAALSDGWP VVSNRVPIPW VSGTSASTPV	480
FGGILSLINE HRILSGRPPPL GFLNPRLYQQ HGAGLFDVTR GCHESLDDE VEGQGFCSP	540
GWDPVTGWGT PNFPALLKTL LNP	563
 SEQ ID NO: 488	moltype = AA length = 177
FEATURE	Location/Qualifiers
source	1..177
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 488	
MGLQACLLGL FALILSGKCS YSPEPDQRRT LPPGWVSLGR ADPEEELSLT FALRQQNVER	60
LSELVQAVSD PSSPQYKGYL TLENADLVR PSPLTLHTVQ KWLLAAGAQK CHSVITQDFL	120
TCWLSIRQAE LLLPGAEFHH YVGGPTETHV AGMRDRSPSC SGSCCSVMSQ PCHMCIL	177
 SEQ ID NO: 489	moltype = AA length = 39
FEATURE	Location/Qualifiers
source	1..39
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 489	
MGLQACLLGL FALILSGKCS YSPEPDQRRT KIPDPRECG	39
 SEQ ID NO: 490	moltype = AA length = 30
FEATURE	Location/Qualifiers
source	1..30
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 490	
MGLQACLLGL FALILSGKCS YSPEPDQRRT	30
 SEQ ID NO: 491	moltype = AA length = 387
FEATURE	Location/Qualifiers
source	1..387
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 491	
MREPLEAFKL ADLDFRKSSL ASGWRMASGA FTMDQFPESV TENFEYDDLA EACYIGDIVV	60
FGTVFLSIFY SVIFAIQLVG NLLUVFALTN SKKPKSVDI YLLNLALSDL LFVATLPFWT	120
HYLINEKGLH NAMCKFTTAFF FIGFFGSI FITVISIDRY LAIVLAANSM NNRTVQHGV	180
ISLGWAAAI LVAAPQFMFT KQKENECLGD YPEVLQEIWP VLRLVETNFL GFLLPLLIMS	240
YCYFRIIQTQ FSCKNHKKAK AIKLILLVVI VFPLFWTPYN VMIFLETLKL YDFFPSCDMR	300

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KDLRLALSVT	ETVAFSHCCL	NPLIYAFAGE	KFRRYLYHLY	GKCLAVLCGR	SVHVDSSSE	360
SQSRHRGSQL	SSNFTYHTSD					387
SEQ ID NO: 492		moltype = AA	length = 355			
FEATURE		Location/Qualifiers				
source		1..355				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 492						
MDQFPESVTE	NFEYDDLAEA	CYIGDIVVFG	TVPLSIFYSV	IFAIGLVGNL	LVVFALTNSK	60
KPKSVTDIYL	LNLALSDLFF	VATLPFWTHY	LINEKGLHNA	MCKFTTAFFF	IGFFGSIFFI	120
TVVISIDRYLA	IVLAANSMNN	RTVQHGVITIS	LGVWAAAAILV	AAPQFMFTKQ	KENECLGDYP	180
EVLQEIWVPL	RNVETNFLGF	LLPPLLIMSYC	YFRRIIQTLS	CKNHKKAKAI	KLILLVVIVF	240
FLFWTPYNVNM	IFLETLKLYD	FFPSCDMRKD	LRLALSVTET	VAFSHCCLNP	LIYAFAGEKF	300
RYLYHLYGK	CLAVLCGRSV	HVDSSSESQ	RSRHGSVLSS	NFTYHTSDGD	ALLLL	355
SEQ ID NO: 493		moltype = AA	length = 106			
FEATURE		Location/Qualifiers				
source		1..106				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 493						
MDQFPESVTE	NFEYDDLAEA	CYIGDIVVFG	TVPLSIFYSV	IFAIGLVGNL	LVVFALTNSK	60
KPKSVTDIYL	LNLALSDLFF	VATLPFWTHY	LINEKGLHNA	MCKFTTAFFF	IGFFGSIFFI	106
SEQ ID NO: 494		moltype = AA	length = 166			
FEATURE		Location/Qualifiers				
source		1..166				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 494						
MDQFPESVTE	NFEYDDLAEA	CYIGDIVVFG	TVPLSIFYSV	IFAIGLVGNL	LVVFALTNSK	60
KPKSVTDIYL	LNLALSDLFF	VATLPFWTHY	LINEKGLHNA	MCKFTTAFFF	IGFFGSIFFI	120
TVVISIDRYLA	IVLAANSMNN	RTVQHGVITIS	LGVWAAAAILV	AAPQFMFTKQ	KENECLGDYP	166
SEQ ID NO: 495		moltype = AA	length = 355			
FEATURE		Location/Qualifiers				
source		1..355				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 495						
MDQFPESVTE	NFEYDDLAEA	CYIGDIVVFG	TVPLSIFYSV	IFAIGLVGNL	LVVFALTNSK	60
KPKSVTDIYL	LNLALSDLFF	VATLPFWTHY	LINEKGLHNA	MCKFTTAFFF	IGFFGSIFFI	120
TVVISIDRYLA	IVLAANSMNN	RTVQHGVITIS	LGVWAAAAILV	AAPQFMFTKQ	KENECLGDYP	180
EVLQEIWVPL	RNVETNFLGF	LLPPLLIMSYC	YFRRIIQTLS	CKNHKKAKAI	KLILLVVIVF	240
FLFWTPYNVNM	IFLETLKLYD	FFPSCDMRKD	LRLALSVTET	VAFSHCCLNP	LIYAFAGEKF	300
RYLYHLYGK	CLAVLCGRSV	HVDSSSESQ	RSRHGSVLSS	NFTYHTSDGD	ALLLL	355
SEQ ID NO: 496		moltype = AA	length = 355			
FEATURE		Location/Qualifiers				
source		1..355				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 496						
MDQFPESVTE	NFEYDDLAEA	CYIGDIVVFG	TVPLSIFYSV	IFAIGLVGNL	LVVFALTNSK	60
KPKSVTDIYL	LNLALSDLFF	VATLPFWTHY	LINEKGLHNA	MCKFTTAFFF	IGFFGSIFFI	120
TVVISIDRYLA	IVLAANSMNN	RTVQHGVITIS	LGVWAAAAILV	AAPQFMFTKQ	KENECLGDYP	180
EVLQEIWVPL	RNVETNFLGF	LLPPLLIMSYC	YFRRIIQTLS	CKNHKKAKAI	KLILLVVIVF	240
FLFWTPYNVNM	IFLETLKLYD	FFPSCDMRKD	LRLALSVTET	VAFSHCCLNP	LIYAFAGEKF	300
RYLYHLYGK	CLAVLCGRSV	HVDSSSESQ	RSRHGSVLSS	NFTYHTSDGD	ALLLL	355
SEQ ID NO: 497		moltype = AA	length = 268			
FEATURE		Location/Qualifiers				
source		1..268				
		mol_type = protein				
		organism = Homo sapiens				
 SEQUENCE: 497						
MSGKHKGPE	VSCCIKYFIF	GPNVIFWFLG	ITPLGIGLWA	WNEKGVLNSNI	SSITDLGGFD	60
PVWLFLVGG	VMFILGFAGC	IGALRENTPL	LKFPSVFLGI	IFFLELTAGV	LAFVFKDWIK	120
DQLYFFINNN	IRAYRDDIDL	QNLIDFTQEY	WQCCGAFGAD	DWNLNIIYFNC	TDSNASRERC	180
GVPFSCCTKD	PAEDVINTQC	GYDARQKPEV	DQQIVIYTKG	CVPQFEKWQ	DNLTIVAGIF	240
IGIALLQIFG	ICLAQNLVSD	IEAVRASW				268
SEQ ID NO: 498		moltype = AA	length = 197			
FEATURE		Location/Qualifiers				
source		1..197				

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mol_type = protein
organism = Homo sapiens
SEQUENCE: 498
MFILGFAGCI GALRENTFLL KFFSVFLGII FFLELTAGVL AFVFKDWIKD QLYFFINNNI 60
RAYRDDIDLQ NLIDFTQEYW QCCGAFGADD WNLNIYFNCT DSNASRERCG VPFSCTKDP 120
AEDVINTQCG YDARQKPEVD QQIVIYTKGC VPQFEKWLDQ NLTIVAGIFI GIALLQIFGI 180
CLAQNLVSDI EAVRASW 197

SEQ ID NO: 499      moltype = AA length = 193
FEATURE           Location/Qualifiers
source            1..193
mol_type = protein
organism = Homo sapiens
SEQUENCE: 499
MSGKHYKGPE VSCCIKYFIF GFNVIFWFLG ITFLGIGLWA WNEKGVLSSI SSITDLGGFD 60
PVWLFLVVGG VMFILGFAGC IGALRENTFL LKFFSVFLGI IFFLELTAGV LAFVFKDWIK 120
DQLYFFINNN IRAYRDDIDL QNLIDFTQEY IPMQVESDVA FHSPAALKIP QKMSSTLSVA 180
MMPGKNQKLT SRL 193

SEQ ID NO: 500      moltype = AA length = 60
FEATURE           Location/Qualifiers
source            1..60
mol_type = protein
organism = Homo sapiens
SEQUENCE: 500
MFILGFAGCI GALRENTFLL KFFSVFLGII FFLELTAGVL AFVFKDWIKD QLYFFINNNI 60

SEQ ID NO: 501      moltype = AA length = 38
FEATURE           Location/Qualifiers
source            1..38
mol_type = protein
organism = Homo sapiens
SEQUENCE: 501
MFILGFAGCI GALRENTFLL KFLKSPVLTE QAENYTFL 38

SEQ ID NO: 502      moltype = AA length = 110
FEATURE           Location/Qualifiers
source            1..110
mol_type = protein
organism = Homo sapiens
SEQUENCE: 502
MFILGFAGCI GALRENTFLL KFFSVFLGII FFLELTAGVL AFVFKDWIKD QLYFFINNNI 60
RAYRDDIDLQ NLIDFTQEYW QCCGAFGADD WNLNIYFNCT DSNASRERCG 110

SEQ ID NO: 503      moltype = AA length = 87
FEATURE           Location/Qualifiers
source            1..87
mol_type = protein
organism = Homo sapiens
SEQUENCE: 503
XVSCCIYFI PGFNVIFWFL GITFLGIGLW AWNEKGVLSSI ISSITDLGGF DPVWLFLVVG 60
GVMFILGFAG CIGALRENTF LLKFDKQ 87

SEQ ID NO: 504      moltype = AA length = 29
FEATURE           Location/Qualifiers
source            1..29
mol_type = protein
organism = Homo sapiens
SEQUENCE: 504
SFASLKSGTC ACTQTGRAGE AGGLRKAGS 29

SEQ ID NO: 505      moltype = AA length = 37
FEATURE           Location/Qualifiers
source            1..37
mol_type = protein
organism = Homo sapiens
SEQUENCE: 505
MLLYPAGFSF ASLKSGTCAC TQTGRAGEAG GLRKAGS 37

SEQ ID NO: 506      moltype = AA length = 677
FEATURE           Location/Qualifiers
source            1..677
mol_type = protein
organism = Homo sapiens
SEQUENCE: 506
MPGFLVRILP LLLVLLLLGP TRGLRNATQR MFEIDYSRDS FLKDQPFY IGSIHYSRV 60

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PRFYWKDRLL	KMKGMLNAl	QTYVPWNFHE	PWPGQYQFSE	DHDVEYFLRL	AHELGLLVIL	120
RPGPYICAED	EMGGGLPAWLL	EKESELLRSS	DPDYLAAVDK	WLGVLPLPKMK	PLLYQNGGPV	180
ITVQVENEYG	SYFACDFDYL	RFLQKRFRHH	LGDDVVLFIT	DGAHKTFLKC	GALQGLYTTV	240
DEFTGTSNITD	AFLSQRKCEP	KGPLINSEFY	TGWLDSHWGQP	HSTIKTEAVA	SSLYDILARG	300
ASVNLYMFIG	GTNFAYWNGA	NSPYAAQPTS	YDYDAPLSEA	GDLTEKYFAL	RNIIQKFEKV	360
PEGPIPSTP	KFAYGKVTL	KLKTVGAALD	IICPSGPPIKS	LYPLTFIQVK	QHYGFVLYRT	420
TLPQDCSNPA	PLSSPLNGVH	DRAYVADGI	PQGVLERNNV	ITLNITGKAG	ATLDLLVENM	480
GRVNYGAYIN	DFKGLVSNLT	LSSNILTDTW	IFPLDTEADV	CSHLGGWGH	DSGHHDEAWA	540
HNSSNYTLP	FYMGNFSIPS	GIPDLPQDTF	IQFPGWTKGQ	VWINGFNGLR	YWPARGPQLT	600
LFVPQHILMT	SAPNTITVLE	LEWAPCSSDD	PELCAVTFVD	RPVIGSSVTY	DHPSPKVEKR	660
LMPPPPQKRN	DWLHDHV					677

SEQ ID NO: 507 moltype = AA length = 546
 FEATURE Location/Qualifiers
 source 1..546
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 507
 MPGFLVRILP LLLVLLLLGP TRGLRNATQR MFEIDYSRDS FLKDQGPFRY ISGSIHYSRV 60
 PRFYWKDRLL KMKGMLNAl QTLPGSCGOV VGSPSAQDEA SPLSEWRASY NSAGSNITDA 120
 FLSQRKCEPK GPLINSEFYT GWLDSHWGQPH STIKTEAVAS SLYDILARGA SVNLYMFIGG 180
 TNFAYWNANG SPYAAQOPTS DYDAPLSEAG DLTEKYFALR NIIQKFEKV PEGPIPSTPK 240
 FAYGKVTLK LKTVGAALDI LCPSPGIKSL YPLTFIQVKQ HYGFVLYRTT LPQDCSNPAP 300
 LSSPLNGVHD RAYVADGIP QGVLERNNVI TLNITGKAGA TLDLLVENMG RVNYGAYIND 360
 FKGLVSNLT SSNIILTDTWI FPLDTEADV SHLGGWGH

DSGHHDEAWAH NSSNYTLP

AF 420

YMGNFSIPSQ IPDLPQDTF QFPGWTKGQV WINGFNGLRY WPARGPQLT FVPQHILMTS 480

APNTITVLEL EWAPCSSDDP ELCAVTFVD PVIGSSVTYD HPSKPVEKRL MPPPQQKRNKD 540

SWLDHV 546

SEQ ID NO: 508 moltype = AA length = 647
 FEATURE Location/Qualifiers
 source 1..647
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 508
 MFEIDYSRDS FLKDQGPFRY ISGSIHYSRV PRFYWKDRLL KMKGMLNAl QTYVPWNFHE 60
 PWPGQYQFSE DHDVEYFLRL AHELGLLVIL RPGPYICAED EMGGGLPAWLL EKESELLRSS 120
 DPDYLAAVDK WLGVLLPKMK PLLYQNGGPV ITVQVENEYG SYFACDFDYL RFLQKRFRHH 180
 LGDDVVLFIT DGAHKTFLKC GALQGLYTT DFPTGSNITD AFLSQRKCEP KGPLINSEFY 240
 TGWLDSHWGQP HSTIKTEAVA SLYDILARG ASVNLYMFIG GTNFAYWNGA NSPYAAQPTS 300
 YDYDAPLSEA GDLTEKYFAL RNIIQKFEKV PEGPIPSTP KFAYGKVTL KLKTVGAALD 360
 IICPSGPPIKS LYPLTFIQVK QHYGFVLYRT TLPQDCSNPA PLSSPLNGVH DRAYVADGI 420
 PQGVLERNNV ITLNITGKAG ATLDLLVENM GRVNYGAYIN DFKGLVSNLT LSSNILTDTW 480
 IFPLDTEADV CSHLGGWGH DS GH HDEAWA HNSSNYTLP 540

AF 440

IQFPGWTKGQ VVINGFNGLR YWPARGPQLT FVPQHILMT SAPNTITVLE LEWAPCSSDD 600

PELCAVTFVD RPVIGSSVTYD DHPSPKVEKR LMPPPPQKRN DWLDHV 647

SEQ ID NO: 509 moltype = AA length = 185
 FEATURE Location/Qualifiers
 source 1..185
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 509
 MPGFLVRILP LLLVLLLLGP TRGLRVENEY GSYFACDFDYL LRFLQKRFH HLGDVVLFIT 60
 TDGAHKTFLK CGALQGLYTT VDFGTGSNIT DAFLSQRKCE PKGPLINSEF YTGWLDHWGQ 120
 PHSTIKTEAV ASSLYDILAR GASVNLYMFII GGTFNAYWN ANSPYAAQPT SYDYDAPLSE 180
 AGDLT 185

SEQ ID NO: 510 moltype = AA length = 147
 FEATURE Location/Qualifiers
 source 1..147
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 510
 MPGFLVRILP LLLVLLLLGP TRGLRSRFLP WAFHLPQRQPK SQLPLHKRG TKTAPNEHAS 60
 SNRSGRRRRR QOWNATORMF EIDYSRDSL KDGQPFRYIS GSIHYSRVPR FYWKDRLLKM 120
 KMAGLNAIQT YVPWNFHEPW PGQYQFS 147

SEQ ID NO: 511 moltype = AA length = 41
 FEATURE Location/Qualifiers
 source 1..41
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 511
 MPGFLVRILP LLLVLLLLGP TRGLRITWQL WTSGWESFCP R 41

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SEQ ID NO: 512	moltype = AA length = 114	
FEATURE	Location/Qualifiers	
source	1..114	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 512		
MGGGLPAWLLE KESILLRSSD	PDYLAADVWK LGVLLPKMKP LLYQNGGPVI TVQVENEYGS	60
YFACDFDYLLR	FLQKRFRRHHL GDDVVLFDTD GAHKTFLKCG ALQGLYTTVD FGTG	114
SEQ ID NO: 513	moltype = AA length = 84	
FEATURE	Location/Qualifiers	
source	1..84	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 513		
MFEIDYSRDS	FLKDQGPFRY ISGSIHYSRV PRFYWKDRLL KMKMAGLNAI QTLPGSCGQV	60
VGSPSAQDEA	SPLSEWRASY NSAG	84
SEQ ID NO: 514	moltype = AA length = 102	
FEATURE	Location/Qualifiers	
source	1..102	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 514		
MFEIDYSRDS	FLKDQGPFRY ISGSIHYSRV PRFYWKDRLL KMKMAGLNAI QTYVPWNFHE	60
PWPGQYQFSE	DHDVEYFLRL AHIELGLLVL RPGPYICAEM	102
SEQ ID NO: 515	moltype = AA length = 150	
FEATURE	Location/Qualifiers	
source	1..150	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 515		
XLGWSKAGSG	SVCLALDQLR DVIESQEELI HQLRNVMVLQ DENFVSKEEF QAVEKKLVEE	60
KAHAHAKTKVL	LAKEEEKLQF ALGEVEVLSK QLEKEKLAPE KALSSVKSKV LQESSKKDQL	120
ITKCNGITCL	TSGSRSSRRRA TWPRCWTRSI	150
SEQ ID NO: 516	moltype = AA length = 63	
FEATURE	Location/Qualifiers	
source	1..63	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 516		
MAASGEPEQRQ	WQEEVAAVVV VGSCMTDLVR RMCMRICYVH FCCQPTPQLQ NCSSLCVITC	60
QEN		63
SEQ ID NO: 517	moltype = AA length = 518	
FEATURE	Location/Qualifiers	
source	1..518	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 517		
MALERLCVLS	KVLLITVLVV EGIAVAQKTQ DGQNIGIKHI PATQCGIWVR TSNGGHFASP	60
NYPDSYPPNK	ECIYILEAAP RQRIELTDFE HYIIEPSFEC RFDHLEVRDG PFGFSPLIDR	120
YCGVKSPPLI	RSTGRPMWIK FSSDDEELEGGL GFRAKYSFIP DPDFTYLGDQ QFELSGADGI	180
VRSSQVEQEE	IWTIKATPKA KIYLRFLDYQ MEHSNECKRN FVAVYDGSSS	240
IENLKAKEPCS	TVANDVMLKT GIGIVIRMWAD EGSRSLSRFRM LFTSFVEPPC TSSTFFCHSN	300
MCINNSLVCN	GVQNCAYPWD ENHCKEKKKA GVFEQITKTH GTIIGITSGI VLVLIIISIL	360
VQVKQPRKVK	MACKTAFNKT GFQEVFDPPH YELFSLRDKE ISADLADLSE ELDNYQKMRR	420
STASRCIHD	HHCGSQASSV KQSRTNLSSM ELPFRNDFAQ PQPMKTFNST FKKSSYTFKQ	480
GHECPEQALE	DRVMEHIPCE IYVRGREDSA QASISIDF	518
SEQ ID NO: 518	moltype = AA length = 525	
FEATURE	Location/Qualifiers	
source	1..525	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 518		
MALERLCVLS	KVLLITVLVV EGIAVAQKTQ DGQNIGIKHI PATQCGIWVR TSNGGHFASP	60
NYPDSYPPNK	ECIYILEAAP RQRIELTDFE HYIIEPSFEC RFDHLEVRDG PFGFSPLIDR	120
YCGVKSPPLI	RSTGRPMWIK FSSDDEELEGGL GFRAKYSFIP DPDFTYLGGI LNPIPDCQFE	180
LSGADGIVRS	SVQEKEEKT PGQAVDCIWT IKATPKAKIY LRFLDYQMEH SNECKRNFA	240
VYDGSSSIEN	LKAKFCSTVA NDVMLKTGIG VIRMWADEGS RLSRFRMLFT SFVEPPCTSS	300
TEFCHSNMCI	NNSLVCNGVQ NCAYPWDENH CKEKKKAGVF EQITKTHGFI IGITSGIVLV	360
LLIISILVQV	KQPRKKVMAC KTAFNKTGFQ EVFDPPHYEL FSLRDKEISA DLADLSEELD	420
NYQKMRSSRT	ASRCIHDHHC GSQASSVKQS RTNLSSMELP FRNDFAQPQP MKTFNSTFKK	480

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SSYTFKQGHE CPEQALEDRV MEEIPCEIYV RGREDSAQAS ISIDF	525
SEQ ID NO: 519	moltype = AA length = 365
FEATURE	Location/Qualifiers
source	1..365
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 519	
XLIDRYCGVK SPPLIRSTGR FMWIKFSSDE ELEGLGFRAK YSFIPDPDFT YLGDCQFELS	60
GADGIVRSSQ VEQEETKPGQ QAVDCIWTIK ATPKAKIYLRL FLDYQMEHSN ECKRNFVAVY	120
DGSSSIENLK AKFCSTVAND VMLKTGIGVI RMWADEGSRL SRFRMLFTSF VEQKKKAGVF	180
EQTITKTHGTI IGITSGIVLV LLIISILVQV KOPRKVVMAC KTAFNKTGFQ EVFDPHYLE	240
FSLRDKEISA DLADLSEELD NYQKMRSSST ASRCIHDHHC GSQASSVKQS RTNLSSMELP	300
FRNDFAQPQP MKTFNSTFKK SSYTFKQGHE CPEQALEDRV MEEIPCEIYV RGREDSAQAS	360
ISIDF	365
SEQ ID NO: 520	moltype = AA length = 194
FEATURE	Location/Qualifiers
source	1..194
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 520	
XTYLGGLN P IPDCQFELSG ADGIVRSSQV EQEEEKTPKGQ AVDCIWTIKA TPKAKIYLRF	60
LDYQMEHSNE CKRNFVAVYD GSSSIENLK A KFCSTVANDV MLKTGIGVIR MWADEGSRLS	120
RFRMLFTSFV EQKKKAGVF E QITKTHGTII GITSGIVLV L LIISILVQVK QPRKKVMA	180
TAPNKTGFQE VFDP	194
SEQ ID NO: 521	moltype = AA length = 228
FEATURE	Location/Qualifiers
source	1..228
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 521	
XSSSIENLK A KFCSTVANDV MLKTGIGVIR MWADEEKKKA GVFEQITKTH GTIIGITSGI	60
VLVLLIISIL VQVKQPRKKV MACKTAFNKT GFQEVDPPH YELFSLRDE ISADLADLSE	120
ELDNYQKMR SSTASRCIHD HHCGSQASSV KQSRTNLSSM ELPFRNDFAQ PQPMKTFNST	180
FKSSSYTFQ G HECPEQALE DRVMECIPCE IYVRGREDSA QASISIDF	228
SEQ ID NO: 522	moltype = AA length = 347
FEATURE	Location/Qualifiers
source	1..347
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 522	
MSSWSRQRPK SPGGIQPHVS RTLFLLLLLA ASA WGVTLSP KDCQVFRSDH GSSISCPA	60
EIPGYLPADT VHLAVEFFNL THLPANLLQG ASKLQELHLS SNGLESLSPE FLRPVPQLRV	120
LDLTRNALTG LPPGLFQASA TLDLTVLKBN QLEVLEVSLL HGLKA LGHLD LSGNRRLRKL	180
PGLLANFTLL TLDLGENQL ETLPDDLLRG PIQLERLHLE GNKLQVLGKD LLLPQPDLY	240
LFLNGNKLAR VAAGAFQGLR QLDMLDLSNN SLASVPEGLW ASLGQPWNWDM RDGFDISGNP	300
WICDQNLSDL YRWLQAQKDK MFSQNDTRCA GPEAVKGQTL LAVAKSQ	347
SEQ ID NO: 523	moltype = AA length = 330
FEATURE	Location/Qualifiers
source	1..330
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 523	
MRGPPEPGQP TMEGDVLDL EALGYKGPLL EEQALT KAAE GGLSSPEFSE LCIWLGSQIK	60
SICNLLEESIT SAGR DLESF QLEISGFLKE MACPYSVLIS GDIKDR LK K EDCLKL LFL	120
STELQASQIL QNKHKHNSQ DKNSEVYQEV QAMFD TLGIP KSTTS DIPHM LNQVESKVKD	180
IILSKVQKHNV GKPLLKMDLN SEQA EQLERI NDALS CEYEC RRRMLMKR LD VTVQSF GWSD	240
RAKVKTDDIA RIYQPKRYAL SPKTTITMAH LLAAREDL SK II R TSSG TS R EKTACAIN KV	300
GVSFSTVENE LMISYLMFLQ ILVYFSFMSW	330
SEQ ID NO: 524	moltype = AA length = 101
FEATURE	Location/Qualifiers
source	1..101
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 524	
ISGDIKDRLK KKEDCLKLLL FLSTELQASQ ILQNKHHKNS QLDKNSEVYQ EVQAMFD TLG	60
IPKSTTS DIP HMLNQVESKV KDILSKIHME E VVVVVVVVV E	101
SEQ ID NO: 525	moltype = AA length = 352
FEATURE	Location/Qualifiers
source	1..352

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mol_type = protein
organism = Homo sapiens
SEQUENCE: 525
MKPALLEVMR MNRICRMVLA TCLGSFILVI FYFQSMMLHPV MRRNPFVGDI CCRKGSRSP 60
QELYNPQIQL ELSNTAVLHQHM RRDQVTDTCR ANSATSRKR VLTPNDLKHL VVDEDHELIY 120
CYVPKVACTN WKRLLMVLTG RGKYSDPMEI PANEAHVSAN LKTLNQYSIP EINHRLKSYM 180
KFLFVREPFE RLVSAYRNKF TQKYNISFHK RYGTKIIRQK RNATQEALR KGDDVKFEEF 240
VAYLIDPHTQ REEPFNEHWQ TVYSLCHPCH IHYDLVKGTYE TLEEDSNYVL QLAGVGSYLK 300
FPTYAKSTRT TDEMTEFFQ NISSEHQQTQL YEVYKLDFLM FNYSVP SYLK LE 352

SEQ ID NO: 526      moltype = AA length = 72
FEATURE           Location/Qualifiers
source            1..72
mol_type = protein
organism = Homo sapiens
SEQUENCE: 526
MKPALLEVMR MNRICRMVLA TCLGSFILVI FYFQIMRRNP FGVDICCRKG SRSPLQELYN 60
PIQVSFKHSV SM 72

SEQ ID NO: 527      moltype = AA length = 77
FEATURE           Location/Qualifiers
source            1..77
mol_type = protein
organism = Homo sapiens
SEQUENCE: 527
MKPALLEVMR MNRICRMVLA TCLGSFILVI FYFQSMMLHPV MRRNPFVGDI CCRKGSRSP 60
QELYNPQIVS FKHSVSM 77

SEQ ID NO: 528      moltype = AA length = 347
FEATURE           Location/Qualifiers
source            1..347
mol_type = protein
organism = Homo sapiens
SEQUENCE: 528
MKPALLEVMR MNRICRMVLA TCLGSFILVI FYFQIMRRNP FGVDICCRKG SRSPLQELYN 60
PIQLELSNTA VLHQMRDQV TDTCRANSAT SRKRRVLTNP DLKHLVVDED HELIYCVPK 120
VACTNWKRLM MVLTRGRGKYS DPMEIPANEA HVSANLKTLM QYSIPEINHR LKSYMKFV 180
REPFERLVS A YRNKFTQKYN ISFHKKRYGTK IIKRQRKNAT QEALRKGDV KFEEFVAYLI 240
DPHTQREEPF NEHWQTVYSL CHPCHIHYDL VGKYETLEED SNYVLQLAGV GSYLFKPTYA 300
KSTRTTDEMT TEFFQNISSE HQTQLYEVYK LDFLMFNFYNSV PSYKLE 347

SEQ ID NO: 529      moltype = AA length = 775
FEATURE           Location/Qualifiers
source            1..775
mol_type = protein
organism = Homo sapiens
SEQUENCE: 529
MEPPYSLTAH YDEFQEVKVV SRCGAGGARG ASLPPGFPLG AARSATGARS GLPRWNRREV 60
CLLSGLVFAA GLCAILAAAL ALKYLGPVAA GGGACPEGCP ERKAFAARAAR FLAANLDASI 120
DPCQDFYSFA CGGWLRRHAI PDDKLTYGTI AAIGEQNEER LRRLLARP GGPGAAQRKV 180
RAAFFRSCLDM REIERLGPGRP MLEVIEDCGG WD LGGAERGP GVAARWDLNR LLYKAQGVYS 240
AAALFSLSTVS LDDRNRSSRYV IRIDQDGTL PERTLYLAQD EDSEKILAAY RVFMERVLSL 300
LGADAVEQKA QEILOVEQQI ANITVSEHDD LRRDVSSMYN KVTLGQLQKI TPHLRWKWL 360
DQIFQEDFSE EEEVVLATD YMQQVSQLIR STPHRVLHNY LVWRVVVVL EHLSPPFREA 420
LHELAQEMEG SDKPQELARV CLGQANRHFV MALGALFVHE HFSAAASKAKV QQLVEDIKYI 480
LGQRLEELDW MDAETRAAAR AKLQYMMVMV GYPDFLKKPD AVDKEYFEV HEKTYFKNL 540
NSIRFSIQLS VKKIRQEVDE STWLLPPQAL NAYLPNKNQ MVFPAGILQP TLYDDFPQS 600
LNYGGIGTII GHETHGYDD WGGQYDRSGN LLHWWTEASY SRFLRKAECI VRYLDNFTVY 660
NQRVNGKHTL GENIADMGGI KLAYHAYQK WREHGPEHPL PRLKYTHDQL FFIFAQNW 720
IKRRSQSIYL QVLTDKHAPE HYRVLGSVQ FEEFGRAFH PKDSPMNPAH KCSVW 775

SEQ ID NO: 530      moltype = AA length = 773
FEATURE           Location/Qualifiers
source            1..773
mol_type = protein
organism = Homo sapiens
SEQUENCE: 530
MEPPYSLTAH YDEFQEVKVV SRCGAGGARG ASLPPGFPLG AARSATGARS GLPRWNRREV 60
CLLSGLVFAA GLCAILAAAL ALKYLGPVAA GGGACPEGCP ERKAFAARAAR FLAANLDASI 120
DPCQDFYSFA CGGWLRRHAI PDDKLTYGTI AAIGEQNEER LRRLLARP GGPGAAQRKV 180
RAAFFRSCLDM REIERLGPGRP MLEVIEDCGG WD LGGAERGP GVAARWDLNR LLYKAQGVYS 240
AAALFSLSTVS LDDRNRSSRYV IRIDQDGTL PERTLYLAQD EDSEKILAAY RVFMERVLSL 300
LGADAVEQKA QEILOVEQQI ANITVSEHDD LRRDVSSMYN KVTLGQLQKI TPHLRWKWL 360
DQIFQEDFSE EEEVVLATD YMQQVSQLIR STPHRVLHNY LVWRVVVVL EHLSPPFREA 420
LHELAQEMEG SDKPQELARV CLGQANRHFV MALGALFVHE HFSAAASKAKV QQLVEDIKYI 480
LGQRLEELDW MDAETRAAAR AKLQYMMVMV GYPDFLKKPD AVDKEYFEV HEKTYFKNL 540

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NSIRFSIQLS VKKIRQEVDK WLLPPQALNA YYLPNKNQMV FPAGILQPTL YDPDFPQSLN	600
YGGIGITIIGH ELTHGYDDWG GQYDRSGNLL HWWTEASYSR FLRKACIVR LYDNPVYVHQ	660
RVNGKHTLGE NIADMGGKLK AYHAYQKWR EHGPHEPLPR LKYTHDQLFF IAFQAQNWCIK	720
RRSQSIYLQV LTDKHAPEHY RVLGSVSQFE EFGRAFHCKP DSPMNPAHKC SVW	773
SEQ ID NO: 531 moltype = AA length = 233	
FEATURE Location/Qualifiers	
source 1..233	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 531	
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DSPA VNGATG HSSSLDAREV IPMAAVKQAL REAGDEFELR YRRAFSDLTS QLHITPGTAY	120
QSFEQVNVNL FRDGVNWGRI VAFFSFQGGAL CVESVDKEMQ VLVSRIAAMW ATYLNHDLEP	180
WIQE NGGWD T FVEL YGNNAAES AESRKGQERF NRWF LTGM TVAGV AGV VLLGSLF SRK	233
SEQ ID NO: 532 moltype = AA length = 170	
FEATURE Location/Qualifiers	
source 1..170	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 532	
MSQSNRELVV DFLSYKLSQK GYSWSQFSDV EENRTEAPEG TESEMETPSA INGNPSWHLA	60
DSPA VNGATG HSSSLDAREV IPMAAVKQAL REAGDEFELR YRRAFSDLTS QLHITPGTAY	120
QSFEQDTFVE LYGNNAAES RKGQERFNRW FLTGMTVAGV VLLGSLFSRK	170
SEQ ID NO: 533 moltype = AA length = 233	
FEATURE Location/Qualifiers	
source 1..233	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 533	
MSQSNRELVV DFLSYKLSQK GYSWSQFSDV EENRTEAPEG TESEMETPSA INGNPSWHLA	60
DSPA VNGATG HSSSLDAREV IPMAAVKQAL REAGDEFELR YRRAFSDLTS QLHITPGTAY	120
QSFEQVNVNL FRDGVNWGRI VAFFSFQGGAL CVESVDKEMQ VLVSRIAAMW ATYLNHDLEP	180
WIQE NGGWD T FVEL YGNNAAES AESRKGQERF NRWF LTGM TVAGV AGV VLLGSLF SRK	233
SEQ ID NO: 534 moltype = AA length = 813	
FEATURE Location/Qualifiers	
source 1..813	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 534	
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AGSRRGRRLRS CLDLEQCSLK VLEPEGSPSL CLLKLMGEKG CTVTELSDFL QAMEHTEVLQ	120
LLSPPG KIT VN PESKAVLA GQFVKLCCRA TGHPFVQYQW FKMNKEIPNG NTSELIFNAV	180
HVKDAGFVVC RVNNNNTFEF SQWSQLDVCD IPESFQRSVDF GVSESKLQIC VEPTSQKLMP	240
GSTLVLCQVA VGSPIPHYQW FKNELPLTHE TKKLYMVPVY DLEHQGTWYC HVYNDRDSQD	300
SKKVEIIIDE LN NLGHPDN EQTTDQPLAK DKVALLIGN NYREHPKLKA PLVDVYELTN	360
LLRQLDFKVV SLLDLTEYEM RNAVDEFLLL LDKGVYGLLY YAGHGYENFG NSFMVPVDAP	420
NPYRSENCLC VONILKLMQE KETGLNVLDI DMCRKRNNDY DTIPILDALK VTANIVFGYA	480
TCQGAEAEFI QHSGLANGMKE MKFLKDRRL DKKITVLLDE VAEDMGKCHL TKGKQALEIR	540
SSLSEKRAL DPIQGTEYSA ESLVRNLQWA KAHELPESMC LKFDCGVQIQ LGFAAEFSNV	600
MIIYTSIVYK PPEIIMCDAY VTDFFPLLDI DPKDANKGP EETGSYLVSK DL PKHCLYTR	660
LSSLQKLKEH LVFTVCLSYQ YSGLEDTVED KQEVNVGKPL IAKLDMHRGL GRKTCFQTCL	720
MSNGPYQSSA ATSGGAGHYH SLQDPFHGVY HSHPGNPSNV TPAD SCHCSR TPDAFISSFA	780
HHASCHFSRS NVPVETTDEI PFSFSDRLRI SEK	813
SEQ ID NO: 535 moltype = AA length = 824	
FEATURE Location/Qualifiers	
source 1..824	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 535	
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AGSRRGRRLRS CLDLEQCSLK VLEPEGSPSL CLLKLMGEKG CTVTELSDFL QAMEHTEVLQ	120
LLSPPG KIT VN PESKAVLA GQFVKLCCRA TGHPFVQYQW FKMNKEIPNG NTSELIFNAV	180
HVKDAGFVVC RVNNNNTFEF SQWSQLDVCD IPESFQRSVDF GVSESKLQIC VEPTSQKLMP	240
GSTLVLCQVA VGSPIPHYQW FKNELPLTHE TKKLYMVPVY DLEHQGTWYC HVYNDRDSQD	300
SKKVEIIIGR TDEAVECTED ELNNLGHPDN KEQTTDQPLA DKVALLIGN MNYREHPKLK	360
APL LVDVYELT NLLRQLDFKV VSLLDLTEYE MRNAVDEFLL LLDKGVYGLLY YYAGHGYENF	420
GNSFMVPVDA PN PYRSENCL CVQNLKLMQ EKETGLNVFL LDMCRKRNNDY DDTIPILDAL	480
KV TANIVFEGY AT CQGAEAEFI IQHSGLANGI FMKFLKDRRL EDKKITVLLD EVAEDMGKCH	540
LTKGKQALEI RSSLSEKRAL TDPIQGTEYS AESLVRNLQW AKAHELPESMC CLKFD CGVQI	600
QLGFAAEFSN VMIIYTSIVY KPPEIIMCD A YVTDFPLLD IDPKDANKGT PEETGSYLV	660
KDLPKHCLYT RLSSLQKLKE HLVFTVCLSY QYSGLEDTVE DKQEVNVGKP LIAKLDMH RG	720

