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ganSpe1 hub_175539_Ganaspis sp. 1: SPALN Alignments to N. vitripennis RefSeq Proteins (XP_001607669.1)

NCBI Details: [XP_001607669.1](#)

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alpha-crystallin A chain isoform X2 [Nasonia vitripennis]

NCBI Reference Sequence: XP_001607669.1
[Identical Proteins](#) [FASTA](#) [Graphics](#)

[Go to:](#)

LOCUS XP_001607669 190 aa linear INV 29-FEB-2020
DEFINITION alpha-crystallin A chain isoform X2 [Nasonia vitripennis].
ACCESSION XP_001607669
VERSION XP_001607669.1
DBLINK BioProject: PRJNA594415
DBSOURCE REFSEQ: accession XM_001607619.6
KEYWORDS RefSeq.

[Analyze this sequence](#)
Run BLAST
Identify Conserved Domains
Highlight Sequence Features
Find in this Sequence
Show in Genome Data Viewer

Item: XP_001607669.1
Score: 959
Position: [scaffold_432402:214818-241200](#)
Genomic Size: 26383
Strand: +



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ganSpe1 hub_175539_Ganaspis sp. 1: SPALN Alignments to N. vitripennis RefSeq Proteins (XP_001607669.1)

NCBI Details: XP_001607669.1

<u>Region</u>	94..175	-	-	Conserved Domains (Concise)
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	/note="Alpha-crystallin domain (ACD) of metazoan alpha-crystallin-type small(s) heat shock proteins (Hsps). sHsps are small stress induced proteins with monomeric masses between 12 -43 kDa, whose common feature is the Alpha-crystallin domain (ACD). sHsps are...; cd06526"			Domain Relatives
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	/site_type="other"			Gene
	/note="putative dimer interface [polypeptide binding]"			Genome
	/db_xref="CDD:107247"			PubMed (RefSeq)
<u>CDS</u>	1..190			PubMed (Weighted)
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	/coded_by="XM_001606198.6:437..1009"			Related Structures (Summary)
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	/db_xref="NASONIABASE:NV12521"			
<u>ORIGIN</u>	1 madsgikrni piklgdfsvi dsefsnirer fdaemrkmeem emsrfrrselm nresnffkst 61 tstttqqqss qnsslspghq sntwldglns plqdegdnk mklrlfdvsq ytpreevvkt 121 vdnkllvhak heektdtksv yreynrefill pkgtntpetik sslskdgvlt veaplpalgg 181 geklipiahh			
//				

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alpha-crystallin A chain isoform X2 [Nasonia vitripennis] Protein

See more...

Item: XP_001607669.1
Score: 959
Position: scaffold_432402:214818-241200
Genomic Size: 26383
Strand: +

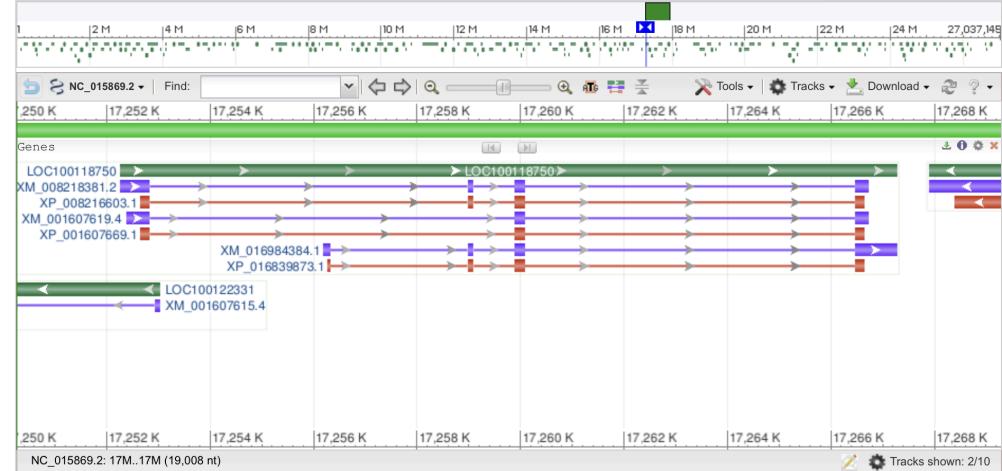
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26%

NCBI Sequence Viewer:

