BLAST ® » blastp suite » RID-308VMTX401R

BLAST Results

crp4PBO

RID 308VMTX401R (Expires on 11-20 17:03 pm)

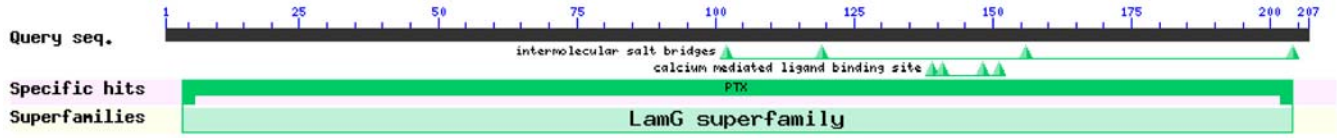
Query ID lcl|Query_314267
Description crp4PBO
Molecule type amino acid
Query Length 207

Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.5.1+

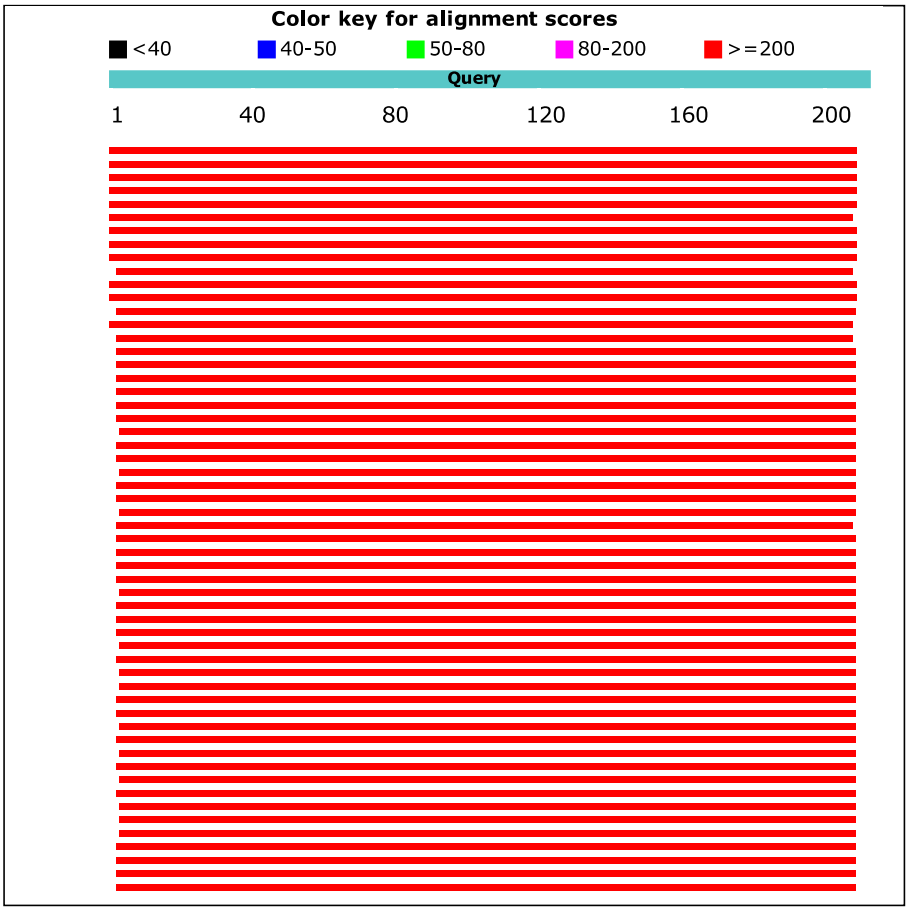
New Analyze your query with SmartBLAST

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 104 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
C-reactive protein [Danio rerio]	429	429	100%	3e-152	100%	AET80950.1
Chain A, Crystal Structure Of Zebrafish Short-chain Pentraxin Protein Without Calcium Ions	428	428	100%	4e-152	100%	4PBO_A
Chain A, Crystal Structure Of Zebrafish Short-chain Pentraxin Protein	428	428	100%	4e-152	100%	4PBP_A
uncharacterized protein LOC751795 precursor [Danio rerio]	426	426	100%	1e-150	99%	NP_001039325.1
Zgc:152809 protein [Danio rerio]	424	424	100%	2e-150	99%	AAH95616.1
pentraxin-related C-reactive protein [Danio rerio]	422	422	99%	2e-149	99%	AGB69039.1
Zgc:152809 protein [Danio rerio]	422	422	100%	3e-149	99%	AAH81513.1
pentraxin-related C-reactive protein [Danio rerio]	412	412	100%	2e-145	96%	AGB69035.1
Zgc:136389 [Danio rerio]	395	395	100%	8e-139	91%	AAI15138.1
pentraxin-related C-reactive protein [Danio rerio]	395	395	98%	8e-139	94%	AGB69040.1
uncharacterized protein LOC678562 precursor [Danio rerio]	392	392	100%	2e-137	91%	NP_001035410.1
LOC570524 protein [Danio rerio]	392	392	100%	3e-137	91%	AAH93242.1
pentraxin-related C-reactive protein [Danio rerio]	381	381	99%	4e-133	91%	AGB69036.1
PREDICTED: pentraxin fusion protein [Danio rerio]	373	373	99%	4e-130	86%	XP_005162945.1
C-reactive protein 3 [Danio rerio]	367	367	98%	2e-127	88%	AGB69037.1
uncharacterized protein LOC327615 precursor [Danio rerio]	363	363	99%	3e-126	85%	NP_001020468.1
PREDICTED: uncharacterized protein LOC327615 isoform X1 [Danio rerio]	363	363	99%	4e-126	85%	XP_005162934.1
pentraxin-related C-reactive protein [Danio rerio]	358	358	99%	3e-124	83%	AHV85507.1
Unknown (protein for IMAGE:7242112) [Danio rerio]	353	353	99%	8e-122	82%	AAH83428.1
uncharacterized protein LOC100141336 precursor [Danio rerio]	343	343	99%	2e-118	81%	NP_001108373.1
C-reactive protein 3 [Danio rerio]	337	337	99%	1e-115	80%	AGB69038.1
pentraxin-related C-reactive protein [Danio rerio]	330	330	98%	7e-113	77%	AHV85509.1
uncharacterized protein LOC100141350 precursor [Danio rerio]	325	325	99%	5e-111	76%	NP_001108387.1
Si:ch211-234p6.12 protein [Danio rerio]	325	325	99%	6e-111	76%	AAI54042.1
pentraxin-related C-reactive protein [Danio rerio]	323	323	98%	4e-110	76%	AHV85508.1
uncharacterized protein LOC678538 precursor [Danio rerio]	322	322	99%	6e-110	76%	NP_001035387.1
PREDICTED: uncharacterized protein LOC100141350 isoform X1 [Danio rerio]	320	320	99%	3e-109	75%	XP_017209283.1
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	316	316	98%	3e-107	73%	XP_018958886.1
PREDICTED: pentraxin fusion protein-like isoform X1 [Cyprinus carpio]	314	314	98%	1e-106	72%	XP_018964461.1
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	313	313	99%	2e-106	73%	XP_018958893.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	313	313	99%	2e-106	73%	XP_016095272.1