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LGRKTCFQTC LMSNGPYQSS AATSGGAGHY HSLQDPFHGV YHSPGNPSN VTPADSCHCS RTPDAFISSF AHHASCHFSR SNVPVETTDE IPFSFSDRLR ISEK	780 824
SEQ ID NO: 536 moltype = AA length = 119 FEATURE Location/Qualifiers source 1..119 mol_type = protein organism = Homo sapiens	
SEQUENCE: 536 MGEKGCTVTE LSDFLQAMEH TEVLQLLSPP GIKITVNPES KAVLAGQFVK LCCRATGHPF VQYQWFKMNK EIPNGNTSEL IFNAHVVKDA GFYVCRVNNN FTFEFQSWSQ LDVCDIPES	60 119
SEQ ID NO: 537 moltype = AA length = 506 FEATURE Location/Qualifiers source 1..506 mol_type = protein organism = Homo sapiens	
SEQUENCE: 537 MAGEVSAATG RFSLERLGLP GLALAAAALL LALCLLVRRT RRPGEPLIK GWLPYLGVVL NLRKDPLRFM KTLQKQHGDT FTVLGGKVYI TFILDPFQYQ LVIKNHKQLS FRVFSNKLL KAFSISQLQK NHDMNDELHL CYQFLQGKSL DILLESMMQN LKQVFEPQLL KTTSWDTAEL YPCSSIIFE ITFTTIYGVK IVCDNNKPFIS ELRDDFLKPD DKFAYLVSNI PIELLGNVKS IREKIIKCGW SEKLAQMCGW SEVFQSRQDV LEKYVYHEDL EIGAHHLGFL WASVANTIPT MFWMAMYLLR HPEAMAAVRD EIDRLLQSTG QKKGSGFPIH LTREQLDLSI CLESSIFEA RLSSYSTIR FVEEDELTLS ETGDYCVRKG DLVAIFPPVLL HGDPEIFEAAP EEFRYDRFIE DGKKTTFK RGKKLKCYLM PFGTGTSKCP GRFFPALMEIK QLLVILLTYF DLEIIDDKPI GLNYSRLLFG IQYPDSDVLF RYKVKS	60 120 180 240 300 360 420 480 506
SEQ ID NO: 538 moltype = AA length = 543 FEATURE Location/Qualifiers source 1..543 mol_type = protein organism = Homo sapiens	
SEQUENCE: 538 MLRSKPALP PPLMLLLLGP GPLSPGALP RPAQAQDVDD LDFFTQEPLH LVSPSFLSVT IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS QVNQDICKYG SIPPDVEEKL RLEWPYQEQL LLREHYQKFF KNSTYSRSSV DVLYTFANCS GLDLIFGLNA LLRTADLQWN SSNAQLLDY CSSKGYNISW ELGNEPNSFL KKADIFINGS QLGEDFIQLH KLLRKSTFKN AKLYGPDVGQ PRRKTAKMLK SFLKAGGEVI DSVTWHYYL NGRTATKEFD LNPDVLDIFI SSVQKVFQVV ESTRPKGKVV LGETSSAYGG GAPLLSDTFA AGFMWLDKLG LSARMGIEVV MRQVFFGAGN YHLVDENFDP LPDYWLSSLF KKLVGTKVLM ASVQGSKRK LRVYLHCTNT DNPRYKEGDL TLYAINLHNV TKYLRLLPYPF SNKQVDKYLL RPLGPHGLLS KSVQLNGLTL KMVDDQTLP LMEKPLRPGS SLGLPAFSYS FFVIRNAKVA ACI	60 120 180 240 300 360 420 480 540 543
SEQ ID NO: 539 moltype = AA length = 543 FEATURE Location/Qualifiers source 1..543 mol_type = protein organism = Homo sapiens	
SEQUENCE: 539 MLRSKPALP PPLMLLLLGP GPLSPGALP RPAQAQDVDD LDFFTQEPLH LVSPSFLSVT IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS QVNQDICKYG SIPPDVEEKL RLEWPYQEQL LLREHYQKFF KNSTYSRSSV DVLYTFANCS GLDLIFGLNA LLRTADLQWN SSNAQLLDY CSSKGYNISW ELGNEPNSFL KKADIFINGS QLGEDFIQLH KLLRKSTFKN AKLYGPDVGQ PRRKTAKMLK SFLKAGGEVI DSVTWHYYL NGRTATKEFD LNPDVLDIFI SSVQKVFQVV ESTRPKGKVV LGETSSAYGG GAPLLSDTFA AGFMWLDKLG LSARMGIEVV MRQVFFGAGN YHLVDENFDP LPDYWLSSLF KKLVGTKVLM ASVQGSKRK LRVYLHCTNT DNPRYKEGDL TLYAINLHNV TKYLRLLPYPF SNKQVDKYLL RPLGPHGLLS KSVQLNGLTL KMVDDQTLP LMEKPLRPGS SLGLPAFSYS FFVIRNAKVA ACI	60 120 180 240 300 360 420 480 540 543
SEQ ID NO: 540 moltype = AA length = 226 FEATURE Location/Qualifiers source 1..226 mol_type = protein organism = Homo sapiens	
SEQUENCE: 540 MLRSKPALP PPLMLLLLGP GPLSPGALP RPAQAQDVDD LDFFTQEPLH LVSPSFLSVT IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS QVNQDICKYG SIPPDVEEKL RLEWPYQEQL LLREHYQKFF KNSTYSRSSV DVLYTFANCS GLDLIFGLNA LLRTADLQWN SSNAQLLDY CSSKGYNISW ELGNAS	60 120 180 226
SEQ ID NO: 541 moltype = AA length = 168 FEATURE Location/Qualifiers source 1..168	

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mol_type = protein
organism = Homo sapiens
SEQUENCE: 541
MLRSKPALP PPLMLLLLGP LGPLSPGALP RPAQAQDVVD LDFFTQEPLH LVSPSFLSVT 60
IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS 120
QVNQDICKYG SIPPDVEEKL RLEWPyQEQL LLREHYQKKF KNSTYSTS 168

SEQ ID NO: 542      moltype = AA length = 380
FEATURE          Location/Qualifiers
source           1..380
mol_type = protein
organism = Homo sapiens
SEQUENCE: 542
MLRSKPALP PPLMLLLLGP LGPLSPGALP RPAQAQDVVD LDFFTQEPLH LVSPSFLSVT 60
IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS 120
QVNQDICKYG SIPPDVEEKL RLEWPyQEQL LLREHYQKKF KNSTYRSSV DVLYTFANCS 180
GLDLIFGLNA LLRTADLQWN SSNAQLLDY CSSKGYNISW ELGNEPNSFL KKADIFINGS 240
QLGEDFIQLH KLLRKSTFKN AKLYGPDVCGQ PRRKTAKMLK AFLKAGGEVI DSVTWHHYL 300
NGRTATKEDF LNPDVLDIFI SSVQKVFDQY WSLLFKKLV GTKVLMASVQ GSKRRLRVY 360
AGFMIIGYL CSRNWWAPRC GAPLLSDTFA 380

SEQ ID NO: 543      moltype = AA length = 469
FEATURE          Location/Qualifiers
source           1..469
mol_type = protein
organism = Homo sapiens
SEQUENCE: 543
MLRSKPALP PPLMLLLLGP LGPLSPGALP RPAQAQDVVD LDFFTQEPLH LVSPSFLSVT 60
IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS 120
QVNQDICKYG SIPPDVEEKL RLEWPyQEQL LLREHYQKKF KNSTYRSSV DVLYTFANCS 180
GLDLIFGLNA LLRTADLQWN SSNAQLLDY CSSKGYNISW ELGNEPNSFL KKADIFINGS 240
QLGEDFIQLH KLLRKSTFKN AKLYGPDVCGQ PRRKTAKMLK AFLKAGGEVI DSVTWHHYL 300
NGRTATKEDF LNPDVLDIFI SSVQKVFDQY WSLLFKKLV GTKVLMASVQ GSKRRLRVY 360
LHCTNTDNPY YKEGDLTLYA INLNHNTVKYL RLPPFESNKQ VDKYLLRPLG PHGLLSKSVQ 420
LNGLTLKMVD DQTLPPLMEK PLRPGLSSLGL PAFSYSPFVI RNAKVAACI 469

SEQ ID NO: 544      moltype = AA length = 485
FEATURE          Location/Qualifiers
source           1..485
mol_type = protein
organism = Homo sapiens
SEQUENCE: 544
MLRSKPALP PPLMLLLLGP LGPLSPGALP RPAQAQDVVD LDFFTQEPLH LVSPSFLSVT 60
IDANLATDPR FLILLGSPKL RTLARGLSPA YLRFGGTKTD FLIFDPKES TFEERSYWQS 120
QVNQDICKYG SIPPDVEEKL RLEWPyQEQL LLREHYQKKF KNSTYSPKNS FLKKADIFIN 180
GSQLEDFIG LHKLLRKSTF KNAKLYGPDV GQPRRKTAKM LKSFLKAGGE VIDSVTWHHY 240
YLNGRATDFE DFLNPDVLDI FISSVQKVFDQY VVESTRPGCKV WLGETSSAY GGGAPLLSDT 300
FAAGFMWLKD LGLSARMGIE VVMRQVFFGA GNYHLVDENF DPLPDWLSL LFKKLVGTKV 360
LMAHSVQGSKR RKLRLVYLHCT NTNDNPRYKEG DLTLYAINLH NVTKYLRPLY PFSNKQVDKY 420
LLRPLGPGL LSKSVQLNGL TLKMVDDQTL PPLMEKPLRP GSSLGLPALS YSFVIRNAK 480
VAACI 485

SEQ ID NO: 545      moltype = AA length = 524
FEATURE          Location/Qualifiers
source           1..524
mol_type = protein
organism = Homo sapiens
SEQUENCE: 545
MDTESTYSGY SYYSSHSKKS HRQGERTRER HKSPRNKDGR GSEKSVTIQP PTGEPLLGN 60
STRTEEVQDD NWGETTTAIT GTSEHSISQE DIARISKDME DSVGLDCKRY LGTVASF 120
LIVFLTPIAF ILLPPILWRD ELEPCGTICE GLFISMAMFL LILLIGTWAL FFRKRADMP 180
RVFVFRALLL VLIFLFWVSY WLIFYGVRILD SRDRNYQGIV QYAVSLVDL LFIHYLAIVL 240
LELRQLQPMF TLQVVRSTDG ESRFYSLGHL SIQRAALVVL ENYYKDFTIY NPNNLTASKF 300
RAAKHMAGLK VYNVNDGPSNN ATGQSRAMIA AAARRRDSSH NELYEEAEH ERRVKKRKR 360
LVAVVEEAFI HIQRQLQAEQQ QKAPGEVMDP REAAQAIFFPS MARALQKYL ITRQQNYHSM 420
ESTLQHLAFC ITNGMTPKAF LERYLSSAGPT LOYDKDRWLS TQWRLVSDEA VTNGLIRDGIV 480
FVLKCLDFSL VVNVKKIPFI ILSEEFIDPK SHKFVLRQLS ETSV 524

SEQ ID NO: 546      moltype = AA length = 524
FEATURE          Location/Qualifiers
source           1..524
mol_type = protein
organism = Homo sapiens
SEQUENCE: 546
MDTESTYSGY SYYSSHSKKS HRQGERTRER HKSPRNKDGR GSEKSVTIQP PTGEPLLGN 60
STRTEEVQDD NWGETTTAIT GTSEHSISQE DIARISKDME DSVGLDCKRY LGTVASF 120

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LLVFLTPIAF	ILLPPILWRD	ELEPCGTICE	GLFISMFKL	LILLIGTWAL	FFRKRRADMP	180
RVFVFRALLL	VLIIFLPVSY	WLFYGVRIILD	SDRNYQGIV	QYAVSLVDAL	LFIHYLAIVL	240
LELRQLQPMF	TLOVVRSTDG	ESRFYSLGHL	SIQRAALVVL	ENYYKDFTIY	NPNLLTASKF	300
RAAKHMGALK	VYNVDPGSNN	ATGQSRAMITA	AAARRRDSHH	NELYYYEEAEH	ERRVKKRKAR	360
LVVAVEEAFI	HIQRLQAEQQ	QKAPGEVMDP	REAAQAIFPS	MARALQKYLR	ITRQQNYHSM	420
ESILQHLAFC	ITNGMTPKAF	LERYLSAGPT	LQYDKDRWLS	TQWRLVSDEA	VTNGLRDGIV	480
FVLKCLDFSL	VVNVKKIPFI	ILSEEFIDPK	SHKFVRLQSQS	ETSV		524

SEQ ID NO: 547	moltype = AA	length = 524				
FEATURE	Location/Qualifiers					
source	1..524					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 547						
MDTESTYSGY	SYYSSHSKKS	HRQGERTRER	HKSPRNKDGR	GSEKSVTIOP	PTGEPLLGN	60
STRTEEVQDD	NWGETTTAIT	GTSEHSISQ	DIARISKDME	DSVGLCKRY	LGLTVASFLG	120
LLVFLTPIAF	ILLPPILWRD	ELEPCGTICE	GLFISMFKL	LILLIGTWAL	FFRKRRADMP	180
RVFVFRALLL	VLIIFLPVSY	WLFYGVRIILD	SDRNYQGIV	QYAVSLVDAL	LFIHYLAIVL	240
LELRQLQPMF	TLOVVRSTDG	ESRFYSLGHL	SIQRAALVVL	ENYYKDFTIY	NPNLLTASKF	300
RAAKHMGALK	VYNVDPGSNN	ATGQSRAMITA	AAARRRDSHH	NELYYYEEAEH	ERRVKKRKAR	360
LVVAVEEAFI	HIQRLQAEQQ	QKAPGEVMDP	REAAQAIFPS	MARALQKYLR	ITRQQNYHSM	420
ESILQHLAFC	ITNGMTPKAF	LERYLSAGPT	LQYDKDRWLS	TQWRLVSDEA	VTNGLRDGIV	480
FVLKCLDFSL	VVNVKKIPFI	ILSEEFIDPK	SHKFVRLQSQS	ETSV		524

SEQ ID NO: 548	moltype = AA	length = 522				
FEATURE	Location/Qualifiers					
source	1..522					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 548						
MDTESTYSGY	SYYSSHSKKS	HRQGERTRER	HKSPRNKDGR	GSEKSVTIOP	PTGEPLLGN	60
STRTEEDDNW	GETTTAITGT	SEHSISQEDI	ARISKDMEDS	VGLDCKRYLG	LTVASFLGL	120
VFLTPIAFIL	LPPILWRDEL	EPCGTICEGL	FISMFKLII	LLIGTWALFF	RKRRADMPRV	180
FVPRALLLVL	IPLFLPVSYWL	FYGVRIILSR	DRNYQGIVQY	AVSLVDALLF	IHYLAIVLLE	240
LRQLQPMFTL	QVVRSTDGES	RFYSLGHLSI	QRAALVVLEN	YYKDFTIYNP	NLLTASKFRA	300
AHKMAGLKVY	NVDGPSNNAT	QGSRAMIAAA	ARRRDSSHNE	LYYEEAEHER	RVKKRKARLV	360
VAVEEAFIHI	QRLQAEQQK	APGEVMDPRE	AAQAIFPSMA	RALQKYLRIT	RQQNYHSMES	420
ILQHLAFCIT	NGMTPKAFL	RYLSAGPTLQ	YDKDRWLSTQ	WRLVSDEAVT	NGLRDGIVFV	480
LKCLDFSLVV	NVKKIPFIIL	SEEFIDPKSH	KFVRLRLQSET	SV		522

SEQ ID NO: 549	moltype = AA	length = 240				
FEATURE	Location/Qualifiers					
source	1..240					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 549						
MAGPPRLLLL	PLLLALARGL	PGALAAQEVQ	QSPHCTTVPV	GASVNITCST	SGGLRGYIYL	60
QLGPQPQDII	YYEDGVVPTT	DRRFGRIDF	SGSQDNLTIT	MHRLQLSDTG	TYTCQAITEV	120
NVYGSGLTQLV	VTEEQSQGWH	RCSDAPPRAS	ALPAPPTGSA	LPDPQTASAL	PDPPAASALP	180
AALAVISFLL	GLGLGVACVL	ARTQIKKLCS	WRDKNSAACV	VYEDMSH SRC	NTLSSPNQYQ	240

SEQ ID NO: 550	moltype = AA	length = 121				
FEATURE	Location/Qualifiers					
source	1..121					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 550						
MHRLQLSDTG	TYTCQAITEV	NVYGSGLTQLV	VTEEQSQGWH	RCSDAPPRAS	ALPAPPTGSA	60
LPDPQTASAL	PDPPAASALP	AALAVISFLL	GLGLGVACVL	ARTQVSVSPS	CHLHPKDCSL	120
S						121

SEQ ID NO: 551	moltype = AA	length = 35				
FEATURE	Location/Qualifiers					
source	1..35					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 551						
MAGPPRLLLL	PLLLALARGL	PGALAAQAGA	CVGST			35

SEQ ID NO: 552	moltype = AA	length = 160				
FEATURE	Location/Qualifiers					
source	1..160					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 552						
MAGPPRLLLL	PLLLALARGL	PGALAAQGRT	FSVLLARLMV	TAQVLPRGAA	VSPLHD C PRG	60

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SLRQHHLLHQ RGPWDLPEA ARATAPRHHL LRGRGGAHYG QTVPGPYHLL RVPGQPDYHH	120
APPAAVGHWH LHLPGHGGQ CLRLRHPGPG DRGTVPRMAQ	160
SEQ ID NO: 553	moltype = AA length = 140
FEATURE	Location/Qualifiers
source	1..140
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 553	
MHRQLQSDTG TYTCQAITEV NVYGSGTLVL VTEEQSQGWH RCSDAPPRAS ALPAPPTGSA	60
LPDPQTASAL PDPPAASALP AALAVISFLL GLGLGVACVL ARTQIKKLCs WRDKNSAACV	120
YVYEDMSHSRC NTLSSPNQYQ	140
SEQ ID NO: 554	moltype = AA length = 221
FEATURE	Location/Qualifiers
source	1..221
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 554	
MAGPPRLLLL PLLLALARGL PGALAAQEVO QSPHCTTVPV GASVNITCST SGGLRGIVYL	60
QLGPQPQDII YYEDGVVPTT DRRFRGRIDF SGSDQNLTT MHRQLQSDTG TYTCQAITEV	120
NVYGSGTLVL VTEEQSQGWH RCSDAPPRAS ALPAPPTGSA LPDPQTASAL PDPPAASALP	180
AALAVISFLL GLGLGVACVL ARTQVSVSPS CHLHPKDSDL S	221
SEQ ID NO: 555	moltype = AA length = 40
FEATURE	Location/Qualifiers
source	1..40
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 555	
XNYEMPRGDT SSLRAPAEDL RWVEKTLSLL YSPQVAGSSR	40
SEQ ID NO: 556	moltype = AA length = 107
FEATURE	Location/Qualifiers
source	1..107
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 556	
MQCQGYVALL GSDDQSWGWN LVDNNNLLHNG EVNGSFPQCN NAPKYQIGER IRVILDMEDK	60
TLAFLERGYEF LGVAFRGLPK VCLYPAVSAV YGNTEVTLVY LGKPLDG	107
SEQ ID NO: 557	moltype = AA length = 530
FEATURE	Location/Qualifiers
source	1..530
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 557	
MSRSQPQLP PGALPRLQAA APAAA PALL PQWPRRPGRW WPASPLGMKV FRRKALVLCA	60
GYALLLVLTM LNLLDYKWHI EPLQQCNPDG PLGAAAGAAG GSWGRGP PPP AGPPRAHARL	120
DLRTPYRPPA AAVGAAPAAA AGMAGVAAPP GNGTRGTGGV GDKRQLVYVF TTWRSGSSFF	180
GELFNQNPEV FFLYEPVWHW WQKLIPGDAV SLOGAARDML SALYRCDLSV FQLYS PAGSG	240
GRNLTTLGF GAATNKVVCS SPLCPAYRKE VVGLVDDRVC KKC PQR LAR FEEECRKYRT	300
LVIKGVRVFD VAVLAPLLRD PALDLKVIHL VRDPRAVASS RIRS RHLIR ESLQVVR SRD	360
PRAHRMPFLE AAGHKLGAKK EG VGGP ADYH ALG AMEVICN SMAK TQLT AL QPPDWLQGHY	420
LV VRYE DLVG DPVKTLRRVY DFVGLL VSPE MEQFAL NM TS GSGSSSKPFV VSARNATQAA	480
NAWRTALTFO QIKQVEEFCY QPM AVL GYER VNSPEEV KDL SKTLLRKPKRL	530
SEQ ID NO: 558	moltype = AA length = 84
FEATURE	Location/Qualifiers
source	1..84
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 558	
MKQTQVGSLF SLGIRNPEPG PVSGTAVPRQ LAWKSGKYVM VMGVVQACSP EPCLQAVKMT	60
DLSDNPIHES MWELEVEDLH RNIP	84
SEQ ID NO: 559	moltype = AA length = 313
FEATURE	Location/Qualifiers
source	1..313
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 559	
MALLVDRVRG HWRIAAGLLF NLLVSICIVF LNKWIYVYHG FPNMSLTLVH FVVTWLGLYI	60
CQKLDIFAPK SLPPSRLLLL ALSFCGFVVF TNLSLQNNTI GTYQLAKAMT TPVIIAIQTF	120
CYQKTFSTRI QLT LIPI TLG VILNSYYDVK FNFLGMVFAA LGVLVTSLYQ VVVGAKQHEL	180
QVNNSMQLYY QAPMSSAMLL VAVPFFEPVF GEGGIFGPWS VSALLMVLLS GVIAPMVNLS	240

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SEQ ID NO: 560	moltype = AA length = 125	
FEATURE	Location/Qualifiers	
source	1..125	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 560		
QAPMSSAMLL VAVPFFEPVF GEGGIFGPWS VSALSTRLEC SGTIMAHCSL SLLGSSNPPA	60	
STSPVAGTTG AHQHTWLIFI FFVETEFCHV AQADLKLLSS SHLSASARS AGITGLSHHT	120	
WPVIS	125	
SEQ ID NO: 561	moltype = AA length = 34	
FEATURE	Location/Qualifiers	
source	1..34	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 561		
MTVMSLSRDL KDDFHSDTTL SILNEQRIRG ILCD	34	
SEQ ID NO: 562	moltype = AA length = 193	
FEATURE	Location/Qualifiers	
source	1..193	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 562		
MAEAEESPGD PGTASPRPLM RDLKAVGKKF MHVLYPRKSN TLLRDWDLWG PLILCVTLAL	60	
MLQRDSADSE KDGGPQFAEV FVIWWFGAVT ITLNSKLGG NISFFQSLCV LGYCILPLTV	120	
AMLIICRLVLL ADPGPVNFMV RLFVVIVMFA WSIVASTAFL ADSQPPNRRA LAVYPVFLFY	180	
FVISWMILTF TPQ	193	
SEQ ID NO: 563	moltype = AA length = 188	
FEATURE	Location/Qualifiers	
source	1..188	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 563		
MAEAEESPGD PGTASPRPLM RDLKAVGKKF MHVLYPRKSN TLLRDWDLWG PLILCVTLAL	60	
MLQRDSADSE KDGGPQFAEV FVIWWFGAVT ITLNSKLGG NISFFQSLCV LGYCILPLTV	120	
AMLIICRLVLL ADPGPVNFMV RLFVVIVMFA WSIVASTAFL ADSQPPNRRA LAVYPVFLFY	180	
FVISWMIL	188	
SEQ ID NO: 564	moltype = AA length = 236	
FEATURE	Location/Qualifiers	
source	1..236	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 564		
MAEAEESPGD PGTASPRPLF AGLSDISIISQ DIPVEGEITI PMRSRIREFD SSTLNESVRN	60	
TIMRDLKAVG KKKFMHVLYPR KSNTLLRWD LWGPLILCVT LALMLQRDSA DSEKDGGPQF	120	
AEVFVIVWFG AVTITLNKL LGGNISFFQZ LCVLGYCILP LTVAMLICRL VLLADPGPVN	180	
FMVRLFVVIV MFAWSIVAST AFLADSQPPN RRALAVYVF LFYFVISWMI LTFTPQ	236	
SEQ ID NO: 565	moltype = AA length = 520	
FEATURE	Location/Qualifiers	
source	1..520	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 565		
MEVLESGEQG VLQWDRKLSE LSEPGDGEAL MYHTHFSELL DEFSQNVLGQ LLNDPFLSEK	60	
SVSMEVEPSP TSPAPLIQAE HSYSLCEEPR AQSPFTHITT SDSFNDDEVE SEKWYLSTDF	120	
PSTSIIKEPV TDEPPPGLVP SVTILTITAIS TPLEKEEPPL EMNTGVDS SC QTIIPKIKLE	180	
PHEVDQFLNF SPKEMPVDH HLPPPTPSSH GSDSEGSLSNP NFRHLHPFSLP QTHSPSRRAAP	240	
RAPSALLSSP LLTAPHKLQG SGPLVLTEEE KRTLIAEGYP IPTKLPLSKS EEKALKKIRR	300	
KIKKNKISAQE SRKKKEYMD SLEKKVESCS TENLELRKKV EVLENTRNL LQQQLQLQTL	360	
VMGKVSRTCK LAGTQTGTCL MVVVLCAVA FGSFFQGYGP YPSATKMALP SQHSLQEPYT	420	
ASVVRSRNLL IYEEHSPPEE SSSPGSAGEL GGWDRGSSL RVSGLESRPD VDLPHFIISN	480	
ETSLEKSVLL ELQQHLVSAK LEGNETLKVV ELDRRVNTTF	520	
SEQ ID NO: 566	moltype = AA length = 240	
FEATURE	Location/Qualifiers	
source	1..240	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 566		

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MNPLRRPRLS	SRLSTATPCA	RSLGSPRSP	TLPPTVTSMT	ICYINSKWMY	GPPSLCLGFA	60
SYEYCFNP	LFEKNLVLSG	PAWFKTRVQQ	GPTAYFFSY	EVESEKWL	TDFPSTSIIK	120
EPVTDEPPP	LVPSTLTIT	AISTPLEKEE	PPELMNTGVD	SSCQTIIIPKI	KLEPHEVDQF	180
LNFSPKEGLS	ALPVSLWVMD	MVGSTEREY	GERAGMSLYH	RCCSWLYEIA	LFLKNKNFAS	240
SEQ ID NO:	567	moltype = AA	length = 460			
FEATURE	source	Location/Qualifiers				
		1..460				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	567					
MEVLESQEQQ	VHQWDRKLSE	LSEPGDGAEAL	MYHTHFSELL	DEFSQNVLGQ	LLNDPFLSEK	60
SVSMEVEPSP	TSPAPLIQAE	HSYSLCEEPR	AQSPFTHTTT	SDSFVNDEVE	SEKWNVLSTDF	120
PSTSIIKTEPV	TDEPPPGLVP	SVTLTITAIS	TPLEKEEPPL	EMNTGVDSSC	QTIIPKIKLE	180
PHEVQDFNLN	SPKEAPVDSL	HLPPTPPSSH	GSDESGLSP	NPRLHFFSPL	QTHNSPRAAP	240
RAPSALSSSP	LLTAPHKLQG	SGPLVLTEEE	KRTLIAEPIG	IPTKLPLSKS	EEKALKIIRR	300
IJKNKISQAQ	SRRKKKEYMD	SLEKKVESCS	TENLELRKVV	EVLENTRRTL	LQQLQKLOLTL	360
VMGKVSRCK	LAGTGTGTCL	MVVVLCAVA	FGSFFQGYGP	YPSATKMALP	SQHSLQEPTY	420
ASVGKTACGK	LGRVLFYFP	AGFLSLPKGI	FCESPMPFKW			460
SEQ ID NO:	568	moltype = AA	length = 449			
FEATURE	source	Location/Qualifiers				
		1..449				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	568					
MDRVYEIPEE	PNVDPVSSL	EDVIRGANPR	FTFPFSILFS	TFLYCGEAAS	ALYMVRIYRK	60
NSETYWMYT	FSFFMFSSIM	VQLTLIFVHR	DLAKDPLSL	FMHILLGPV	IRCLEAMIK	120
LTLWKKEEQE	EPYVSLTRKK	MLIDGEEVIL	EWEVGHHSIRT	MLAHRNAYKR	MSQIQAFGLS	180
VPQLTYOLV	SLISAEPVLC	RVVLMVFSLV	SVTYVGATCN	MLAIQIKYDD	YKIRLGPLEV	240
LCITIWRTLE	ITSRLLLILVL	FSATLKLAV	PFLVLNFLL	LFEPWIKFWR	SGAQMPNNIE	300
KNFSRVTGLV	VLISVITLYA	GINFSCSAL	QLRLADRDVL	DKGQNWGHMG	LHYSVRLVEN	360
VIMVLFKFK	GVKVLLNYCH	SLIALQIIA	YLISIGFM	FFQYLPPLRS	LFTHNVVVDYL	420
HCVCCHQHPR	TRVENSEPP	ETEARQSVV				449
SEQ ID NO:	569	moltype = AA	length = 139			
FEATURE	source	Location/Qualifiers				
		1..139				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	569					
MDRVYEIPEE	PNVDPVSSL	EDVIRGANPR	FTFPFSILFS	TFLYCGEAAS	ALYMVRIYRK	60
NSETYWMYT	FSFFMFSSIM	VQLTLIFVHR	DLAKDPLSL	FMHILLGPV	ISCANGIFPG	120
ICHLWGHPLQ	YVGYPDQVR					139
SEQ ID NO:	570	moltype = AA	length = 471			
FEATURE	source	Location/Qualifiers				
		1..471				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	570					
MASVVLPSGS	QCAAAAAAAA	PPGLRLRLLL	LLFSAAALIP	TGDGQNLFTK	DVTVIEGEVA	60
TISCOVNKSD	DSVIQLLNPN	RQTIYFRDFR	PLKDSRFQLL	NFSSSELKVS	LTVNVISDEG	120
RYFCQLYTD	PQESYTTITV	LPVPRNLIMID	IQKDTAVEGE	EIEVNCTAMA	SKPATTIRWF	180
KGNTELKGKS	EVEEWSDMYT	VTSQMLKVKH	KEDDGVPVIC	QVEHPAVTGN	LQTQRYLEVQ	240
YKPQVHIQMT	YPLQGLTREG	DALELTCEAI	GKPQPVMVTV	VRVDDEMPQH	AVLSPGNLFI	300
NNLNKTDNGT	YRCEASNIVG	KAHSDYMLIV	YDPPTTIPPP	TTTTTTTTTT	TTTILTIITD	360
TTATTEPAVH	GLTQLPNSAE	ELDSEDLSDS	RAGEEGSIRA	VDHAVIGGGV	AVVVFAMLCL	420
LIILGRYFAR	HKGTYFTHEA	KGADDAADAD	TAIINAEGQ	NNSEEKKEYF	I	471
SEQ ID NO:	571	moltype = AA	length = 442			
FEATURE	source	Location/Qualifiers				
		1..442				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	571					
MASVVLPSGS	QCAAAAAAAA	PPGLRLRLLL	LLFSAAALIP	TGDGQNLFTK	DVTVIEGEVA	60
TISCOVNKSD	DSVIQLLNPN	RQTIYFRDFR	PLKDSRFQLL	NFSSSELKVS	LTVNVISDEG	120
RYFCQLYTD	PQESYTTITV	LPVPRNLIMID	IQKDTAVEGE	EIEVNCTAMA	SKPATTIRWF	180
KGNTELKGKS	EVEEWSDMYT	VTSQMLKVKH	KEDDGVPVIC	QVEHPAVTGN	LQTQRYLEVQ	240
YKPQVHIQMT	YPLQGLTREG	DALELTCEAI	GKPQPVMVTV	VRVDDEMPQH	AVLSPGNLFI	300
NNLNKTDNGT	YRCEASNIVG	KAHSDYMLIV	YDPPTTIPPP	TTTTTTTTTT	TTTILTIITD	360
SRAGEEGSIR	AVDHAVIGGV	VAVVVFAML	LIILGRYFA	RHKGYFTHE	AKGADDAADA	420
DTAIINAEGG	QNNSEEKKEY	FI				442
SEQ ID NO:	572	moltype = AA	length = 443			

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FEATURE	Location/Qualifiers
source	1..443
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 572	
MASVVLPSGS	QCACAAAAAAA PPGLRLRLLL LLFSAAALIP TGDGQNLFTK DVTVIEGEVA 60
TISCQVNKSD	D SVIQLLNPN R QTIYFRDFR PLKDSRFQLL NFSSSELKVS LTNVISDEG 120
RYFCQLYTDP	PQESYTTITV LVPPRNLMID IQKDTAVEGE EIEVNCTAMA SKPATTIRWF 180
KGNTELKGKS	EVEEWSDMYT VTSQMLKVH KEDDGVPVIC QVEHPAVTGN LQTQRYLEVQ 240
YKPQVHIQMT	YPLQGLTREG DALELTCEAI GKPQPVMVTW VRVDDEMPQH AVLSPGNLFI 300
NNLNKTNDGT	YRCEASINVG KAHSDYMLVV YDTTATTEPA VHGLTQLPNS AEELDSEDL 360
DSRAGEEGSI	R A V D H A V I G G V V A V V V F A M L C L L I I L G R Y F A R H K G T Y F T H E A K G A D D A A D 420
ADTAIIAEG	G Q N N S E E K K E Y F I 443
SEQ ID NO: 573	moltype = AA length = 453
FEATURE	Location/Qualifiers
source	1..453
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 573	
MASVVLPSGS	QCACAAAAAAA PPGLRLRLLL LLFSAAALIP TGDGQNLFTK DVTVIEGEVA 60
TISCQVNKSD	D SVIQLLNPN R QTIYFRDFR PLKDSRFQLL NFSSSELKVS LTNVISDEG 120
RYFCQLYTDP	PQESYTTITV LVPPRNLMID IQKDTAVEGE EIEVNCTAMA SKPATTIRWF 180
KGNTELKGKS	EVEEWSDMYT VTSQMLKVH KEDDGVPVIC QVEHPAVTGN LQTQRYLEVQ 240
YKPQVHIQMT	YPLQGLTREG DALELTCEAI GKPQPVMVTW VRVDDEMPQH AVLSPGNLFI 300
NNLNKTNDGT	YRCEASINVG KAHSDYMLVV YDPPTTIPPP TTTTTTTTT TTTILTITD 360
TTATTEPAVH	D S R A G E E G S I R A V D H A V I G G V V A V V V F A M L C L L I I L G R Y F A R H K G T Y F T H 420
ADTAIIAEG	G Q N N S E E K K E Y F I 453
SEQ ID NO: 574	moltype = AA length = 67
FEATURE	Location/Qualifiers
source	1..67
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 574	
MASVVLPSGS	QCACAAAAAAA PPGLRLRLLL LLFSAAALIP T GLTSSPRLE CGGTISAHCS 60
LGLPVLR	67
SEQ ID NO: 575	moltype = AA length = 414
FEATURE	Location/Qualifiers
source	1..414
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 575	
MASVVLPSGS	QCACAAAAAAA PPGLRLRLLL LLFSAAALIP TGDGQNLFTK DVTVIEGEVA 60
TISCQVNKSD	D SVIQLLNPN R QTIYFRDFR PLKDSRFQLL NFSSSELKVS LTNVISDEG 120
RYFCQLYTDP	PQESYTTITV LVPPRNLMID IQKDTAVEGE EIEVNCTAMA SKPATTIRWF 180
KGNTELKGKS	EVEEWSDMYT VTSQMLKVH KEDDGVPVIC QVEHPAVTGN LQTQRYLEVQ 240
YKPQVHIQMT	YPLQGLTREG DALELTCEAI GKPQPVMVTW VRVDDEMPQH AVLSPGNLFI 300
NNLNKTNDGT	YRCEASINVG KAHSDYMLVV YDSRAGEEGS I R A V D H A V I G G V V A V V V F A M 360
LCLLIILGRY	F A R H K G T Y F T H E A K G A D D A A D A D T A I I N A E G Q N N S E E K K E Y F I 414
SEQ ID NO: 576	moltype = AA length = 111
FEATURE	Location/Qualifiers
source	1..111
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 576	
MIDIQKDTAV	E G E E I E V N C T A M A S K P A T T I R W P K G N T E L K G K S E V E E W S D M Y T V T S Q M L 60
KVHKEDDGVP	V I C Q V E H P A V T G N L Q T Q R Y L E V Q Y K P Q V H I Q M T Y P L Q G L T R 111
SEQ ID NO: 577	moltype = AA length = 79
FEATURE	Location/Qualifiers
source	1..79
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 577	
MIDIQKDTAV	E G E E I E V N C T A M A S K P A T T I R W P K G N T E L K G K S E V E E W S D M Y T V T S Q M L 60
KVHKEDDGVP	V I C Q V E H P A V T G N L Q T Q R Y L E V Q Y K P Q V H I Q M T Y P L Q G L T R 79
SEQ ID NO: 578	moltype = AA length = 413
FEATURE	Location/Qualifiers
source	1..413
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 578	

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XSVVLPSGSQ	CAAAAAAAAP	PGLRLRLLLL	LFSAAALIPT	GDGQNLFTKD	VTVIEGEVAT	60
ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	FSSSELKVSL	TNVSIISDEGR	120
YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	IENCTAMAS	KPATTIRWFK	180
GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	VEHPAVTGNL	QTQRYLEVQY	240
KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	RVDDEMPQHA	VLSGPNLFIN	300
NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DSRAGEEGSI	RAVDHAVIGG	VVAVVVFAML	360
CLLIILGRYF	ARHKGTYFTH	EAKGADDAAD	ADTAIIAEG	GQNNSEEKKE	YFI	413

SEQ ID NO: 579	moltype = AA	length = 346				
FEATURE	Location/Qualifiers					
source	1..346					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 579						
GDGQNLFTKD	VTVIEGEVAT	ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	60
FSSSELKVSL	TNVSIISDEGR	YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	120
IENCTAMAS	KPATTIRWFK	GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	180
VEHPAVTGNL	QTQRYLEVQY	KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	240
RVDDEMPQHA	VLSGPNLFIN	NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DSRAGEEGSI	300
RAVDHAVIGG	VVAVVVFAML	CLLIILGRYF	ARHKGTYFTH	EAKGADDAAD	ADTAIIAEG	360
					SSPRIK	346

SEQ ID NO: 580	moltype = AA	length = 373				
FEATURE	Location/Qualifiers					
source	1..373					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 580						
GDGQNLFTKD	VTVIEGEVAT	ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	60
FSSSELKVSL	TNVSIISDEGR	YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	120
IENCTAMAS	KPATTIRWFK	GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	180
VEHPAVTGNL	QTQRYLEVQY	KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	240
RVDDEMPQHA	VLSGPNLFIN	NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DSRAGEEGSI	300
RAVDHAVIGG	VVAVVVFAML	CLLIILGRYF	ARHKGTYFTH	EAKGADDAAD	ADTAIIAEG	360
					GQNNSEEKKE	373