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Select a row to display the corresponding transcript and peptide details:

mRNA Accession	Scaffold Accession	5' Start	3' End	Strand	Protein Accession	Graphical Viewer
XM_008218381.2	NC_015869.2	17,252,267	17,266,721	+	XP_008216603.1	View in Sequence Viewer
XM_001607619.4	NC_015869.2	17,252,373	17,266,741	+	XP_001607669.1	View in Sequence Viewer
XM_016984384.1	NC_015869.2	17,256,175	17,267,274	+	XP_016839873.1	View in Sequence Viewer

[Transcript Details](#) [Polypeptide Details](#)Options: [Export All Unique CDS to FASTA](#) [Export All CDS for Selected Isoform to FASTA](#) [Download CDS Workbook](#)



Select a row to display the corresponding transcript and peptide details:

mRNA Accession	Scaffold Accession	5' Start	3' End	Strand	Protein Accession	Graphical Viewer
XM_008218381.2	NC_015869.2	17,252,267	17,266,721	+	XP_008216603.1	View in Sequence Viewer
XM_001607619.4	NC_015869.2	17,252,373	17,266,741	+	XP_001607669.1	View in Sequence Viewer
XM_016984384.1	NC_015869.2	17,256,175	17,267,274	+	XP_016839873.1	View in Sequence Viewer

[Transcript Details](#) | [Polypeptide Details](#)

Options: [Export All Unique CDS to FASTA](#) | [Export All CDS for Selected Isoform to FASTA](#) | [Download CDS Workbook](#)

CDS usage map:

Isoform	1_7737_0	2_7737_0	3_7737_1	4_7737_1	5_7737_0
XP_008216603.1	1		2	3	4
XP_001607669.1	1			2	3
XP_016839873.1		1	2	3	4

Select a row to display the corresponding CDS sequence:

CDS ID	5' Start	3' End	Strand	Phase	Size (aa)
1_7737_0	17,252,652	17,252,836	+	0	61
3_7737_1	17,258,974	17,259,093	+	1	39
4_7737_1	17,259,891	17,260,083	+	1	64
5_7737_0	17,266,463	17,266,657	+	0	65

| [GEP Home Page](#) |

mySt | Paras | ganS | alpha | PRED | GEP | tblas | NCB | +

gander.wustl.edu/~wilson/nvitrefseqrecord/retrievegenerecord.php?se...

XM_001607615.4

NC_015869.2: 17M..17M (19,008 nt)

Select a row to display the corresponding transcript and peptide details:

mRNA Accession	Scaffold Accession	5' Start	3' End	Strand	Protein Accession	Graphical Viewer
XM_008218381.2	NC_015869.2	17,252,267	17,266,721	+	XP_008216603.1	View in Sequence Viewer
XM_001607619.4	NC_015869.2	17,252,373	17,266,741	+	XP_001607669.1	View in Sequence Viewer
XM_016984384.1	NC_015869.2	17,256,175	17,267,274	+	XP_016839873.1	View in Sequence Viewer

Transcript Details | **Polypeptide Details**

Options: Export All Unique CDS to FASTA | Export All CDS for Selected Isoform to FASTA | Download CDS Workbook

CDS usage map:

Isoform	1_7737_0	2_7737_0	3_7737_1	4_7737_1	5_7737_0
XP_008216603.1	1		2		
XP_001607669.1	1				
XP_016839873.1		1	2		

Select a row to display the corresponding CDS sequence:

CDS ID	5' Start	3' End	Strand	Phase
1_7737_0	17,252,652	17,252,836	+	0
3_7737_1	17,258,974	17,259,093	+	1
4_7737_1	17,259,891	17,260,083	+	1
5_7737_0	17,266,463	17,266,657	+	0

