

Table S6. Neurexin AS4 dbEST TBLASTN search results, alignment score table and list of validated hits for human, mouse, *Xenopus*, zebrafish, sea lamprey and *Ciona* ESTs.

In parentheses are given the number of AS4 splice variants vs. number of hits fulfilling the search criteria and containing at least part of this sequence area. The AS4 exon sequence is highlighted in yellow. The alignments were generated using a 160 residue mouse neurexin-1 fragment as a query (described in Fig. S5) using BLOSUM62 matrix and default Entrez BLAST settings.

HUMAN (9/23 splice variants)

Sequences producing significant alignments:	(Bits)	Value
emb BX431035.2 BX431035 Homo sapiens FETAL BRAIN Homo sapien...	216	8e-70
gb CN262436.1 17000600092091 GRN_PRENEU Homo sapiens cDNA 5'...	206	2e-66
dbj DB171492.1 DB171492 TKIDN2 Homo sapiens cDNA clone TKIDN...	198	3e-62
dbj DB488484.1 DB488484 RIKEN full-length enriched human cDN...	196	6e-62
dbj DB218625.1 DB218625 TRACH3 Homo sapiens cDNA clone TRACH...	183	3e-56
dbj DB462876.1 DB462876 RIKEN full-length enriched human cDN...	178	1e-54
emb BX431034.2 BX431034 Homo sapiens FETAL BRAIN Homo sapien...	177	2e-54
dbj HY001490.1 HY001490 RIKEN full-length enriched human cDN...	177	4e-54
dbj DB476019.1 DB476019 RIKEN full-length enriched human cDN...	172	2e-52
gb CB154877.1 K-EST0212952 B2N807043 Homo sapiens cDNA clone...	166	7e-50
gb BF345183.1 602018394F1 NCI_CGAP_Brn67 Homo sapiens cDNA c...	161	1e-46
dbj DA747306.1 DA747306 NT2RP7 Homo sapiens cDNA clone NT2RP...	157	5e-46
dbj HY037592.1 HY037592 RIKEN full-length enriched human cDN...	144	2e-41
dbj DB465352.1 DB465352 RIKEN full-length enriched human cDN...	139	8e-40
gb BF529228.1 602041680F1 NCI_CGAP_Brn67 Homo sapiens cDNA c...	94.7	1e-37
dbj HY044110.1 HY044110 RIKEN full-length enriched human cDN...	134	2e-37
gb BQ723058.1 AGENCOURT_8109177 Lupski sympathetic trunk Hom...	127	2e-33
gb BG913108.1 602811713F1 NCI_CGAP_Brn67 Homo sapiens cDNA c...	120	9e-31
dbj HY135994.1 HY135994 RIKEN full-length enriched human cDN...	116	2e-30
dbj DA690044.1 DA690044 NT2NE2 Homo sapiens cDNA clone NT2NE...	105	3e-26
gb AW894889.1 CM1-NN0033-110400-181-e04 NN0033 Homo sapiens ...	100	2e-24
gb BQ879316.1 AGENCOURT_8113386 Lupski dorsal root ganglion ...	99.8	3e-23
dbj DA745012.1 DA745012 NT2RP7 Homo sapiens cDNA clone NT2RP...	94.4	8e-22
gb AA984057.1 am76b03.s1 Stratagene schizo brain S11 Homo sa...	63.9	4e-21
gb CB991846.1 AGENCOURT_13618102 NIH_MGC_148 Homo sapiens cD...	92.8	7e-21
gb CB994026.1 AGENCOURT_13617369 NIH_MGC_148 Homo sapiens cD...	93.2	8e-21
gb EL737097.1 14205 Full Length cDNA from the Mammalian Gene...	91.7	9e-21
gb CB994400.1 AGENCOURT_13642788 NIH_MGC_148 Homo sapiens cD...	92.4	1e-20
gb BM724595.1 UI-E-E01-aiz-1-10-0-UI.r1 UI-E-E01 Homo sapien...	88.6	4e-20
gb BG820026.1 602782573F1 NCI_CGAP_Brn67 Homo sapiens cDNA c...	88.2	6e-20
gb BM801146.1 AGENCOURT_6422532 NIH_MGC_92 Homo sapiens cDNA...	85.5	6e-18
dbj DB464606.2 DB464606 RIKEN full-length enriched human cDN...	82.4	3e-17
gb BF346913.1 602021742F1 NCI_CGAP_Brn67 Homo sapiens cDNA c...	71.2	9e-14