SEQ ID NO: 581	moltype = AA	length = 412				
FEATURE	Location/Qualifiers					
source	1..412					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 581						
GDGQNLFTKD	VTVIEGEVAT	ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	60
FSSSELKVSL	TNVSIISDEGR	YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	120
IENCTAMAS	KPATTIRWFK	GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	180
VEHPAVTGNL	QTQRYLEVQY	KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	240
RVDDEMPQHA	VLSGPNLFIN	NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DPPTIPPP	300
TTTTTTTTTT	TTILTIIITDT	TATTEPAVHD	SRAGEEGSI	AVDHAVIGGV	VAVVVFAML	360
LLILGRYFA	RHKGTYFTH	AKGADDAADA	DTAIINAEGG	QNNSEEKKEY	FI	412

SEQ ID NO: 582	moltype = AA	length = 430				
FEATURE	Location/Qualifiers					
source	1..430					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 582						
GDGQNLFTKD	VTVIEGEVAT	ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	60
FSSSELKVSL	TNVSIISDEGR	YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	120
IENCTAMAS	KPATTIRWFK	GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	180
VEHPAVTGNL	QTQRYLEVQY	KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	240
RVDDEMPQHA	VLSGPNLFIN	NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DPPTIPPP	300
TTTTTTTTTT	TTILTIIITDT	TATTEPAVHG	LTLQPNAAE	LSDSELDSDR	AGEEGSIRAV	360
DHAVIGGVVA	VVVFAMLCLL	IILGRYFARH	KGTYFTHEAK	GADDAADADT	AIINAEGGQN	420
NSEEKKEYFI						430

SEQ ID NO: 583	moltype = AA	length = 401				
FEATURE	Location/Qualifiers					
source	1..401					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 583						
GDGQNLFTKD	VTVIEGEVAT	ISCVNKSDD	SVIQLLNPNR	QTIFYFRDFRP	LKDSRFQLLN	60
FSSSELKVSL	TNVSIISDEGR	YFCQLYTDPP	QESYTTITV	VPPRNLMDI	QKD TAVEGEE	120
IENCTAMAS	KPATTIRWFK	GNTELKGSE	VEEWSDMYTV	TSQMLLKVKH	EDDGVPVICQ	180
VEHPAVTGNL	QTQRYLEVQY	KPVHQIMTY	PLQGLTREGD	ALELTCEAIG	KPQPMVTVW	240
RVDDEMPQHA	VLSGPNLFIN	NLNKTNGTY	RCEASNIVGK	AHSDYMLVYV	DPPTIPPP	300
TTTTTTTTTT	TTILTIIITDS	RAGEEGSIRA	VDHAVIGGV	VVVFAMLCL	LIILGRYFAR	360

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HKGTYFTHEA KGADDAADAD TAIINAEGGQ NNSEEKKEYF I	401
SEQ ID NO: 584 moltype = AA length = 200	
FEATURE Location/Qualifiers	
source 1..200	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 584	
MASSLTCTGV IWALLSFLCA ATSCVGFMP YWLWGSQQLGK PVSFGTFRRC SYPVHDESRQ 60	
MMVMVEECGR YASFQGIPSA EWRRICTIVG LGCGLLLVA LTALMGCCVS DLISRTVGRV 120	
AGGIQFLGGL LIGAGCALYP LGWDSEEVHQ TCYGTSGQFD LGKCEIGWAY YCTGAGATAA 180	
MLLCTWLACF SGKKQKHYPY 200	
 SEQ ID NO: 585 moltype = AA length = 554	
FEATURE Location/Qualifiers	
source 1..554	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 585	
MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLLIDSQME 60	
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRLK 120	
SCFTKDYEHH DKACVRTFYE TPLQLLEVKV NVFNETKNLL DKDWNIIFSKN CNNSFAECSS 180	
QDVVTKPDCN CLYPKAIPSS DPASVSPHQD LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP 240	
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG 300	
TNWVPEEASG EASEIPVPGQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA 360	
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPEP GSPIRISSLRP QGLSNPSTLS 420	
AQQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTG 480	
HERQSEGSFS PQLQESVFHL LVPSVILVLL AVGGLLFYRW RRRSHQEPQR ADSPLEQPEG 540	
SPLTQDDRQV ELPV 554	
 SEQ ID NO: 586 moltype = AA length = 119	
FEATURE Location/Qualifiers	
source 1..119	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 586	
MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLLIDSQME 60	
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRL 119	
 SEQ ID NO: 587 moltype = AA length = 438	
FEATURE Location/Qualifiers	
source 1..438	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 587	
MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLLIDSQME 60	
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRLK 120	
SCFTKDYEHH DKACVRTFYE TPLQLLEVKV NVFNETKNLL DKDWNIIFSKN CNNSFAECSS 180	
QDVVTKPDCN CLYPKAIPSS DPASVSPHQD LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP 240	
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG 300	
TNWVPEEASG EASEIPVPGQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA 360	
DVTGHHERQSE GSFSQQLQES VFHLLVPSVI LVLLAVGGGL FYRWRSSHQ EPQRADSPLE 420	
QPEGSPLTQD DRQVELPV 438	
 SEQ ID NO: 588 moltype = AA length = 554	
FEATURE Location/Qualifiers	
source 1..554	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 588	
MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLLIDSQME 60	
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAIAIV QLQELSLRLK 120	
SCFTKDYEHH DKACVRTFYE TPLQLLEVKV NVFNETKNLL DKDWNIIFSKN CNNSFAECSS 180	
QDVVTKPDCN CLYPKAIPSS DPASVSPHQD LAPSMAPVAG LTWEDSEGTE GSSLLPGEQP 240	
LHTVDPGSAK QRPPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFNPG MEDILDSAMG 300	
TNWVPEEASG EASEIPVPGQG TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA 360	
DVTGTALPRV GPVRPTGQDW NHTPQKTDHP SALLRDPEP GSPIRISSLRP QGLSNPSTLS 420	
AQQLSRSHS SGSVLPLGEL EGRRSTRDRR SPAEPEGGPA SEGAARPLPR FNSVPLTDTG 480	
HERQSEGSFS PQLQESVFHL LVPSVILVLL AVGGLLFYRW RRRSHQEPQR ADSPLEQPEG 540	
SPLTQDDRQV ELPV 554	
 SEQ ID NO: 589 moltype = AA length = 256	
FEATURE Location/Qualifiers	
source 1..256	
mol_type = protein	
organism = Homo sapiens	

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SEQUENCE: 589
MTAPGAAGRC PPTTTLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME 60
TSCQITFEFV DQEQLKDPVC YLKKAFLLVQ DIMEDTMRFR DNTPNAAIAIV QLQELSLRK 120
SCFTKDYEEH DKACVRTFYE TPLQLLEVKV NVPNETKNL DKDWNIFSKN CNNSFAECSS 180
QGHERQSEGS FSPQLQESVF HLLVPSVLV LLAVGGLLFY RWRRRSHQEP QRADSPLEQP 240
EGSPLTQDDR QVELPV 256

SEQ ID NO: 590 moltype = AA length = 285
FEATURE Location/Qualifiers
source 1..285
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 590
MTAPGAAGRC PPTIDSQMET SCQITFEFVD QEQLKDPVCY LKKAFLLVQD IMEDTMFRD 60
NTPNAIAIVQ LQELSLRLKS CFTKDYEHD KACVRTFYET PLQLLEKVKN VFNETKNLLD 120
KDWNIIFSKNC NNSFAECSSQ DVVTKPDNC LYPKAIPSSD PASVSPHQPL APSMAPVAGL 180
TWEDSEGTEG SSSLPGEQPL HTVDPGSAKQ RPPRSTCQSF EPPETPVVKD STIGGSPQPR 240
PSVGAFNPGM EDILDSAMGT NWVPEEASGE ASEIPVPGT ELSPS 285

SEQ ID NO: 591 moltype = AA length = 113
FEATURE Location/Qualifiers
source 1..113
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 591
MIGSGHLQSL QRLIDSQMET SCQITFEFVD QEQLKDPVCY LKKAFLLVQD IMEDTMFRD 60
NTPNAIAIVQ LQELSLRLKS CFTKDYEHD KACVRTFYET PLQLLEKVKN VFN 113

SEQ ID NO: 592 moltype = AA length = 150
FEATURE Location/Qualifiers
source 1..150
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 592
MGWGRQLQRIS LPSQCLSLLS TWLGSLLL LV CLLASRSITE EVSEYCSHMI GSGHLQSLQR 60
LIDSQMETSC QITFEVDQE QLKDPCYLYK KAFLLVQDIM EDTMRFRDNT PNAIAIVQLQ 120
ELSLRLKSCF TKDYEEHDKA CVRTFYETPL 150

SEQ ID NO: 593 moltype = AA length = 173
FEATURE Location/Qualifiers
source 1..173
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 593
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIEDLKYY GATTVVRVCE VTYDKTPLEK 60
DGITVVWDWPF DDGAPPGKV VEDWLSSLVKA KFCEAPGSCV AVHCVAGLGR APVLVALALI 120
ESGMKYEDAI QFIRQKRRGA INSQQLTYLE KYRPKQRLRF KDPHTHKTRC CVM 173

SEQ ID NO: 594 moltype = AA length = 148
FEATURE Location/Qualifiers
source 1..148
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 594
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIEDLKYY GATTVVRVCE VTYDKTPLEK 60
DGITVVWDWPF DDGAPPGKV VEDWLSSLVKA KFCEAPGSCV AVHCVAGLGR KRRGAINSKQ 120
LTYLEKRYPK QRLRFKDPHT HKTRCCVM 148

SEQ ID NO: 595 moltype = AA length = 148
FEATURE Location/Qualifiers
source 1..148
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 595
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIEDLKYY GATTVVRVCE VTYDKTPLEK 60
DGITVVWDWPF DDGAPPGKV VEDWLSSLVKA KFCEAPGSCV AVHCVAGLGR KRRGAINSKQ 120
LTYLEKRYPK QRLRFKDPHT HKTRCCVM 148

SEQ ID NO: 596 moltype = AA length = 173
FEATURE Location/Qualifiers
source 1..173
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 596
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIEDLKYY GATTVVRVCE VTYDKTPLEK 60
DGITVVWDWPF DDGAPPGKV VEDWLSSLVKA KFCEAPGSCV AVHCVAGLGR APVLVALALI 120

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ESGMKYEDAI QFIRQKRRGA INSKQLTYLE KYRPKQRLRF KDPHTHKTRC CVM	173
SEQ ID NO: 597	moltype = AA length = 70
FEATURE	Location/Qualifiers
source	1..70
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 597	
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIEDLKKY GATTVVRVCE VTYDKTPLEK	60
DGTVVWDWPF	70
SEQ ID NO: 598	moltype = AA length = 87
FEATURE	Location/Qualifiers
source	1..87
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 598	
MARMNRPAPV EVSYKHMRFI ITHNPTNATL STFIESGMKY EDAIQFIQK RRGAINSQK	60
TYLEKYRPPQ RLRFKDPHTH KTRCCVM	87
SEQ ID NO: 599	moltype = AA length = 25
FEATURE	Location/Qualifiers
source	1..25
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 599	
MINACRDFLE LAEIHSRKWQ RALQY	25
SEQ ID NO: 600	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 600	
MELTIFILRL AIYIILTFPLY LLNFLGLWSW ICKKKWFPPYFL VRFTVIYNEQ MASKKRELFS	60
NLQEFAFPSSG KLSLLEVVGCG TGANFKFYPP GCRVTCIDPN PNFEKFELIKS IAENRHLQFE	120
RFVVAAGENNM HQVADGSVDV VVCTLVLCMV KNQERILREV CRVLRPCGGAF YFMMEHVAEC	180
STWNYFWQOV LDPAWHLFD GCNLTRRESWK ALERASFSKL KLQHIQAPLS WELVRPHIYG	240
YAVK	244
SEQ ID NO: 601	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 601	
MELTIFILRL AIYIILTFPLY LLNFLGLWSW ICKKKWFPPYFL VRFTVIYNEQ MASKKRELFS	60
NLQEFAFPSSG KLSLLEVVGCG TGANFKFYPP GCRVTCIDPN PNFEKFELIKS IAENRHLQFE	120
RFVVAAGENNM HQVADGSVDV VVCTLVLCMV KNQERILREV CRVLRPCGGAF YFMMEHVAEC	180
STWNYFWQOV LDPAWHLFD GCNLTRRESWK ALERASFSKL KLQHIQAPLS WELVRPHIYG	240
YAVK	244
SEQ ID NO: 602	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 602	
MELTIFILRL AIYIILTFPLY LLNFLGLWSW ICKKKWFPPYFL VRFTVIYNEQ MASKKRELFS	60
NLQEFAFPSSG KLSLLEVVGCG TGANFKFYPP GCRVTCIDPN PNFEKFELIKS IAENRHLQFE	120
RFVVAAGENNM HQVADGSVDV VVCTLVLCMV KNQERILREV CRVLRPCGGAF YFMMEHVAEC	180
STWNYFWQOV LDPAWHLFD GCNLTRRESWK ALERASFSKL KLQHIQAPLS WELVRPHIYG	240
YAVK	244
SEQ ID NO: 603	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 603	
XELTIFILRL AIYIILTFPLY LLNFLGLWSW ICKKKWFPPYFL VRFTVIYNEQ MASKKRELFS	60
NLQEFAFPSSG KLSLLEVVGCG TGANFKFYPP GCRVTCIDPN PNFEKFELIKS IAENRHLQFE	120
RFVVAAGENNM HQVADGSVDV VVCTLVLCMV KNQERILREV CRVLRPCGGAF YFMMEHVAEC	180
STWNYFWQOV LDPAWHLFD GCNLTRRESWK ALERASFSKL KLQHIQAPLS WELVRPHIYG	240
YAVK	244

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SEQ ID NO: 604	moltype = AA length = 180
FEATURE	Location/Qualifiers
source	1..180
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 604	
MELTIFILRL AIYIILTFPLY LLNFLGLWSW ICKKWFPYFL VRFTVIYNEQ MASKKRELFS	60
NLQEFGAGSG KLSLLLEVCGC TGANFKFVPP GCRVTCIDPN PNFEKFELIKS IAENRHLQFE	120
RFVVAAGENM HQVADGSVDV VVCTLVLCV KNQERILREV CRVLRPGGAF YFMEHVAEC	180
SEQ ID NO: 605	moltype = AA length = 811
FEATURE	Location/Qualifiers
source	1..811
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 605	
MLLLFHSKRM PVAEAPQVAG GQGDGGDGE AEPEGMFKC EDSKRKARGY LRLVPLFVLL	60
ALLVLASAGV LLWYFLGYKA EVMVSQVYS GLSRVLNRHS QDLTRRESSA FRSETAKAQ	120
MLKELITSTR YSFGEGLPTE FFWFILQIPE HRRMLMSPEV VQALLVEELL	180
STVNSSAAVP YRAEYEVDP EGLVILEASVK DIAALNSTLG CYRYSYVGQ QVRLRLKGPDH	240
LASSCLWHLQ GPKDMLKLRL LEWTLAECRD RLAAMYDVAG LEKRLITSVY GCSRQEPVVE	300
VLASGAIMAV VWKKGLHSY DPFLVLSVQPV VFQACEVNLT LDNRRLDSQGV LSTPYFPSYY	360
SPQTHCSWHL TVPSLDYGLA LWFDAYALRR QKYDLPCTQ GQWTIQNRRLC GLRILQPYAE	420
RIPVVATAGI TINFTSQISL TGPGVRVHYG LYNNQSDPCPG EFLCSVNGLC VPACDGVKDC	480
PNGLDERNCV CRATFQCKED STCISLKPVC DGQPDCLNNG DEEQCQEGVP CGTFTFQCED	540
RSCVKKPNPQ CDGRPDRCRD SDEEEHCDCLG QGPSSRIVGG AVSSEGEWPW QASLQVRGRH	600
IICGGALIADR WVITAACFCQ EDSMASTVL TVFLGKVWN SRWPGEVSK VSRLLLLHPYH	660
EEDSHDYDVA LLQLDHPVVR RSAAVRPVCL PARSHFFEPG HCWITGWAL REGGPISNAL	720
QKDVQQLIPQ DLCSEVYRYQ VTPRMLCAGY RKGKKDACQG DSGGPLVCKA LSGRWFLAGL	780
VSWGLGCRP NYFGVYTRIT GVISWIQQV T	811
SEQ ID NO: 606	moltype = AA length = 824
FEATURE	Location/Qualifiers
source	1..824
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 606	
MPVAEAPQVA GGQGDGGDGE EAEPEGMFK A CEDSKRKARG YLRLVPLFVL LALLVLASAG	60
VLLWYFLGYK AAEVMVSQVYS GSLRVLNRHF SQDLTRRESS AFRSETAKAQ KMLKELITST	120
RLGTYYNNSS VVSFGEGLPTE CFFFWLQIPE EHRRMLMSPE VVQALLVEEL LSTVNSSAAV	180
PYRAEYEVDP EGLVILEASVK DIAALNSTLG GCYRYSYVGQ QVRLRLKGPD HLASSCLWHL	240
QGPKDMLKLRL RLEWTLAECRD DRLAMYDVAG PLEKRLITSV YGCSRQEPVVE EVLASGAIMA	300
VVWKKGLHSY YDPFLVLSVQP VVFQACEVNLT LDNRRLDSQGV VLSTPYFPSYY YSPQTHCSWH	360
LTVPSLDYGL ALWFDAYALR RQKYDLPCTQ GQWTIQNRRLC GLRILQPYAE ERIPVVATAG	420
ITINFTSQISL TGPGVRVHY GLYNQSDPCPG GEFLCSVNGLC VPACDGVKDC CPNGLDERNC	480
VCRATFQCKE DSTCISLKPVC CDGQPDCLNNG SDEEQCQEGV PCGTFTFQCE DRSCVKKPNP	540
QCDGRPDRCRD GSDEEEHCDCG LQGPSSRIVG GAVSSEGEWPW WQASLQVRGR HICGGALIAD	600
RWVITAACFC QEDSMASTVL WTVFLGKVWQ NSRWPGEVSK KVSRLLLLHPY HEEDSHDYDV	660
ALLQLDHPVV RSAAVRPVCL PARSHFFEPG LHCWITGWGA LREGGPISNA VALFYGWRNQ	720
GSETCCCPIS NALQKVDVQL IPQDLCSEVY RYQVTPRMLC AGYRKGGKDA CQGDGGPLV	780
CKALSGRWFL AGLVSWGLGC GRPNYFGVYT RITGVISWIQQV T	824
SEQ ID NO: 607	moltype = AA length = 802
FEATURE	Location/Qualifiers
source	1..802
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 607	
MPVAEAPQVA GGQGDGGDGE EAEPEGMFK A CEDSKRKARG YLRLVPLFVL LALLVLASAG	60
VLLWYFLGYK AAEVMVSQVYS GSLRVLNRHF SQDLTRRESS AFRSETAKAQ KMLKELITST	120
RLGTYYNNSS VVSFGEGLPTE CFFFWLQIPE EHRRMLMSPE VVQALLVEEL LSTVNSSAAV	180
PYRAEYEVDP EGLVILEASVK DIAALNSTLG GCYRYSYVGQ QVRLRLKGPD HLASSCLWHL	240
QGPKDMLKLRL RLEWTLAECRD DRLAMYDVAG PLEKRLITSV YGCSRQEPVVE EVLASGAIMA	300
VVWKKGLHSY YDPFLVLSVQP VVFQACEVNLT LDNRRLDSQGV VLSTPYFPSYY YSPQTHCSWH	360
LTVPSLDYGL ALWFDAYALR RQKYDLPCTQ GQWTIQNRRLC GLRILQPYAE ERIPVVATAG	420
ITINFTSQISL TGPGVRVHY GLYNQSDPCPG GEFLCSVNGLC VPACDGVKDC CPNGLDERNC	480
VCRATFQCKE DSTCISLKPVC CDGQPDCLNNG SDEEQCQEGV PCGTFTFQCE DRSCVKKPNP	540
QCDGRPDRCRD GSDEEEHCDCG LQGPSSRIVG GAVSSEGEWPW WQASLQVRGR HICGGALIAD	600
RWVITAACFC QEDSMASTVL WTVFLGKVWQ NSRWPGEVSK KVSRLLLLHPY HEEDSHDYDV	660
ALLQLDHPVV RSAAVRPVCL PARSHFFEPG LHCWITGWGA LREGGPISNA LQKDVQQLIP	720
QDLCSEVYRY QVTPRMLCAG YRKGGKDACQG DSGGPLVCKA ALSGRWFLAG LVSWGLGCR	780
PNYFGVYTRI TGVISWIQQV T	802
SEQ ID NO: 608	moltype = AA length = 824
FEATURE	Location/Qualifiers
source	1..824

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mol_type = protein
organism = Homo sapiens

SEQUENCE: 608
MPVAEAPQVA GGQGDGGDGE EAEPEGMFKA CEDSKRKARG YLRLVPLFVL LALLVLASAG 60
VLLWYFLGYK AEVMVSVQYS GSLRVLNRHF SQDLTRRESS AFRSETAKAQ KMLKELITST 120
RLGTYYNSSS VYSFGEGLPT CFFWFILQIP EHRLRMLSPPE VVQALLVEEL LSTVNSSAAV 180
PYRAEYEVDP EGLVILEAVS DIAALNSTL GCYRYSYVGQ GQVLRLKGPQ HASSCLWHL 240
QGPKDMLKL RLEWTIAECR DRLAMYDVAG PLEKRLITSV YGCSRQEPVV EVLASGAIMA 300
VWWKGLHSY YDPFVLSVQP VVFQACEVNL TLDNRLLDSQG VLSTPYFPsy YSPQTHCSWH 360
LTVPSLDYGL ALWFDAYAL RRQKYDLPCTQ GWTIQRNRL CGLRILQPYA ERIPVATAG 420
ITINFTSQIS LTGPGVRVHY GLYNQSDPCP GEFLCSVNGL CVPAACGVKD CPNGLDERNC 480
VCRATFQCKE DSTCISLPKV CDGQPDCLNG SDEEQCQEGV PCGTFTQCK DRSCVKKPNP 540
QCDGRPDCRD GSDEEHDCDG LQGPSSRIVG GAVSSEGEWP WQASLQVGR HICGGALIAD 600
RWVITAACHF QEDDSMASTVL WTVFLGKVMQ NSRWPGEVFS KVSRLLLHPY HEEDSHDYDV 660
ALLQLDHPVV RSAAVRPVCL PARSHFFEPG LHCWITGWGA LREGALRADA VALFYGWRNQ 720
GSETCCCPIS NALQKVDVQL IPQDLCSEVY RYQVTPRMLC AGYRKGKDA CGQDSGGPLV
CKALSGRWFL AGLVSWGLGC GRPNYFGVYT RITGVISWIQ QVVT 824

SEQ ID NO: 609      moltype = AA length = 141
FEATURE             Location/Qualifiers
source              1..141
mol_type = protein
organism = Homo sapiens

SEQUENCE: 609
MPVAEAPQVA GGQGDGGDGE EAEPEGMFKA CEDSKRKARG YLRLVPLFVL LALLVLASAG 60
VLLWYFLGYK AEVMVSVQYS GSLRVLNRHF SQDLTRRESS AFRSETAKAQ KMLKELITST 120
RLGTYYNSSS VYSFGEGLPT C 141

SEQ ID NO: 610      moltype = AA length = 71
FEATURE             Location/Qualifiers
source              1..71
mol_type = protein
organism = Homo sapiens

SEQUENCE: 610
LTLDNRLLDSQ GVLSPTYFPS YYSPQTHCSW HLTVPSLDYAL RRQKYDLPCT 60
QGQWTIQNRR V 71

SEQ ID NO: 611      moltype = AA length = 461
FEATURE             Location/Qualifiers
source              1..461
mol_type = protein
organism = Homo sapiens

SEQUENCE: 611
MLLFHHSKRM PVAEAPQVAG GQGDGGDGE AEPEGMFKAC EDSKRKARGY LRLVPLFVLL 60
ALLVLASAGV LLWYFLGYKA EVMVSVQVSG SLRVLNRHFS QDLTRRESSA FRSETAKAQ 120
MLKELITSTR LGTYYNSSS YSFGEGLPTC FFWFILQIPE HRRMLMSPEV VQALLVEELL 180
STVNSSAAVP YRAEYEVDP GLVILEAVS DIAALNSTLG CYRYSYVGQ GQVLRLKGPDH 240
LASSCLWHLQ GPKDMLKL RLEWTIAECR DRLAMYDVAGP LEKRLITSVY GCSRQEPVVE 300
VLASGAIMAV VWWKGLHSYY DPFLVLSVQP VVFQACEVNL TLDNRLLDSQG VLSTPYFPsy 360
SPQTHCSWHL TVPSLDYGLA LWFDAYALRR QKYDLPCTQG QWTIQRNRRYH FLSSLWLPFL 420
PPPPSLPSSI VTPSLEAQVP NLRGAARGAS RGWGWCQACC P 461

SEQ ID NO: 612      moltype = AA length = 428
FEATURE             Location/Qualifiers
source              1..428
mol_type = protein
organism = Homo sapiens

SEQUENCE: 612
MLRTLLRRRL FSYPTKYYFM VLVLSSLITFS VLRIHQKPEF VSVRHLELAG ENPSSDINCT 60
KVLQGDVNEI QKVKLEILTV KFKKRPRWTP DDYINMTSDC SSFIKRRKYI VEPLSKEEAE 120
FPIAYSVIVHH HKIEMDLRLL RAIYMPQNFY CIHVDTKSED SYLAAMVGIA SCFSNVFVAS 180
RLESVVYAW SRVQADLNMC KDLYAMSANW KYLINLCGMD FPIKTNLEIV RKLKLLMGEN 240
NLETTERMPSH KEERWKRYE VVNKGKLTNTG TVKMLPPLET PLFSGSAYFV VSREYVGYVL 300
QNEKIQKLMW WAQDTYSPDE YLWATIQRIP EVPGSLPASH KYDLSDMQAV ARFVKWQYFE 360
GDVSKGAPYP PCDGVHVRSP CIFGAGDLNW MLRKHHLFAN KFDVVDVLFA IQCLDEHLRH 420
KAETLK 428

SEQ ID NO: 613      moltype = AA length = 428
FEATURE             Location/Qualifiers
source              1..428
mol_type = protein
organism = Homo sapiens

SEQUENCE: 613
MLRTLLRRRL FSYPTKYYFM VLVLSSLITFS VLRIHQKPEF VSVRHLELAG ENPSSDINCT 60
KVLQGDVNEI QKVKLEILTV KFKKRPRWTP DDYINMTSDC SSFIKRRKYI VEPLSKEEAE 120
FPIAYSVIVHH HKIEMDLRLL RAIYMPQNFY CIHVDTKSED SYLAAMVGIA SCFSNVFVAS 180

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RLESVVYASW SRVQADLNCM KDLYAMSANW KYLINLCMD FPIKTNLEIV RKLKLLMGEN NLETERMPSH KEERWKRYE VVNNGKLTNTG TVKMLPPLET PLFSGSAYFV VSREYVGYVL QNEKIQKLME WAQDTYSPDE YLWATIQRIP EVPGSLPASH KYDLSDMQAV ARFVKWQYFE GDVSKGAPYP PCDGVHVRSV CIFGAGDLNW MLRKHHHLFAN KFDVDVDLFA IQCLDEHLRH KALETLKH	240 300 360 420 428
 SEQ ID NO: 614 moltype = AA length = 428 FEATURE Location/Qualifiers source 1..428 mol_type = protein organism = Homo sapiens	
SEQUENCE: 614 MLRTLRLRRRL FSYPTKYYFM VLVLSSLITFS VLRIHQKPEF VSVRHLELAG ENPSSDINCT KVLFQGDVNEI QKVKEILTV KFKKRPRWRTP DDYINMTSDC SSFIKRKYI VEPLSKEEAE FPIAYSVNVH HKEIMLDRLL RAIYMPQNFY CIHVDTKSED SYLAAMGIA SCFSNVFVAS RLESVVYASW SRVQADLNCM KDLYAMSANW KYLINLCMD FPIKTNLEIV RKLKLLMGEN NLETERMPSH KEERWKRYE VVNNGKLTNTG TVKMLPPLET PLFSGSAYFV VSREYVGYVL QNEKIQKLME WAQDTYSPDE YLWATIQRIP EVPGSLPASH KYDLSDMQAV ARFVKWQYFE GDVSKGAPYP PCDGVHVRSV CIFGAGDLNW MLRKHHHLFAN KFDVDVDLFA IQCLDEHLRH KALETLKH	60 120 180 240 300 360 420 428
 SEQ ID NO: 615 moltype = AA length = 219 FEATURE Location/Qualifiers source 1..219 mol_type = protein organism = Homo sapiens	
SEQUENCE: 615 MPGRKRKSRR RNARAAEENR NNRKIQASEA SETPMMAASV ASTPEDDL SG PEEDPSTPEE ASTTPEEASS TAQAQKPSVP RSNFQGTKK SLLMSILALIF IMGNSAKEAL VWKVLGKLG QPGRQHSIFG DPKKIVTEEF VRRGYLIYKP VPRSSPVYE FFWGPRAHVE SSKLKVMHFV ARVRNRCSKD WPCNYDWDSD DDAEVEAILN SGARGYSAP	60 120 180 219
 SEQ ID NO: 616 moltype = AA length = 85 FEATURE Location/Qualifiers source 1..85 mol_type = protein organism = Homo sapiens	
SEQUENCE: 616 MGPGRQRWWL LLWLPLPLATL PVRGEAAAAA LSVRCKALK EKDLIRTSES DCYCYNQNSQ VEWKYIWSTM QGDCVLLCGA CQEDI	60 85
 SEQ ID NO: 617 moltype = AA length = 417 FEATURE Location/Qualifiers source 1..417 mol_type = protein organism = Homo sapiens	
SEQUENCE: 617 MGPGRQRWWL LLWLPLPLATL PVRGEAAAAA LSVRCKALK EKDLIRTSES DCYCYNQNSQ VEWKYIWSTM QVKITSPLGL RIVVIAERHN CQYEPENILSF IKCVIHNFWI PKESNEITII INPYRETVCF SVEPVKKIFN YMIVHNRNIM DFKLFLVFVA GVFLFFYART LSQSPTFYYS SGTGVLGVLMT LVFVLLLVKPF FIPKYSTFWA LMVGCWFASV YIVCQLMEDL KWLWENRIY VLGYVLVIVGF PSFVVCYKHG PLADDRSRSL LMWMLRLLSL VLVYAGVAVP QFAYAAILL MSSWSLHYPL RACSYMRWKM EQWFTSKELV VKYLTDEYR EQADAETNSA LEELRACRK PDFPSWLVVS RLHTPSKFAD FVLGGSHLSP EEISLHEEQY GLGGAFLEEQ LFNPSTA	60 120 180 240 300 360 417
 SEQ ID NO: 618 moltype = AA length = 138 FEATURE Location/Qualifiers source 1..138 mol_type = protein organism = Homo sapiens	
SEQUENCE: 618 MQVKITSPLGL FRIVVIAERH NCQYEPENILS FIKCVIHNFWI IPKESNEITI IINPYRETVC FSVEPVKKIF NYMIHNRNIM DFKLFLVFVA AGVFLFFYART TLSQSPTFYYS SSGTGVLGVL TLVFVLLLVK RFIPKAMS	60 120 138
 SEQ ID NO: 619 moltype = AA length = 24 FEATURE Location/Qualifiers source 1..24 mol_type = protein organism = Homo sapiens	
SEQUENCE: 619 MQVKITSPLGL FRIVVIAERH NCQY	24
 SEQ ID NO: 620 moltype = AA length = 35 FEATURE Location/Qualifiers source 1..35	

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SEQUENCE: 620 <code>mol_type = protein organism = Homo sapiens</code> SEQ ID NO: 621 FEATURE source <code>moltype = AA length = 422 Location/Qualifiers 1..422 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 621 <code>MLHLLALFLH CLPLASG DYD ICKSWVT TDE GPTWEFYACQ PKVMRLKDYY KVVKVEPS GIT 60 CGDP PERFC S HENPYLCSNE CDASNPD LAH PPRLMFD KEE EGLAT YWQSI TWSRYP SPLE 120 ANITLSWNKT VELTDDVVMT FEYGRPTVMV LEKSLDN GR T WQPYQFYAED CMEA FGMSAR 180 RARDMSSSA HRVLCTE EYS RWAGSKKEKH VRFEVDRFRA IFAGPDLRN M DNLYTRLES A 240 KGLKEFFFTL DLRMRLRPA LGGGTYVQREN LYKYFYAISN IEVIGRCKCN L HANLC S MRE 300 GSLQCECEHN TTGPDCGKCK KNFRTRSWRA GSYLPLPHGS PNACATAGSF GTLQT PPPG R 360 SPS ALRG SRR GLANVKEPAG SRPQISEMLL GCTVTLHQGS VGPHIPPKLS LPDPGG PWLG 420 SQ 422</code>	35
SEQ ID NO: 622 FEATURE source <code>moltype = AA length = 530 Location/Qualifiers 1..530 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 622 <code>MLHLLALFLH CLPLASG DYD ICKSWVT TDE GPTWEFYACQ PKVMRLKDYY KVVKVEPS GIT 60 CGDP PERFC S HENPYLCSNE CDASNPD LAH PPRLMFD KEE EGLAT YWQSI TWSRYP SPLE 120 ANITLSWNKT VELTDDVVMT FEYGRPTVMV LEKSLDN GR T WQPYQFYAED CMEA FGMSAR 180 RARDMSSSA HRVLCTE EYS RWAGSKKEKH VRFEVDRFRA IFAGPDLRN M DNLYTRLES A 240 KGLKEFFFTL DLRMRLRPA LGGGTYVQREN LYKYFYAISN IEVIGRCKCN L HANLC S MRE 300 GSLQCECEHN TTGPDCGKCK KNFRTRSWRA GSYLPLPHGS PNACATAGSF GNCE CYGH SN 360 RC SYCIDFLNV VTCVSKHNT RGQHCQH CRL GYYRNG SAEL DDENVCIECN CNQIG SVH DR 420 CNETGF CECR EGAAGPKCDD CLPTH YWR QG CYPNVC DDD Q LLCQNGGTCL QNQRCAC PRG 480 YTGVRCBQPR CDPADDDGGL DCDRAPGAAP RPATLLGCLL LLGLAARLGR 530</code>	
SEQ ID NO: 623 FEATURE source <code>moltype = AA length = 211 Location/Qualifiers 1..211 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 623 <code>MRTLACLLL GCGYLAHVLA EEA EIPREVI ERLARSQIHS IRDLQRLLEI DSVGSEDSL D 60 TSLRAHGVHA TKHVPEKRPL PIRRKRSIEE AVPAVCKTRT VIYEIPRSQV DPTSANFLI W 120 PPC VEVKR CT GCCNTSSV KC QPSRVHHR SV KVA KEVQVR LEEH LECACA 180 TTSLNPDY RE EDTGRPRESG KKRKRKRLKP T 211</code>	
SEQ ID NO: 624 FEATURE source <code>moltype = AA length = 205 Location/Qualifiers 1..205 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 624 <code>QRQAAALGSQ SPSPAGL RAG AVPPARA CLQ EAEI PPREVI RLARSQIHSI RD LQLR LEID 60 SVGS EDSL DT SLRAHGVH AT KH VP EKRPL PIRRK RSIEE AVPAVCKTRT IYEIPRSQV D 120 PTS ANFLI WP PC VEVKR CTG CCNTSSV KC QPSRVHHR SV KVA KEVQVR K PKL KEVQ VR 180 EEH LECACAT TS LNP DY RE EDT D VR 205</code>	
SEQ ID NO: 625 FEATURE source <code>moltype = AA length = 196 Location/Qualifiers 1..196 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 625 <code>MRTLACLLL GCGYLAHVLA EEA EIPREVI ERLARSQIHS IRDLQRLLEI DSVGSEDSL D 60 TSLRAHGVHA TKHVPEKRPL PIRRKRSIEE AVPAVCKTRT VIYEIPRSQV DPTSANFLI W 120 PPC VEVKR CT GCCNTSSV KC QPSRVHHR SV KVA KEVQVR LEEH LECACA 180 TTSLNPDY RE EDT D VR 196</code>	
SEQ ID NO: 626 FEATURE source <code>moltype = AA length = 86 Location/Qualifiers 1..86 mol_type = protein organism = Homo sapiens</code> SEQUENCE: 626 <code>MRTLACLLL GCGYLAHVLA EEA EIPREVI ERLARSQIHS IRDLQRLLEI DSVGSEDSL D 60</code>	

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TSRLRAHGVHA	TKHVPEKRPL	PIRRKR	86
SEQ ID NO: 627	moltype = AA length = 273		
FEATURE	Location/Qualifiers		
source	1..273		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 627			
MIFLLLMLSL ELQLHQIAAL FTVTVPKELY IIEHGSNVTL ECNFDTGSHV NLGAITASLQ	60		
KVENDTSPHR ERATLLEEQL PLGKASFHIP QVQRDQEQY QCIIIVGVAW DYKYLTALKVK	120		
ASYRKINTHI LKVPETDEVE LTCQATGYPL AEVSWPNVSV PANTSHSRTP EGLYQVTSVL	180		
RLKPPPGRNF SCVFVNTHVR ETLASIDLQ SQUEPRTHPT WLLHIFIPFC IIAFIFIATV	240		
IALRKQLCQK LYSSKDTTKR PVTTTKREVN SAI	273		
SEQ ID NO: 628	moltype = AA length = 423		
FEATURE	Location/Qualifiers		
source	1..423		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 628			
MDRGQPSLEP AAAAPRASGR CVIAPVRAVL RLRRRVCVLR KRRRLQPAGGG PDVGTGAPRP	60		
GCSPPRPRAD LDQPKFTFPL SPAELPSRTP RKKRRRSRLV LYPETSRKYL PRVEHRSRAQ	120		
RCLLLNLAIV GFQVILNAIEN LDDNAQRYDL DGLEKALQRA VFQGPAAVSR IVALMRDYL	180		
THVHSRPLL ALHGPGSGVKG SHVGRLLARH FRSVLEDSAL VLQYHARHHC PEARAAQDCR	240		
EELARRVADV VARAEAEKKT PLLVLDDELH MPRPLLDELH GFLQPQRSHH FNHNAIYVLLS	300		
GAGGAEVTRF VLQNARALP LRPDGFRSAE AAAAQAEEDL RASLLAVLSR EHPLWQAAAI	360		
VPFLLLDKRD VVSCFRDEMA GEGFFPDQAR AENLAAQLSF YRVAGREFAV TGCKQVVATV	420		
NLL	423		
SEQ ID NO: 629	moltype = AA length = 69		
FEATURE	Location/Qualifiers		
source	1..69		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 629			
XISEAEKAKQ KIAPVFFREE YMLNNAVGSC QKPYVALIHG ITMGGDCSLM WVEVISCHDS	60		
KENLVTS LH	69		
SEQ ID NO: 630	moltype = AA length = 52		
FEATURE	Location/Qualifiers		
source	1..52		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 630			
DVGGGYLPRL QGKLGYFLA LTGFRLKGRD VYRAGIATHF VDSEKNGDDT IT	52		
SEQ ID NO: 631	moltype = AA length = 793		
FEATURE	Location/Qualifiers		
source	1..793		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 631			
MLRGGRRGQL GWHSWAAGPG SLLAWLILAS AGAAPCPDAC CPHGSSGLRC TRDGALDSLH	60		
HLPGAENLTE LYIENQHQLQ HLELRDLRGL GELRNLTIKV SGLRFVAPDA FHFTPRLSRL	120		
NLSFNNALESL SWKTVQGLSL QELVLSGNPL HCSCALRWLQ RWEEEGLGGV PEQKLQCHQ	180		
GPLAHMPNAS CGVPTLKQV PNASVWDGG VLLRCQVEGR GLEQAGWILT ELEQSATVMK	240		
SGLLPSLGLT LANVTSDLNK KNVTCAEND VGRAEVSVQV NVSFPASVQL HTAVEMHHWC	300		
IPFSVDGQPA PSLRWLFGNS VLNETSFIFT EFLEPAANET VRHGCLRLNQ PTHVNNGNYT	360		
LIAANPFGQA SASIMAAFMND NPFEERNPDEPD IPDTNSTSGD PVEKKDETTFV GVSVAVGAV	420		
FACLFLSTLL LNWKCGRRN KFGINRPAVL APEDGLAMSL HFMTLGGSSL SPTEGKGSSL	480		
OQHIIENPQY FSDASPSGVH HIKRDRDIVLK WELGEAGPKV VFLAECHNLN PEQDKMLVAV	540		
KALKEASESA RQDFQREAEI LTMLQHQHIV RFFGVCTEGR PLLMVFEYMR HGDLNRLFLRS	600		
HGDPAKLLAG GEDVAPGPLG LGQLLAVASQ VAAGMVYLAG LHFVHRDLAT RNCLVGQGLV	660		
VKIGDFGMSR DIYSTDYYRV GGRTMLPIRW MPPEISLYRK FTTESDVWSF GVVLWEIFTY	720		
GKQPWYQLSN TEAIDCITQG RELERPRACP PEVYAIMRGC WQREPQQRHS IKDVHARLQA	780		
LAQAPPVYLD VLG	793		
SEQ ID NO: 632	moltype = AA length = 790		
FEATURE	Location/Qualifiers		
source	1..790		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 632			
MLRGGRRGQL GWHSWAAGPG SLLAWLILAS AGAAPCPDAC CPHGSSGLRC TRDGALDSLH	60		
HLPGAENLTE LYIENQHQLQ HLELRDLRGL GELRNLTIKV SGLRFVAPDA FHFTPRLSRL	120		
NLSFNNALESL SWKTVQGLSL QELVLSGNPL HCSCALRWLQ RWEEEGLGGV PEQKLQCHQ	180		