PREDICTED: uncharacterized protein LOC100124600 isoform X1 [Danio rerio]	306	306	99%	3e-103	72%	XP_005162932.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	305	305	99%	5e-103	70%	XP_016092021.1
C-reactive protein [Carassius auratus]	304	304	98%	2e-102	71%	AKO22072.1
uncharacterized protein LOC100124600 precursor [Danio rerio]	303	303	99%	2e-102	71%	NP_001096097.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus rhinocerous]	303	303	99%	2e-102	69%	XP_016417986.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus anshuiensis]	302	302	99%	7e-102	69%	XP_016314329.1
pentraxin-related C-reactive protein [Danio rerio]	301	301	98%	2e-101	72%	AHV85510.1
uncharacterized protein LOC797437 precursor [Danio rerio]	300	300	99%	7e-101	70%	NP_001122266.1
pentraxin-related C-reactive protein [Danio rerio]	297	297	98%	1e-99	71%	AHV85513.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus anshuiensis]	296	296	98%	1e-99	69%	XP_016314345.1
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	295	295	99%	2e-99	68%	XP_018958887.1
hypothetical protein cypCar_00034430 [Cyprinus carpio]	296	296	99%	3e-99	68%	KTF91385.1
pentraxin-related C-reactive protein [Danio rerio]	295	295	98%	3e-99	71%	AHV85511.1
pentraxin-related C-reactive protein [Danio rerio]	295	295	99%	5e-99	70%	AHV85512.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	293	293	98%	2e-98	68%	XP_016092045.1
pentraxin [Ctenopharyngodon idella]	291	291	99%	2e-97	67%	ACM04449.1
PREDICTED: pentraxin fusion protein-like isoform X1 [Sinocyclocheilus anshuiensis]	290	290	98%	6e-97	67%	XP_016327552.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus rhinocerous]	288	288	99%	2e-96	68%	XP_016380387.1
PREDICTED: pentraxin fusion protein-like isoform X2 [Sinocyclocheilus anshuiensis]	288	288	98%	3e-96	66%	XP_016327553.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus rhinocerous]	287	287	98%	3e-96	66%	XP_016411205.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	287	287	98%	5e-96	67%	XP_016095271.1
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	286	286	99%	9e-96	66%	XP_018964465.1
PREDICTED: pentraxin fusion protein-like [Pygocentrus nattereri]	284	284	99%	6e-95	66%	XP_017544190.1
pentraxin [Cyprinus carpio]	283	283	99%	2e-94	66%	BAB69039.1
PREDICTED: pentraxin fusion protein-like [Astyanax mexicanus]	284	284	99%	3e-94	67%	XP_007239597.1
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	280	280	99%	3e-93	65%	XP_018947993.1
PREDICTED: pentraxin fusion protein-like isoform X3 [Cyprinus carpio]	278	278	99%	1e-92	65%	XP_018964464.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	278	278	99%	2e-92	65%	XP_016095275.1
hypothetical protein cypCar_00034570 [Cyprinus carpio]	281	425	97%	4e-92	66%	KTG44527.1
PREDICTED: pentraxin fusion protein-like [Clupea harengus]	276	276	99%	1e-91	64%	XP_012686483.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus anshuiensis]	276	276	99%	2e-91	64%	XP_016327551.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus anshuiensis]	276	276	98%	2e-91	65%	XP_016314330.1
PREDICTED: pentraxin fusion protein [Danio rerio]	275	275	99%	2e-91	64%	XP_699087.5
PREDICTED: pentraxin fusion protein-like [Cyprinus carpio]	275	275	99%	3e-91	64%	XP_018958894.1