Sequence viewer for LOC100118750: LOC100118750:1_7737_0

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>LOC100118750:1_7737_0
MADSGIKRNIPIKLGDFSVIDSEFSNIRERFDAEMRKMEEEMSFRSELM
NRESNFFKSTT
```

blast.ncbi.nlm.nih.gov/Blast.cgi

Query Descri

LOC100118750:1_7737_0

Query Length

61

Subject ID

Icl|Query_6389893 (dna)

Subject Descr

hub_175539_ganSpe1_dna range ...

Subject Length

300939

Other reports

?

Descriptions Graphic Summary Alignments Dot Plot

Sequences producing significant alignments

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Select columns

Show 100

?

select all 1 sequences selected

Graphics

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	hub_175539_ganSpe1_dna range=scanno...		119	119	100%	1e-35	96.72%	300939	Query_6389893

Feedback

blast.ncbi.nlm.nih.gov/Blast.cgi

hub_175539_ganSpe1_dna range=...

Subject Length
300939

Other reports

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Alignment view Pairwise [Restore defaults](#)

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1 sequences selected ?

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hub_175539_ganSpe1_dna range=scaffold_432402:1-300939 5'pad=0 3'pad=0
strand=+ repeatMasking=None
Sequence ID: Query_6389893 Length: 300939 Number of Matches: 1

Range 1: 214818 to 215000 [Graphics](#) [Next Match](#) [Previous Match](#)

Score	Expect	Identities	Positives	Gaps	Frame
119 bits(299)	1e-35	59/61(97%)	61/61(100%)	0/61(0%)	+3

Query 1 MADSGIKRNIPIKLGDFSVIDSEFSNIRERFDAEMRKMEEMSR
Sbjct 214818 MADSGIKRNIPIKLGDFSVID+EFSNIRERFDAEMRKME+EMSR

Query 61 T 61
Sbjct 214998 T 215000

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Range: 214818-215000

Descriptions Graphic Summary Alignments **Alignments** Dot Plot

Alignment view Pairwise ? **Restore defaults** Download ▾

1 sequences selected ?

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hub_175539_ganSpe1_dna range=scaffold_432402:1-300939 5'pad=0 3'pad=0 strand=+ repeatMasking=none