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GPLAHMPNAS	CGVPTLKQVQ	PNASVDVGDD	VLLRCQVEGR	GLEQAGWILT	ELEQSATVMK	240
SGGLPSLGLT	LANVTSDLNK	KNVTCWAEND	VGRAEVSVQV	NVSFPASVQL	HTAVEMHHWC	300
IPFSVDGQPA	PSLRWLNFNGS	VLNETSIFT	EFLEPAANET	VRHGCLRLNQ	PTHVNNGNYT	360
LIAANPFGQA	SASIMAAFMD	NPFEENPEDP	IPDTNSTSGD	PVEKKDETPE	GVSVAVGLAV	420
FACLFLSTLL	LVLNKCGRRN	KFGINRPAVL	APEDGLAMSL	HFMTLGGSSL	SPTEKGGSGL	480
QGHIIENPQY	FSDACVHHIK	RRDIVLKWEI	GEAGAFGVFEL	AECHNLLPEQ	DKMLVAVKAL	540
KEASESARQD	FQREAEELLTM	LQHQHIVRFF	GVCTEGRPLL	MVFEYMRHGD	LNRFRLSHGP	600
DAKLLAGGED	VAPGPLGLGQ	LLAVASQVA	GMVYLAGLHF	VHRDLATRNC	LVGQGLVVKI	660
GDFGMSRDIY	STDYRVGGR	TMLPIRWMP	ESILYRKFTT	ESDVWSFGVV	LWEIFTYGKQ	720
PWYQLSNTEA	IDCITQGREL	ERPRACPPEV	YAIMRGCWQR	EPQQRHSIKD	VHARLQALAQ	780
APPVYLDVLG						790

SEQ ID NO: 633	moltype = AA	length = 760				
FEATURE	Location/Qualifiers					
source	1..760					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 633						
MKEAALICLA	PSVPPILTVK	SWDTMQLRAA	RSRCTNLLAA	SYIENQQHLQ	HLELRLRLGL	60
GELRNLTIVK	SGLRFVAPDA	FHFTPRLSRL	NLSFNALES	SWKTVQGLSL	QELVLSGNPL	120
HCSCALRWLQ	RWEEEGLGGV	PEQKLQCHGQ	GPLAHMPNAS	CGVPTLKQVQ	PNASVDVGDD	180
VLLRCQVEGR	GLEQAGWILT	ELEQSATVMS	SGGLPSLGLT	LANVTSDLNR	KNVTCWAEND	240
VGRAEVSVQV	NVSFPASVQL	HTAVEMHHWC	IPFSVDGQPA	PSLRWLNFNGS	VLNETSIFT	300
EFLEPAANET	VRHGCLRLNQ	PTHVNNGNYT	LIAANPFGQA	SASIMAAFMD	NPFEENPEDP	360
IPDTNSTSGD	PVEKKDETPE	GVSVAVGLAV	FACLFLSTLL	LVLNKCGRRN	KFGINRPAVL	420
APEDGLAMSL	HFMTLGGSSL	SPTEKGGSGL	QGHIIENPQY	FSDACVHHIK	RRDIVLKWEI	480
GEGAFGVFEL	AECHNLLPEQ	DKMLVAVKAL	KEASESARQD	FQREAEELLTM	LQHQHIVRFF	540
GVCTEGRPLL	MVFEYMRHGD	LNRFRLSHGP	DAKLLAGGED	VAPGPLGLGQ	LLAVASQVA	600
GMVYLAGLHF	VHRDLATRNC	LVGQGLVVKI	GDFGMSRDIY	STDYRVGGR	TMLPIRWMP	660
ESILYRKFTT	ESDVWSFGVV	LWEIFTYGKQ	PWYQLSNTEA	IDCITQGREL	ERPRACPPEV	720
YAIMRGCWQR	EPQQRHSIKD	VHARLQALAQ	APPVYLDVLG			760

SEQ ID NO: 634	moltype = AA	length = 388				
FEATURE	Location/Qualifiers					
source	1..388					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 634						
MKEAALICLA	PSVPPILTVK	SWDTMQLRAA	RSRCTNLLAA	SYIENQQHLQ	HLELRLRLGL	60
GELRNLTIVK	SGLRFVAPDA	FHFTPRLSRL	NLSFNALES	SWKTVQGLSL	QELVLSGNPL	120
HCSCALRWLQ	RWEEEGLGGV	PEQKLQCHGQ	GPLAHMPNAS	CGVPTLKQVQ	PNASVDVGDD	180
VLLRCQVEGR	GLEQAGWILT	ELEQSATVMS	RPVCSCTRWW	RCTTGAPS	WMGSRHRLCA	240
GSSMAPCSMR	PASSLSSWS	RQPMAPCGTIG	VCASTSPPTS	TTATTTRCWLW	TPSARPPPS	300
WLPWTTLSS	STPRTPSLT	TAHLETRWRR	RTKHLLGSRW	LWAWPSPLPAS	SFLRCSLCST	360
NVDGETSLGS	TARLCWLQRM	GWPCPCIS				388

SEQ ID NO: 635	moltype = AA	length = 796				
FEATURE	Location/Qualifiers					
source	1..796					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 635						
MLRGGRGSQL	GWHWSAACPG	SLLAWLILAS	AGAAPCPDAC	CPHGSSGLRC	TRDGALDSLH	60
HPGAENLTE	LYIENQQHLQ	HLELRLRLGL	GELRNLTIVK	SGLRFVAPDA	FHFTPRLSRL	120
NLSFNALES	SWKTVQGLSL	QELVLSGNPL	HCSCALRWLQ	RWEEEGLGGV	PEQKLQCHGQ	180
GPLAHMPNAS	CGVPTLKQVQ	PNASVDVGDD	VLLRCQVEGR	GLEQAGWILT	ELEQSATVMK	240
SGGLPSLGLT	LANVTSDLNK	KNVTCWAEND	VGRAEVSVQV	NVSFPASVQL	HTAVEMHHWC	300
IPFSVDGQPA	PSLRWLNFNGS	VLNETSIFT	EFLEPAANET	VRHGCLRLNQ	PTHVNNGNYT	360
LIAANPFGQA	SASIMAAFMD	NPFEENPEDP	IPVSFSPVDT	NSTSGDPVEK	KDETFPGVSV	420
AVGLAVFACL	FLSTLLLVLN	KCGRNRNKFGL	NRPAVLAPED	GLAMSLHFM	LGGSSLSPTE	480
GKGSGLQH	IENPQYFSDA	CVHHIKRDR	VLPWELGEG	FGKVFLAEC	NLLPQDKML	540
VAVKALKEAS	ESARQDFQE	AELLTMLHQH	HIVRFFGVCT	EGRPLLMVFE	YMRHGDLNRF	600
LRSHGPDAKL	LAGGEDVAPG	PLGLGQLLAV	ASQVAAGMVY	LAGLHFVHRD	LATRNCLVGQ	660
GLVVKIGDFG	MSRDYISTDY	YRVGGRTMLP	IRWMPPESIL	YRKFTTESDV	WSFGVVLWEI	720
FTYGKQPWYQ	LSNTEAIDCI	TQGRELERPR	ACPPEVYAIM	RGCWQREPOQ	RHSIKDVHAR	780
LQALAQAPPV	YLDVLG					796

SEQ ID NO: 636	moltype = AA	length = 131				
FEATURE	Location/Qualifiers					
source	1..131					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 636						
MSKRYLQKAT	KGKLLIIIFI	VTLWGKVSS	ANHHKAHHVK	TGTCEVVALH	RCCNKNKIEE	60
RSQTVKSCSF	PGQVAGTTRA	APSCVDASIV	EQKWWCHMQP	CLEGEECKVL	PDRKGWSCSS	120
GNKVKTTRVT	H					131

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SEQ ID NO: 637      moltype = AA length = 87
FEATURE
source
1..87
mol_type = protein
organism = Homo sapiens
SEQUENCE: 637
MSKRYLQKA TKGKLLIIIF IVTLWGKVVS SANHHKAHHV KTGTCEVVAL HRCCNKNKIE 60
ERSQTVKCSC FPGQVAGTTR AAPSCVD 87

SEQ ID NO: 638      moltype = AA length = 131
FEATURE
source
1..131
mol_type = protein
organism = Homo sapiens
SEQUENCE: 638
MSKRYLQKAT KGKLLIIIFI VTLWGKVVS ANHHKAHHV TGTCVVALH RCCNKNKIEE 60
RSQTVKCSFC PGQVAGTTRA APSCVDASIV EQKWWCHMQP CLEGEECKVL PDRKGWSCSS 120
GNKVKTTTRAN V 131

SEQ ID NO: 639      moltype = AA length = 101
FEATURE
source
1..101
mol_type = protein
organism = Homo sapiens
SEQUENCE: 639
MVPITRMSK RYLQKATKGK LIIIFIVTL WGKVSSANH HKAHHVKTGT CEVVALHRCC 60
NKNKIEERSQ TVKCSCFPGQ VAGTTRAAPS CVDASIVEQK W 101

SEQ ID NO: 640      moltype = AA length = 34
FEATURE
source
1..34
mol_type = protein
organism = Homo sapiens
SEQUENCE: 640
MQPCLEGEEC KVLPDRKGWS CSSGNKVKTT RVTH 34

SEQ ID NO: 641      moltype = AA length = 49
FEATURE
source
1..49
mol_type = protein
organism = Homo sapiens
SEQUENCE: 641
MSKRYLQKAT KGKLLIIIFI VTLWGKVVS ANHHKGPNLT QEKSDDPQG 49

SEQ ID NO: 642      moltype = AA length = 131
FEATURE
source
1..131
mol_type = protein
organism = Homo sapiens
SEQUENCE: 642
MSKRYLQKAT KGKLLIIIFI VTLWGKVVS ANHHKAHHV TGTCVVALH RCCNKNKIEE 60
RSQTVKCSFC PGQVAGTTRA APSCVDASIV EQKWWCHMQP CLEGEECKVL PDRKGWSCSS 120
GNKVKTTRVTH 131

SEQ ID NO: 643      moltype = AA length = 110
FEATURE
source
1..110
mol_type = protein
organism = Homo sapiens
SEQUENCE: 643
MSKRYLQKA TKGKLLIIIF IVTLWGKVVS SANHHKAHHV KTGTCEVVAL HRCCNKNKIE 60
ERSQTVKCSC FPGQVAGTTR AAPSCVDASI VEQKWWCHMQP CLEGEECKV 110

SEQ ID NO: 644      moltype = AA length = 2229
FEATURE
source
1..2229
mol_type = protein
organism = Homo sapiens
SEQUENCE: 644
MFPGCPRLWV LVVLGTSWVG WGSQGTEAAQ LRQFYVAAQG ISWSYRPEPT NSSLNLSVTS 60
FFKKIVYREYE PYFKKEKPQS TISGLLGPTL YAEVGDIIKV HFKNKADKPL SIHPQGIRYS 120
KLSEGASYLD HTFPKAEMDD AVAPGREYTY EWSISEDSGP THDDPPCLTH IYYSHENLIE 180
DFNSGLIGPL LICKKGTLTE GGTQKTFDKQ IVLLFAVFDE SKSWSQSSL MYTVNGYVNG 240
DFMPDITVCAH DHISWHLLGM SSGPELEFSIH FNGQVLEQNH HKVSAITLVS ATSTTANMTV 300
GPEGKWISS LTPKHLQAGM QAYIDIKNCP KKTRNLKKIT REQRHHMKRW EYFIAAEVI 360

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WDYAPVIPAN	MDKKYRSQHL	DNFSNQIGKH	YKKVMYTQYE	DESFTKHTVN	PNMKEDGILG	420
PIIIRAQRDT	LKIVFKNMAS	RPYSIYPHG	TFSFYEDEVN	SSFTSGRNT	MIRAVQPGET	480
YTYYKWNILEF	DEPTENDAQ	LTRPYYSVD	IMRDIAASGLI	GLLLICKSRS	LDRRGIQRAA	540
DIEQQAVFAV	FDENKSWYLE	DNINKFCNP	DEVKRDDPKF	YESNIMSNTF	LSAINGYVPE	600
SITTLGFCFD	DTVQWHFCV	GQNEILTIH	FTGHSFIYKG	RHEDTTLFP	MRGESVTVM	660
DNVGTWMLTS	MNSSPRSKKL	RLKFRDVKCI	PDDDEDSEYI	FEPPESTVMA	TRKMHDRLEP	720
EDEESDADYD	YQNRLAAALG	IRSFRNSSLN	QEEEEFNLT	LAELNGTEFV	SSNTDIIVGS	780
NYSSPSNISK	FTVNNLAEPO	KAPSHQATT	AGSPLRLHIG	KNSVLNSSTA	EHSSPYSED	840
IEDPLQPDVT	GIRLLSLGAG	EFKSQEHAHK	KGPKVERDQA	AKHRFSWMKL	LAHKVGRHLS	900
QDTGSPSGMR	PWEDELPSQD	GSPSPMRWK	DPPSDLLLK	QSNSSKILVG	RWHLASEKGS	960
YEIIQDTDED	TAVNNWLISP	QNASRANGES	TPLANKPGKQ	SGHPKPFPRVR	HKSLOVQRQDG	1020
GKSRLKKSQF	LIKTRKKKK	KHTHHAPLSP	RTPHPLRSEA	YNTFSERRL	HSLVLHKNSNE	1080
TSLPTDLNQT	LPSMDFGWIA	SLPDHNQNSS	NDTGQASC	GLYQTVPPPE	HYQTFPIQDP	1140
DQMHSSTDPS	HRSSSPSELSE	MLEYDRSHKS	FPTDISQMS	SSEHEVWQTV	ISPDLSQVTL	1200
SPELSQTNLN	PDLSHTLSP	ELIQRNLSPA	LGQMPISPDL	SHTTSLPDSL	HTTLSLDSQ	1260
TNLSPELSLQ	NLSPALGQMP	LSPDLSHTTL	SLDFSQTNL	PELSHMTLSP	ELSQTNLSPA	1320
LGQMPISPDL	SHTTLSLDF	QTNLSPELSQ	TNLSPALGQM	PLSPDPSSH	LSLDLSQTNL	1380
SPELSQTNLN	PDLSEMLP	DLSQIPLPTD	LDQMTLSPDL	GETDLSPNFG	QMSLSPDLSQ	1440
VTLNDTFLSK	TLLPDLSQIS	PPPDLQDIFY	PSESSQSLL	QEFNEFPPV	DLGQMPSPSS	1500
PTLNNDTFLSK	EFPNPLVIGL	SKDGTDYIEI	I PKEEVQSS	DDYAEIDYVP	YDDPYKTDVD	1560
TNINSSRDPD	NIAAWYLRSN	NGNRRNYYIA	AEEISWDYSE	FVQRETDIED	SDDIPEDDTY	1620
KKVVFRRKYLD	STFTKRDPRG	EYEEHLGLIG	PIIIRAEVDDV	I QVRFKNLAS	R PYSLHAGL	1680
SYEKSYEWSPEWFK	EDNAVQPNSS	YTYYVWHATER	SGPESPGSAC	RAWAYYSAVN	1740	
PEKDIHSGLI	CPLLCQKGL	LHKDSDNMPMD	MREFVLLPMT	FDEKKSWYYE	KKSRSWRLLT	1800
SSEMKKSHF	HAINGMIYSL	PGLKMYEQEW	VRLHLLNIGG	SDQIHVVHFH	GQTLLENGNK	1860
QHOLGVWPLL	PGSFKTELEM	ASKPGWLLN	TEVGONQRG	MOTPFELIMDR	DCRMPMGLST	1920
GIISDSQIKA	SEFLGYWEPR	LARLNDSQSY	NAWSVEKLA	EFA SKPWIQV	DMQKEVITG	1980
IQTQGAKHLY	KSCYTYEFFV	AYSSNQINWQ	I FGKNSTRNV	MFNGNSDAS	TIKENQFDPP	2040
IVARYIRISP	TRAYNRPTLR	LELQGCEVNG	CSTPLGMENG	KIENQKITAS	SFKKSWWGDY	2100
WEPFRARLNA	QGRVNAWQAK	ANNNKQWLEI	DLLKIKKITA	I ITQGCKSLS	SEMYVKSYTI	2160
HYEQSGVEWK	PYRLKSSMVD	KIFEGNTNTK	GHVKNFFNPP	I ISRFIRVIP	KTWNQSI ALR	2220
LELFGCDIY						2229

SEQ ID NO: 645 moltype = AA length = 2224
 FEATURE Location/Qualifiers
 source 1..2224
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 645
 MFPGCPRLWV LVVLGTSWVG WGSQGTEAAQ LRQFYVAAQG ISWSYRPEPT NSSLNLSVTS 60
 FKKIVYREYE PYFKKEKPQS TISGLLGTL YABVGDIIVK HFKNKADKPL SIHPQGIRYS 120
 KLSEGASYLD HTFPKAEMDD AVAPGREYTY EWSISEDSGP THDDPPCLTH IYYSHENLIE 180
 DFNSGLIGPL LICKKGTLT GGTQKTFDKQ IVLLFAVFD E SKWSWSQSSL MYTVNGYVNG 240
 TMPDITVCAH DHISWLLGM SSGPELFSV FNQGVLEQNH KVHSAITLVS ATSTTANMTV 300
 GPEGKWISS LTPKHLQAGN QAYIDIKNCP KKTRNLKKT REQRRHMKRW EYFIAEAEVI 360
 WDYAPVIPAN MDKKYRSQHL DNFSNQIGKH YKKVMYTQYE DESFTKHTVN PNMKEDGILG 420
 PIIIRAQRDT LKIVFKNMAS RPYSIYPHG TFSFYEDEVN SSFTSGRNT MIRAVQPGET 480
 YTYYKWNILEF DEPTENDAQ LTRPYYSVD IMRDIAASGLI GLLLICKSRS LDRRGIQRAA 540
 DIEQQAVFAV FDENKSWYLE DNINKFCNP DEVKRDDPKF YESNIMSNTF GYVPESTITL 600
 GFCFDDTVQW HFCVGQTNE ILTIHFTGHS FIYGKRHEDT LTLEPFRMGEV VTVTMDNVGT 660
 WMLTSMNNSP RSKKLRLKFR DVKCI PDDDE DSYEIFPEP STVMATRKMH DRLEPDEES 720
 DADYDYQNRL AAALGIRNSR NSSLNQEEE FNLTALALEN GTEFVSSNTD II VGSNYSSP 780
 SNISKFTVNN LAEPOKAPSQ QQATTAGSPL RHLIGKNSVL NSSTA EHSSP YSEDPIEDPL 840
 QPDVTGIRL SLGAGEFKSQ EHAKHKGPKV ERDQAAKHRF SWMKLLAHKV GRHLSQDTGS 900
 PSGMRPBDL PSQDTGSPS MRWPDKDPSL LLLLKQSNSS KILVGRWHLA SEKGSYEEIQ 960
 DTDEDTAVNN WLISPQNASR AWGSTEPLAN PGKQSGHPK FPRVRHKSLQ VRQDGKKSRL 1020
 KKSQFLKTR KKKKEKHTH APLSPRTFH LRSEAYNTFS ERRKLHSLVL HKSNETSLPT 1080
 DLNQTLPSMD FGWIASLPDH NQNSNDTQ ASCPPGlyQT VPPEEHYQTF PIQDPDQMH 1140
 TSDPSHRSSS PELSEMELEYI RSHKSFPDTI SQMSPSEHEE VWQTVISPD L SQVTLSPELS 1200
 QTNLSPDL SH TLSPELIQR NLSPALGQMP ISPDLSSHTL SPDLSSHTL L DLSQTNLSP 1260
 ELSQTNLSPS LQGMLPLSPDL SHTTSLD FS QTNLSPELSH MTLSQELSPQT NLSPALGQMP 1320
 ISPDLSHTTL SLDFSQTNL PELSQTNLSP ALGQMPISPDL PSHTTSLDL SQTNLSPELS 1380
 QTNLSPDLSE MPLFADLSQI PLT PDLQDMT LSPDLGETDL SPNFGQMSL PDLSQVTLS 1440
 DISDTTLPSD LSQISPPPD L DQIFYPSESS QSLLLQEFNE SF PYPDQGM PSPSSPTLND 1500
 TFLSKEFNPL VIVGLSKDGT YEIIPEKSE VQSSSEDDY VD YD YVPPDYPY KTDVRTNINS 1560
 SRDPDNIAAW YLRSNNNGNR NYIYIAEELI WDYSEFVSE D TIEDSDIP ED TTYKVVF 1620
 RKYLDSTFTK RDPRGEYEEH LGILGPIIRA EVDDVIQVRF KNLASRPSL HAHGLSYEKS 1680
 SEKGTYEDDS PEWFKE DNAQ QPNSSYTYW HATERSGPES PGSACRAWAY YSAVNPEKDI 1740
 HSGLIGPLLI CQKGILHKDS NM PDM DREFV LLFMTFDEKK SWYYEKRSR SWRLTSSEM 1800
 KSHEFHAI NG MIYSLPGLKM YE QEWVRLHL LNIGGSQDIH VVHFHQGTL ENGNKQHQLG 1860
 VWPLLPGFSK TLEMKASKPG WWLNLTEVGE N QAGMOTPF LIMDRDCRM MGLSTGIISD 1920
 SQIKASEFLG YWEPLRLARLN NGGSYNAWSV EKLAEEFASK PWI QVDMQKE VIITGIQTC 1980
 AKHYLKSCYT TEFYVAYSSN QINQWIFKGN STRNVMYFNG NSDASTIKEN QFDPIVARY 2040
 IRISPTRAYN RPTLRLELQG CEVNGCSTPL GMENGKIE N QITASSFKS WWG DYWE PFR 2100
 ARLNAQGRVN AWQAKANNK QWLEIDL LK KITAIITQG CKSLSS EMV KSYTIHYSEQ 2160
 GVEWKPYRLK SSMVDKIFEG FFNNPPIISRF IRVPIK TWNQ SIALRLELFG 2220

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CDIY

2224

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SEQ ID NO: 646      moltype = AA length = 553
FEATURE          Location/Qualifiers
source           1..553
mol_type = protein
organism = Homo sapiens

SEQUENCE: 646
MAASKKAVLG PLVGAVDQGT SSTRFLVFNS KTAELLSHHQ VEIKQEFPRE GWVEQDPKEI 60
LHSVYECIEK TCEKLGQLNI DISNIKAIGV SNQRETTVVW DKITGEPLYN AVVWLDRTO 120
STVESLSKRI PGNNNPFVKSK TGLPLSTYFS AVKLRWLLDN VRKVQKAVEE KRALFGTIDS 180
WLIWSLTGGV NGGVHCTDVT NASRTMLFNI HSLEWDKQLC EFFFGIPMEIL PNVRSSSEIY 240
GLMKAGALEG VPISGCLGDQ SAALVGQMCF QIGQAKNTYG TGCFLLCNTG HKCVFSDHGL 300
LTTVAYKLGR DKPVYYALEG SVAIAGAVIR WLRDNLGIK TSEEIEKLAK EVGTSYGCYF 360
VPAFSGLYAP YWEPSARGII CGLTQFTNKC HIAFAALEAV CFQTREILDA MNRDGIPLS 420
HQLOVDGGMTS NKILMQLQAD ILYIPVVKPS MPETTALGA MAAGAAEGVG VWSLEPEDL 480
AVTMERFEPO INAEEESEIRY STWKKAVMKS MGWVTTQSPE SGDPSIFCSDL PLGFFIVSSM 540
VMLIGARYIS GIP 553

SEQ ID NO: 647      moltype = AA length = 559
FEATURE          Location/Qualifiers
source           1..559
mol_type = protein
organism = Homo sapiens

SEQUENCE: 647
MAASKKAVLG PLVGAVDQGT SSTRFLVFNS KTAELLSHHQ VEIKQEFPRE GWVEQDPKEI 60
LHSVYECIEK TCEKLGQLNI DISNIKAIGV SNQRETTVVW DKITGEPLYN AVVWLDRTO 120
STVESLSKRI PGNNNPFVKSK TGLPLSTYFS AVKLRWLLDN VRKVQKAVEE KRALFGTIDS 180
WLIWSLTGGV NGGVHCTDVT NASRTMLFNI HSLEWDKQLC EFFFGIPMEIL PNVRSSSEIY 240
GLMKISHSVK AGALEGPVIS GCLGDQSAAL VGMQCFQIGQ AKNTYGTGCF LLCNTGHKCV 300
FSDHGLLTTV AYKLGRDKPV YYALEGSVAI AGAVIRWLND NLGIIKTSEE IEKLAKEVGT 360
SYGCYFVPAP SGLYAPYWEV SARGIICGLT QFTNKCHIAF AALEAVCFQT REILDAMNRD 420
CGIPLSHLQV DGGMTSNKIL MQLQADILYI PVVKPSMPET TALGAAMAAG AAEGVGWSL 480
EPEDDLASAVTM ERFEPQINAE ESEIRYSTWK KAVMKSMSGWV TTQSPESGDP SIFCSLPLGF 540
FIVSSVMMLI GARYISGIP 559

SEQ ID NO: 648      moltype = AA length = 41
FEATURE          Location/Qualifiers
source           1..41
mol_type = protein
organism = Homo sapiens

SEQUENCE: 648
SARVAKFRCC LIPDSDSITC IPLKPAFSGM APDVAYSTPT S 41

SEQ ID NO: 649      moltype = AA length = 57
FEATURE          Location/Qualifiers
source           1..57
mol_type = protein
organism = Homo sapiens

SEQUENCE: 649
MRHLHYRYKEA SGYFHTLRAV MRNPEEDGKD TLQCIAEMLQ ITKQAMGSDL PIIEKKL 57

SEQ ID NO: 650      moltype = AA length = 183
FEATURE          Location/Qualifiers
source           1..183
mol_type = protein
organism = Homo sapiens

SEQUENCE: 650
MPRS SHRPPPT AQRAATAAAA EPKSEGVVAM TFKIFLFLAG LMVKVPVGLY FSCKLLLQFS 60
LMLMSPEDSG FYATIVAVVG LHQQFSECT LIDATHRDVD VLLLLNSNAY YVAYYDDEV 120
KVNQYQRSL ENLEKIEIGP EPTLFGKPKF SCMRLHYRYK EASGYFHTLR AVMRNPEEDG 180
KDT 183

SEQ ID NO: 651      moltype = AA length = 145
FEATURE          Location/Qualifiers
source           1..145
mol_type = protein
organism = Homo sapiens

SEQUENCE: 651
MSAVLLLALL GFILPLPGVQ ALLCQFGTVQ HVWKVSDLPR QWTPKNTSCD SGLGCQDTLM 60
LIESGPQVSL VLSKGCTEAK DQEPRVTEHR MGPGLSLISY TFVCRQEDFC NNVLVNSLPLW 120
APQPPPAPDMM GAAEGPFGKA EQVDS 145

SEQ ID NO: 652      moltype = AA length = 139
FEATURE          Location/Qualifiers
source           1..139

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mol_type = protein
organism = Homo sapiens
SEQUENCE: 652
MSAVLLLALL GFILPLPGVQ ALLCQFGTVQ HVWKVSDLPR QWTPKNTSCD SGLGCQDTLM 60
LIESGPQVSL VLSKGCTEAK DQEPRVTEHR MGPGLSILSY TFVCRQEDFC NNLVNSLPLW 120
APQPPAGACG RVGRRGRGC 139

SEQ ID NO: 653      moltype = AA length = 437
FEATURE           Location/Qualifiers
source            1..437
mol_type = protein
organism = Homo sapiens
SEQUENCE: 653
MSAVLLLALL GFILPLPGVQ ALLCQFGTVQ HVWKVSDLPR QWTPKNTSCD SGLGCQDTLM 60
LIESGPQVSL VLSKGCTEAK DQEPRVTEHR MGPGLSILSY TFVCRQEDFC NNLVNSLPLW 120
APQPPADPGS LRCPVCLSME GCLECTTEEI CPKGTTTHCYD GLLRLRGGGI FSNLDRVQGCM 180
PQPVCNLLNG TQEIGPGMT ENCDMKDFLT CHRGGTMITH GNLAQEPTDW TTSNTEMCEV 240
GQVCQETLLL LDVGLTSTLV GTKGSTVGA QNSQKTTIHS APPGVLVASY THFCSSDLGN 300
SASSSSVLLN SLPPQAAPVP GDRQCPTCVQ PLGTCSSGSP RMTCPRGATH CYDGYIHLSG 360
GGLSTKMSIQ GCVAQPSSFL LNHTRQIGIF SAREKRDVQ PASQHEGGGA EGLESLTWGV 420
GLALAPALWW GVVCPSC 437

SEQ ID NO: 654      moltype = AA length = 131
FEATURE           Location/Qualifiers
source            1..131
mol_type = protein
organism = Homo sapiens
SEQUENCE: 654
MAGVKALVAL SFSGAIGLTF LMLGCALEDY GYVWPLFVL1 FHAISPIPHF IAKRVTYDSD 60
ATSSACRELA YFFTTGIVVS AFGFPVILAR VAVIKWGACG LVLAGNAVIF LTIQGFFLIF 120
GRGDDDFSWEQ W 131

SEQ ID NO: 655      moltype = AA length = 140
FEATURE           Location/Qualifiers
source            1..140
mol_type = protein
organism = Homo sapiens
SEQUENCE: 655
MRDGKGFLQG PLYFALVALS FSGAIGLTF MLGCALEDYG VYWPLFVLIF HAISPIPHFI 60
AKRVTYDSDA TSSACRELAY FFTTGIVVSA FGFPVILARV AVIKWGACGL VLAGNAVIFL 120
TIQGFFLIFG RGDDDFSWEQW 140

SEQ ID NO: 656      moltype = AA length = 140
FEATURE           Location/Qualifiers
source            1..140
mol_type = protein
organism = Homo sapiens
SEQUENCE: 656
MQFGEELAAV RKAQANVMLF LEEKEQAAALS QANGIKAHLE YRSAEMEKSK QELERMAAIS 60
NTVQFLEMRM TSRLTRTQHT SISGCRRTA RSPTPRPGSI PTRTSPAGSC TGGRCCPSRV 120
CTCTGTILRW RSSGQAPMLA 140

SEQ ID NO: 657      moltype = AA length = 205
FEATURE           Location/Qualifiers
source            1..205
mol_type = protein
organism = Homo sapiens
SEQUENCE: 657
MTPPERLFLP RVCGETTLHLL LLGLLLVLLP GAQGLPGVGL TPSAAQTARQ HPKMHLAHEST 60
LKPAAHLLGD PSKQNSLLWR ANTDR AFLQD GFSLSNNSLL VPTSGIYFVY SQVVFSGKAY 120
SPKATSSPLY LAHEVQLFSS QYPFHVPILLS SQKMVYPGLQ EPWLHSMYHG AAFQLTQGDQ 180
LSTHTDGIPH LVLSPTVFF GAFAL 205

SEQ ID NO: 658      moltype = AA length = 205
FEATURE           Location/Qualifiers
source            1..205
mol_type = protein
organism = Homo sapiens
SEQUENCE: 658
MTPPERLFLP RVCGETTLHLL LLGLLLVLLP GAQGLPGVGL TPSAAQTARQ HPKMHLAHEST 60
LKPAAHLLGD PSKQNSLLWR ANTDR AFLQD GFSLSNNSLL VPTSGIYFVY SQVVFSGKAY 120
SPKATSSPLY LAHEVQLFSS QYPFHVPILLS SQKMVYPGLQ EPWLHSMYHG AAFQLTQGDQ 180
LSTHTDGIPH LVLSPTVFF GAFAL 205

SEQ ID NO: 659      moltype = AA length = 1015
FEATURE           Location/Qualifiers

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source          1..1015
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 659
MLTALAPPAL PGIPRQLPTA PARRQDSSGS SGSYYTAPGS PEPPDVGPDA KGPANWPWVA 60
PGRGAGAQPR LSVSAQNSRQ RHGPQSGFPR GPGSGPRPQ PQLRTLPSGR MEVIFGVGPL 120
FGCSGADDRE AQQQFTEPAF ISPLPPGPAS PAAVPRQSQV PDGGSRWATY LELRPRGPSP 180
AAPAQFECVE VALEEGAAPA RPRTVPKROI ELRPRPQSPP RAAGAPRPLL LLRTGSLDES 240
LGPLQAAAGF VQTALARLKS PEAPAPSSAT FGSTGRSEPE TRETARSTHV VLEAKSRPL 300
RVRDNTSAPAK APPRPWPSLRK RAIIRDKPAP GTEPLGPVSS SIFLOSEEKQ QEARKTRFPR 360
EAPDRTVQRA RSPPFECRIP SEVPSRAVRP RSPSPPRQTP NGAVRGPRCP SPQNLSPWDR 420
TTRRVSSPLF PEASSEWENQ NPAVEETVSR RSPSPPLILSQ NWQCVAGERS PSLEAPSLWE 480
IPHSAVADAV EPRSSPSPPA FFPWEAPDRP IGTWGPSPQE TWDPMPGSS IAFTQEAQNG 540
LTQEELAPPT PSAPGTPPEPT EMQSPSTREI SDLAFFGGSQO SPEVAAPEPP GHSPVGTLLDA 600
DKCPEVLGPI EAASGRPRMA IPRPRDVKL VKTTTYAPGFP AGAQGSGLPA PPADPCGEEG 660
GESKTQEPPA LGPPAPAHY SVFIKDFLPV VPHPYEPPEP SFDTVARDAS QPNGLRRRA 720
ENSTAKPFKR TEIRLPGALA LGRRPEVTSR VRARGPGGEN RDVEAQRLVP DGDGRTSPLG 780
GARSSSQRSR VGPAGVRSP PGSPOMQASP SPGIAPKPKT PPTAEPAAA VQAPLPREPL 840
ALAGRRTAPAQ PRAASAPPTD RSPQSPSQGA RRQPGAAPLG KVLDVPESGR YYFVEAPRQP 900
RLRVLFDPES QYVEVLLPP SSPGPQPHRVY TPLALGLGLY PPAYGPISL SLPPSPGPQA 960
LGSPQLPWVS EAGPLDGTYY LPVSGTPNPA PPLLCCAPS SSGPTQPGKG SLFPL 1015

SEQ ID NO: 660      moltype = AA length = 418
FEATURE           Location/Qualifiers
source            1..418
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 660
MDMLHPSSVS TTSEHENASS AWPPDATLGN VSAGPSPAGL AVSGVLIPLV YLVVCVVGLL 60
GNSLVIYVVL RHTASPVTN VYILNLALAD ELFMLGLPFL AAQNALSYWP FGSLMCRLLVM 120
AVDGINQFTS IFCLTVMSVD RYLAHVHPTR SARWRATPVA RTVSAAVWVA SAVVVLPPVV 180
FSGVPRGMST CHMQWPEAA AWRAGFIIYT AALGFFGPLL VICLCYLLIV VKVRSAGRRV 240
WAPSCQRERRR SERRVTRMVV AVVALFVLCW MPFYVLNIVN VVCPLPEEPA FFGLYFLVVA 300
LPYANSANCANP ILYGFLSYRF KQGFRRVLLR PSRVRVSQEP TVGPPEKTEE EDEEEEDGEE 360
SREGGKGKEM NGRVSQITQP GTSGQERPPS RVASKEQQLL PQEASTGEKS STMRI SYL 418

SEQ ID NO: 661      moltype = AA length = 418
FEATURE           Location/Qualifiers
source            1..418
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 661
MDMLHPSSVS TTSEHENASS AWPPDATLGN VSAGPSPAGL AVSGVLIPLV YLVVCVVGLL 60
GNSLVIYVVL RHTASPVTN VYILNLALAD ELFMLGLPFL AAQNALSYWP FGSLMCRLLVM 120
AVDGINQFTS IFCLTVMSVD RYLAHVHPTR SARWRATPVA RTVSAAVWVA SAVVVLPPVV 180
FSGVPRGMST CHMQWPEAA AWRAGFIIYT AALGFFGPLL VICLCYLLIV VKVRSAGRRV 240
WAPSCQRERRR SERRVTRMVV AVVALFVLCW MPFYVLNIVN VVCPLPEEPA FFGLYFLVVA 300
LPYANSANCANP ILYGFLSYRF KQGFRRVLLR PSRVRVSQEP TVGPPEKTEE EDEEEEDGEE 360
SREGGKGKEM NGRVSQITQP GTSGQERPPS RVASKEQQLL PQEASTGEKS STMRI SYL 418