hypothetical protein cypCar_00034571 [Cyprinus carpio]	280	461	99%	4e-91	65%	KTG44526.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	275	275	99%	4e-91	64%	XP_016093745.1
PREDICTED: pentraxin fusion protein isoform X2 [Esox lucius]	267	267	99%	3e-88	61%	XP_010887108.1
PREDICTED: pentraxin fusion protein-like [Scleropages formosus]	267	267	99%	4e-88	61%	XP_018590420.1
PREDICTED: pentraxin fusion protein isoform X1 [Esox lucius]	267	267	99%	5e-88	61%	XP_010887107.1
pentraxin fusion protein-like [Scleropages formosus]	267	267	100%	1e-87	61%	KPP70264.1
PREDICTED: pentraxin-4 [Ictalurus punctatus]	261	261	99%	7e-86	59%	XP_017332852.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus grahami]	258	258	78%	1e-85	74%	XP_016122205.1
PREDICTED: pentraxin fusion protein-like [Salmo salar]	261	261	99%	2e-85	60%	XP_014014357.1
PREDICTED: pentraxin fusion protein-like [Oreochromis niloticus]	259	259	99%	4e-85	60%	XP_005448311.1
PREDICTED: pentraxin fusion protein-like [Maylandia zebra]	259	259	99%	4e-85	60%	XP_014265248.1
PREDICTED: pentraxin fusion protein-like [Neolamprologus brichardi]	259	259	99%	4e-85	60%	XP_006801140.1
unnamed protein product [Oncorhynchus mykiss]	260	260	99%	6e-85	59%	CDQ58740.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: pentraxin fusion protein-like [Haplochromis burtoni]	261	261	99%	1e-84	60%	XP_005950593.1
PREDICTED: pentraxin fusion protein-like [Sinocyclocheilus rhinocerous]	256	256	80%	1e-84	72%	XP_016403417.1
PREDICTED: pentraxin fusion protein-like [Pundamilia nyererei]	260	260	99%	2e-84	60%	XP_005753943.1
PREDICTED: pentraxin fusion protein-like [Poecilia mexicana]	257	257	99%	4e-84	60%	XP_014862563.1
PREDICTED: pentraxin fusion protein-like [Poecilia latipinna]	259	259	99%	5e-84	60%	XP_014888132.1
PREDICTED: pentraxin fusion protein-like [Poecilia formosa]	258	258	99%	6e-84	60%	XP_007578065.2
PREDICTED: LOW QUALITY PROTEIN: pentraxin fusion protein-like [Lates calcarifer]	256	256	99%	7e-84	58%	XP_018537343.1
putative pentraxin [Gasterosteus aculeatus]	255	255	99%	9e-84	60%	ACF39478.1
putative pentraxin [Gasterosteus aculeatus]	255	255	99%	1e-83	60%	ACF39477.1
PREDICTED: pentraxin fusion protein-like [Fundulus heteroclitus]	256	256	99%	1e-83	60%	XP_012718484.1
putative pentraxin [Gasterosteus aculeatus]	255	255	99%	1e-83	60%	ACF39494.1
putative pentraxin [Gasterosteus aculeatus]	255	255	99%	1e-83	60%	ACF39482.1
PREDICTED: pentraxin fusion protein-like [Poecilia reticulata]	256	256	99%	1e-83	60%	XP_008434594.1
putative pentraxin [Gasterosteus aculeatus]	255	255	99%	1e-83	60%	ACF39495.1
PREDICTED: pentraxin fusion protein-like isoform X2 [Oryzias latipes]	256	256	99%	1e-83	59%	XP_011486435.1
PREDICTED: pentraxin fusion protein-like [Xiphophorus maculatus]	256	256	99%	1e-83	60%	XP_005812087.1
putative pentraxin [Gasterosteus aculeatus]	254	254	99%	1e-83	60%	ACF39486.1
PREDICTED: pentraxin fusion protein-like isoform X1 [Oryzias latipes]	255	255	99%	2e-83	60%	XP_004080389.1
PREDICTED: pentraxin fusion protein-like [Larimichthys crocea]	255	255	99%	2e-83	60%	XP_010730071.1
Pentraxin fusion protein [Larimichthys crocea]	255	255	99%	2e-83	60%	KKF19124.1
PREDICTED: pentraxin fusion protein-like [Takifugu rubripes]	255	255	99%	3e-83	58%	XP_011601826.1
pentraxin [Monopterus albus]	256	256	99%	4e-83	58%	AJT49024.1