ALIGNMENTS

>emb|BX431035.2| BX431035 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone CS0DF015YG21 5-PRIME, mRNA sequence. Length=451

Score = 216 bits (551), Expect = 8e-70, Method: Compositional matrix adjust.
 Identities = 114/148 (77%), Positives = 117/148 (79%), Gaps = 30/148 (20%)
 Frame = +1

Query	1	QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA GNND	60
Sbjct	4	QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA----	171
Query	61	NERLAIARQRIPYRLGRVVDEWLLDK GRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN	120
Sbjct	172	-----GRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN	273

Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
GL+ L+MAAENDA+IAIVGNVRLVGEVP
Sbjct 274 GLESLDMAAENDAHAIAIVGNVRLVGEVP 357

>gb|CN262436.1| 17000600092091 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
Length=307

Score = 206 bits (525), Expect = 2e-66, Method: Compositional matrix adjust.
Identities = 101/101 (100%), Positives = 101/101 (100%), Gaps = 0/101 (0%)
Frame = +1

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNND 60
QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNND
Sbjct 4 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNND 183

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII 101
NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII
Sbjct 184 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII 306

>dbj|DB171492.1| DB171492 TKIDN2 Homo sapiens cDNA clone TKIDN2006442 5', mRNA
sequence. Length=569

Score = 198 bits (504), Expect = 3e-62, Method: Compositional matrix adjust.
Identities = 92/131 (70%), Positives = 110/131 (84%), Gaps = 0/131 (0%)
Frame = +2

Query 18 EESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGR 77
+E +NDGKYHVVRFTR+GGNATLQVD+WPV E YP GN DNER + +Q+IP++ R
Sbjct 2 KEERTPVNDGKYHVVRFTRNGGNATLQVDNWPVNEHYPTGNTDNERFQMVKQKIPFKYNR 181

Query 78 VVDEWLLDKGRQLTIFNSQATIIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIAI 137
V+EWL +KGRQLTIFN+QA I IGK++G+ FQGQLSGLYY+GLKVLNMAAEN+ NI I
Sbjct 182 PVEEWLQEKGRLTIFNTQAQIAIGGKDKGRLFQGLSGLYYDGLKVLNMAAENNPNIKI 361

Query 138 VGNVRLVGEVP 148
G+VRLVGEVP
Sbjct 362 NGSVRLVGEVP 394

>dbj|DB488484.1| DB488484 RIKEN full-length enriched human cDNA library,
hypothalamus Homo sapiens cDNA clone H033022N07 5', mRNA sequence. Length=453

Score = 196 bits (499), Expect = 6e-62, Method: Compositional matrix adjust.
Identities = 94/94 (100%), Positives = 94/94 (100%), Gaps = 0/94 (0%)
Frame = +1

Query 54 YPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIIGGKEQGQPFQGG 113
YPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIIGGKEQGQPFQGG
Sbjct 1 YPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIIGGKEQGQPFQGG 180

Query 114 LSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV 147
LSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV
Sbjct 181 LSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV 282

>dbj|DB218625.1| DB218625 TRACH3 Homo sapiens cDNA clone TRACH3008421 5', mRNA
sequence. Length=560

Score = 183 bits (465), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 95/125 (76%), Positives = 95/125 (76%), Gaps = 30/125 (24%)

Frame = +1

```
Query 24 INDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWL 83
INDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAG
Sbjct 1 INDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAG----- 102

Query 84 LDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRL 143
RQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRL
Sbjct 103 ----RQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRL 270

Query 144 VGEVP 148
VGEVP
Sbjct 271 VGEVP 285
```

>dbj|DB462876.1| DB462876 RIKEN full-length enriched human cDNA library, hippocampus
Homo sapiens cDNA clone H023002C01 5', mRNA sequence. Length=480

Score = 178 bits (451), Expect = 1e-54, Method: Compositional matrix adjust.
Identities = 85/85 (100%), Positives = 85/85 (100%), Gaps = 0/85 (0%)
Frame = +3

```
Query 64 LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLK 123
LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLK
Sbjct 3 LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLK 182

Query 124 VLNMAAENDANIAIVGNVRLVGEVP 148
VLNMAAENDANIAIVGNVRLVGEVP
Sbjct 183 VLNMAAENDANIAIVGNVRLVGEVP 257
```

>emb|BX431034.2| BX431034 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF015YG21 5-PRIME, mRNA sequence. Length=420