SEQ ID NO: 662      moltype = AA length = 526
FEATURE           Location/Qualifiers
source            1..526
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 662
MGHLSAPLHR VRVPWQGLLL TASLLTFWNP PTTAQLTTES MFPNVAEKVE VLLLHVHNLPO 60
QLFGYSWYKG ERVDGNRQIV GYAIGTQQAT PGPANGREI IYPNASLLIQ NVTQNDTGFY 120
TLQVIKSDLV NEEATGQFH YPELPKPSIS SNNSNPVEDK DAVAFTCEPE TQDFTYLWWI 180
NNQSLPVSPR LQLSNGNRTL TLLSVTRNDT GPYECEIQNP VSANRSDPVT LNVTYGPDT 240
TISPSDPTYR PGANLSSLCA AASNPNAQOVS WLINGTFQOS TQELFIPNIT VNNSGSYTC 300
ANNSVTGCNR TTVKTIIVTE LSPVVAKPQI KASKTTVTD KDSVNLCTST NDTGISIRWF 360
FNQSLSPSSE RMKLSQGNNT LSINPVKRED AGTYWCEVFN PISKNQSDPI MLNVNNALP 420
QENGLSPGAI AGIVIGVVAL VALIATALAC FLHFGKTGRA SDQRDLTEHK PSVSNHTQDH 480
SNDPPNKMNE VTYSTLNFEA QQPTQPTSAS PSLTAIEIYI SEVKKQ 526

SEQ ID NO: 663      moltype = AA length = 430
FEATURE           Location/Qualifiers
source            1..430
               mol_type = protein
               organism = Homo sapiens
SEQUENCE: 663
MGHLSAPLHR VRVPWQGLLL TASLLTFWNP PTTAQLTTES MFPNVAEKVE VLLLHVHNLPO 60
QLFGYSWYKG ERVDGNRQIV GYAIGTQQAT PGPANGREI IYPNASLLIQ NVTQNDTGFY 120
TLQVIKSDLV NEEATGQFH YPELPKPSIS SNNSNPVEDK DAVAFTCEPE TQDFTYLWWI 180
NNQSLPVSPR LQLSNGNRTL TLLSVTRNDT GPYECEIQNP VSANRSDPVT LNVTYGPDT 240

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TISPSDTYYY	PGANLSLSCY	AASNNPPAQS	WLINGTFFQOS	TQEELFIPNIT	VNNNSGSYTC	300
ANNSVTGCNR	TTVKTIIIVTD	NALPQENG	LS PGAIAGIVIG	VVALVALIAV	ALACPLHF	360
TGRASDQRDL	TEHKPSVSNH	TQDHSDNPPN	KMNEVTYSTL	NFEAQOPTQP	TSASPSTAT	420
EIYJSVEVKKO						430

SEQ ID NO: 664 moltype = AA length = 461
FEATURE Location/Qualifiers
source 1..461
mol_type = protein
organism = Homo sapiens

SEQUENCE:	664					
MGHLSLAPHLR	VRVPWQGLLL	TASLLTFWNP	PTTAQLTTES	MPFNVAEKG	VLLLHVHNLPO	60
QLFGYSWYKG	ERVDGMRQIV	GYAIGTQQAT	PGPANSRGRET	IYPNASLLIQ	NVTQNDTGFY	120
TLQVKSSDLV	NEEATQCFHV	YPELPKPSIS	SNNSNPVEDK	DAVAFTCEPE	TQDITTYLWWI	180
NNQSLPVSPR	LQLSGNRRL	TLLSVTRNDT	GPYECEIQNP	VSANRSDPVT	LNVTYGPDTP	240
TISPSDTYYR	PGANLSSLSCY	AASNPAPAQS	WLINGTFQOS	TQELFLIPNIT	VNNNSGSYTC	300
AMNSVTGCRN	TTVKTIITVE	RQNLTMLPRL	DSNSWAQAIL	PSVSQSAAEIT	DNALPQEGL	360
SKPMAGIVI	GVVALVALIA	VALACFLHFG	KTRGRASDRLQ	LTEHKPSVSN	HQTQDHSDNPP	420
NKMEVNTYST	LNFEAQOPTQ	PTSASPSTIA	TEIIYSEVKK	Q		461

SEQUENCE: 665							
MGHLSAPLHR	VRVPWQGLLL	TASLLTFWNP	PTTAQLTTES	MPFNVAEKG	VLLLHVHNL	PQ	60
QLFGWSYWK	ERVDGNRQIV	GYAIGTQQAT	PGPANSGRET	IYPNASLIIQ	NVTQNDTG	FY	120
TLOVQIKSDLV	NEEAATGQFHV	YPELPKPSIS	SNNNSNPVEDK	DAVAFTCEPE	TQDITTYLWWI		180
NNQSLPVSPR	LQLSGNRTL	TLLSVTRNDT	GPYECEIQNP	VSANRSDPVT	LNVTYGPDT		240
TISPSPDTYR	PGANLSSLSCV	AASNPQAOS	WLINGTFCQS	TQELFIPNIT	VNNNSGSY	TC	300
ANNSVTGCNR	TTVKTIIVTE	LSPVVAKPQI	KASKTTVGD	KDSVNLTCST	NDTGISIRWF		360
FKNQSLPSSE	RMKLKSQGNNT	LSSVNPKRED	AGTYWCEVPIRN	PISKNQSDPI	MLNVNLYNALP		420
QENGLSPGAI	AGIVIGVVAL	VALIAVALAC	FLHFGKTGSS	GPLQ			464

SEQ ID NO: 666 moltype = AA length = 368
FEATURE Location/Qualifiers
source 1..368
mol_type = protein
organism = Homo sapiens

SEQUENCE: 666						
MGHLSAPLHR	VRVPWQGLLL	TASLLTFWNP	PTTAQLTTES	MPFNVAEKG	VLLLHVHNLQ	60
QLFGYSWYKG	ERVDGNRQIV	GYAIGTQQAT	PGPANSGRET	IYPNASLIIQ	NVTQNDTGFY	120
TLQVKISDLV	NEEATGQFHV	YPELPKPSIS	SNNNSNPVEDK	DAVAFTCEPE	TQDTTYLWWI	180
NNQSLPVSPR	LQLSGNRTL	TLLSVTRNDT	GPYECEIQNP	VSANRSDPVT	LNVTYGPDP	240
TIPSPDSTYY	PGANLSSLSCY	AASNPQAQYS	WLINGTFQOS	TQELFTPNIT	VNNSSGSYTC	300
ANNSVTCGCR	TTVKTIIVTD	NALPQENGLS	PGAIAGIVIG	VVALVALIAV	ALACPLHFGK	360
TGSSGPLQ						368

SEQ ID NO: 667 moltype = AA length = 94
FEATURE Location/Qualifiers
source 1..94
mol_type = protein
organism = Homo sapiens
SEQUENCE 667

MFPFVNAECKE VLLLVLHNLPQ QLFPGYSWYKG ERVDGNGRQIV GYAIGTQQAT PGPANSGRE 60
IYPNASLLIQ NVTQNDTGFY TLQVIKSDLV NEEA 94

SEQ ID NO: 668 moltype = AA length = 399
FEATURE Location/Qualifiers
source 1..399
mol_type = protein
organism = Homo sapiens

Organism - HOMO sapiens	
SEQUENCE:	668
MGHLSAPLHR	VRVPWQGLLL TASLLTFWNP PTTAQLTTES MPFNVAEGKE VLLLVHNLPO
QLFGWSYWKG	ERVDGNRQIV GYAIGTQQAT PGPNASGRET IYPNASLIIQ NVTQNDTGFY
TLOVIKSDLV	NEEATQFHV YPELPKPSIS SNNNSPNVEDK DAVAFTCEPE TDQDTTYLWWI
NNQSLPVSPIR	LQLSNGNRTL TLLSVTRNDT GPYECEIQNP VSANRSPVT LNVTYGPDTP
TISPSTDYYR	PGANLSSLCY AASNPNAQYS WLINGTFFQS TQEFLIPNIT VNNNSGSYTC
ANNSVCGNR	TTVKTIIVTE MAFHVAKAG LKLKSSSNPP ASTSQSAKIT DNALPQENGL
SPGAIAGIVI	GVVALVALIA VALACFLHFG KTGGSGPLQ

SEQ ID NO: 669 moltype = AA length = 99
FEATURE Location/Qualifiers
source 1..99
mol type = protein

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SEQUENCE: 669	organism = Homo sapiens
MPFNVAEKGKE VLLLVLHNLPO QLFGYSWYKG ERVDGNRQIV GYAIGTQQAT PGPANSGRET	60
IYPNASLLIQ NVTQNDTGFY TLQVKSSDLV NEEATGQPH	99
 SEQ ID NO: 670	moltype = AA length = 174
FEATURE	Location/Qualifiers
source	1..174
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 670	
MACLGFRQRHK AQLNLATRTW PCTLLFFLLF IPVFCCKAMHV AQPAVVLAASS RGIAASFVCEY	60
ASPGKATEVR VTVLQRQADSQ VTEVCAATYM MGNELTFLDD SICTGTSSGN QVNLTIQGLR	120
AMDTGLYICK VELMYPYPPYY LGIGNGTQIY VIDPEPCPD SDFLLWLAAV SSGLPFYFSL	180
LTAVALSLSKML KKRSPLLTGV YVKMPPTEPE CEKQFQPYFI PIN	223
 SEQ ID NO: 671	moltype = AA length = 223
FEATURE	Location/Qualifiers
source	1..223
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 671	
MACLGFRQRHK AQLNLATRTW PCTLLFFLLF IPVFCCKAMHV AQPAVVLAASS RGIAASFVCEY	60
ASPGKATEVR VTVLQRQADSQ VTEVCAATYM MGNELTFLDD SICTGTSSGN QVNLTIQGLR	120
AMDTGLYICK VELMYPYPPYY LGIGNGTQIY VIDPEPCPD SDFLLWLAAV SSGLPFYFSL	180
LTAVALSLSKML KKRSPLLTGV YVKMPPTEPE CEKQFQPYFI PIN	223
 SEQ ID NO: 672	moltype = AA length = 137
FEATURE	Location/Qualifiers
source	1..137
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 672	
MHVAQPAVVL ASSRGIAFV CEYASPGKAT EVRVTVLRQA DSQVTEVCAA TYMMGNELT	60
LDDSICTGTS SGNVNLTIQ GLRAMDTGLY ICKVELMYPY PPYIYGIGNGT QIYVIAKEKK	120
PSYNRGLCEN APNARM	137
 SEQ ID NO: 673	moltype = AA length = 79
FEATURE	Location/Qualifiers
source	1..79
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 673	
MACLGFRQRHK AQLNLATRTW PCTLLFFLLF IPVFCCKAMHV AQPAVVLAASS RGIAFSVSKE	60
KKPSYNRGLC ENAPNARM	79
 SEQ ID NO: 674	moltype = AA length = 244
FEATURE	Location/Qualifiers
source	1..244
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 674	
MWRCLLLIWA QGLRQAPLAS GMMTGTIETT GNISAEKGGSII ILQCHLSST TAQVTQVNWE	60
QDQDQLLAICN ADLGHWHISPS FKDRVAPGPGL LGLTLQSLTVN NDTGEYFCIY HTYPDGTYTG	120
RIFLEVLESS VAEHGARFQI PLLGAMAATL VVICTAVIVV VALTRKKAL RIHSVEGDLR	180
RKSAGQEEWS PSAPSPPGSC VQAEAAPAGL CGEQRGEDCA ELHDYFNVL S YRSLGNCSFF	240
TETG	244
 SEQ ID NO: 675	moltype = AA length = 169
FEATURE	Location/Qualifiers
source	1..169
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 675	
MMTGTIETTG NISAEKGGSII ILQCHLSSTT AQVTQVNWEQ QDQDQLLAICNA DLGWHISPSF	60
KDRVAPGPGL GLTLQSLTVN DTGEYFCIYH TYPDGTYTGR IFLEVLESSV AEHGARFQIP	120
LLGAMAATLV VICTAVIVVV ALTRKKKALR IHSVEGDLR KSAGQEEWS	169
 SEQ ID NO: 676	moltype = AA length = 311
FEATURE	Location/Qualifiers
source	1..311
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 676	
MAFLVAHPMQ FVYLLTTLCV FNMVFAKLG SETVFSQRSL FTVLSAVGYF QWQKRPHL	60
VGPLGRSMRW CLLLIWAQGL RQAPLASGMM TGTIETTGNI SAEKGGSIL QCHLSSTTAQ	120
VTQVNWEQQD QLLAICNADL GWHSISPFKD RVAPGPGL GL TLQSLTVNDT GEYFCIYHTY	180

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PDGTYTGRIF LEVLESSVAE HGARFQIPLL GAMAATLVVI CTAVIVVVAL TRKKKALRIH	240
SVEGDLRRKS AGQEEWPSA PSPPGSCVQA EAAPAGLCGE QRGEDCAELH DYFNVL SYRS	300
LGNCSFFTET G	311
SEQ ID NO: 677 moltype = AA length = 163	
FEATURE Location/Qualifiers	
source 1..163	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 677	
MMTGTIETTG NISAEKGGSI ILQCHLSSTT AQVTQVNWEQ QDQLLAICNA DLGWHISPSF	60
KDRVAPGPGL CLTQLSLSLTVN DTGEYFCIYH TYPDGTYTGR IFLEVLESSV AEHGARFQIP	120
LLGAMAATLV VICTAVIVVV ALTRKKKALR IHSVEGDLRR KSA	163
SEQ ID NO: 678 moltype = AA length = 244	
FEATURE Location/Qualifiers	
source 1..244	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 678	
MRCWCLLIWA QGLRQAPLAS GMMTGTIETT GNISAEKGGS IIILQCHLSST TAQVTQVNWE	60
QQDQLLAICN ADLGWHISPS FKDRVAPGPGL LGTLTQLSLSLTV NDTGEYFCIY HTYPDGTYTG	120
RIFLEVLESS VAEHGARFQI PLLGAMAATL VVICTAVIVV VALTRKKKAL RIHSVEGDLR	180
RKSAGQEEWS PSAPSPPGSC VQAEAAPAGL CGEQRGEDCA ELHDYFNVL S YRSLGNCSFF	240
TETG	244
SEQ ID NO: 679 moltype = AA length = 263	
FEATURE Location/Qualifiers	
source 1..263	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 679	
MDSYLLMWGL LTFIMVPGCQ AELCDDDPPE IPHATFKAMA YKEGTMNLNE CKRGFRRIKS	60
GSLYMLCTGN SSHSSWDNQC QCTSSATRNT TKQVTPQPEE QKERKTTEMQ SPMQPVDQAS	120
LPGHCREPPP WENEATERIY HFVVGQMYY QCVCQGYRALH RGPAESVCKM THGKTRWTQP	180
QLICTGEEKP QASPEGRPES ETSCLVTTTD FQIQTEMAAT METSIFTTEY QVAVAGCVFL	240
LISVLLSGL TWQRQRKSR RTI	263
SEQ ID NO: 680 moltype = AA length = 200	
FEATURE Location/Qualifiers	
source 1..200	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 680	
MDSYLLMWGL LTFIMVPGCQ AELCDDDPPE IPHATFKAMA YKEGTMNLNE CKRGFRRIKS	60
GSLYMLCTGN SSHSSWDNQC QCTSSATRNT TKQVTPQPEE QKERKTTEMQ SPMQPVDQAS	120
LPGEEEKPOAS PEGRPSESETS CLVTTTDFQI QTTEMAATMET SIFTTEYQVA VAGCVLLIS	180
VLLLSGLTWQ RRQRKSRRTI	200
SEQ ID NO: 681 moltype = AA length = 272	
FEATURE Location/Qualifiers	
source 1..272	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 681	
MDSYLLMWGL LTFIMVPGCQ AELCDDDPPE IPHATFKAMA YKEGTMNLNE CKRGFRRIKS	60
GSLYMLCTGN SSHSSWDNQC QCTSSATRNT TKQVTPQPEE QKERKTTEMQ SPMQPVDQAS	120
LPGHCREPPP WENEATERIY HFVVGQMYY QCVCQGYRALH RGPAESVCKM THGKTRWTQP	180
QLICTGEMET SQFPGEEKPK ASPEGRPES ETSCLVTTDF QIQTTEMAATM ETSIFTTEYQ	240
VAVAGCVFL ISVLLLSGLT WQRQRKSR TI	272
SEQ ID NO: 682 moltype = AA length = 510	
FEATURE Location/Qualifiers	
source 1..510	
mol_type = protein	
organism = Homo sapiens	
 SEQUENCE: 682	
MEDTKESNVK TFC SKNILAI LGFSSIIAVI ALLAVGLTQN KALPENVKYG IVLDAGSSHT	60
SLIYIKWPAE KENDITGVVHQ VEECRVKGPQ ISKFVQKVNE IGIYLTDCE RAREVIPRSQ	120
HQETPVYLGA TAGMRLRME SEELADRVL VVERSLSNYP FDFQGARIT GQEEGAYGWI	180
TINYLLGKFS QKTRWFSIVP YETNNQETPG ALDLGGASTQ VTFVPQNQTI ESPDNALQFR	240
LYGKDYNVYT HSFLCYGDQ ALWQKLAKDI QVASNEILRD PCFHGPYKKV VNVS DLYKTP	300
CTKRFEMTLP FQQFEIQQGIG NYQQCHQSIL ELPNTSYCPY SQCAFNGIFL PPLQGDFGAF	360
SAFYFVMKFL NLTSEKVSQE KVTEMMKKFC AQPWEI KTS YAGVKEKYL EYCFSGTYIL	420
SFLQGYHFT ADSWEHIHFI GKIQGSDAGW TLGYMLNLTN MIPAEQPLST PLSHSTYVFL	480
MVLFSLVLFT VAIIGLLIFH KPSYFWKDMV	510

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SEQ ID NO: 683      moltype = AA  length = 522
FEATURE
source          Location/Qualifiers
1..522
mol_type = protein
organism = Homo sapiens
SEQUENCE: 683
MGREELFLTF SFSSGFQESN VKTFCSKNIL AILGFSSIIIA VIALLAVGLT QNKALPENVK 60
YGIVLDAAGS HTSLIYIKWP AEKENDTGVV HQVEECRVKG PGISKFVQKV NEIGIYLTD 120
MERAREVIPR SQHQETPVYL GATAGMRLLR MESEELADR V LDVVERSLSN YPFDFQGARI 180
ITGQEEGAYG WITINYLLGK FSQKTRWFSI VPYETNNQET FGALDLGGAS TQVTFVPQNQ 240
TIESPDNALQ PRLYGDYDNY YTHSFLCYGK DQALWQKLAK DIQVASNEIL RDPCPHPGYK 300
KVVNVSDLYK TPCTKRFEMT LPFQQFEIQG IGNYQQCHQS ILELFNTSYC PYSQCAFNGI 360
FLPPLQGDFG AFSAFYFVMI FLNLTSEKVS QEKTTEMKKF FCAQPWEEIK TSYAGVKEKY 420
LSEYCFSGTY ILSLLLQGYH FTADSWEIH FIGKIQGSDA GWTLGYMLNL TNMIPAEQPL 480
STPLSHSTYV FLMVLFSLVL FTVAIIGLLI FHKPSYFWKD MV 522

SEQ ID NO: 684      moltype = AA  length = 517
FEATURE
source          Location/Qualifiers
1..517
mol_type = protein
organism = Homo sapiens
SEQUENCE: 684
MKGTKDQLTSQ QKESNVKTF SKNILAILGF SSIIAVIALL AVGLTQNKA PENVKYGIN 60
DAGSSHSTS LYKWPAAKEN DTGVVHQVEE CRVKPGPIK FVQKVNEIGI YLTDCMERAR 120
EVIPRSHQEE TPVYLGATAG MRLLRMESEE LADRVLVDVVE RSLSNYPDF QGARIITGQE 180
EGAYGWITIN YLLGKFSQKT RWFSIVPYET NNQETFGALD LGGASTQVTF VPQNQTIESP 240
DNALQFRLYK KDYNVYTHSF LCYGKDQALW QKLAKDIOVA SNEILDPCF HPGYKKVNV 300
SDLYKTPCTK RFEMTLPFQQ FEIQCIGNYQ OCHQSILELF NTSYCPYSQC AFNGIFLPP 360
QGDFGAFSAF YFVMKFLNLT SEKVSQEKVT EMMKKFCAQW WEEIKTSYAG VKEKYLSEYC 420
FSGTYIILSSL LQGYHFTADS WEHIHFIGKI QGSDAGWTLG YMLNLTNMIP AEQPLSTPLS 480
HSTYVFMLV FSLVLFPTVAI IGLLIFHKPS YFWKDMV 517

SEQ ID NO: 685      moltype = AA  length = 63
FEATURE
source          Location/Qualifiers
1..63
mol_type = protein
organism = Homo sapiens
SEQUENCE: 685
MERAREVIPR SQHQETPVYL GATAGMRLLR VPGSLLAKRK VPMAGLLSTI CWANSVRKQG 60
GSA 63

SEQ ID NO: 686      moltype = AA  length = 402
FEATURE
source          Location/Qualifiers
1..402
mol_type = protein
organism = Homo sapiens
SEQUENCE: 686
MERAREVIPR SQHQETPVYL GATAGMRLLR MESEELADR V LDVVERSLSN YPFDFQGARI 60
ITGQEEGAYG WITINYLLGK FSQKTRWFSI VPYETNNQET FGALDLGGAS TQVTFVPQNQ 120
TIESPDNALQ PRLYGDYDNY YTHSFLCYGK DQALWQKLAK DIQVASNEIL RDPCPHPGYK 180
KVVNVSDLYK TPCTKRFEMT LPFQQFEIQG IGNYQQCHQS ILELFNTSYC PYSQCAFNGI 240
FLPPLQGDFG AFSAFYFVMI FLNLTSEKVS QEKTTEMKKF FCAQPWEEIK TSYAGVKEKY 300
LSEYCFSGTY ILSLLLQGYH FTADSWEIH FIGKIQGSDA GWTLGYMLNL TNMIPAEQPL 360
STPLSHSTYV FLMVLFSLVL FTVAIIGLLI FHKPSYFWKD MV 402

SEQ ID NO: 687      moltype = AA  length = 51
FEATURE
source          Location/Qualifiers
1..51
mol_type = protein
organism = Homo sapiens
SEQUENCE: 687
MEDTKESNVK TFC SKNILAI LGFSSIIAVI ALLAVGLT QNKALPENVKDG K 51

SEQ ID NO: 688      moltype = AA  length = 199
FEATURE
source          Location/Qualifiers
1..199
mol_type = protein
organism = Homo sapiens
SEQUENCE: 688
MSKGLWYFPL FCLRIKVLTG EINGSANYEM FIFHNGGVQI LCKYPDIVQQ FKMOLLKGGQ 60
ILCDLTKTKG SGNTVSIKSL KFCHSQLSNN SVSFFLYNLD HSHANYYFCN LSIFDPPPDK 120
VTLTGGYLHI YESQLCCQLK FWLPIGCAAF VVVCILGCIL ICWLTKKKYS SSVHDPNGEY 180
MFMRAVN TAK KSRLTDVTL 199

SEQ ID NO: 689      moltype = AA  length = 168

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FEATURE	Location/Qualifiers
source	1..168
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 689	
MKSGLWYFFL PCLRIKVLTG EINGSANYEM FIFHNGGVQI LCKYPDIVQQ FKMQLLKGGQ	60
ILCDLTKTKG SGNTVSIKSL FKCHSQLSNN SVSFFLYNLD HSHANYYFCN LSIFDPPPK	120
VTLTGGYLHI YESQLCCQLK FWLPIGCAAF VVVCILGCIL ICWLTKKM	168
SEQ ID NO: 690	moltype = AA length = 277
FEATURE	Location/Qualifiers
source	1..277
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 690	
MCVGARRLGR GPCAALLLLG LGLSTVTGLH CVGDTYPSND RRCHECRPGN GMVSRCRSQ	60
NTVCRPCPGF FYNDVVSSKP CKPCTWCNLR SGSERKQLCT ATQDTCRCCR AGTQPPLDSYK	120
PGVDCAPCPP GHFSPGDNQA CKPWTNCTLA GKHTLQPAQN SSDAICEDRD PPATQPQETQ	180
GPPARPIVTQ PTEAWPRTSQ GPSTRPVVEP GGRAVAAILG LGLVLGLGP LAILLALYLL	240
RRDQRLLPPDA HKPPGGGSFR TPIQEQQADA HSTLAKI	277
SEQ ID NO: 691	moltype = AA length = 255
FEATURE	Location/Qualifiers
source	1..255
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 691	
MAQHGAMGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTNDARCC RVHTTRCCRD	60
YPGEECCSEW DCMCVQPEFH CGDPCTTCTR HHPCPPGQGV QSQGKFSFGF QCIDCASGTF	120
SGGHEGHCKP WTDCCWRCRR RPPTPEAASS PRKSGASDRQ RRRGGWETCG CEPGRPPGPP	180
TAASPSPGAP QAAGALRSAL GRALLPWQQK WVQEGGSQDR PGPCSSAAAA GPCRERETQ	240
SWPSSLALGP DGVGS	255
SEQ ID NO: 692	moltype = AA length = 234
FEATURE	Location/Qualifiers
source	1..234
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 692	
MAQHGAMGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTNDARCC RVHTTRCCRD	60
YPGEECCSEW DCMCVQPEFH CGDPCTTCTR HHPCPPGQGV QSQGKFSFGF QCIDCASGTF	120
SGGHEGHCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL	180
TSAQLGLHIW QLRKTQLLLE VPPSTEDARS CQFPPEERGE RSAEEKGRIG DLWV	234
SEQ ID NO: 693	moltype = AA length = 241
FEATURE	Location/Qualifiers
source	1..241
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 693	
MAQHGAMGAF RALCGLALLC ALSLGQRPTG GPGCGPGRLL LGTGTNDARCC RVHTTRCCRD	60
YPGEECCSEW DCMCVQPEFH CGDPCTTCTR HHPCPPGQGV QSQGKFSFGF QCIDCASGTF	120
SGGHEGHCKP WTDCTQFGFL TVFPGNKTHN AVCVPGSPPA EPLGWLTVVL LAVAACVLLL	180
TSAQLGLHIW QLRSQCMWPR ETQLLLEVPP STEDARSCQF PEEERGERSA EEKGRLGDLW	240
V	241
SEQ ID NO: 694	moltype = AA length = 169
FEATURE	Location/Qualifiers
source	1..169
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 694	
MCVQPEFHCG DPCCTTCRH PCPPGQGVQS QGKFSFGFQ IDCASGTFSG GHEGHCKPWT	60
DCTQFGFLTV FPGNKTHNAV CVPGSPPAEP LGWLTVVLLA VAACVLLLTS AQLGLHIWQL	120
RSQCMWPRET QLLLEVPPST EDARSCQFPE EERGERSAAE KGRGLGDLWV	169
SEQ ID NO: 695	moltype = AA length = 595
FEATURE	Location/Qualifiers
source	1..595
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 695	
MRVLLAALGL LFLGALRAFP QDRPFEDTCH GNPSHYYDKA VRRCCYRCPM GLFPTQQCPQ	60
RPTDCRKQCE PDYYLDEADR CTACVTCRD DLVEKTPCAW NSSRVCECRP GMFCSTSABN	120
SCARCFHFHSV CPAGMIVKFP GTAQKNTVCE PASPGVSPAC ASPENCKEPS SGTIPQAKPT	180
PVSPATSSAS TMPVRRGTRL AQEEASKLTR APDSPSSVGR PSSDPLGLSPT QPCPEGSGDC	240

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RKQCEPDYLYL DEAGRCTACV SCSRDDLVEK TPCAWNSSRT CECRPGMIC A TSATNSCARC 300
VYPYPICAET VTKPQDMAET DTTFEAPPLG TQDCNPTPE NGEAPASTSP TQSLLVDSQA 360
SKTLPPIPTSA PVALSSTGKP VLDAGPVLFW VILVLVVVVG SSAFLLCRRR ACRKRIRQKL 420
HLCYPVQTSQ PKLELVDSRP RRSSTQLRSG ASVTEPVAAE RGLMSQPLME TCHSVGAAYL 480
ESLPLQDASP AGGPSSPRDL PEPRVSTEHT NNKIEKIJIM KADTVIVGTV KAELPEGRGL 540
AGPAEPELEE ELEADHTPHY PEQETEPPPLG SCSDVMLSVE EEGKEDPLPT AASGK 595

SEQ ID NO: 696	moltype = AA length = 483
FEATURE	Location/Qualifiers
source	1..483
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 696	
MFCSTSAVNS CARCFFHSVC PAGMIVKFPG TAQKNTVCEP ASPGVSPACA SPENKEPSS 60	
GTIPQAKPTP VSPATSSAST MPVRGGTRLA QEAASKLTRA PDSPSSVGRP SSDPGLSPTQ 120	
PCPEGSGDCCR KQCEPDYLYLD EAGRCTACVS CSRDDLVEKT PCAWNSSRTC ECRPGMICAT 180	
SATNSCARCV PYPICAETV TKPQDMAEKD TTDFEAPPLGT QPDCNPTPE GEAPASTSP 240	
QSLLVDSQAS KTLPIPTSA VALSSTGKPV LDAGPVLFWV ILVLVVVVG SAFLLCRRRA 300	
CRKRIRQKLH LCYPVQTSQP KLELVDSRP RSSTLRSGAS VTEPVAAEERG LMSQPLMETC 360	
HSGVAAYLES LPLQDASPAG GPSSPRDLPE PRVSTEHTNN KIEKIJIMKA DTVIVGTVKA 420	
ELPEGRGLAG PAEPELEE EADHTPHYPE QETEPPLGSC SDVMLSVEEE GKEDPLPTAA 480	
SGK	483

SEQ ID NO: 697	moltype = AA length = 55
FEATURE	Location/Qualifiers
source	1..55
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 697	
MVRLLAALGL LFLGALRAFP QGCSRHHSSA RGLLTAGSSV SLTTTWMRPT AVQPA 55	

SEQ ID NO: 698	moltype = AA length = 176
FEATURE	Location/Qualifiers
source	1..176
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 698	
MRIFAVFIFM TYWHLNNAPY NKINQRLILV DPVTSEHELT CQAEGYPKAE VIWTSSDHQV 60	
LSGKTTTNTS KREEKLFNVT STLRINTTTN EIFYCTFRRL DPEENHTAEL VIPELPLAHP 120	
PNERTHLVL GAILLCLGVA LTFIFRLRKG RMMDVKKCGI QDTNSKKQSD THLEET 176	

SEQ ID NO: 699	moltype = AA length = 290
FEATURE	Location/Qualifiers
source	1..290
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 699	
MRIFAVFIFM TYWHLNNAFT VTVPKDLYVV EYGSNMTIEC KPPVEKQLDL AALIVYWEME 60	
DKNIIIQFVHG EEDLKQVHSS YRQRARLLKD QLSLGNAALQ ITDVKLQDAG VYRCMISYGG 120	
ADYKRITKVK NAPYNKINQR ILVVDPTSE HELTCQAEGY PKAEVIWSS DHQVLSGKTT 180	
TTSNSKREKEL FNVTSTLRIN TTTNEIFYCT FRRLDPEENH TAEELVIEPLP LAHPPNERTH 240	
LVLGAILLC LGVALTFIFR LRKGRRMMDVK KCGIQDTNSK KQSDTHLEET 290	

SEQ ID NO: 700	moltype = AA length = 551
FEATURE	Location/Qualifiers
source	1..551
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 700	
MAAPALSWRL PLLILLPLA TSWASAANVG TSQFTCFYNS RANISCVWSQ DGALQDTSCQ 60	
VHAWPDRRRW NQTCELLPVS QASWACNLIL GAPDSQKLTT VDIVTLRVL REGVRWRVMA 120	
IQDFKPFENL RLMAPISLQV VHVEHRCNI SWEISQASHY FERHLEFEAR TLSPGHTWEE 180	
APPLTLKQKQ EWICLETLTP DTQYEFQVRV KPLQGEFTTW SPWSQPLAFR TKPAALGKDT 240	
IPWLQHLLVG LSGAFIGIIL VYLLINCRNT GPWLKKVLKC NTPDPSKFQS QLSSEHGGDV 300	
QKWLSSPGGLAP EISPLEVLER DKVTQLLLQQ DVKPEPASLS SNHSLTSCFT 360	
NQGYFFFHLP DALEIBACQV YFTYDPYSEE DPDEGVAGAP TGSSPQPLQP LSGEDDAYCT 420	
FPSRDDLLF SPSLLGGPSP PSTAPGGSGA GEERMPPSLQ ERVPRDWDPQ PLGPPTPGVP 480	
DIVDFQPPPE LVLREAGEEV PDAGPREGVS FPWSRPPCGQ EFRALNARLP LNTDAYLSQ 540	
EIQGQDPHTL V	551

SEQ ID NO: 701	moltype = AA length = 146
FEATURE	Location/Qualifiers
source	1..146
	mol_type = protein
	organism = Homo sapiens

SEQUENCE: 701	
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MAAPALSWRL PLLLLLLPLA TSWASAAVNG TSQFTCFYNS RANISCVWSQ DGALQDTSCQ	60
VHAWPDRRRW NQTCELLPVS QASWACNLIL GAPDSQKLTT DIVTTLRVLC REGVRWRVMA	120
IQDFKPFENL RLMAPISLQV VHVELTH	146
SEQ ID NO: 702	moltype = AA length = 88
FEATURE	Location/Qualifiers
source	1..88
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 702	
MAAPALSWRL PLLLLLLPLA TSWASAAVNG TSQFTCFYNS RANISCVWSQ DGALQDTSCQ	60
VHAWPDRRRW NQTCELLPVS QASWACNL	88
SEQ ID NO: 703	moltype = AA length = 188
FEATURE	Location/Qualifiers
source	1..188
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 703	
MAAPALSWRL PLLLLLLPLA TSWASAAVNG TSQFTCFYNS RANISCVWSQ DGALQDTSCQ	60
VHAWPDRRRW NQTCELLPVS QASWACNLIL GAPDSQKLTT DIVTTLRVLC REGVRWRVMA	120
IQDFKPFENL RLMAPISLQV VHVELTHRCNI SWEISQASHY FERHLEFEAR TLSPGHTWE	180
APLLTLKQ	188
SEQ ID NO: 704	moltype = AA length = 255
FEATURE	Location/Qualifiers
source	1..255
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 704	
MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSCPFP NSFSSAGGQR	60
TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCQKQQ ELTKKGCKDC	120
CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE	180
PGHSPQIISF FLALTSTALL FLLFFLTLRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG	240
CSCRFPPEEE GGCEL	255
SEQ ID NO: 705	moltype = AA length = 87
FEATURE	Location/Qualifiers
source	1..87
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 705	
ERDVVCGPSP ADLSPGASSV TPPAPAREPG HSPQIISFFL ALTSTALLFL LFFLTLRFSV	60
VKRGRKKLLY IFKQHGSSGD TFTILES	87
SEQ ID NO: 706	moltype = AA length = 255
FEATURE	Location/Qualifiers
source	1..255
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 706	
MGNSCYNIVA TLLLVLNFER TRSLQDPCSN CPAGTFCDNN RNQICSCPFP NSFSSAGGQR	60
TCDICRQCKG VFRTRKECSS TSNAECDCTP GFHCLGAGCS MCEQDCQKQQ ELTKKGCKDC	120
CFGTFNDQKR GICRPWTNCS LDGKSVLVNG TKERDVVCGP SPADLSPGAS SVTPPAPARE	180
PGHSPQIISF FLALTSTALL FLLFFLTLRF SVVKRGRKKL LYIFKQPFMR PVQTTQEEDG	240
CSCRFPPEEE GGCEL	255
SEQ ID NO: 707	moltype = AA length = 92
FEATURE	Location/Qualifiers
source	1..92
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 707	
MHCQLTMETE AIDGYITCDN ELSPEREHSN MAIDLTSSTP NGQHASPSHM TSSKSSFYDF	60
FLCVCVSPAT DFNLGLWGP LTLWYSYCYR FC	92
SEQ ID NO: 708	moltype = DNA length = 660
FEATURE	Location/Qualifiers
source	1..660
	mol_type = genomic DNA
	organism = Homo sapiens
SEQUENCE: 708	
atgcctcggg gacgaaagag tcggccggc cgtaatgcga gagccgcaga agagaaccgc	60
aacaatcgca aaatccaggc ctcagaggcc tccgagacc ctagggccgc ctctgtggta	120
gcgagcaccc ccgaagacga cctgagccgc cccgaggaaag acccgagcac tccagaggag	180
gcctctacca cccctgaaga agcctcgacg actgccccaa cacaaaaagcc ttcaagtggcc	240

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cgaggcaatt ttcagggcac caagaaaagt ctccctgatgt ctatattagc gctcatcttc 300
atcatggca acagcggcaa ggaagaaatg gtcgtggaaa tgctggggaa gtttagaatg 360
cagcctggac gtcagcacag catcttggaa gatccgaaga agatcgtcac agaagagttt 420
gtgcgcagag ggtacctgat ttataaaccg gtgcggcgtt gcaactccgtt ggagtatgag 480
ttcttcgtggg ggccccggac acacgtggaa tcgagcaaac tgaaagtcat gcatttgc 540
gcaagggttc gtaaccgatg ctctaaagac tggcccttgta attatgactg ggattcggac 600
gatgtgcac aggttgaggc tatttcataat tcaggtgcta ggggttatttc cgcccttaa 660

SEQ ID NO: 709      moltype = AA length = 219
FEATURE           Location/Qualifiers
source            1..219
mol_type = protein
organism = Homo sapiens
SEQUENCE: 709
MPRGRKRSRRR RNARAAEENR NNRKIQASEA SETPMMAASVV ASTPEDDLGG PEEDPSTPEE 60
ASTTPEEASS TAQAOKPSVP RSNFQGTKKS LLMSILALIF IMGNSAKEAL VWKVLGKLM 120
QPGRQHSIFG DPKKIVTEEF VRRGYLIYKP VPRSSPVEYE FFWGPRAHVE SSKLKVMHFV 180
ARVRNRCSDKD WPCNYWDSD DDAEVEAILN SGARGYSAP 219

SEQ ID NO: 710      moltype = DNA length = 64
FEATURE           Location/Qualifiers
misc_feature      1..64
note = Adapter sequence
source            1..64
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 710
agatcggaaag agcacacgtc tgaactccag tcacnnnnnnn atctcgatg ccgtttctg 60
cttg                                         64

SEQ ID NO: 711      moltype = DNA length = 58
FEATURE           Location/Qualifiers
misc_feature      1..58
note = Adapter sequence
source            1..58
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 711
agatcggaaag agcgtcggtt agggaaagag tgttagatctc ggtggcgcc gtatcatt 58

SEQ ID NO: 712      moltype = AA length = 116
FEATURE           Location/Qualifiers
source            1..116
mol_type = protein
organism = Homo sapiens
SEQUENCE: 712
MLRLQMTDGH ISCTAVEFSY MSKISLNTPP GTKVKLSGIV DIKNGFLLLN DSNTTVLGGE 60
VEHLIEKWEL QRSLSKHNRS NIGTEGGPPP FVPGQFGRR NSQDKRKCEV LWCDPC 116