Alignments

C-reactive protein, partial [Danio rerio]

Sequence ID: **AET80950.1** Length: 224 Number of Matches: 1
Range 1: 18 to 224

Score	Expect	Method	Identities	Positives	Gaps	Frame
429 bits(1104)	3e-152()	Compositional matrix adjust.	207/207(100%)	207/207(100%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  18   FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  77

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  78   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  137

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  138  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  197

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLVVPDN
Sbjct  198  NRVKGNVFDWDTIEYDVTGNVLVVPDN  224
```

Chain A, Crystal Structure Of Zebrafish Short-chain Pentraxin Protein Without Calcium Ions

Sequence ID: **4PBO_A** Length: 207 Number of Matches: 1
Range 1: 1 to 207

Score	Expect	Method	Identities	Positives	Gaps	Frame
428 bits(1101)	4e-152()	Compositional matrix adjust.	207/207(100%)	207/207(100%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
```

```
Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLVVPDN
Sbjct  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
```

Chain A, Crystal Structure Of Zebrafish Short-chain Pentraxin Protein

Sequence ID: **4PBP_A** Length: 210 Number of Matches: 1

See 2 more title(s)

Range 1: 4 to 210

Score	Expect	Method	Identities	Positives	Gaps	Frame
428 bits(1101)	4e-152()	Compositional matrix adjust.	207/207(100%)	207/207(100%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  4    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  63

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  64   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  123

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  124  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  183

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLVVPDN
Sbjct  184  NRVKGNVFDWDTIEYDVTGNVLVVPDN  210
```

uncharacterized protein LOC751795 precursor [Danio rerio]

Sequence ID: **NP_001039325.1** Length: 225 Number of Matches: 1

See 2 more title(s)

Range 1: 19 to 225

Score	Expect	Method	Identities	Positives	Gaps	Frame
426 bits(1094)	1e-150()	Compositional matrix adjust.	205/207(99%)	205/207(99%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  19   FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  78

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  79   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  138

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  139  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  198

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLV  DN
Sbjct  199  NRVKGNVFDWDTIEYDVTGNVLVATDN  225
```

Zgc:152809 protein, partial [Danio rerio]

Sequence ID: **AAH95616.1** Length: 211 Number of Matches: 1

Range 1: 5 to 211

Score	Expect	Method	Identities	Positives	Gaps	Frame
424 bits(1090)	2e-150()	Compositional matrix adjust.	205/207(99%)	205/207(99%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  5    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  64

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  65   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  124

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  125  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  184

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLV  DN
Sbjct  185  NRVKGNVFDWDTIEYDVTGNVLVATDN  211
```

pentraxin-related C-reactive protein [Danio rerio]

Sequence ID: **AGB69039.1** Length: 231 Number of Matches: 1

Range 1: 25 to 230

Score	Expect	Method	Identities	Positives	Gaps	Frame
422 bits(1086)	2e-149()	Compositional matrix adjust.	204/206(99%)	204/206(99%)	0/206(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  25   FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  84

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  85   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  144

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  145  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  204

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPD  206
            NRVKGNVFDWDTIEYDVTGNV V PD
Sbjct  205  NRVKGNVFDWDTIEYDVTGNVPVAPD  230
```