Sequence ID: **Query_999187** Length: **300939** Number of Matches: **1**

Range 1: 241009 to 241203 [Graphics](#) ▾ [Next Match](#) [Previous Match](#)

Score 124 bits(312)	Expect 2e-37	Identities 60/65(92%)	Positives 64/65(98%)	Gaps 0/65(0%)	Frame +1
Query 1	VHAKHEEKTDKSVYREYNREFLLPKGTNPETIKSSLSDGVLTVEAPL				
Sbjct 241009	VHAKHEEK++TKSVYREYNREFLLPKGTNPETIKSSLSDGVLTVEAPL				
Query 61	IAHH* 65				
Sbjct 241189	IAHQ* 241203				

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Range: 241009-241203

Descriptions Graphic Summary Alignments Dot Plot

Alignment view Pairwise ? Restore defaults Download

1 sequences selected ?

[Download](#) [Graphics](#) ▼ Next ▲ Previous [Descriptions](#)

hub_175539_ganSpe1_dna range=scaffold_432402:1-300939 5'pad=0 3'pad=0 strand=+ repeatMasking=none

Sequence ID: **Query_3923443** Length: **300939** Number of Matches: **1**

Range 1: 228861 to 228968 [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Positives	Gaps	Frame
52.0 bits(123)	3e-12	26/38(68%)	28/38(73%)	2/38(5%)	+3

Query 2 HHTSSSEHRTSTTSKTEGWDSSKPDGVPPMRSAFDSFK 39
H TSSSEHRTSTTSKTE WD K + P RS+FD FK
Sbjct 228861 HHTSSSEHRTSTTSKTESWD--KTETSKPTRSSFDCFK 228968

back

Range: 228861-228968

?

Descriptions Graphic Summary Alignments Dot Plot

Alignment view Pairwise ▾ [Restore defaults](#) [Download](#) ▾

1 sequences selected ?

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hub_175539_ganSpe1_dna range=scaffold_432402:1-300939 5'pad=0 3'pad=0 strand=+ repeatMasking=none

Sequence ID: **Query_3997417** Length: **300939** Number of Matches: **1**

Range 1: 231885 to 232073 [Graphics](#) [Next Match](#) [Previous Match](#)

Score 120 bits(300)	Expect 9e-36	Identities 58/63(92%)	Positives 61/63(96%)	Gaps 0/63(0%)	Frame +3
Query 2	TTQQQSSQNSSLSPQHDSNTWLDGLNSPLIQDEGDNKMLKLRFDVSQYT +T QS+QNSSLSPQHDSNTWLDGLNSPLIQDEG+NKMLKLRFDVSQYT				
Sbjct 231885	STTTQSNQNSSLSPQHDSNTWLDGLNSPLIQDEGNNKMLKLRFDVSQYT				