SEQ ID NO: 713      moltype = AA length = 651
FEATURE           Location/Qualifiers
source            1..651
mol_type = protein
organism = Homo sapiens
SEQUENCE: 713
MLRLQMTDGH ISCTAVEFSY MSKISLNTPP GTKVKLSGIV DIKNGFLLLN DSNTTVLGGE 60
VEHLIEKWEL QRSLSKHNRS NIGTEGGPPP FVPGQFGRS HVQVDSRELD RRKTLQVTMP 120
VKPTNDNDEF EKQRTAAIAE VAKSKETKTF GGGGGGARSN LNMNAAGNRN REVLPKEKST 180
KSEKGKHGVY RELVDEKALE HITEMGFSKE ASRQALMDNG NNLEAALNVL LTSNKQKPVM 240
GPLLRGRGKQ RGRIRSEDEE DLGNARPSAP STLFDFLESQ MGTLNVEEPQ SQPQLHQGQ 300
YRSSNTTQONG VKDNNNHLRHP PRNDRTRQPRN EKPPRFQRDS QNSKSVLEGQ GLPDRNGSER 360
PSTSSVSEWV AEDRIKCDRP YSRYDRTKDT SYPLGSQHSN GAFKKRDNSM QSRSGKGPSF 420
AEAKENPLPQ GSVDYNNQKR GKRESQTSIP DYFYDRKSQT INNEAFSGIK IEKHPNVNTD 480
YQNPVRSNSF IGVPGNEVEM PLKGRRIGPI KPAGPVTAAP CDDKIFYNSG PKRRSGPIKP 540
EKILESSIMP EYAKMWKPGD ECFALYWEDN KFYRAEVEAL HSSGMTAVVK FIDYGNYEEV 600
LLSNIKPIQT EAWEEGTYD QTLEFRRGGD GQPRRSTRPT QQFYQPXRAR N 651

SEQ ID NO: 714      moltype = AA length = 651
FEATURE           Location/Qualifiers
source            1..651
mol_type = protein
organism = Homo sapiens
SEQUENCE: 714
MLRLQMTDGH ISCTAVEFSY MSKISLNTPP GTKVKLSGIV DIKNGFLLLN DSNTTVLGGE 60
VEHLIEKWEL QRSLSKHNRS NIGTEGGPPP FVPGQFGRS HVQVDSRELD RRKTLQVTMP 120
VKPTNDNDEF EKQRTAAIAE VAKSKETKTF GGGGGGARSN LNMNAAGNRN REVLPKEKST 180

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KSEGKHEGVY	RELVDEKALK	HITEMGFSKE	ASRQALMDNG	NNLEAALNVL	LTSNKQKPVM	240
GPPLRGRGKG	RGRIRSEDEED	DLGNARPSAP	STLFDFLESK	MGTLSNVEEPK	SQPQLHQQQ	300
YRSSNTEQNG	VKDNNHLRHP	PRNDTRQPRN	EKPPRFQRDS	QNSKSVLEGS	GLPRNRGSER	360
PSTSSVSEWV	AEDRIKCDRP	YSRYDRTKDT	SYPLGSQHSQ	GAFKKRDNSM	QSRSGKGPSF	420
AEAKENPLPQ	GSDVYDNNQKR	GKRESQTSIP	DYFYDRKSQT	INNEAFSGIK	IEKHFNVNTD	480
YQNPVRSNSF	IGVPNGELEM	PLKGRRIGPI	KPAGPVTA	CDDKIFYNSG	PKRRSGPIKP	540
EKILESSIPM	EYAKMWKPGD	ECFALYWEDN	KFYRAEVEAL	HSSGMTAVVK	FIDYGNYEEV	600
LLSNIKPIQT	EAWEEGTYD	QTLEFRGGD	GQPRRSTRPT	QQFYQPPRAR	N	651

SEQ ID NO: 715	moltype = AA	length = 129				
FEATURE	Location/Qualifiers					
source	1..129					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 715						
MLRLQMTDGH	ISCTAVEFSY	MSKISLNTPP	GTKVKLSGIV	DIKNGFLNN	DSNTTVLGGE	60
VEHLIEKWEL	QRSLSKHNRS	NIGTEGGPPP	FVPGQKCVS	HVQVDSRELD	RRKTLQVTMP	120
VKPTNDNDE						129

SEQ ID NO: 716	moltype = AA	length = 744				
FEATURE	Location/Qualifiers					
source	1..744					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 716						
MAQVAGAALS	QAGWYLSDEG	I EACTSSPDK	VNVNDIILIA	LNTDLRTIGK	KFLPSDINS	60
KVEKLEGPCV	LQIQKIRNVA	APKDNEESQA	A P R M L R I Q M T	D G H I S C T A V E	F S Y M S K I S L N	120
TPPPGTVKL	SIVVDIKNGFL	L L N D S N T T V L	G G E V E H L I E K	W E L Q R S L S K H	N R S N I G T E G G	180
PPPFVPFGQK	CVSHVQVDSR	E L D R R K T L Q V	T M P V K P T N D N	D E F E K Q R T A A	I A E V A K S K E T	240
KTFGGGGGGA	RSNLNNMNAAG	N R N R E V L Q K E	K S T K S E G K H E	G V Y R E L V D E K	A L K H I T E M G F	300
SKEASRQALM	DNGNNLNEAAL	N V L L R T S N K Q K	P V M G P P L R G R	G K G R G R I R S E	D E E D L G N A R P	360
SAPSTLDFD	ESKMGTLNVE	E P K S Q P Q Q L H	Q G Q Y R S S N T E	Q N G V K D N N H L	R H P P R N D T R Q	420
PRNEKPPRFQ	RDSQNSKSVL	E G S G L P R N R G	S E R P S T S S V S	E V W A E D R I K C	D R P Y S R Y D R T	480
KDTSYPLGSQ	HSDGAFKKRD	N S M Q S R S G K G	P S F A E A K N P	L P Q G S V D Y N N	Q K R G K R E S Q T	540
SIPDYFYDRK	SQTINNEAFS	G I K I E K H P N V	N T D Y Q N P V R S	N S F I G V P N G E	V E M P L K G R R I	600
GPIKPAGPVT	AVPCDDKIFY	N S G P K R R S G P	I K P E K I L E S S	I P M E Y A K M W K	P G D E C F A L Y W	660
EDNKFYRAEV	EALHSSGMA	V V K F I D Y G N Y	E E V L L S N I K P	I Q T E A W E E E G	T Y D Q T L E F R R	720
GGDGQPRRST	RPTQQFYQPP	R A R N				744

SEQ ID NO: 717	moltype = AA	length = 651
FEATURE	Location/Qualifiers	
source	1..651	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 717		

MLRLQMTDGH	ISCTAVEFSY	MSKISLNTPP	GTKVKLSGIV	DIKNGFLNN	DSNTTVLGGE	60
VEHLIEKWEL	QRSLSKHNRS	NIGTEGGPPP	FVPGQKCVS	HVQVDSRELD	RRKTLQVTMP	120
VKPTNDNDE	E K Q R T A A I A E	A K S K E T K T P G	G G G G G A R S N L	N M M A A G N R N R	E V L Q K E K S T K	180
KSEGKHEGVY	RELVDEKALK	HITEMGFSKE	ASRQALMDNG	NNLEAALNVL	LTSNKQKPVM	240
GPPLRGRGKG	RGRIRSEDEE	DLGNARPSAP	STLFDFLESK	MGTLSNVEEPK	SQPQLHQQQ	300
YRSSNTEQNG	VKDNNHLRHP	PRNDTRQPRN	EKPPRFQRDS	QNSKSVLEGS	GLPRNRGSER	360
PSTSSVSEWV	AEDRIKCDRP	YSRYDRTKDT	SYPLGSQHSQ	GAFKKRDNSM	QSRSGKGPSF	420
AEAKENPLPQ	GSDVYDNNQKR	GKRESQTSIP	DYFYDRKSQT	INNEAFSGIK	IEKHFNVNTD	480
YQNPVRSNSF	IGVPNGELEM	PLKGRRIGPI	KPAGPVTA	CDDKIFYNSG	PKRRSGPIKP	540
EKILESSIPM	EYAKMWKPGD	ECFALYWEDN	KFYRAEVEAL	HSSGMTAVVK	FIDYGNYEEV	600
LLSNIKPIQT	EAWEEGTYD	QTLEFRGGD	GQPRRSTRPT	QQFYQPPRAR	N	651

SEQ ID NO: 718	moltype = AA	length = 650
FEATURE	Location/Qualifiers	
source	1..650	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 718		

MLRLQMTDGH	ISCTAVEFSY	MSKISLNTPP	GTKVKLSGIV	DIKNGFLNN	DSNTTVLGGE	60
VEHLIEKWEL	QRSLSKHNRS	NIGTEGGPPP	FVPGQKCVS	HVQVDSRELD	RRKTLQVTMP	120
VKPTNDNDE	E K Q R T A A I E V	A K S K E T K T P G	G G G G G A R S N L	N M M A A G N R N R	E V L Q K E K S T K	180
SEGKHEGVY	RELVDEKALK	HITEMGFSKE	S R Q A L M D N G	N L E A A L N V L L	T S N K Q K P V M G	240
PPLRGRGKG	RGRIRSEDEE	LGNARPSAPS	T L D F F L E S K M	G T L N V E E P K S	Q P Q Q L H Q G Q Y	300
RSSNTEQNGV	KDNNHLRHP	R N D T R Q P R N E	K P P R F Q R D S Q	N S K S V L E G G S G	L P R N R G S E R P	360
STSSVSEWVA	EDRIKCDRPY	S R Y D R T K D T S	Y P L G S Q H S D G	A F K K R D N S M Q	S R S G K G P S F A	420
EAKENPLPQG	SVDYDNNQKRG	K R E S Q T S I P D	Y F Y D R K S Q T I	N N E A F S G I K I	E K H F N V N T D Y	480
QNPVRSNSFI	GVPNGELEM	L K G R R I G P I K	P A G P V T A V P C	D D K I F Y N S G P	K R R S G P I K P E	540
KILESSIPME	YAKMWKPGDE	C F A L Y W E D N K	F Y R A E V E A L H	H S S G M T A V V K F	I D Y G N Y E E V L	600
LSNIKPIQTE	AWEEEGTYDQ	T L E F R R G G D	Q P R R S T R P T Q	Q F Y Q P P R A R N		650

SEQ ID NO: 719	moltype = AA	length = 832
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FEATURE	Location/Qualifiers	
source	1..832	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 719		
MEAGGGAGPG CCGAGAGAGA GPGALPPQPA ALPPAPPQGS PCAAAAGGSG ACGPATAVAA	60	
AGTAEGPGGG GSARIAVKKA QLRSAPRAKK LEKLGVYSAC KAEESCKCNG WKNPNPSPPTP	120	
PRADLQQIIV SLTESCRSCS HALAHVSHL ENVSEEMNR LLGIVLDVET LFTCVHKEED	180	
ADTKQVYFYL FKLLRKSILO RGKPVVEGSL EKKPPFEKPS IEQGVNNFVQ YKFSHLPAKE	240	
RQITIVELAKM FLNMRINYWHI EAPSQRRLRS PNDISGYKE NYTRWLCYCVP VPQFCDSLPR	300	
YETTQVFGRT LLRSVFTVMP RQLLEQARQE KDKLPLEKRT LILTHFPKFL SMLEEVYVSQ	360	
NSPIWDQDFL SASSRTSQLG IQTVINPPPPV AGTISYNSTS SSLEQPNAGS SSPACKASSG	420	
LEANPGEKRK MTDHSVLEEA KKPRVMGDIP MELINEVMST ITDPAAMLGP ETNFLSAHSA	480	
RDEAERLEER RGVIEPHVVG NSLNQKPNKK ILMWLVLQVN VFSHQLPRMP KEYITRLVFD	540	
PKHKTTLALIK DGRVIGGICF RMFPNSQGFTIE IVPCAVTSNE QVKGYGTHLM NHLKEYHIKH	600	
DILNFLTLYAD EYAIGYFKKQ GFSKEIKIPK TKVGYIKEYD EGATLMGCEL NPRIPYTEFS	660	
VIKKQKEII KKLERKQAO IRKVYPGLSC FKDGVRQIPI ESIPGIRETG WKPSGKEKSK	720	
EPRDPDOLYS TLKSILQQVK SHQSAPWPMB PVKRTEAHPGY YEVIRPFMDL KTMSERLKNR	780	
YYVSKKLFMA DLQRVFTNCK EYNPPESEYY KCANILEKFF FSKIKEAGLI DK	832	
SEQ ID NO: 720	moltype = AA length = 472	
FEATURE	Location/Qualifiers	
source	1..472	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 720		
MIGTVKMEGH ETSDWNSYYA DTQEAYSSV PVSMMNSGLGS MNSMNNTYMTM NTMTTSGNMT	60	
PASFNMSYAN PGLGAGLSPG AVAGMPGGS GAMNSMTAAG VTAMGTALSP SGMGAMGAQQ	120	
AASMNGLGPV AAAMNPPCMSP MAYAPSNLGR SRAGGGDAK TFKRSYPHAK PPYSYISLIT	180	
MAIQQAPSXKMLT LTLSEIYQWI MDLFPYYRQN QQRWQNSIRH SLSFNDCFVK VARSPDKPGK	240	
GSYWTLHPDS GNMFENGSYKL RRQKRFKCEP QPGAGGGGGS GSGGSGAKGG PESRKDPSGA	300	
SNSPADSPLH RGVHGKTQGL EGAPAPGPA SPQTLHDHSGA TATGGASELK TPASSTAPP	360	
SSGPALASV PASHPAHGLA PHESQHLKG DPHYSFNHFP SINNLMSSSE QQHKLDFKAY	420	
EQALQYSPYRG STLPASLPLG SASVTTRSPI EPSALEPAYY QGVYSRPVLN TS	472	
SEQ ID NO: 721	moltype = AA length = 36	
FEATURE	Location/Qualifiers	
source	1..36	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 721		
MIGTVKMEGH ETSDWNSYYA DTQELAITLQ KFNYHY	36	
SEQ ID NO: 722	moltype = AA length = 531	
FEATURE	Location/Qualifiers	
source	1..531	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 722		
MVDVGKWPIF TLLSPQEIAS IRKACVFGTS ASEALYVTDN DEVVFVGLNY SNCLGTGDNQ	60	
STLVPKKLEG LCGKKIKSLS YGSGPHVLLS TEDGVVYAWG HNGYSQLGNG TTNQGIAPVQ	120	
VCTNLLIKQV VEVACGSHHS MALAADGEVF AWGYNNCQGV GSGSTANQPT PRKVTNCLHI	180	
KRVVGIACQQ TSSMAVLNDG EVYGWGYGNQ GQLGLGNNGN QLTPVRVAAL HSVCVNQIVC	240	
GYAHTLALTD EGLLYAWGAN TYQQLGTGNK NNLLSPAHIK VEKERVVEIA ACHSAHTSAA	300	
KTGQGHVYMW QCRCGOSVIL PHLTHFSCTD DVFAFCFATPA VSWRLLSVEH EDFLTVAESEL	360	
KKEFDSPETA DLKFRIDGKY IHVHKAVLKI RCEHFRSMFQ SYWNEDMKEV IEIDQFSYPV	420	
YRAFLQYLYT DTVDLPPEDA IGLLDDLATSY CENRLKKLCQ HIIKRGITVE NAFSLFSAAV	480	
RYDAEDLEEF CFKFCINHLT EVTQTAAFWQ MDGPLLKEFI AKASKCGAFK N	531	
SEQ ID NO: 723	moltype = AA length = 531	
FEATURE	Location/Qualifiers	
source	1..531	
	mol_type = protein	
	organism = Homo sapiens	
SEQUENCE: 723		
MVDVGKWPIF TLLSPQEIAS IRKACVFGTS ASEALYVTDN DEVVFVGLNY SNCLGTGDNQ	60	
STLVPKKLEG LCGKKIKSLS YGSGPHVLLS TEDGVVYAWG HNGYSQLGNG TTNQGIAPVQ	120	
VCTNLLIKQV VEVACGSHHS MALAADGEVF AWGYNNCQGV GSGSTANQPT PRKVTNCLHI	180	
KRVVGIACQQ TSSMAVLNDG EVYGWGYGNQ GQLGLGNNGN QLTPVRVAAL HSVCVNQIVC	240	
GYAHTLALTD EGLLYAWGAN TYQQLGTGNK NNLLSPAHIK VEKERVVEIA ACHSAHTSAA	300	
KTGQGHVYMW QCRCGOSVIL PHLTHFSCTD DVFAFCFATPA VSWRLLSVEH EDFLTVAESEL	360	
KKEFDSPETA DLKFRIDGKY IHVHKAVLKI RCEHFRSMFQ SYWNEDMKEV IEIDQFSYPV	420	
YRAFLQYLYT DTVDLPPEDA IGLLDDLATSY CENRLKKLCQ HIIKRGITVE NAFSLFSAAV	480	
RYDAEDLEEF CFKFCINHLT EVTQTAAFWQ MDGPLLKEFI AKASKCGAFK N	531	
SEQ ID NO: 724	moltype = AA length = 420	

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FEATURE	Location/Qualifiers
source	1..420
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 724	
MSGRPRRTSF AESCKPVQQP	SAFGSMKVSR DKDGSKVTTV VATPGQGPDR PQEVSYTDTK 60
VIGNGSFGVV YQAKLCDSGE	LVAIKKVLQD KRFKNRELQI MRKLDHCNIV RLRYFFYSSG 120
EKKDEVYLNL VLDYVPETVV	RVARHYSRAK QTLPIVIYVKL YMYQLFRSLA YIHSGICCHR 180
DIKPQNLLD PDTAVLKLCD	FGSAKQLVRG EPNVSYICSR YYRAPELIFG ATDYTFSSIDV 240
WSAGCVAELA LLGQPFFPGD	SGVDQLVEII KVLGTPTRREQ IREMNPNTYE FKFPQIKAHP 300
WTKVFRPRTP PEAIALCSRL	LEYPTPALARL PLEACAHNSF DELRDPNVKL PNGRDTPALF 360
NFTTQELESSN PPLATILIPP	HARIQAAAST PTNATAASDA NTGDRGQTNN AASASASNST 420
SEQ ID NO: 725 moltype = AA length = 433	
FEATURE	Location/Qualifiers
source	1..433
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 725	
MSGRPRRTSF AESCKPVQQP	SAFGSMKVSR DKDGSKVTTV VATPGQGPDR PQEVSYTDTK 60
VIGNGSFGVV YQAKLCDSGE	LVAIKKVLQD KRFKNRELQI MRKLDHCNIV RLRYFFYSSG 120
EKKDEVYLNL VLDYVPETVV	RVARHYSRAK QTLPIVIYVKL YMYQLFRSLA YIHSGICCHR 180
DIKPQNLLD PDTAVLKLCD	FGSAKQLVRG EPNVSYICSR YYRAPELIFG ATDYTFSSIDV 240
WSAGCVAELA LLGQPFFPGD	SGVDQLVEII KVLGTPTRREQ IREMNPNTYE FKFPQIKAHP 300
WTKDSSGTGH FTSGVRVFRP	RTPPEAIALC SRLEYTEPTA RLTPLEACAH SFFDELRDPN 360
VKLPGNRDTP ALFNFTTQEL	SSNPPLATIL IPPHARIQAA ASTPTNATAA SDANTGDRGQ 420
TNNAAASASAS NST	433
SEQ ID NO: 726 moltype = AA length = 326	
FEATURE	Location/Qualifiers
source	1..326
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 726	
MEKDGLCRAD QQYECVAEIG	EGAYGKVFKA RDLKNNGGRFV ALKRVRRVQTG EEMPLSTIR 60
EVAVLRLHLET FEHPNVVRLF	DVCTVSRTDR ETKLTLVFEH VDQDLTTYLD KVPEPGVPT 120
TIKDMMFQLL RGLDFLHSRH	VVHRDLKPQN ILVTSSGQIK LADFGLARIY SFQMALTSSV 180
VTLWYRAPEV LLQSSYATPV	DLWSVGCIFA EMFRRKPLFR GSSDVQLGK ILDVIGLPGE 240
EDWPRDVALP RQAFHSKSAQ	PIEKFVTDID ELGKDLLLKC LTFNPAKRIS AYSALSHPYF 300
QDLERCKENL DSHLPPSQNT	SELNTA 326
SEQ ID NO: 727 moltype = AA length = 326	
FEATURE	Location/Qualifiers
source	1..326
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 727	
MEKDGLCRAD QQYECVAEIG	EGAYGKVFKA RDLKNNGGRFV ALKRVRRVQTG EEMPLSTIR 60
EVAVLRLHLET FEHPNVVRLF	DVCTVSRTDR ETKLTLVFEH VDQDLTTYLD KVPEPGVPT 120
TIKDMMFQLL RGLDFLHSRH	VVHRDLKPQN ILVTSSGQIK LADFGLARIY SFQMALTSSV 180
VTLWYRAPEV LLQSSYATPV	DLWSVGCIFA EMFRRKPLFR GSSDVQLGK ILDVIGLPGE 240
EDWPRDVALP RQAFHSKSAQ	PIEKFVTDID ELGKDLLLKC LTFNPAKRIS AYSALSHPYF 300
QDLERCKENL DSHLPPSQNT	SELNTA 326
SEQ ID NO: 728 moltype = AA length = 113	
FEATURE	Location/Qualifiers
source	1..113
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 728	
MRSLGQNPTE AELQDMINEV	DADGNGTIDF PEFLTMMARK MKDTDSEEEI REAFRVDKD 60
GNGYISAAEL RHVMTNLGEK	LTDEEVDEMI READIDGDQV NYEEFVQMM TAK 113
SEQ ID NO: 729 moltype = AA length = 149	
FEATURE	Location/Qualifiers
source	1..149
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 729	
MADQLTEEQI AEFKEAFSLF	DKDGDGTITT KELGTVMRSL GQNPTEAELO DMINEVDADG 60
NGTIDFPEFL TMMARKMDT	DSEEEIREAF RVFDKDGNGY ISAAELRHVM TNLGEKLTD 120
EVDEMIREAD IDGDGQVN	YE EFVQMMTAK 149
SEQ ID NO: 730 moltype = AA length = 83	
FEATURE	Location/Qualifiers
source	1..83

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mol_type = protein
organism = Homo sapiens
SEQUENCE: 730
MADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMSRL GQNPTAEELQ DMINEVDEMI 60
READIDGDGQ VNYEEFVQMM TAK 83

SEQ ID NO: 731      moltype = AA length = 113
FEATURE           Location/Qualifiers
source            1..113
mol_type = protein
organism = Homo sapiens
SEQUENCE: 731
MRSLGQNPTE AELQDMINEV DADGNNTIDF PEFLTMMARK MKDTDSEEEI REAFRVDKD 60
GNGYISAAEL RHVMTNLGEK LTDEEVDEMI READIDGDGQ VNYEEFVQMM TAK 113

SEQ ID NO: 732      moltype = AA length = 113
FEATURE           Location/Qualifiers
source            1..113
mol_type = protein
organism = Homo sapiens
SEQUENCE: 732
MRSLGQNPTE AELQDMINEV DADGNNTIDF PEFLTMMARK MKDTDSEEEI REAFRVDKD 60
GNGYISAAEL RHVMTNLGEK LTDEEVDEMI READIDGDGQ VNYEEFVQMM TAK 113

SEQ ID NO: 733      moltype = AA length = 113
FEATURE           Location/Qualifiers
source            1..113
mol_type = protein
organism = Homo sapiens
SEQUENCE: 733
MRSLGQNPTE AELQDMINEV DADGNNTIDF PEFLTMMARK MKDTDSEEEI REAFRVDKD 60
GNGYISAAEL RHVMTNLGEK LTDEEVDEMI READIDGDGQ VNYEEFVQMM TAK 113

SEQ ID NO: 734      moltype = AA length = 149
FEATURE           Location/Qualifiers
source            1..149
mol_type = protein
organism = Homo sapiens
SEQUENCE: 734
MADQLTEEQI AEFKEAFSLF DKDGDGTITT KELGTVMSRL GQNPTAEELQ DMINEVDAAG 60
NGTIDPFPEFL TMMARKMKDT DSEEEIREAF RVFDKGNGY ISAAELRHVM TNLGEKLTD 120
EVDEMIREAD IDGDGQVNYE EFVQMMTAK 149

SEQ ID NO: 735      moltype = AA length = 474
FEATURE           Location/Qualifiers
source            1..474
mol_type = protein
organism = Homo sapiens
SEQUENCE: 735
MVQQTNNNAEN TEALLAGESS DSGAGLELGI ASSPTPGSTA STGGKADDPS WCKTPSGHIK 60
RPMNAFMWRS QIERRKIMEQ SPDMHNAEIS KRLGKRWKLL KDSDKIPFIR EAERURLKHM 120
ADYPDYKYRP RKKVKSGNAN SSSSSAASSK PGEKGDKVGG SGGGHHGGGG GGGSSNAGGG 180
GGGASGGGGAN SKPAQKSCG SKVAGGAGGG VSXPHAKLIL AGGGGGGKAA AAAAASFAAE 240
QAGAAALLPL GAAADHHSLY KARTPSASAS ASSAASASAA LAAPGKHLAE KKVKRVYLF 300
GLGTSSSPVG CGVGAGADPSD PLGLYEEEAGA GCSPDAPSLS GRSSAASSPA AGRSPADHRG 360
YASLRRAASPA PSSAPSHASS SASSHSSSSS SSGSSSSDDE FEDDLDDLNP SSNFESMSLG 420
SSSSSSALDR DLDNFNEPGS GSHFEFPDYC TPEVSEMISG DWLESSISNL VFYI 474

SEQ ID NO: 736      moltype = AA length = 680
FEATURE           Location/Qualifiers
source            1..680
mol_type = protein
organism = Homo sapiens
SEQUENCE: 736
MKMKKFQIPV SFQDLTVNFT QEEWQQLDPA QRLLYRDVML ENYSNLVSVG YHVSKPVDIF 60
KLEQGEEPWI VEEFSQNQYP DIDDALEKKNK EIQDKHLQT VFFSNKTLIT ERENVFGKTL 120
NLGMNSVPSR KMPYKCNPGG NSLTKNSEVI VAKKSKENRK IPDGYSGFK HEKSHLGMKK 180
YRYNPMRKAS NQNONENLILHQ NIQILKQPFD YNKCGKTFKK RAILITQKGR QTERKPNECN 240
ECRKTFSKRS TLIVHQRIHT GEKPYVCSDC RKTFRVKTSL TRHRRRIHTGE RPYECSECRK 300
TFIDKSALIV HQKIHGGEKS YECNECGKTF FRKSALAEHF RSHTGEKPYE CKECGNAFSK 360
KSYLVVHQRT HRGEKPNCEK ECGKTFFCQSL ALTAHQRIHT GEKPYECSEC EKTFCCQSL 420
NVHRRSHTGE KPYECSQCGK FLCTKSALIA HQITHRGKKS YECNECGKFF CHKSTLTIHQ 480
RTHTGEKHGV FNKCGRISIV KSNCSQCKRM NTKENLYECS EHGHAVSKNS HLIVHQRTIW 540
ERPYPECNECG RTYCRKSALT HHQRHTGQR PYECNECGKT FCQKFSFVEH QRTHTGEKPY 600
ECNECGKSF C HKSARFRVHRR IHTGEKPYEC NQCGKTYRRL WTLTEHQKIH TGEKPYECNK 660
CEKTFRHKS N PLLHQKSHKE 680

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SEQ ID NO: 737      moltype = AA length = 642
FEATURE          Location/Qualifiers
source           1..642
                 mol_type = protein
                 organism = Homo sapiens
SEQUENCE: 737
MLENYSNLVS VGYHVSYPD 1FKLEQEEP WIVEEFSNQN YPDIDDALEK NKEIQDKHLT 60
QTVFFSNKTL ITERENVFGK TLNLGMNSVP SRKMPYKCNP GGNSLKTNSE VIVAKKSKEN 120
RKIPDGYSGF GKHEKSHLGK KKYRYNPMRK ASNQNEENLIL HQNIQILKQP FDYDYNKGKTF 180
FKRAILITQK GRQTERKPN CNECRKTSK RSTLIVHQRI HTGEKPVCS DCRKTFRVKT 240
SLTRHRRHT GERPYPECSEC RKTFTDKSAL IVEHQKIHGGE KSYECNECGF TFFRKSLAEL 300
HFRSHTGEKP YECKECGNAF SKKSYLVHQ RTHRGEKPNE CKECGKTFCC QSALTAHQRI 360
HTGEKPYEC ECEKTFFCQ ALVNQHRRSHT GEKPYECFCQ GKFLCTKSAL IAHQITHRGK 420
KSYECNECGK FFCHKSTLT HQRTHTGEKH GVFNKCGRIS IVKSNCSQCK RMNTKENLYE 480
CSEHGHAVSK NSHLIVHQRT IWERPYECNE CGRTYCRKSA LTHHQRTHTG QRPyECNECG 540
KTFQCQKFSVH EHQRHTGEK PYECNECGKS FCHKSAFRVH RRIHTGEKPY ECNQCGKTYR 600
RLWTLTEHQK IHTGEKPYEC NKCEKTFRHK SNFLLHQKS KE 642

SEQ ID NO: 738      moltype = AA length = 703
FEATURE          Location/Qualifiers
source           1..703
                 mol_type = protein
                 organism = Homo sapiens
SEQUENCE: 738
MCVFLHLLSY IKDTSFIPGP DCELHPRGMA ATGPCSEAPV QGCDAGELQQ LGLCGVSDVQ 60
RSWSKFCNFP LTGYHVSYPD VIFKLEQGEE PWIVEEFSNQ NYPDIDDALE KNKEIQDKH 120
TQTVFFSNKTL LITERENVFGK TLNLGMNSVP PSRKMPYKCN PGGNSLKTNS EVIVAKKSKE 180
NRKIPDGYSGF PGKHEKSHLG MKKYYRNPMR KASNQNEENLIL LHQNIQILKQ PFDDYNKGKTF 240
FFKRAILLTQ KGRQTERKPN ECNCRKTSK RSTLIVHQRI HTGEKPVVC SDCRKTFRVK 300
TSLTRHRRHT GERPYPECSEC CRKTFIDKSAL LIVHQKIHGGE EKSYECNECGF KTFFRKSLAEL 360
EHPRSHTGEK PYECKECGNA FSKSYLVHQ RTHRGEKPNE EKECGKTFCC CQSALTAHQRI 420
IHTGEKPYEC SECEKTFFCQ SALNVHRRSH TGEKPYECQ CGKFLCTKSAL LIAHQITHRG 480
KSYECNECGK KFCHKSTLT IHQRTHTGEK HGVFNKCGRIS SIVKSNCSQCK RMNTKENLYE 540
ECSEHGHAVSK NSHLIVHQRT IWERPYECN ECGRTYCRKSA ALTHHQRTHTG QRPyECNECG 600
GKTFQCQKFSVH VEHQRHTGEK PYECNECGK SFCHKSAFRVH RRIHTGEKPY YECNQCGKTY 660
RLWTLTEHQK IHTGEKPYEC CNKCEKTFRHK KSNFLLHQKS KE 703

SEQ ID NO: 739      moltype = AA length = 679
FEATURE          Location/Qualifiers
source           1..679
                 mol_type = protein
                 organism = Homo sapiens
SEQUENCE: 739
MENEKEIPVS PQDLTVNFQTQ EEWQQLDPAQ RLLYRDVMLE NYSNLVSVGY HVSKPDVIFK 60
LEQGEEPWIV EEFSENQNPDPD IDDALEKNKE IQDKHLTQTV FFSNKTLLITE RENVFGKTLN 120
LGMSNVPSRK MPYKCNPGGN SLKTNSEIV AKKSKENRKI PDGYSGFGKH EKSHLGMKKY 180
RYNPMRKSNSLQENLILHQNIQILKQFIDKSALIV QKIHGGEKSY ECNECGKTFCC AILITQKGRQ TERKPNECNE 240
CRKTFSKRST LIVHQRIHTG EKPVVCSDCR KTFRVKTSLT RHRRHTGER PYECSECRKT 300
FIDKSALIV QKIHGGEKSY ECNECGKTFCC RKSALAEHFR SHTGEKPYEC KECGNAFSKK 360
SYLUVHORTH RGEKPNECKE CGKTFCCQSA LTAHQRIHTG EKPYECSECE KTFCCQSAALN 420
VHRRSHTGEK PYECQSCQGF LTKTSALIAH QITHRGKKSY ECNECGKFC HKSTLTIHQRI 480
THTGEKHGVF MKCGRISIV SNCQCKRMN TKEENLYCSE EGHAVSKNSH LIVHORTIWE 540
RPYECNECGR TYCRKSALTH HQRTHTGQRP YECNECGKTF CCQKFSFVEHQ RTHTGEKPYE 600
CNECGKSFCH KSAFRVHRRSI HTGEKPYECN QCGKTYRRLW TLTEHQKIHT GEKPYECNKC 660
EKTFRHKSNF LLHQKSHKE 679

SEQ ID NO: 740      moltype = AA length = 173
FEATURE          Location/Qualifiers
source           1..173
                 mol_type = protein
                 organism = Homo sapiens
SEQUENCE: 740
MLENYSNLVS VGYHVSYPD 1FKLEQEEP WIVEEFSNQN YPDIDDALEK NKEIQDKHLT 60
QTVFFSNKTL ITERENVFGK TLNLGMNSVP SRKMPYKCNP GGNSLKTNSE VIVAKKSKEN 120
RKIPDGYSGF GKHEKSHLGK KKYRYNPMRK ASNQNEENLIL HQNIQILKQP FDY 173

SEQ ID NO: 741      moltype = AA length = 679
FEATURE          Location/Qualifiers
source           1..679
                 mol_type = protein
                 organism = Homo sapiens
SEQUENCE: 741
MENEKEIPVS PQDLTVNFQTQ EEWQQLDPAQ RLLYRDVMLE NYSNLVSVGY HVSKPDVIFK 60
LEQGEEPWIV EEFSENQNPDPD IDDALEKNKE IQDKHLTQTV FFSNKTLLITE RENVFGKTLN 120
LGMSNVPSRK MPYKCNPGGN SLKTNSEIV AKKSKENRKI PDGYSGFGKH EKSHLGMKKY 180

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RYNPMRKASN	QNENLILHQN	IQILKQPFDY	NKGKTFKKR	AILITQKGRQ	TERKPNECNE	240
CRKTFSKRT	LIVHORIHTG	EKPVVCSDCR	KTRFRVKTSLT	RHRRHTGER	PYECSECRKT	300
FIDKSALIVH	QKIHGGEKSY	ECNECGKTF	RKSALAEHFR	SHTGEKPYEC	KECGNAFSKK	360
SYLUVHVQRT	RGEKPNECKE	CGKTFCCQSA	LTAHQRIHTG	EKPYECSECE	KTFFCQSALN	420
VHRRSHTGEK	PYECSQCGKF	LCTKSALIAH	QITHRGKKSY	ECNECGKFC	HKSTLTIHQR	480
THTGEKHGVF	NKCGRISIVK	SNCSCQCKRMN	TKENLYECSE	HGHAVSKNSH	LIVHQRTIWE	540
RPYECNECGR	TYCRKSALT	HQRHTGQRP	YECNECGKTF	CQKFSFVEHQ	RTHTGEKPYE	600
CNECGKSFCH	KSAFRVHRRI	HTGEKPYECN	QCQKTYRRLW	TLTEHQKIHT	GEKPYECNKC	660
EKTFRHKSNF	LLHQKSHKE					679

SEQ ID NO: 742	moltype = AA	length = 1455				
FEATURE	Location/Qualifiers					
source	1..1455					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 742						
MGGACSSFTT	SSSPTIYSTS	VTDSKAMQVE	SCSSAVGVSN	RGVSEKQLTS	NTVQQHPSTP	60
KRHTVLYISP	PPEDLLDNSE	MSCDQEGCGL	ESEQSCSMW	EDSPSNFSNM	STSSYNDNTE	120
VPRKSRKRNP	KQRPVGKRRD	CEESNMDIFD	ADSAKAPHYV	LSQLTTDNKG	NSKAGNGTLE	180
NQKGTVKKS	PLMCGQYPVK	SEGKELKIVV	QPETQHARRY	LTEGSRGSVK	DRTQOGFPTV	240
KLEGHNEPVP	LQVFVGNDSG	RVKPHGFYQA	CRVTGRNTP	CKEV DIEGTT	VIEVGLDPSEN	300
NMTLAVDCVG	ILKLERNADVE	ARIGIAGSKK	KSTRARLVFR	VNIMRKDGST	LTLQTQPSPI	360
LCTQPAGPVE	ILKKSLHSCS	VKGEEEVFL	GKNFLKGTKV	IFQENVSDEM	SWKSEAEIDM	420
ELPHQNHLIV	KVPPYHDQHI	TLPVSVGIYV	VTNAGRSHDV	QPFTYTPDPA	AAGALNVNVK	480
KEISSPARPC	SFEEAMKAMK	TTGCNLDKV	IIPNALMTP	IPSSMIKSE	VTPMVEVTAEK	540
RSSTIFKTKT	SVGSTQOTLE	NISNIAGNS	FSSPSSSHLP	SENEKQQQIQ	PKAYNPETLT	600
TJQTQDISQP	GTTPAVSASS	QLPNSDALLQ	QATQFQTRRET	QSREIQLQSDG	TVVNLSQLTE	660
ASQQQQQSQPL	QEQAQTLLQQQ	ISSNIFPPSN	SVSQLQNTIQ	QLQAGSFRTGS	TASGSSGSD	720
LVQQVLEAQO	QLSSVLFsap	DGNENVQEQL	SADIFQQVQS	IQSGVSPGMF	SSTEPTVHTR	780
PDNLLPGRAE	SVHPQSENTL	SNQQQQQQQQ	QOVMESSAAM	VMEMQQSICQ	AAAQIQSELF	840
PSTASANGNL	QOSPVYQOTS	HMMMSALSTNE	DMQMOCELFS	SPPAVSGNET	STTTTQQVAT	900
PGTTMFQTS	SGDGEETGTQ	AKQI0NSVFC	TMVQMQHSGD	NQPQVNLFSS	TKSMSVQNS	960
GTQQQGNGLF	QQGNEEMMSLQ	SGNFLQQSSH	SQAOQFLHPQN	PIADAQNLQ	ETQGSLFHSP	1020
NPIVHSQTST	TSSEMQOPPM	FHSQSTIAVL	QGSVPQDQQ	STNIFLSQSP	MNNLQTNTVA	1080
QEAFFAPNS	ISPLQSTSNS	EQQAAFPQQA	PISHIQTPTML	SQEQAQPPQQ	GLFQPOVALG	1140
SLPNPNMPQS	QQGTMFQSQH	SIVAMQSNSP	SQEQQQQQQQ	QQQQQQQQQQ	SILFSNQNTM	1200
ATMASPKQPP	PNMIFNPNNQ	PMANQEQQNQ	SIFHQQSNMA	PMNQEQQPMQ	FQSQSTVSSL	1260
QNPGBTQSES	SQTPLPHSSP	QIQLVQGSPS	SQEQQVTLFL	SPASMSALQT	SINQODMQQS	1320
PLYSQPNNMP	GIQGATSSPQ	PQATLFHNTA	GGTMNQLQNS	PGSSQQTSGM	FLFGIQNNCS	1380
QLLTSGPATL	PDQLMAISQP	GQPQNEQGPQ	VTTLLSQQMP	ENSPLASSIN	TNQNIEKIDL	1440
LVSLQNQGNN	LTGSF					1455