Zgc:152809 protein, partial [Danio rerio]

Sequence ID: **AAH81513.1** Length: 234 Number of Matches: 1
Range 1: 28 to 234

Score	Expect	Method	Identities	Positives	Gaps	Frame
422 bits(1085)	3e-149	Compositional matrix adjust.	204/207(99%)	204/207(98%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDR VILFAYYTPDVD
Sbjct  28   FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDRGVILFAYYTPDVD  87

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  88   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  147

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD
Sbjct  148  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  207

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNVLV  DN
Sbjct  208  NRVKGNVFDWDTIEYDVTGNVLVATDN  234
```

pentraxin-related C-reactive protein [Danio rerio]

Sequence ID: **AGB69035.1** Length: 225 Number of Matches: 1
Range 1: 19 to 225

Score	Expect	Method	Identities	Positives	Gaps	Frame
412 bits(1059)	2e-145	Compositional matrix adjust.	198/207(96%)	203/207(98%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD
Sbjct  19   FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  78

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ
Sbjct  79   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  138

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEI ++QMWDYVL S QIKAVY NQD
Sbjct  139  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEITDVQMWDYVLPSTQIKAVYSNQD  198

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            +RVKGNVFDW+TI+YDVTGNVLVVPDN
Sbjct  199  DRVKGNVFDWNTIKYDVTGNVLVVPDN  225
```

Zgc:136389 [Danio rerio]

Sequence ID: **AAI15138.1** Length: 225 Number of Matches: 1
Range 1: 19 to 225

Score	Expect	Method	Identities	Positives	Gaps	Frame
395 bits(1016)	8e-139	Compositional matrix adjust.	189/207(91%)	198/207(95%)	0/207(0%)	

Features:

```
Query  1    FKNLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVD  60
            +K+LSGKVLQFKTATDNSYVKL P+KPLSLSAFTLCMRVATELPLDR+VILFAYY PDVD
Sbjct  19   YKDLSGKVLQFKTATDNSYVKLTPQKPLSLSAFTLCMRVATELPLDRDVILFAYYVPDVD  78

Query  61   ELNVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQ  120
            ELNVWRE+DGRVSLYI+SSKDAAFFRL PLSTLQTHLCV WESATG TAFWMDGRRSLHQ
Sbjct  79   ELNVWREKDGRVSLYIRSSKDAAFFRLHPLSTLQTHLCVTWESATGATAFWMDGRRSLHQ  138

Query  121  VYRKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQD  180
            VYRKG+SIR GGTVVLGQDPDSY+GSFDVDQSFVGEIANLQMWDYVLS+AQIKAVYYNQD
Sbjct  139  VYRKGFSIRPGGTVVLGQDPDSYLGSFDVDQSFVGEIANLQMWDYVLSTAQIKAVYYNQD  198

Query  181  NRVKGNVFDWDTIEYDVTGNVLVVPDN  207
            NRVKGNVFDWDTIEYDVTGNV V  DN
Sbjct  199  NRVKGNVFDWDTIEYDVTGNVPVATDN  225
```

pentraxin-related C-reactive protein [Danio rerio]

Sequence ID: **AGB69040.1** Length: 229 Number of Matches: 1
Range 1: 25 to 228

Score	Expect	Method	Identities	Positives	Gaps	Frame

395 bits(1016) 8e-139() Compositional matrix adjust. 192/204(94%) 195/204(95%) 0/204(0%)

Features:

```
Query  3    NLSGKVLQFKTATDNSYVKLYPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVDEL  62
            L GK L F T TD+SYV++ PEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVDEL
Sbjct  25   GLGGKSLFFPTNTDSSYVQIDPEKPLSLSAFTLCMRVATELPLDREVILFAYYTPDVDEL  84

Query  63   NVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQVY  122
            NVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQVY
Sbjct  85   NVWRERDGRVSLYIQSSKDAAFFRLPPLSTLQTHLCVAWESATGLTAFWMDGRRSLHQVY  144

Query  123  RKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQDNR  182
            RKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQDNR
Sbjct  145  RKGYSIRSGGTVVLGQDPDSYVGSFDVDQSFVGEIANLQMWDYVLSSAQIKAVYYNQDNR  204

Query  183  VKGNVFDWDTIEYDVTGNVLVVPD  206
            VKGNVFDWDTIEYDVTGNV V PD
Sbjct  205  VKGNVFDWDTIEYDVTGNVPVAPD  228
```