Query 62	KLL 64				
Sbjct 232065	KLL 232073				

◀ ▶

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Range: 231885-232073

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Alignment view Pairwise [?](#) [Restore defaults](#) [Download](#)

1 sequences selected [?](#)

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hub_175539_ganSpe1_dna range=scaffold_432402:1-300939 5'pad=0 3'pad=0 strand=+ repeatMasking=none

Sequence ID: **Query_4274255** Length: 300939 Number of Matches: 1

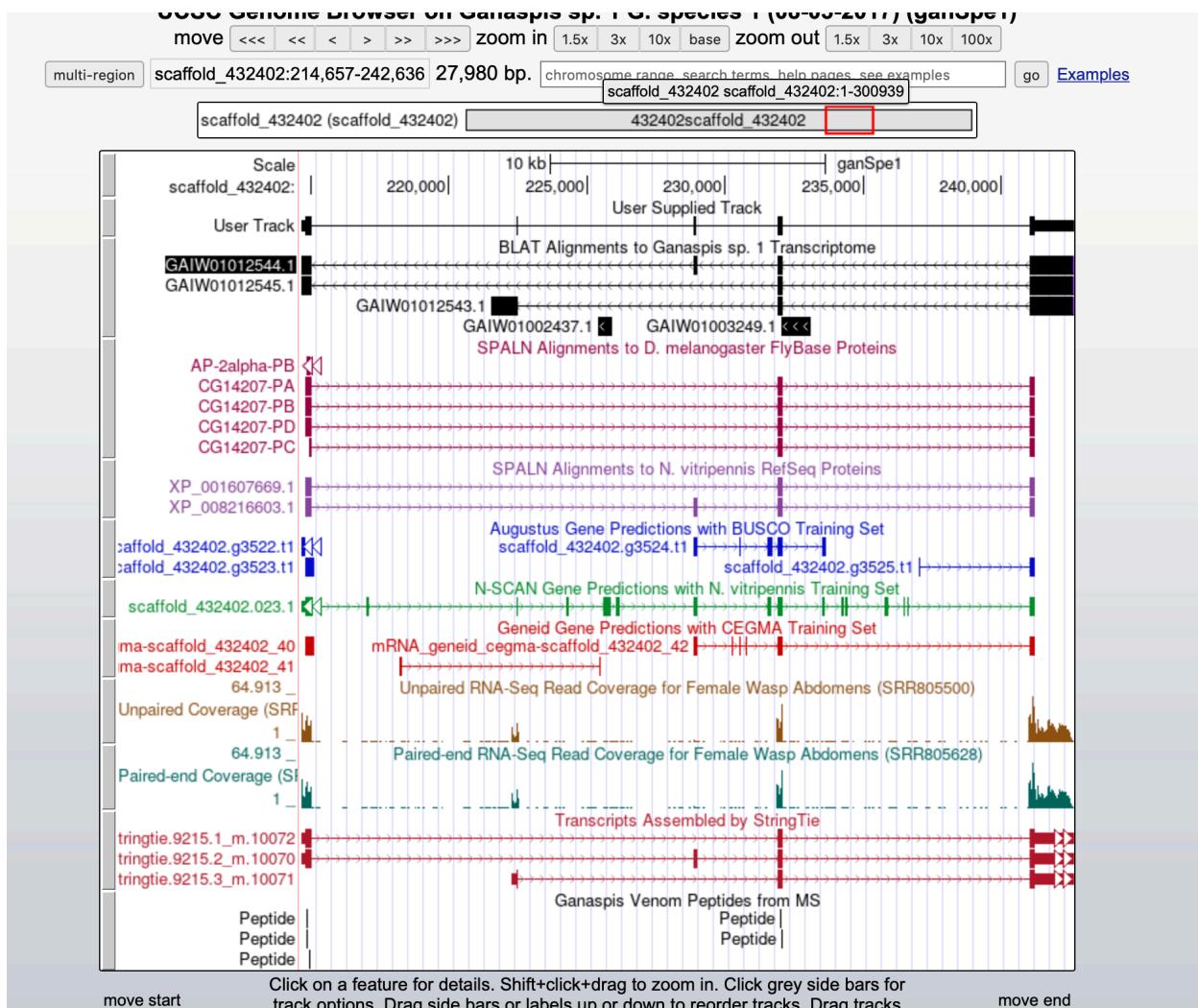
Range 1: 222458 to 222511 [Graphics](#) [Next Match](#) [Previous Match](#)

Score 33.9 bits(76)	Expect 2e-06	Identities 12/18(67%)	Positives 17/18(94%)	Gaps 0/18(0%)	Frame +2
Query 1	MIVDEDLYPPRHKTIVKY	18			
Sbjct 222458	MI+ E+LYPPRHKTV++				
	MILGEELYPPRHKTVVRF	222511			

[Feedback](#)

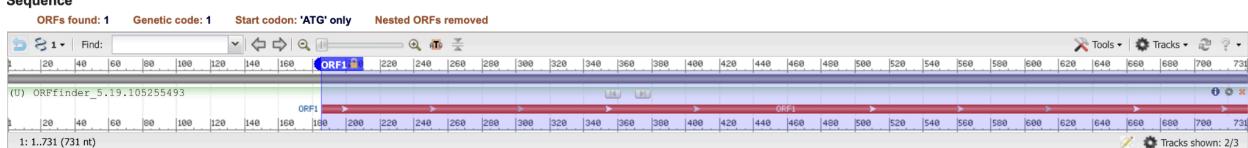
Range: 222458-222511

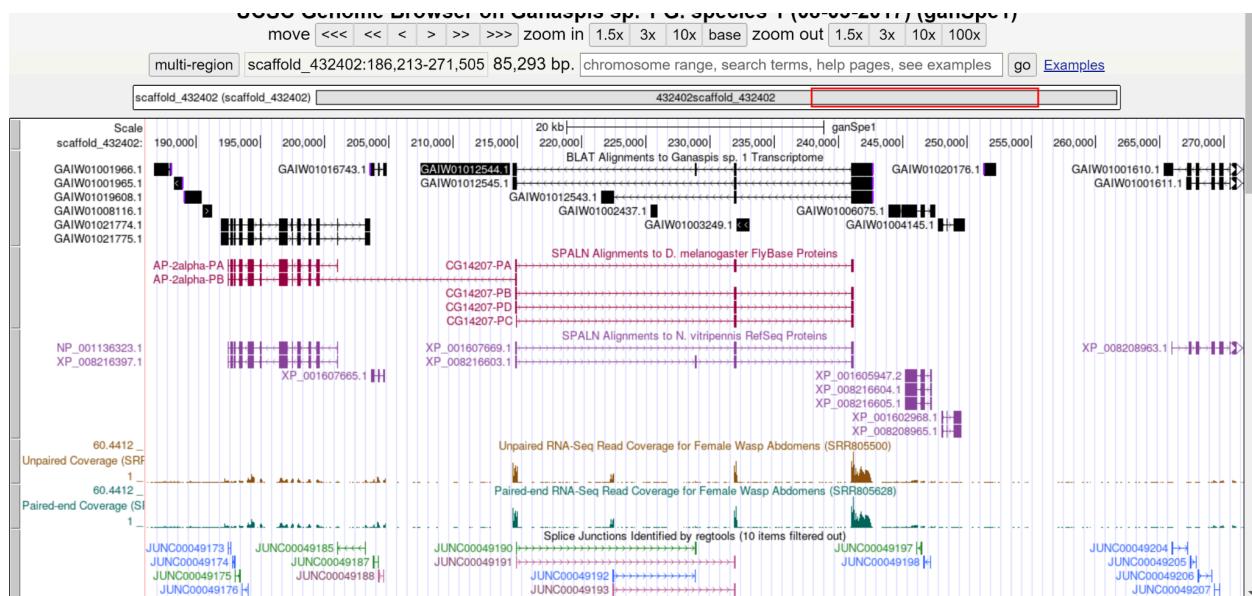
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AGATGAGGAAGATGGAGGACGAAATGTCCCGTTCAGGAGTGAACTCATG
AACCGTGAGAGCAACTTTCAAGAGCACTACAAGATGATCCTGGAGAG
GAACTCTACCCCCCGAGACACAAAACGTGCGTTCTACTCGACAAG
CAGCTCCGAACACAGGACCTCGACGACCTCCAAAACGTGAGAGTTGGATA
AAACTGAAACCTCAAACCAACGAGGTCTTCTCGACTGTTTAAAGC
ACCACCAACGCAGAGTAACCAAAACAGCTCTGAGCCCACAGCACGATT
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GAAATCGTCGTAAAACCGTCGACAATAAATTACTGGTGCACGCCAAGCA
TGAGGAAAAATCTGAAACTAAATCGGTCTACAGAGAGTATAACAGGGAAT
TCCTTCTTCCCAAAGGAACCAATCCTGAGAGCATTAAATCCTCATTGAGC
AAGGACGGAGTCCTCACCGTGGAAAGCACCTTGCCGCCATTGGACAAGG
CGAAAAACTCATCCCTATCGCCCACCAATAA
```



Open Reading Frame Viewer

Sequence





This has the gene model checker custom tracks in red

Xxxx protein

MILGEELYPPRHKTVVFHSTSSEHRTSTSKTESWDKTETSKPTRSSF
DCFKSTTQSQNQSSLSPQHDSNTWLDGLNSPLIQDEGNNKMLKLRFDVS
QYTPPEEVVKTVDNKLLVHAKHEEKSETKSVYREYNREFLLPKGTPESI

KSSLSKDGVLTVEAPLPAIGQGEKLIPIAHQ

xxxxx_mRNA

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