SEQ ID NO: 743	moltype = AA	length = 70				
FEATURE	Location/Qualifiers					
source	1..70					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 743						
XIIPTLPSDK	LSKIQLTLKLA	ARYIDFLYQV	LQSDELDSDKM	ASCSYVAHER	LSYAFSVWRM	60
EGAWSMSASH						70

SEQ ID NO: 744	moltype = AA	length = 135				
FEATURE	Location/Qualifiers					
source	1..135					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 744						
XPAQGKRGKK	SAGCGGGGGA	GGGGGSSSGG	GSPQSYEELQ	TQRVMANVRE	RQRTQSLNEA	60
FAALRKIIP	LPSDKLISKI	QKRGKKSAG	CGGGGGAGGG	GGSSSGGGSP	QSYEELQTQR	120
SVWRMEGAW	MSASH					135

SEQ ID NO: 745	moltype = AA	length = 202				
FEATURE	Location/Qualifiers					
source	1..202					
	mol_type = protein					
	organism = Homo sapiens					
SEQUENCE: 745						
MMDDVSSSPV	SPADDLSNS	EEEPDRQQPP	SGKRGGRKRR	SSRRSAGGG	GPGGAAGGGV	60
GGGDEPGSPA	QKRGKKSAG	CGGGGGAGGG	GGSSSGGGSP	QSYEELQTQR	VMANVRERQR	120
TQSLNNEAA	LRKIIPTLPS	DKLSKIQLTK	LAARYIDFLY	QVLQSDLDS	KMASCSYVAH	180
ERLSYAFSVW	MEGAWSMSA	SH				202

SEQ ID NO: 746	moltype = AA	length = 636
FEATURE	Location/Qualifiers	
source	1..636	
	mol_type = protein	

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		organism = Homo sapiens	
SEQUENCE: 746			
MAQSTATSPD GGTTFEHLWS	SLEPDSTYFD LPQSSRGNNNE VVGGTDSSMD VFHLEGMTTS		60
VMAQFNLLSS TMDQMSSRAA	SASPYTPEHA ASVPTHSPYA QPSSTFDTMS PAPVIPSNTD		120
YPGPHHFEVT FQQSSTAKSA	TWTYSPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV		180
YKKAEEHTDV VKRCPNHELG	RDFNEGQSAP ASHLIRVEGN NLSQYVDDPV TGRQSVVVPY		240
EPPQVGTEFT TILYNFMCMNS	SCVGGMNRNP ILIIITLEMR DGQVLGRRSF EGRICACPGR		300
DRKADEDHYR EQQALNESSA	KNGAASKRAF KQSPPAVPAL GAGVKKRRHG DEDTYYLQVR		360
GRENFEILMK LKESLELMEL	VPQLVDSYR QQQLLQRQP HLOQPPSYGPV LSPMNVHGG		420
MNKLPSVNL VGQPPPHSSA	ATPNLGPVGP GMLNNHHGHAV PANGEMSSSH SAQSMVSGSH		480
CTPPPPYHAD PSLVSLTGL	GCPNCIEYFT SQQLSYIYL QNLTIEDLGA LKIPQYRMT		540
WRGLQDLKQ GHDYSTAQQL	LRSSNAATIS IGGSELQRQ RVMEAUVFRV RHTITPNRG		600
GGGGGPDEWA DFGFDLDPCK	ARKQPIKEEF TEAEIH		636
SEQ ID NO: 747	moltype = AA length = 403		
FEATURE	Location/Qualifiers		
source	1..403		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 747			
MAQSTATSPD GGTTFEHLWS	SLEPDSTYFD LPQSSRGNNNE VVGGTDSSMD VFHLEGMTTS		60
VMAQFNLLSS TMDQMSSRAA	SASPYTPEHA ASVPTHSPYA QPSSTFDTMS PAPVIPSNTD		120
YPGPHHFEVT FQQSSTAKSA	TWTYSPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV		180
YKKAEEHTDV VKRCPNHELG	RDFNEGQSAP ASHLIRVEGN NLSQYVDDPV TGRQSVVVPY		240
EPPQVGTEFT TILYNFMCMNS	SCVGGMNRNP ILIIITLEMR DGQVLGRRSF EGRICACPGR		300
DRKADEDHYR EQQALNESSA	KNGAASKRAF KQSPPAVPAL GAGVKKRRHG DEDTYYLQVR		360
GRENFEILMK LKESLELMEL	VPQLVDSYR QQQLLQRQP HLOQPPSYGPV LSPMNVHGG		420
MNKLPSVNL VGQPPPHSSA	ATPNLGPVGP GMLNNHHGHAV PANGEMSSSH SAQSMVSGSH		480
CTPPPPYHAD PSLVRTWGP			403
SEQ ID NO: 748	moltype = AA length = 499		
FEATURE	Location/Qualifiers		
source	1..499		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 748			
MAQSTATSPD GGTTFEHLWS	SLEPDSTYFD LPQSSRGNNNE VVGGTDSSMD VFHLEGMTTS		60
VMAQFNLLSS TMDQMSSRAA	SASPYTPEHA ASVPTHSPYA QPSSTFDTMS PAPVIPSNTD		120
YPGPHHFEVT FQQSSTAKSA	TWTYSPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV		180
YKKAEEHTDV VKRCPNHELG	RDFNEGQSAP ASHLIRVEGN NLSQYVDDPV TGRQSVVVPY		240
EPPQVGTEFT TILYNFMCMNS	SCVGGMNRNP ILIIITLEMR DGQVLGRRSF EGRICACPGR		300
DRKADEDHYR EQQALNESSA	KNGAASKRAF KQSPPAVPAL GAGVKKRRHG DEDTYYLQVR		360
GRENFEILMK LKESLELMEL	VPQLVDSYR QQQLLQRQP HLOQPPSYGPV LSPMNVHGG		420
MNKLPSVNL VGQPPPHSSA	ATPNLGPVGP GMLNNHHGHAV PANGEMSSSH SAQSMVSGSH		480
CTPPPPYHAD PSLVRTWGP			499
SEQ ID NO: 749	moltype = AA length = 555		
FEATURE	Location/Qualifiers		
source	1..555		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 749			
MAQSTATSPD GGTTFEHLWS	SLEPDSTYFD LPQSSRGNNNE VVGGTDSSMD VFHLEGMTTS		60
VMAQFNLLSS TMDQMSSRAA	SASPYTPEHA ASVPTHSPYA QPSSTFDTMS PAPVIPSNTD		120
YPGPHHFEVT FQQSSTAKSA	TWTYSPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV		180
YKKAEEHTDV VKRCPNHELG	RDFNEGQSAP ASHLIRVEGN NLSQYVDDPV TGRQSVVVPY		240
EPPQVGTEFT TILYNFMCMNS	SCVGGMNRNP ILIIITLEMR DGQVLGRRSF EGRICACPGR		300
DRKADEDHYR EQQALNESSA	KNGAASKRAF KQSPPAVPAL GAGVKKRRHG DEDTYYLQVR		360
GRENFEILMK LKESLELMEL	VPQLVDSYR QQQLLQRQP RDAQQWPWRS ASQRDEQQP		420
QRPVHGLGP LHSATPLPQR	PQPRQDLGAL KIPEQYRMTI WRGLQDLKQG HDYSTAQQLL		480
RSSNAATISI GGSGELQRQ	VMEAUVFRV HTITIPNRGG PGGGPDEWAD FGFDLDPCKA		540
RKQPIKEEFT EAEIH			555
SEQ ID NO: 750	moltype = AA length = 540		
FEATURE	Location/Qualifiers		
source	1..540		
	mol_type = protein		
	organism = Homo sapiens		
SEQUENCE: 750			
MAQSTATSPD GGTTFEHLWS	SLEPDSTYFD LPQSSRGNNNE VVGGTDSSMD VFHLEGMTTS		60
VMAQFNLLSS TMDQMSSRAA	SASPYTPEHA ASVPTHSPYA QPSSTFDTMS PAPVIPSNTD		120
YPGPHHFEVT FQQSSTAKSA	TWTYSPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV		180
YKKAEEHTDV VKRCPNHELG	RDFNEGQSAP ASHLIRVEGN NLSQYVDDPV TGRQSVVVPY		240
EPPQVGTEFT TILYNFMCMNS	SCVGGMNRNP ILIIITLEMR DGQVLGRRSF EGRICACPGR		300
DRKADEDHYR EQQALNESSA	KNGAASKRAF KQSPPAVPAL GAGVKKRRHG DEDTYYLQVR		360
GRENFEILMK LKESLELMEL	VPQLVDSYR QQQLLQRQP LTGLCGPNCI EYFTSQGLQS		420
IYHLQNLTI DLGALKIPEQ YRMTIWRGLQ DLKGHDST AQQLLRSNA ATISIGGSQE			480
RQORQMEAV HFRVRHTITI	PNRGPGGGPDE WDAWDFGFDL PDCKARKQPT KEETFEAEIH		540

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SEQ ID NO: 751      moltype = AA length = 450
FEATURE          Location/Qualifiers
source           1..450
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 751
MLYVGDPARH LATAQFNLLS STMDQMSSRA ASASPYTPEH AASVPTHSPY AQPSTFDTM 60
SPAPVIPSN T DYPGPHFEV TFQQSSTAKS ATWTYSPLLK KLYCQIAKTC PIQIKVSTPP 120
PPGTAIRAMP VYKKAEHVTD VVKRCPNHEL GRDFNEGQSA PASHLIRVEG NNLSQYVDDP 180
VTGRQSVVVP YEPPOVGTEF TTILYNFMCN SSCVGGMNRR PILIIITLEM RDGQVLGRRS 240
FEGRICACPG RDRKADEDHY REQQLNESS AKNGAASKRA FKQSPPAVPA LGAGVKRRH 300
GDEDTYYLQV RGRENFEILM KLKESLELME LVPQPLVDSY RQQQQLLQRP SHLQPPSYGP 360
VLSPMNKVGH GMNKLPSVNVQ LVGQPPPHSS AATPNLGPVG PGMLNNHGHA VPANGEMSS 420
HSAQSMVSGS HCTPPPYHA DPSLVRWTGP 450

SEQ ID NO: 752      moltype = AA length = 426
FEATURE          Location/Qualifiers
source           1..426
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 752
MLYVGDPARH LATAQFNLLS STMDQMSSRA ASASPYTPEH AASVPTHSPY AQPSTFDTM 60
SPAPVIPSN T DYPGPHFEV TFQQSSTAKS ATWTYSPLLK KLYCQIAKTC PIQIKVSTPP 120
PPGTAIRAMP VYKKAEHVTD VVKRCPNHEL GRDFNEGQSA PASHLIRVEG NNLSQYVDDP 180
VTGRQSVVVP YEPPOVGTEF TTILYNFMCN SSCVGGMNRR PILIIITLEM RDGQVLGRRS 240
FEGRICACPG RDRKADEDHY REQQLNESS AKNGAASKRA FKQSPPAVPA LGAGVKRRH 300
GDEDTYYLQV RGRENFEILM KLKESLELME LVPQPLVDSY RQQQQLLQRP PRDAQQPWPR 360
SASQRDRDEQQ PQRPVHGLGV PLHSATPLPR RPQPRQFFNR IGVSKLHRVF HLPRVTEHLP 420
PAEPDH 426

SEQ ID NO: 753      moltype = AA length = 587
FEATURE          Location/Qualifiers
source           1..587
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 753
MLYVGDPARH LATAQFNLLS STMDQMSSRA ASASPYTPEH AASVPTHSPY AQPSTFDTM 60
SPAPVIPSN T DYPGPHFEV TFQQSSTAKS ATWTYSPLLK KLYCQIAKTC PIQIKVSTPP 120
PPGTAIRAMP VYKKAEHVTD VVKRCPNHEL GRDFNEGQSA PASHLIRVEG NNLSQYVDDP 180
VTGRQSVVVP YEPPOVGTEF TTILYNFMCN SSCVGGMNRR PILIIITLEM RDGQVLGRRS 240
FEGRICACPG RDRKADEDHY REQQLNESS AKNGAASKRA FKQSPPAVPA LGAGVKRRH 300
GDEDTYYLQV RGRENFEILM KLKESLELME LVPQPLVDSY RQQQQLLQRP SHLQPPSYGP 360
VLSPMNKVGH GMNKLPSVNVQ LVGQPPPHSS AATPNLGPVG PGMLNNHGHA VPANGEMSS 420
HSAQSMVSGS HCTPPPYHA DPSLVSFLTG LGCPNCIEFY TSQGLQSIYH LQNLTIEDLG 480
ALKIPEQYRM TIWRGLQDLK QGDYSTAQQ LLRSSNAATI SIGGSGELQR QRVMEAVHFR 540
VRHTITIPN R GPGGGPDEW ADFGFDPDCKA KARKQPIKEE FTEAEIH 587

SEQ ID NO: 754      moltype = AA length = 565
FEATURE          Location/Qualifiers
source           1..565
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 754
MDQMSSRAAS ASPTYTPEAA SVPTHSPYAQ PSSTFDTMSP APVIPSNTDY PGPHHFETVF 60
QQSSTAKSAT WTYSPLKKL YCQIAKTCPI QIKVSTPPPP GTAIRAMPVY KKAEHVTDV 120
KRCPNHELGR DFNEGOSAPA SHLIRVEGNN LSQYVDDPVT GRQSVVVPYE PPQVGTEFTT 180
IILYNFMCNSS CVGGMNRRPI LIIIITLEMRD GQVLGRRSF E GRICACPGRD RKADEDHYRE 240
QQALNESSAK NGAASKRAFI QSPPAVPALG AGVKKRHRGD EDTYYLQVRG RENFEILMKL 300
KESLELMELV PQPLVDSYRQ QQQLLQRPSH LQPPSYGPV SPMLNVHGGM NKLPSVNQLV 360
GQPPPHSSAA TPNLGPVGPG MLNNHGHA VPANGEMSSHS AQSVMVSGSHC TPPPPYHADP 420
SLVSFLTGLG CPNCIEYFTS QGLQSIYHLQ NLTIEDLGLA KIPEQYRMTI WRGLQDLKQG 480
HDYSTAQOLL RSSNAAATISI GGSGELQRQR VMEAVHFRVR HTITIPNRGG PGGGPDEWAD 540
FGFDLDPCKA RKQPIKEEFT EAEIH 565

SEQ ID NO: 755      moltype = AA length = 555
FEATURE          Location/Qualifiers
source           1..555
                  mol_type = protein
                  organism = Homo sapiens
SEQUENCE: 755
MAQSTATSPD GGTTFEHLWS SLEPDSTYFD LPQSSRGNNN VVGGTDSSMD VFHLEGMTTS 60
VMAQFNLLSS TMDQMSSRAA SASPYTPEHA ASVPTHSPY AQPSTFDMS PAPVIPSNTD 120
YPGPHHFETV FQQSSTAKSA TWTYSPPLKK LYCQIAKTCP IQIKVSTPPP PGTAIRAMPV 180
YKKAEHVTDV VVKRCPNHELGR DFNEGQSAF ASHLIRVEGN NLSQYVDDP TGRQSVVVPY 240
EPPQVGTEFT T ILYNFMCNSS CVGGMNRRP ILLIITLEMRD DGQVLGRRSF EGRICACPGR 300

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DRKADEDHYR	EQQALNESSA	KNGAASKRAF	KQSPPAVPAL	GAGVKKRHG	DEDTYLQVR	360
GREENFEILMK	LKESLELMEL	VPQLPLVDSYR	QQQQLLQRPP	RDAQQPWRS	ASQRDDEQQP	420
QRPVHGLGP	LHSATPLPRR	PQPRQDLGAL	KIPEQYRMTI	WRGLQDLKQG	HDYSTAQQLL	480
RSSNAATISI	CGSGELQRQR	VMEA VHF RVR	HTTIPNRRGG	PGGGPDEWAD	FGFDLPDCKA	540
RKQPIKEEFT	EAEIH					555

SEQ ID NO: 756 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 756

MAQSTATSPD	GGTTFEHLWS	SLEPDSTYFD	LPQSSSRGNNE	VVGTDSSMD	VFHLEGMTTS	60
VMFAQFNLSS	TMDQMSRRAA	SASPYTPEHA	ASVPTHSPYA	QPSSTFDTMS	PAPVIPSTND	120
YPGPHHFLSS	TQQSSTAKSA	TWTYPLLLKK	LYCQIAKTC	IQIKVSTPPP	PGTAIRAMPV	180
YKKAEHTDVT	VKRCNPHELG	RDFNEGQSAP	ASHLIRVEGN	NLSQYVDDPV	TGRQSVVVPY	240
EPPQVGTEFT	TILYNFM CNS	SCVGGMNRPP	ILIIITLEMR	DGQVLGRRSF	EGRICACPGR	300
DRKADEDHYR	EQQALNESSA	KNGAASKRAF	KQSPPAVPAL	GAGVKKRHG	DEDTYLQVR	360
GREENFEILMK	LKESLELMEL	VPQLPLVDSYR	QQQQLLQRPF	LTGLGCPNCI	EYFTSQGLQS	420
IYHLQNLTIE	DLGALKIPEQ	YRMTIWRGLQ	DLKQGHDYST	AQQLRERSSNA	ATISIGGSGE	480
LQRQRVMEAV	HFRVRHTITI	PNRGPGGGP	DEWADFGFDL	PDCKARKQPI	KEEFTEAEIH	540

SEQ ID NO: 757 moltype = AA length = 602
 FEATURE Location/Qualifiers
 source 1..602
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 757

MAAEEEAAAG	GKVLREENQC	IAPVVSSRVS	PGRPTAMG	FSSHMTTEFP	KRKGSDDPS	60
QVEDGEHQVK	MKAFAREAHSQ	TEKRRDKMN	NLIEELSAMI	PQCNPMARKL	DKLTVLRMAV	120
QHRLSLKGLT	NSYVGNSYR	SFLQDNELRH	LILKTAEGFL	FVVGCERGKI	LFVSKSVSKI	180
LNDQASLTG	QSLFDPLHPK	DVAVKVEQLS	SFDISPREKL	IDAKTGLQVH	SNLHAGRTRV	240
YSGSRRSFFC	RIKSCKISVK	EEHGCLPNSK	KKEHRKFYTI	HCTGYLRSWP	PNIVGMEER	300
NSKKDNTSFT	CLVAIGRLQP	YIVPQNSGEI	NVKPTEFITE	FAVNGKEVYY	DQRATAILGY	360
LPQELLGTSC	YEYFHQDDHN	NLTQKAVL	QSKEKILTD	YKFRAKDGSF	VTLKSQWFSF	420
TNPWTKELEY	IVSVNTLVLG	HSEPEASFL	PCSSQSSSEES	SROQCMSVPG	MSTGTVLGAG	480
SIGTDIANEI	LDLQLRQSSS	YLDDSSPTGL	MKDTHTVNCR	SMSENKELFPP	SPSEMGLEEA	540
TRQNQSTVAV	HSHEPLLSDG	AQLDFDALCD	NDDTAMAAMF	NYLEAEGLG	DGDFDSIQW	600
TL						602

SEQ ID NO: 758 moltype = AA length = 599
 FEATURE Location/Qualifiers
 source 1..599
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 758

MAAEEEAAAG	GEVAGGEATA	PGKVLREENQ	CIAPVVSSRV	SPGTRPTAMG	SFSSHMTTEFP	60
RKRKGSDSDP	SQEAHSQTEK	RRRDKMNNLI	EELSAMIPOC	NPMARKLDKL	TVLRMAVQHL	120
RSLKGLTNSY	VGSNYRPSFL	QDNELRHLIL	KTAEGFLFV	GCERGKILFV	SKSVSKILNY	180
DQASLTGSQL	FDFLHPKDVA	KVKEQLSSFD	ISPREKLIDA	KTGLQVHSNL	HAGRTRVYSG	240
SRRSFFCRIK	SCKISVKEE	GCLPNSSKKKE	HRKFYTIHCT	GYLRSWPNTI	VGMEEERNNSK	300
KDNSNFTCLV	AIGRLQPYIV	PQNSGEINVK	PTEFITEFRAV	NGKFVYVDQR	ATAILGYLPQ	360
ELLGTCYEV	FHQDDHNNLT	DKHKAVLQSK	EKILTDYKF	RAKDGFSVTL	KSQWFSFTNP	420
WTKELEYIVS	VNTLVLGHSE	PGEASFLPCS	SQSSEESSRQ	SCMSVPGMST	GTVLGAGSIG	480
TDIANEILDL	QRLQSSSYLD	DSSPTGLMD	THTVNCRSMS	NKELFPSPS	EMGELEATRQ	540
NQSTVAVHSH	EPLLSDGAQL	DFDALCDNDD	TAMAAMFNYL	EAEGGLGDPG	DFSDIQWLT	599

SEQ ID NO: 759 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 organism = Homo sapiens

SEQUENCE: 759

MAAEEEAAAG	GEVAGGEATA	PGKVLREENQ	CIAPVVSSRV	SPGTRPTAMG	SFSSHMTTEFP	60
RKRKGSDSDP	SQEAHSQTEK	RRRDKMNNLI	EELSAMIPOC	NPMARKLDKL	TVLRMAVQHL	120
RSLKGLTNSY	VGSNYRPSFL	QDNELRHLIL	KTAEGFLFV	GCERGKILFV	SKSVSKILNY	180
DQASLTGSQL	FDFLHPKDVA	KVKEQLSSFD	ISPREKLIDA	KTGLQVHSNL	HAGRTRVYSG	240
SRRSFFCRIK	SCKISVKEE	GCLPNSSKKKE	HRKFYTIHCT	GYLRSWPNTI	VGMEEERNNSK	300
KDNSNFTCLV	AIGRLQPYIV	PQNSGEINVK	PTEFITEFRAV	NGKFVYVDQR	ATAILGYLPQ	360
ELLGTCYEV	FHQDDHNNLT	DKHKAVLQSK	EKILTDYKF	RAKDGFSVTL	KSQWFSFTNP	420
WTKELEYIVS	VNTLVLGHSE	PGEASFLPCS	SQSSEESSRQ	SCMSVPGMST	GTVLGAGSIG	480
TDIANEILDL	QRLQSSSYLD	DSSPTGLMD	THTVNCRSV	VHSWISMPYV	TMMTQPWLHL	540

SEQ ID NO: 760 moltype = AA length = 622
 FEATURE Location/Qualifiers
 source 1..622

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mol_type = protein
organism = Homo sapiens

SEQUENCE: 760
MAAEEEAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTTEFPR KRKGSDSDPS 60
QSGIMTEKVV EKLSQNPLTY LLSTRIEISA SSGSREAHQ TEKRRRDKMN NLIEELSAM 120
PQCNPMARKL DKLTVLRMAV QHLRSLKGLT NSYVGNSYRPS SFLQDNELRH LILKTAEGFL 180
FVVGCERGKI LFVSKSVSKI LNYDQASLTG QSLFDLHPK DVAKVKEQLS SFDISPREKL 240
IDAKTGLQVH SNLHAGRTRV YSGSRRSFFC RIKSCKLISVK EEHGCLPNSK KHEHRKFYTI 300
HCTGYLRSWP PNIVGMEEER NSKKDNSNFT CLVAIGRLQP YIVPQNSGEI NVKPTEFITR 360
FAVNNGKVFVY DQRATAILGV LPQQLNLGTSC YEYFHQDDHN NLTDKHKAVL QSKEKILTD 420
YKFRAKDGSF VTLKSQWPSF TNPKWTLVLC HSEPGEASF PCSSQSSEES 480
SRQSCMSVPG MSTGTVLGAG SIGTDIANEI LDLQRLQSS YLDDSSPTGL MKDTHTVNC 540
SMSNKELFPP SPSEMGELEA TRQNQSTVAV HSHEPLLSDG AQLDFDALCD NDDTAMAAMF 600
NLYEAEGGLG DPGDFSDIQW TL 622

SEQ ID NO: 761      moltype = AA length = 588
FEATURE          Location/Qualifiers
source           1..588
mol_type = protein
organism = Homo sapiens

SEQUENCE: 761
MAAEEEAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTTEFPR KRKGSDSDPS 60
QEAHQSOTEKR DRDKMNNLIE ELSAMIPQCN PMARKLDKLT VLRMAVQHLR SLKGLTNSYV 120
GSNYRPSPFLQ DNELRHLLIKE TAEGLFLVVG CERGKILFVS KSVSKILNYD QASLTGQSLF 180
DFLHPKDVAK VKEQLSSFDI SPREKLIDAK TGLQVHSNLHAGRTRVYSGS RRSFFCRIKS 240
CKISVKEEHG CLPNSKKKEH RKFYTIHCTG YLRSWPPNIV GMEEERNSSKK DNSNFTCLVA 300
IGRLQPYIVP QNSGEINVVP TEFITRAFVN GKFVYVDQRA TAILGYLPQE LLGTCYEF 360
HQDDHNNLTD KHKAVLQSKE KILTDSYKFR AKDGSFVTLK SQWFSTNPW TKELEYIVSV 420
NTLVLGHSEP GEASFLPCSS QSSEESSRQCS CMSVPGMSTG TVLGAGSIGT DIANEILDLQ 480
RLQSSSYLDD SSPTGLMKDT HTVNCRSMSN KELFPPSPSE MGELEATRQN QSTVAVHSHE 540
PLLSDGALQD FDALCDNDDT AMAAFMNYLE AEGGLGDPGD FSDIQWTL 588

SEQ ID NO: 762      moltype = AA length = 636
FEATURE          Location/Qualifiers
source           1..636
mol_type = protein
organism = Homo sapiens

SEQUENCE: 762
MAAEEEAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTTEFPR KRKGSDSDPS 60
QSGIMTEKVV EKLSQNPLTY LLSTRIEISA SSGSREVEDGE HQVKMKAFFE AHSQTEKRR 120
DKMNNLIEEL SAMIPOCNPM ARKLDKLT VMAVQHLRS KGLTNSYVGS NYRPSFLQDN 180
ELRHLILKTA EGFLFVVGCE RGKILFVSKS VSKILNYDQA SLTGQSLFDF LHPKDVAVK 240
EQLSSFDISP REKLIDAKTG LQVHSNLHAG RTRVYSGSRR SFFCRIKSCK ISVKEEHGCL 300
PNSKKKEHHRK PTYTIHCTG RSWPPNIV EERENSKKDN SNFTCLVAIG RLQPYIVPQN 360
SGBINVKPTE FITRFAVNFK FVYDQARATA ILGYLPQELL GTSCYEFHQ DDHNNLTDKH 420
KAVLQSKEKI LTDTSYKFRAK DGSFVTLKSQ WFSFTNPWTK ELEYIVSVNT LVLGHSEPGE 480
ASFLPCSSQS SEESSSRQCSM SVPGMSTGTV LGAGSIGTDD ANEILDLQRL QSSSYLDDSS 540
PTGLMKDTHT VNCRSMNKE LFPPSPSEMG ELEATRQNOS TVAVHSHEPL LSDGAQLDFD 600
ALCDNDTAM AAFMNYLEAE GGLGDPGDFS DIQWTL 636

SEQ ID NO: 763      moltype = AA length = 588
FEATURE          Location/Qualifiers
source           1..588
mol_type = protein
organism = Homo sapiens

SEQUENCE: 763
MAAEEEAAAG GKVLREENQC IAPVVSSRVS PGTRPTAMGS FSSHMTTEFPR KRKGSDSDPS 60
QEAHQSOTEKR DRDKMNNLIE ELSAMIPQCN PMARKLDKLT VLRMAVQHLR SLKGLTNSYV 120
GSNYRPSPFLQ DNELRHLLIKE TAEGLFLVVG CERGKILFVS KSVSKILNYD QASLTGQSLF 180
DFLHPKDVAK VKEQLSSFDI SPREKLIDAK TGLQVHSNLHAGRTRVYSGS RRSFFCRIKS 240
CKISVKEEHG CLPNSKKKEH RKFYTIHCTG YLRSWPPNIV GMEEERNSSKK DNSNFTCLVA 300
IGRLQPYIVP QNSGEINVVP TEFITRAFVN GKFVYVDQRA TAILGYLPQE LLGTCYEF 360
HQDDHNNLTD KHKAVLQSKE KILTDSYKFR AKDGSFVTLK SQWFSTNPW TKELEYIVSV 420
NTLVLGHSEP GEASFLPCSS QSSEESSRQCS CMSVPGMSTG TVLGAGSIGT DIANEILDLQ 480
RLQSSSYLDD SSPTGLMKDT HTVNCRSMSN KELFPPSPSE MGELEATRQN QSTVAVHSHE 540
PLLSDGALQD FDALCDNDDT AMAAFMNYLE AEGGLGDPGD FSDIQWTL 588

SEQ ID NO: 764      moltype = AA length = 551
FEATURE          Location/Qualifiers
source           1..551
mol_type = protein
organism = Homo sapiens

SEQUENCE: 764
MGSFSSHMTF PPRKRKGSDS DPSQEAHSQT EKRRRDKMNN LIEELSAMIP QCNPMARKLD 60
FVVGCERGKIL HLRSLKGLTN SYVGNSYRPS FLQDNELRH ILKTAEGFLF VVGCERGKIL 120
FVSKSVSKIL NYDQASLTGQ SLFDFLHPKD VAJVKEQLSS FDISPREKL DAKTGLQVHS 180

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NLHAGRTRVY	SGSRRSFFCR	IKSCKISVKE	EHGCLPNSKK	KEHRKFYTIIH	CTGYLRSWPP	240
IVIGMEEERN	SKKDONSFTC	LVAIGRQLQPY	IVPQNSGEIN	VKPTEFITRF	AVNGKFVYVD	300
QRATAILGYL	PQELLGTLSCY	EYFHQDDHHNN	LTDKHKAVLQ	SKEKILTDSDY	KFRAKDGSFV	360
TLKSQWFSFT	NPWTKELEYI	VSVNTLVLGH	SEPGEASFLP	CSSQSSEESS	RQSCMSVPGM	420
STGTVLGAGS	IGTIDIANEIL	DLQRLQSSSY	LDDSSPTGLM	KDTHTVNCRS	MSNKELFPPS	480
PSEMGELEAT	RQNQSTVAVH	SHEPLLSDGA	QLDFDALCDN	DDTAMAAFVN	YLEAEGLGD	540
PGDFSDIQWT	L					551

SEQ ID NO: 765	moltype = AA	length = 125
FEATURE	Location/Qualifiers	
source	1..125	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 765						
MPHSSDSSDS	SFSRSPPPGK	QDSSDDVRRV	QRREKNRIAA	QKSRQRQTQK	ADTLHLESED	60
LEKQNAALRK	EIKQLTEELK	YFTSVLNSHE	PLCSVLAEST	PSPPEVVYSA	HAFHQPHVSS	120
PRFQP						125

SEQ ID NO: 766	moltype = AA	length = 73
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 766						
MPHSSDSSDS	SFSRSPPPGK	QDSSDDVRRV	QRREKNRIAA	QKSRQRQTQK	SIKKDAQVPW	60
HRARRAGNGY	FSK					73

SEQ ID NO: 767	moltype = AA	length = 202
FEATURE	Location/Qualifiers	
source	1..202	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 767						
MATLIYVDKE	NGEPGTRVVA	KDGLKLGSGP	SIKALDGRSQ	VSTPRFGKTF	DAPPALPKAT	60
RKALGTVNRA	TEKSVTKGP	LKQKQPSFSA	KKMTEKTVKA	KSSVPASDDA	YPEIEKFFPF	120
NPLDFESFDL	PEEHQIAHLP	LSGVPLMILD	EERELEKLFQ	LGPPSPVKMP	SPPWESNLLQ	180
SPSSILSTLD	VELPPVCCDI	DI				202

SEQ ID NO: 768	moltype = AA	length = 121
FEATURE	Location/Qualifiers	
source	1..121	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 768						
MPLPKVGGF	GGERSSSLYTQ	YLSCTGILL	EYSYGKTFSS	AIKALDGRSQ	VSTPRFGKTF	60
DAPPALPKAT	RKALGTVNRA	TEKSVTKGP	LKQKQPSFSA	KKMTEKTVKA	KSSVPASDDA	120
Y						121

SEQ ID NO: 769	moltype = AA	length = 202
FEATURE	Location/Qualifiers	
source	1..202	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 769						
MATLIYVDKE	NGEPGTRVVA	KDGLKLGSGP	SIKALDGRSQ	VSTPRFGKTF	DAPPALPKAT	60
RKALGTVNRA	TEKSVTKGP	LKQKQPSFSA	KKMTEKTVKA	KSSVPASDDA	YPEIEKFFPF	120
NPLDFESFDL	PEEHQIAHLP	LSGVPLMILD	EERELEKLFQ	LGPPSPVKMP	SPPWESNLLQ	180
SPSSILSTLD	VELPPVCCDI	DI				202

SEQ ID NO: 770	moltype = AA	length = 202
FEATURE	Location/Qualifiers	
source	1..202	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 770						
MATLIYVDKE	NGEPGTRVVA	KDGLKLGSGP	SIKALDGRSQ	VSTPRFGKTF	DAPPALPKAT	60
RKALGTVNRA	TEKSVTKGP	LKQKQPSFSA	KKMTEKTVKA	KSSVPASDDA	YPEIEKFFPF	120
NPLDFESFDL	PEEHQIAHLP	LSGVPLMILD	EERELEKLFQ	LGPPSPVKMP	SPPWESNLLQ	180
SPSSILSTLD	VELPPVCCDI	DI				202

SEQ ID NO: 771	moltype = AA	length = 2406
FEATURE	Location/Qualifiers	
source	1..2406	
	mol_type = protein	
	organism = Homo sapiens	

SEQUENCE: 771		
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MDPEQSVKGT	KKAEQSPRKR	LTKGEAIQTS	VSSSPVPYPPGS	GTAATQESPA	QELLAPQPFP	60
GPSSVLREGS	QEKTGQQQKP	PKRPPIEAVS	HISQLPQHPL	TPAFMSPGKP	EHLLEGSTWQ	120
LVDPMPRGPS	GSFVAPGLHP	QSQLLPSHAS	IIPPEDLPGV	PKVFVPRPSQ	VSLKPTEEAH	180
KKERKPQKPG	KYICQYCSR	CAKPSVLQKH	IRSHTGERPY	PCGPGCFSK	TKSNLYKHRK	240
SHAHRIAKGL	ASGMGGEMYP	HGLEMERIPIG	EEFEEEPTEGE	STDSEEETSA	TSGHPAELSP	300
RPKQPLLSSG	LYSSSGSHSS	HERCSSLQSS	TAQSLEDPPP	FVEPSEHPL	SHKPEDTHTI	360
KQKLALRLSE	RKKVIDEQAF	LSPGSKGST	SGYFSRSESA	EQQVSPPNNTN	AKSYAEIIFG	420
KCGRIGQRTA	MLTATSTQPL	LPLSTEDKPS	LVLSPVPRTO	VIEHITKLIT	INEAVVDTSE	480
IDSVVKPRSS	LSRRSSMESP	KSSLYREPLS	SHSEKTKPQE	SLLSLQHPPS	TAPPVPLRS	540
HSMPSAACTI	STPHHPFRGS	YSFDDDHITDS	EALSHSSHVF	TSHPRMLKRQ	PAIELPLGGE	600
YSSSEEPGPSS	KDTASKPSDE	VEPKESELTK	KTKGGLTKKG	VIYECNICGA	RYKKRDNYEA	660
HKKYCYSELQ	IAKPISAGTH	TSPEAEKSQI	EHEPWSQMMH	YKLGTTLELT	PLRKRRKEKS	720
LGDEEEPPAF	ESTKSQFGSP	GPSDAARNLP	LESTKSPAEP	SKSVPSLEGP	TGFQPRTPKP	780
GSGSESGKER	RTTSKEISV	QHTSSFEKSD	SLEQPSGLEG	EDKPLAQFPS	PPPAPHGRSA	840
HSLQPKLVRQ	PNIQVPEILV	TEEPDRDPTE	PEPPPKPEPEK	TEEFQWPQRS	QTLAQLPAEK	900
LPPKKKRLRL	AEMAQSSGES	SFESSVPLSR	SPSQESNVSL	SGSSRSASF	RDDHGKAEP	960
SPSSDMRPKP	LGHMLTVPS	HHPHAREMRR	SASEQSPNVS	HSAHMTETRS	KSFDFGSLSL	1020
TGPSAPAPVA	PPARVAPPER	RKCFLVQRQAS	LSRPPESLE	VAPKGRQESE	EPQPSSSKPS	1080
AKSSLQSISS	AATSHGGPPG	GKPGQDRPP	LGPTVPTYE	LQVFHHPVAQ	TPLHEKPYLP	1140
PPVSLFSFQH	LVQHEPGQSP	EFFSTQAMSS	LLSPSPYSMPP	LPPSLFQAPP	LPLQPTVLHP	1200
GQLHLPQLMP	HPANIPFRQP	PSFLPMPYPT	SSALSSGF	PLQSQFALQL	PGDVESHLPQ	1260
IKTSLAPLAT	GSAGLSPSTE	YSSDIRLPPV	APPASSSAPT	SAPPALPAC	PDTMVLVVP	1320
VRVQTNMPSY	GSAMYTTLSQ	ILVTQSQGSS	ATVALPKFEE	PPSKGTTVCG	ADVHEVGPGP	1380
SGLSEEQSRA	FPTPYLRVPV	TLPERKGTS	SSESILSLEG	SSSTAGGSKR	VLSPAGSLEL	1440
TMETQQQKRV	KEEEASKADE	KLELVKPCSV	VLTSTEDGKR	PEKSHLGQNQ	QGRRELEMLS	1500
SLSSDPSDTK	EIPPLPHPAL	SHGTAPGSEA	LKEYPQPSGK	PHRRGLTPLS	VKKEDSKEQP	1560
DPLSLAPPSS	LPLSETSSRP	AKSQEGLTDK	KVLQFPLSLH	TTNVSWCYLN	YIKPNHIQHA	1620
DRRSSVYAGW	CISLYNPNLP	GVSTKAALSL	LRSKQKVSK	TYTMATAPH	EAGRLOVPS	1680
RKPRMTVEHL	PSLVPEGQK	DLARVEKEEE	RRGEPEEAD	ASQRGEPAR	KIFEGGYKSN	1740
EEVYVVRGRG	RGKYVCEECG	IRCKKPSMLK	KHIRTHTDVR	PYVCKHCHFA	FKTKGNLTKH	1800
MKSKAHSKCC	QETGVLEEL	QETGSDDDL	QDSEGRGSE	AEEHQFSDL	EDSDSDSDDL	1860
EDEDEDEEES	QDELSPRSSE	APPGCPH	RADSPILGP	QPDPAPASGT	EATRGSSVSE	1920
AERLTASSCS	MSSQSMGPLP	WLGPAPLGSV	EKDTGSALS	KPVSPRWPWS	PSKEAGSRPP	1980
LARKHSLTKN	DSSPQRCSPA	REPQASAPSP	PGLHVDPGRG	MGALPCGSPR	LQLSPLTLCP	2040
LGRELAPRAH	VLSKLEGTTD	PGLPRYSPTR	RWSPGQAESP	PRSPAPPKWA	LAGPGSPSAG	2100
EHGPGLGLDP	RVLFPPLAPL	HKLRSRSPET	CASPWQKAES	RSPSPCGPA	HPLSSRPFSA	2160
LHDFGHHLA	RTEENIFSHL	PLHSQHLLTRA	PCPLIPIGGI	QMVQARPGAH	PTLPPGPTAA	2220
WVSGFSGGGS	DLTGAREAQE	RGRWSPTESS	SASVSPVAKV	SKFTLSELE	GGDYPKERER	2280
TGGGPGRRPD	WTPHGTGAPA	EPTPTHSPCT	PPDTLPRPPQ	GRRAAQSWSP	RLESRAPTN	2340
PEPSATPLD	RSSSVGCLAE	ASARFFPARTR	NLSGEPRTRQ	DSPKGSGSE	PRAHPHQPED	2400
RVPPNA						2406

SEQ ID NO:	772	moltype = AA	length = 2405			
FEATURE		Location/Qualifiers				
source		1..2405				
		mol_type = protein				
		organism = Homo sapiens				
SEQUENCE:	772					
MDPEQSVKGT	KKAEQSPRKR	LTKGEAIQTS	VSSSPVPYPPGS	GTAATQESPA	QELLAPQPFP	60
GPSSVLREGS	QEKTGQQQKP	PKRPPIEAVS	HISQLPQHPL	TPAFMSPGKP	EHLLEGSTWQ	120
LVDPMPRGPS	GSFVAPGLHP	QSQLLPSHAS	IIPPEDLPGV	PKVFVPRPSQ	VSLKPTEEAH	180
KKERKPQKPG	KYICQYCSR	CAKPSVLQKH	IRSHTGERPY	PCGPGCF	TKSNLYKHRK	240
SHAHRIAKGL	ASGMGGEMYP	HGLEMERIPIG	EEFEEEPTEGE	STDSEEETSA	TSGHPAELSP	300
RPKQPLLSSG	LYSSSGSHSS	HERCSSLQSS	TAQSLEDPPP	FVEPSEHPL	SHKPEDTHTI	360
KQKLALRLSE	RKKVIDEQAF	LSPGSKGST	SGYFSRSESA	EQQVSPPNNTN	AKSYAEIIFG	420
KCGRIGQRTA	MLTATSTQPL	LPLSTEDKPS	LVLSPVPRTO	VIEHITKLIT	INEAVVDTSE	480
IDSVVKPRSS	LSRRSSMESP	KSSLYREPLS	SHSEKTKPQE	SLLSLQHPPS	TAPPVPLRS	540
HSMPSAACTI	STPHHPFRGS	YSFDDDHITDS	EALSHSSHVF	TSHPRMLKRQ	PAIELPLGGE	600
YSSSEEPGPSS	KDTASKPSDE	VEPKESELTK	KTKGGLTKKG	VIYECNICGA	RYKKRDNYEA	660
HKKYCYSELQ	IAKPISAGTH	TSPEAEKSQI	EHEPWSQMMH	YKLGTTLELT	PLRKRRKEKS	720
LGDEEEPPAF	ESTKSQFGSP	GPSDAARNLP	LESTKSPAEP	SKSVPSLEGP	TGFQPRTPKP	780
GSGSESGKER	RTTSKEISV	QHTSSFEKSD	SLEQPSGLEG	EDKPLAQFPS	PPPAPHGRSA	840
HSLQPKLVRQ	PNIQVPEILV	TEEPDRDPTE	PEPPPKPEPEK	TEEFQWPQRS	QTLAQLPAEK	900
LPPKKKRLRL	AEMAQSSGES	SFESSVPLSR	SPSQESNVSL	SGSSRSASF	RDDHGKAEP	960
SPSSDMRPKP	LGHMLTVPS	HHPHAREMRR	SASEQSPNVS	HSAHMTETRS	KSFDFGSLSL	1020
TGPSAPAPVA	PPARVAPPER	RKCFLVQRQAS	LSRPPESLE	VAPKGRQESE	EPQPSSSKPS	1080
AKSSLQSISS	AATSHGGPPG	GKPGQDRPP	LGPTVPTYE	LQVFHHPVAQ	TPLHEKPYLP	1140
PPVSLFSFQH	LVQHEPGQSP	EFFSTQAMSS	LLSPSPYSMPP	LPPSLFQAPP	LPLQPTVLHP	1200
GQLHLPQLMP	HPANIPFRQP	PSFLPMPYPT	SSALSSGF	PLQSQFALQL	PGDVESHLPQ	1260
IKTSLAPLAT	GSAGLSPSTE	YSSDIRLPPV	APPASSSAPT	SAPPALPAC	PDTMVLVVP	1320
VRVQTNMPSY	GSAMYTTLSQ	ILVTQSQGSS	ATVALPKFEE	PPSKGTTVCG	ADVHEVGPGP	1380
SGLSEEQSRA	FPTPYLRVPV	TLPERKGTS	SSESILSLEG	SSSTAGGSKR	VLSPAGSLEL	1440
TMETQQQKRV	KEEEASKADE	KLELVKPCSV	VLTSTEDGKR	PEKSHLGQNQ	QGRRELEMLS	1500
SLSSDPSDTK	EIPPLPHPAL	SHGTAPGSEA	LKEYPQPSGK	PHRRGLTPLS	VKKEDSKEQP	1560
DPLSLAPPSS	LPLSETSSRP	AKSQEGLTDK	KVLQFPLSLH	TTNVSWCYLN	YIKPNHIQHA	1620
DRRSSVYAGW	CISLYNPNLP	GVSTKAALSL	LRSKQKVSK	TYTMATAPH	EAGRLOVPS	1680

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RKPRMTEVHL	PSLVSPEGQK	DLEARKEEEE	RRGEPEEDAP	ASQRGEPARI	KIFEGGYKSN	1740
EEYVYVRGRG	RGKYVCEECG	IRCKKPSMLK	KHIRTHTSDVR	PYVKCHCHFA	FTKGNLTKH	1800
MKSKAHSKKC	QETGVLEELA	AEEGTSDDLF	QDSEREGSE	AVEEHQFSDL	EDSDSDSDDLD	1860
DEDEDDEEES	QDELRSRSPSE	APPGPGHPLB	RADSSPILGP	QPDPASGST	EARTRGSVSE	1920
AERLTASSCS	MSSQSMQPGLP	WLGPAPLGSV	EKDGTGALSYP	KVPSPRRPWS	PSKEAGSRPP	1980
LARKHSLTKN	DSSPQRCSPA	REPQASAPSP	PGLHVDPGRG	MGALPCGSPR	LQLSPLTLCP	2040
LGRELAAPRA	VLSKLEGTTD	PGLPRYSPTR	RWSPGQAESP	PRSAPGKWA	LAGPGSPSAG	2100
EHGPGLGLDP	RVLFPAPLHK	HKLLSRSPET	CASPTCAESR	SPSCPGPAH	PLSSRPFSA	2160
DFHFHGLILAR	TEENIFSHLP	LHSQHRLTRAP	CPLIPIGGIQ	VMQARQPAH	TLLPGPTAAW	2220
VSGFSGGGSD	LTGAREAQER	GRWSPTESSS	ASVSPVAKVS	KFTLSSELEG	GDYPKERERT	2280
GGGGPGRPPDW	TPHGTGAPAE	PTPTHSPCTP	PDTLPRPPQG	RRAQCSWSPR	LESFRAPTNP	2340
EPSATPPLDR	SSSVGCLAEA	SARFPARTRN	LSGEPRTRQD	SPKPGSGEP	RAHPHQPEDR	2400
VPPNA						2405

SEQ ID NO: 773 moltype = AA length = 801
FEATURE Location/Qualifiers
source 1..801
mol_type = protein
organism = Homo sapiens

SEQUENCE: 773

MKTSBRRLT LKRBLRQARSET

MKISPRRPLI LKRRRLPLPV QNAPSEISEE EPRRSAPAQE SN
GIKIINUVTM RNTQVIAILRN NANIIUCITA ITAKCKECCG C

GIRL IN APTM PR
LEBOSTATSKY JU

LRPQTQTSYD	AKRTEVTLT	LGPKAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
LSNQIQLWRKLN	SSDGLGSRSI	KQEEMEEKHN	HLEQRQVKVE	EPSRSPSASWQ	NSVSRPPYS	240
YAMMIOFAIN	STERKRMTL	DITYIWIEDHF	PYFKHIAKGW	WKNSIRHLNS	LHDMPVRETS	300
ANGKVSFWTI	HPSANRYLTL	DQVFKPLDPG	SPQLPEHLES	QQKRPNPELR	RNMTIKTELP	360
LGARRKMKPL	LPRVFSYLLV	IQFPVNQSLV	LQPSVKVLPA	LAASLMSSEL	ARHSKVRVRIA	420
PKVFGQVWPF	GYMSKFFSGD	DLRFGTPTIS	LNFNIFCLCS	VLLAEBGIAP	LSSAGPGKEE	480
KLLFEGFSP	LLPVOTIKEE	EIQPGEEPMH	RALPIKVEPS	PLEEWPSPAP	SFKKEEHSHW	540
EDSSQSPTPR	PKKSYSGLRS	PTRCVSEMLV	IQRHRERRERS	RSRRKQHLLP	PCVDEPELLF	600
SEGPSTSRWA	AELPPFPADSS	DPAQSOLSYSQ	EVGGPFKTP	KETLPISTP	SKSVLPRTP	660
SWRLTPPKAV	GGLDFSPVDT	SQGASDPLPD	PLGLMDLSTT	PLQSAPPLES	PQRLLSSEPL	720
DLISVPGNNS	SPSDIDVPK	GSPEPQVSGL	AAANRSLTEGL	VLDTMNDSSL	KILLDISFPG	780
LDEDPLGPDN	INWSQFIPEL	Q				801

SEQ ID NO: 774 moltype = AA length = 748
FEATURE Location/Qualifiers
source 1..748
mol_type = protein
organism = Homo sapiens

SEQUENCE: 774

MKTSPRRPLI LK

GIKTIINHPTM PNTQVVAIPN NANIHSTIITA LTAKGKESSGS SG

L-BROTOTESYD AW

LRFQIQTSIS	ARRKKEFLL	LGPFRPAARDV	NFLRPPGALC	EQRKECTACD	EAAGQFTTNS	180
LSNQIWLKRM	SSDGLGGSRSI	KQEMBEKCN	HLEQRQVKVE	EPSRPSASWQ	NSVSERPPYS	240
YMAMIQFAIN	STERKRMTLK	DTIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLS	LHDMFVRETS	300
ANGKVSPWTI	HPSANRYLTL	DQVFQKQQKRP	NPFLRRNMTI	KTELPILGARR	KMKPLLPRVS	360
SYLVLPQFPV	NQSLVLQPSV	VKPLVPLAASL	MSESELARHSK	VRVIAPKVLL	AEEGIAPLSS	420
AGPGKEEKL	FGEGPSPLP	VQTKEEEEIQ	FEPEMPHLAR	PIKVESPPL	EWPSPASPK	480
ESESSHWSEDS	SQSPTPRPKK	SYSGLRSPT	CVSEMLVIQH	RERRRSRSR	RKQHLLPPCV	540
DEPELLFSEG	PSTSRWAEL	PFPADSSDPA	SQLSYSQEVG	GPFKTPIKET	LPISTS PKS	600
VLRPTFESWR	LTPPAKVGGL	DFSPVQTSGQ	ASDPLPDPLG	LMDLSTTPLQ	SAPPLESPQR	660
LLSSEPLLDI	SVPFGNNSDN	DDIVPKPGSP	EPQVSGLAAN	RSLTEGLVLD	TMNDSL SKIL	720
LDISFQGLDE	DPLGPNDNIN	SOFTPELO				748

SEQ ID NO: 775 moltype = AA length = 763
FEATURE Location/Qualifiers
source 1..763
mol_type = protein
organism = Homo sapiens

SEQUENCE: 775
Organism = *homo sapiens*

SEQUENCE: 775
MKTGDRRRRLI LKBRBRI RL DVL QNABRGFT

MRTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQE SN

GIKI INHPTM PM

LRPQTQTSYD	AKRTEVTLET	LGPKPAARDV	NLPRPPGALC	EQKRETCADG	EAAGCTINNS	180
LSNIQWLRKW	SSDGGLGSRSI	KQEMEEKENC	HLEQRQVKVE	EPSRSPSASWQ	NSVSERRPPYS	240
YMANQIFQAIN	STERKRMLTK	DIYTWIEDHF	PYFKHIAKPG	WKNSIRHNLN	LHDMDFVRETS	300
ANGKVSFWTI	HPSANRYLTL	DQVFKPLDQG	SPQLPEHES	QOKRPNPELR	RNMTRIKTELP	360
LGARRKMKPL	LPRVSYSSLV	IQFPVNQSLV	LOPSVKVLP	LAASLMSSEL	ARHSKRVRIA	420
PKVLLAEEGI	APLSSAGPGK	EEKLLFGEGF	SPLLPVQTIK	EEEIQPGEEM	PHLARPIKVE	480
SPPLEEWPS	APSFKEESSH	SWEDSSQSPT	PRPKKSYSGL	RSPTRCVSEM	LVIQHRERRE	540
RSRSRRKQHL	LPPCVDPEL	LFSEGPSTSR	WAELPPFD	SSDPASQLSY	SQEVGCPFKT	600
PIKETLPISS	TPSKSVLPRT	PESWRLTTPA	VKGGLDFDSPV	QTSQGASDPL	PDPLGLMDLS	660
TTPLQSAPPL	ESPQRNLSSS	PLLDLISVPPG	NSSPSDIDTUP	KPGSPFEQVS	GLAANRSLTE	720
GLVLDTMNDS	LSKILLDISP	PGLIDEDPLGP	DNINWSOIP	ELO		780

SEQ ID NO: 776 moltype = AA length = 206

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FEATURE	Location/Qualifiers
source	1..206 mol_type = protein organism = Homo sapiens
SEQUENCE: 776	
XAKPGWKNSI RHNLSLHDMF VRETSANGKV SFWTIHPSAN RYLTLDQVFK PLDPGSPQLP	60
EHLESQQKR PNPELRRNMT IKTTELPLGAR RKMKPPLLPRV SSYLVPIQFP VNQSLVLQPS	120
VVKVPLPLAAS LMSSELARHS KVRVIAPKVLAABEGIAPLS SAGPGKEEKL LFGEGFSPPLL	180
PVQTKEEEEI QPGEEMPHLA RPIKVE	206
SEQ ID NO: 777	moltype = AA length = 80
FEATURE	Location/Qualifiers
source	1..80 mol_type = protein organism = Homo sapiens
SEQUENCE: 777	
TALTAKGKES GSSGPNKFIL ISCGGAPTPQ PGLRPQTQTS YDAKRTEVTL ETLGPKPAAR	60
DVNLPRLPPGA LCEQKRETCG	80
SEQ ID NO: 778	moltype = AA length = 748
FEATURE	Location/Qualifiers
source	1..748 mol_type = protein organism = Homo sapiens
SEQUENCE: 778	
MKTSPRRPLI LKRRRLPLPV QNAPSETSEE EPKRSPAQQE SNQAEASKEV AESNSCKFPA	60
GKIIINHPTM PNTQVVAIPN NANHSIITA LTAKGKESGS SGPNKFILIS CGGAPTQPPG	120
LRLPQTQTYD AKRTEVLET LGPKPAARDV NLPRPPGALC EQKRETCDGE AAGCTINNSL	180
SNIQWLRKMS SDGLGSRSIK QEMEEKENCH LEQRQVKVVEE PSRPSASWQN SVSERPPYSY	240
MAIMIQFAINS TERKRMTLKD IYTWIEDHFP YFKHIAKPGW KNSIRHNLSL HDMFVRETSAA	300
NGKVFSWTIH PSANRYNMTK QVFQKQNRKQ NPELRRNMTI KTELPLGARR KMKPLLPRTVS	360
SYLVPIQPV NQSLVLQPSV KVPLPLAASL MSSELARHSK RVRIAPKVLL AEEGTAPLSS	420
AGPGKEEKLL PGEGEFSPLLP VQTIKEEEEIQ PGEEEMPHLAR PIKVESPPLLE EWPSPPAPSKF	480
EESSHSWEDS SQSPTPRPKK SYSGLRSPTR CVSEMLVIQH RERRERSRSR RKQHLLPPCV	540
DEPELLFSEG PSTSRWAAEL PFPADSSDPA SQLSYSQEVEG GFVKTPIKET LPISSTPSKS	600
VLPRTPEWR LTPPAKVGGL DFSPVQTSGQ ASDPLPDPLG LMDDSTTPLQ SAPPLESPQR	660
LLSSEPLLDI SVPFGNSSPS DIDVPKPGSP EPQVSGLAAN RSLTEGLVLD TMNDLSKIL	720
LDISFPGLDE DPLGPDNINW SQFIPELQ	748
SEQ ID NO: 779	moltype = AA length = 432
FEATURE	Location/Qualifiers
source	1..432 mol_type = protein organism = Homo sapiens
SEQUENCE: 779	
MSELKDCPLQ PHDFKSVVDHL KVCPRTAVL ARSEDDGIGI EELDTLQLEL ETLLSSASRR	60
LRVLEAETQI LTDWQDKKGDRH ELGAPPKHGK PKKQKLEGKA GHGPGPGPGR	120
PKSKNLQPKI QEYEFTDDPI DVPRIPKNDP PNRFWASVEP YCADITSEEV RTLEELLKPP	180
EDEAEHYKIP PLGKHYNSQRW AQEQLLLEEOK DGARAAAADV KKKGLMGPLT ELDTKDVAL	240
LKKSEAQHEQ PEDGCPFGAL TQRLLQALVE ENIISPMEDES PIPDMSGKES GADGASTSPR	300
NQNKPFSPVH TKSLESRIKE ELIAQGLLES EDRPAEDEDSE EVLAELRKRQ AELKALSAHN	360
RTKKHDLLRL AKEEVSRQEL RQRVRMADNE VMDAFRKIMA ARQKKRTPTK KEKDQAWKTL	420
KERESILKLL DG	432
SEQ ID NO: 780	moltype = AA length = 432
FEATURE	Location/Qualifiers
source	1..432 mol_type = protein organism = Homo sapiens
SEQUENCE: 780	
MSELKDCPLQ PHDFKSVVDHL KVCPRTAVL ARSEDDGIGI EELDTLQLEL ETLLSSASRR	60
LRVLEAETQI LTDWQDKKGDRH ELGAPPKHGK PKKQKLEGKA GHGPGPGPGR	120
PKSKNLQPKI QEYEFTDDPI DVPRIPKNDP PNRFWASVEP YCADITSEEV RTLEELLKPP	180
EDEAEHYKIP PLGKHYNSQRW AQEQLLLEEOK DGARAAAADV KKKGLMGPLT ELDTKDVAL	240
LKKSEAQHEQ PEDGCPFGAL TQRLLQALVE ENIISPMEDES PIPDMSGKES GADGASTSPR	300
NQNKPFSPVH TKSLESRIKE ELIAQGLLES EDRPAEDEDSE EVLAELRKRQ AELKALSAHN	360
RTKKHDLLRL AKEEVSRQEL RQRVRMADNE VMDAFRKIMA ARQKKRTPTK KEKDQAWKTL	420
KERESILKLL DG	432
SEQ ID NO: 781	moltype = AA length = 369
FEATURE	Location/Qualifiers
source	1..369 mol_type = protein organism = Homo sapiens
SEQUENCE: 781	
MSELKDCPLQ PHDFKSVVDHL KVCPRTAVL ARSEDDGIGI EELDTLQLEL ETLLSSASRR	60

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LRVLEAETQI LTDWQDKGD RRFLKLRDH ELGAPPKHGK PKKQKLEGKA GHGPGPGPGR	120
PISKNLQPKI QYEYFTDDP1 DVPRIPKNDA PNRFWASVPE YCDAITSEEV RTLELLKPP	180
EDEAEHYKIP PLGKHYNSQRW AQEDLLEEQQ DGARAAAVAD KKKGLMGPLT ELDTKVDAL	240
LKKSEAHQE PEDGCPFGAL TQRLLQALVE ENIISPMBDS PIPDMSGKES GADGASTSPR	300
NQNKPFSVPH TKSLESRIKE ELIAQGLLES EDRAPAEDSED EVLAELRKQ AELKALSAHN	360
RTKKHDLLR	369
SEQ ID NO: 782	moltype = AA length = 95
FEATURE	Location/Qualifiers
source	1..95
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 782	
MSELKDPLQ PHDFKSVDHL KVCPRYTAVL ARSEDDGIGI EELDTLQLEL ETLLSSASRR	60
LRVLEAETQI LTDWQDKGD RRFLKLRDH ELGAP	95
SEQ ID NO: 783	moltype = AA length = 99
FEATURE	Location/Qualifiers
source	1..99
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 783	
MPSDFISLLS ADLDLESPKS LYSRDSLKLH PSQNFHRAGL LEESVYDLLP KELQLPPSRE	60
TSVASMSQTG GGEAGSPPPA VVAAGFASEA GSVCIKNDL	99
SEQ ID NO: 784	moltype = AA length = 1531
FEATURE	Location/Qualifiers
source	1..1531
	mol_type = protein
	organism = Homo sapiens
SEQUENCE: 784	
MPSDFISLLS ADLDLESPKS LYSRESVYDL LPKELQLPPS RETSVASMSQ TSGGEAGSPP	60
PAVVAADASS APSSSSMGG A CSSFTTSSSP TIYSTSVTDS KAMQVESCSS AVGVSNRGV	120
EKQLTSNTVQ QHPSTPKRHT VLYISPPPED LLDNSRMSCQ DEGCGLESEQ SCSTMMDSP	180
SNFNSNMSTSS YNDNTEVPRK SRKRNPQRP GVKRRDCEES NMIDFDADSA KAPHYVLSQL	240
TTDNKGNKSA CNGTLENQKG TGVKKSPMLC QGYPVKSEGK ELKIVVQPET QHRARYLT	300
SRGSVKDRQ QGFPTVKLEG HNEPVLQVF VGNDSGRVKP HGFYQACRTV GRNTPCKEV	360
DIEGTTVIEV GLDPSNNMTL AVDCVGILKL RNADVEARIG IAGSKKKSTR ARLVFRVNIM	420
RKDGSTLTLQ TPSSPILCTQ PAGVPEILKK SLHSCSVKGE EEVFLIGKNF LKGTKVI	480
NVSDENSWLK EAEIDMELFH QNHLLVKVY HWDQHITLPV SVGIVYVTNA GRSHDVQPFT	540
YTPDPAAAGA LNVNVKKEIS SPARPCSFE AMKAMKTTGC NLDKVNIIPN ALMTPLIPSS	600
MIKSEDVTPM EVTAEKRSST IFKTTKSVGS TQQTLENISN IAGNGSFSSP SSSHLPSENE	660
KQQQIQPKAY NPETLTTIQTQ QDISQPGTPP AVSASSQLPN SDALLQQATQ FQTRETQSRE	720
ILQSDGTVVN LSQLEASQQ QTLQQQISSN IFFPSPNSVSQ LQNTIQLQQA	780
GSGTGSTASG SSSGVDLVQQ VLEAQQLSS VLFSAPDGNE NVQEQLSADI FQQVSQLQSG	840
VSPGMFSSTE PTVHTRPDNL LPGRAESVHP QSENTLSNQQ QQQQQQQQVM ESSAAMVMM	900
QSQICQAAAQ IQSELSPKSTA SANGLQSP VYQQTSHMMS ALSTNEDMQM QCELFSSPPA	960
VSGNETSTTT TQVATPGETT MfqTSSSGDG EETGTQAKQI QNSVFQTMVQ MQHSGDNQPO	1020
VNLFSSTKSM MSVQNSGTQQ QGNGLFQQGN EMMSLQSGNF LQOSSHSSQAO LFHPONPIAD	1080
AQNLSQLETQG SLFHSNPPIV HSQTTTSSSE QMOPPMFHQS STIAVLQGSS VPQDQSTNI	1140
FISQSQPMNL QTNTVAQEAF FAAPNSISPL QSTSNSSEQA AFQQQAPISH IQTPLMSQEQ	1200
AQPPQQQLFQ PQVALGSLPP NMPPMSQGQT MFQSQHSIVA MQSNSPSQEQ QQQQQQQQQQ	1260
QQQQQQOSILF SNQNTMATMA SPKOPPPNM1 FNPNQNPMAN QEQQNOISIFH QOSNMAPMNQ	1320
EQQPMQFQSQ STVSSLQNPQ PTQSESSQTP LFHSSPQIQL VQGSPSSSEQ QVTFLSPAS	1380
MSALQTSINQ QDMQQSPLYS PQNNMPGIOQ ATSSPQPOAT LFHNTAGGTN NQLQNSPGSS	1440
QQTSGMFLFG IQNNCQLLTT SGPATLPDQL MAISQPGQPO NEGQPPVTTL LSQQMPENSP	1500
LASSINTNQN IEKIDLVLVSL QNQGNLNTGS F	1531
SEQ ID NO: 785	moltype = AA length = 119
FEATURE	Location/Qualifiers
source	1..119
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	organism = Homo sapiens
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MPSDFISLLS ADLDLESPKS LYSRDSLKLH PSQNFHRAGL LEESVYDLLP KELQLPPSRE	60
TSVASMSQTG GGEAGSPPPA VVAAGIPEMF ILCILMCMIL RFKKGFASEA GSVCIKNDL	119
SEQ ID NO: 786	moltype = AA length = 1548
FEATURE	Location/Qualifiers
source	1..1548
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	organism = Homo sapiens
SEQUENCE: 786	
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TSVASMSQTG GGEAGSPPPA VVAADASSAP SSSSMGGACS SFTTSSPTI YSTSVDKSA	120
MQVESCSSAV GVSNSRGVSEK QLTSNTVQOH PSTPKRHTVL YISPPPEDLL DNSRMSCQDE	180

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GCGLSEQSC	SMWMEDPSN	FSNMSTSSYN	DTEVPRKSR	KRNPKQPGV	KRRDCEESNM	240
DIFDADSAKA	PHYVLSQLTT	DNKGN SKAGN	GTL ENQKG TG	VKKSPMLCGQ	YPVKSEGKEL	300
KIVVQPETQH	RARYLTEGSR	GSVKDRTQQG	FPTVKLEGHN	EPVVLQFVG	NDSGRVKPHG	360
FYQACRVTGR	NTTPCKEVDI	EGTTVIEVGL	DPSNNMTLAV	DCVGILKLRLN	ADVEARIGIA	420
GSKKKSTRAR	LVFRVNIMRK	DGSTLTLQTP	SSPILCTQPA	GVPEILKSSL	HCSVKGEEE	480
VFLIGKNFLK	GTKVIFQENV	SDENSWKSEA	EIDMELFHQN	HLIVKVPPYH	DQHITLPVSV	540
GIYVVTNAGR	SHDVQPFYT	PDPAAGALNV	VNVKEISSPA	RPCSFEEAMK	AMKTTGCNL	600
KVNIIPNALM	TPLIPPSMIK	SEDVTPMEVT	AEKRSSTIFK	TTKSVGSTQQ	TLENISNIAG	660
NGSFSSPSSS	HLPSENEKQQ	QIQPKAYNPE	TLTTIQTQDI	SQPGTGP AVS	ASSQLPNSDA	720
LICQATOFQT	RETQSEIREIL	SDGTVVNL SQ	LT EASQQQQQ	SPLQEQAQTL	QQQIISNIFF	780
SPNSVSQQLQ	TIQQLQAGSF	TGSTASGSSG	SVDLVQQVLE	AQQQLSSVLF	SAPDGNEVQ	840
EQLSADIFQO	VSQIQSGVSP	GMFSSTEPTV	HTRPDNLLPG	RAESVHPQS	NTLSNQQQQQ	900
QQQQQVMESS	AAMVMEMMQS	ICQAAAQIQS	ELFPSTASAN	GNLQQSPVYQ	QTSHMMSALS	960
TNEDDMQMCQE	LFSSPPAVS	NETSTTTTQQ	VATPGTTMFQ	TSSSGDGEET	GTQAKQI QNS	1020
VFQTMVQMQH	SGDNQPVNL	FSSTKSMSSV	QNSGTQQQGN	GLFQQGNE MM	SLQSGNFLQ	1080
SSHQSQAOLFH	PQNPIADAQN	LSQETQGSLF	HSPNPIVHSQ	TSTTSSEQM	PPMFHSQSTI	1140
AVLQGSSVPQ	DQQSTNIFLS	QSPMNNLQTN	TVAQE AFFA	PNSISPLQST	SNSEQQAAFQ	1200
QQA PISHI QT	PMLSQBQAOQ	PQOGLFQPOV	ALGSLPPNPM	PQSQQGTMFQ	SQHSIVAMQS	1260
NSPSQEQQQQ	QQQQQQQQQQ	QQQSI LSFSNQ	NTMATMASPK	QPPP NMIFNP	NQNPMANQEQ	1320
QNQSI FHQQ	NMAPMNEQQ	PMQFOSQSTV	SSLQNP GPTQ	SESSQTPLFH	SSPQIQLVQG	1380
SPSSQEQQVT	LFLSPASMSA	LQTSINQ QDM	QCSPLYS PQN	NMPGIQGAT	SPQPQATLF	1440
NTAGGT MNLQ	QNSPGSSQQT	SGMFLFGI QN	NCSQLLTSGP	ATLPDQLMAI	SQPGQPQNEG	1500
QPVVTTLLSQ	QMPENSPLAS	SINTNQNIEK	IDLLVSLQ	GNLNTGSF		1548

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 mol_type = protein
 organism = Homo sapiens

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TSVASM SQT	GGEAGS PPPA	VVAADASSAP	SSSMGGAC S	SFTTSSSP	TI YSTS VTD SKA	120
MQVESCSA V	GVSNRGVSEK	QLTSNTVQHQH	PSTPKRHTVL	YISPPPEDLL	DNSRMSCQDE	180
GCGLESEQSC	SMWMEDPSN	FSNMSTSSYN	DTEVPRKSR	KRNPKQPGV	KRRDCEESNM	240
DIFDADSAKA	PHYVLSQLTT	DNKGN SKAGN	GTL ENQKG TG	VKKSPMLCGQ	YPVKSEGKEL	300
KIVVQPETQH	RARYLTEGSR	GSVKDRTQQG	FPTVKLEGHN	EPVVLQFVG	NDSGRVKPHG	360
FYQACRVTGR	NTTPCKEVDI	EGTTVIEVGL	DPSNNMTLAV	DCVGILKLRLN	ADVEARIGIA	420
GSKKKSTRAR	LVFRVNIMRK	DGSTLTLQTP	SSPILCTQPA	GVPEILKSSL	HCSVKGEEE	480
VFLIGKNFLK	GTKVIFQENV	SDENSWKSEA	EIDMELFHQN	HLIVKVPPYH	DQHITLPVSV	540
GIYVVTNAGR	SHDVQPFYT	PDPAAGALNV	VNVKEISSPA	RPCSFEEAMK	AMKTTGCNL	600
DKVNIIPNAL	MTPLIPPSMIK	KSEDVTPMEV	TAEKRSSTIF	TTKSVGSTQ	QTLENISNIA	660
GNGSFSSPSS	SHLPSENEKQ	QIQPKAYNPE	ETLTTIQTQD	ISQPGTGP AV	SASSQLPNSD	720
ALLCQATOFQ	RETQSEIREIL	QSDGTVVNL Q	QTEASQQQQ	QSPLQEQAQTL	LOQQIISNIF	780
PSPNVSQSLQ	NTIQQLQAGS	FGTGSTASGSS	GSVDLVQQV	EAQQQLSSVLF	SAPDGNEVQ	840
QEQLSADIFQ	QVSQIQSGV	PGMFSSTEPT	VHTRPDNLLP	GRAESVHPQS	ENTLSNQQQQ	900
QQQQQQVME	SAAMVMEMMQ	SICQAAAQIQ	SELFPSTASA	NGNLQQSPVY	QTSHMMSAL	960
STMEDDMQMC	ELFSSPPAVS	GNETSTTTTQ	VATPGTTMFQ	TSSSGDGEET	TGTQAKQI QN	1020
SVFQTMVQMQ	HSGDNQPVNL	LFSSTKSMMS	VQNSGTQQQG	NGLFQQGNE M	MSLQSGNFLQ	1080
QSSHSQ AOLF	HPQNP IADAQ	NLSQETQGS	FHSHPNPIVHS	QTSTTSS EQM	QPPMPHSQST	1140
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QQA PISHI QT	TPMLSQEQAQ	PPQOGLFQPO	VALGSLPPN	MPSQOQGTM	SQHSIVAMQS	1260
SNSPSQEQQQQ	QQQQQQQQQQ	QQQSI LSFSN	NTMATMASPK	KQPPNMFN	PNQNPMANQEQ	1320
QNQSI FHQQ	NMAPMNEQQ	PMQFOSQSTV	VSSLQNP GPTQ	SESSQTPLFH	HSSPOIQLVQ	1380
GSPSSQEQQV	TFLSPASMSA	ALQTSINQ QD	MQQSPLYSPQ	NNMPGIQGAT	SSPQPQATLF	1440
HNTAGGT MNLQ	QNSPGSSQQT	TSGMFLFGI QN	NCSQLLTSG	PATLPDQLMA	ISQPGQPQNEG	1500
QPVVTTLLSQ	QMPENSPLAS	SSINTNQNIE	KIDLLVSLQ	GNLNTGSF		1549

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NQKGTGVKKS	PMLCGQY PVK	SEGKELKIV	QPETQH RARY	LTEGSRGV	DRTQQGFTV	240
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NMTLAVDCVG	I LKLRNADVE	ARIAGSKK	KSTRARL VFR	VNIMRKDG ST	LTLQTPSSPI	360
LCTQPAGVPE	I LKKSLHSCS	VKEEEVFLI	GKNFLKG TKV	IFQENVS D	SWKSEAEIDM	420
ELFHQNHLIV	KVPPYHDQH	TLPVSVGIV	VTNAGRSHDV	QPF TYTPDPA	AAGALNVNVK	480
KEISSPARPC	SFEEAMKAMK	TTGCNLDKV	IIPN ALMTP	IPSSMI KSED	VTPM EVTA EK	540
RSSTIFKT	SVGSTQ QTLE	NISNIAGNG	FSSPSSSSHL	SENEKQQQIQ	PKAYN PETLT	600
TIQTQDISQP	GTFPAV SASS	QLPNSD ALLQ	QATQFQ TRET	QSREILQ SDG	TVVNL SQLTE	660
ASQQQQQSP	QEQA QTLQ	ISSN IFPSN	SVSQ LQNTI	QLQAGSFTG S	TASGSSGSV D	720
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PGTTMFQTS	SGDGEETGTQ	AKQIQNSVFQ	TMVQMQHSGD	NQPQVNLFSS	TKSMMSVQNS	960
GTQQQGNGLF	QOGNEMMSLQ	SGNFLQQSSH	SQQLFHPON	PIADAQNLSQ	ETQGSLFHSP	1020
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SLPPNPMPQS	QQGTMFQSQH	SIVAMQSNSP	SQEQQQQQQQ	SILFSNQNTM		1200
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QNPGBTQSES	SQTPLFHSSP	QIQLVQGSPS	SQEQQVTLFL	SPASMSALQT	SINQODMQQS	1320
PLYSPQNMM	GIQGATSSPQ	PQATLHFHNTA	GGTMNQLQNS	PGSSQQTSGM	FLFGIQNINCS	1380
QLLTSGPATL	PDQLMAISQP	GQPQNEGQPP	VTTLLSQQMP	ENSPLASSIN	TNQNIEKIDL	1440
LVSLLQNGNN	LTGGSF					1455

SEQ ID NO: 789 moltype = AA length = 1455
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 source 1..1455
 mol_type = protein
 organism = Homo sapiens

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 NMMLAVDCVG ILKLRLNADVE ARIGIAGSKK KSTRARLVFR VNIMRKDGST LTLQTPSSPI 360
 LTCQPAVGPE ILKKSLHSCS VKGEEEVFLI GKNFLKGTVK IFQENVSDEN SWKSEAEIDM 420
 ELFHQNHLLIV KVPPYHHDQH1 TLPVSVGIYV VTNAGRSHDV QPFETYDPA AAGALNVNVK 480
 KEISSPAPC SFEEAMKAMK TTGCNLDKVN IIPNALMTPL IPSSMKSED VTPMVEVTAEK 540
 RSSTIFKTTK SVGSTQQTLE NISNIAGNGS FSSPSSSHLP SENEKQQQIQ PKAYNPETLT 600
 TIQTQDISQP GTFPAVASS QLPNSDALLQ QATQFQTRRET QSREIILQSDG TVVNLSQLTE 660
 ASQQQQQSPN QEQAAQTLQQQ ISSNIFVPPSN SVSOLQNTIQ QLQAGSFTGS TASGSSGSD 720
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 GTQQQGNGLF QOGNEMMSLQ SGNFLQQSSH SQQLFHPON PIADAQNLSQ ETQGSLFHSP 1020
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 QLLTSGPATL PDQLMAISQP GQPQNEGQPP VTTLLSQQMP ENSPLASSIN TNQNIEKIDL 1440
 LVSLLQNGNN LTGGSF 1455

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 IEKIDLLVSL QNQGNNLTG F 141

SEQ ID NO: 791 moltype = AA length = 143
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 DPSNNMMLAS ASRSARNLKE KLA 143

1.25. (canceled)

26. A method for identifying an antibody acting as an anti-tumoral agent that depletes tumor-infiltrating regulatory T cells, comprising the steps of:

- a) assaying candidate antibodies for their binding specificity to CCR8;
- b) selecting antibodies having a specific binding activity to CCR8;

c) testing the specific binding antibodies in a cell system comprising tumor infiltrating regulatory T cells for their capacity of inhibiting proliferation and/or inducing an apoptotic response of the tumor infiltrating regulatory T cells.

27. The method of claim **26**, wherein the depletion of tumor-infiltrating regulatory T cells comprises inducing antibody-dependent cell-mediated cytotoxicity (ADCC).

28. An in vitro method for monitoring the efficacy of a therapeutic treatment in a subject of a solid tumor which is a non-small cell lung cancer or a metastasis derived therefrom, said method comprising the steps of:

- a) obtaining an isolated biological sample containing tumor infiltrating T regulatory cells from the subject;
- b) detecting CCR8 in said biological sample;
- c) comparing the detected CCR8 to a control selected from a biological sample obtained from the same subject before initiation of the therapeutic treatment or taken at a time during the course of the therapeutic treatment, wherein a lower amount of CCR8 in the biological sample than in the control indicates effective treatment of the tumor.

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