Score = 177 bits (448), Expect = 2e-54, Method: Compositional matrix adjust.
Identities = 93/129 (72%), Positives = 97/129 (75%), Gaps = 30/129 (23%)
Frame = +1

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA
Sbjct 4 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA---- 171

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
GRQLTIFNSQA IIGGKEQGQPFQQLSGLYYN
Sbjct 172 -----GRQLTIFNSQAPIIIGGKEQGQPFQQLSGLYYN 273

Query 121 GLKVLNMAA 129
GL+VL++ +
Sbjct 274 GLEVLDLGS 300
```

>dbj|HY001490.1| HY001490 RIKEN full-length enriched human cDNA library, testis
Homo sapiens cDNA clone H04D005J11, mRNA sequence. Length=529

Score = 177 bits (449), Expect = 4e-54, Method: Compositional matrix adjust.
Identities = 85/95 (89%), Positives = 89/95 (94%), Gaps = 0/95 (0%)
Frame = +2

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPA G D
Sbjct 239 QGTGVVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 418
```

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNS 95
NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNS
Sbjct 419 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNS 523

>dbj|DB476019.1| DB476019 RIKEN full-length enriched human cDNA library, hippocampus
Homo sapiens cDNA clone H023069F15 5', mRNA sequence. Length=487

Score = 172 bits (437), Expect = 2e-52, Method: Compositional matrix adjust.
Identities = 83/85 (98%), Positives = 83/85 (98%), Gaps = 0/85 (0%)
Frame = +3

Query 64 LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLK 123
L IARQRIPYRLGRVVDEWLLDKGRQ TIFNSQATIIIGGKEQGQPFQGLSGLYYNGLK
Sbjct 3 LPIARQRIPYRLGRVVDEWLLDKGRQXTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLK 182

Query 124 VLNMAAENDANIAIVGNVRLVGEVP 148
VLNMAAENDANIAIVGNVRLVGEVP
Sbjct 183 VLNMAAENDANIAIVGNVRLVGEVP 257

>gb|CB154877.1| K-EST0212952 B2N807043 Homo sapiens cDNA clone B2N807043-26-H08
5', mRNA sequence. Length=465

Score = 166 bits (419), Expect = 7e-50, Method: Compositional matrix adjust.
Identities = 85/135 (63%), Positives = 96/135 (71%), Gaps = 30/135 (22%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFTSRGGNATLQVDSWPV ERYPA
Sbjct 144 QGTGVIFNVGTDDITIDEPNIAIVSDGKYHVVRFTSRGGNATLQVDSWPVNERYPAAAA 311

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
GRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN
Sbjct 312 -----GRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYN 413

Query 121 GLKVLNMAAENDANI 135
GLKVL +AAE+D N+
Sbjct 414 GLKVLALAAESDPNV 458

>gb|BF345183.1| 602018394F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4153894
5', mRNA sequence. Length=826

Score = 161 bits (408), Expect = 1e-46, Method: Compositional matrix adjust.
Identities = 88/149 (59%), Positives = 99/149 (66%), Gaps = 31/149 (21%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFTSRGGNATLQVDSWPV ERYPA
Sbjct 300 QGTGVIFNVGTDDITIDEPNIAIVSDGKYHVVRFTSRGGNATLQVDSWPVNERYPAAAA 467

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
GRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN
Sbjct 468 -----GRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYN 569

Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
GLKVL E + G++RLVGE P
Sbjct 570 GLKVLAAGRRERPQMLRTEGHLRLVGEVP 656

>dbj|DA747306.1| DA747306 NT2RP7 Homo sapiens cDNA clone NT2RP7012472 5', mRNA sequence. Length=554

Score = 157 bits (396), Expect = 5e-46, Method: Compositional matrix adjust.
Identities = 72/110 (65%), Positives = 88/110 (80%), Gaps = 0/110 (0%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA**GNND** 60
QKIGV FN+GT DI+I+E +NDGKYHVVRFRTR+GGNATLQVD+WPV E YP GN D
Sbjct 225 QGKIGVVFNIGTVDISIKEERTPVNDGKYHVVRFRTRNGGNATLQVDNWPVNEHYPTGNTD 404
Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPF 110
NER + +Q+IP++ R V+EWL +KGRQLTIFN+QA I IGGK++ P
Sbjct 405 NERFQMVKQKIPFKYNRPVEEWLQEKGRQLTIFNTQAQIAIGGKDKRTPL 554

>dbj|HY037592.1| HY037592 RIKEN full-length enriched human cDNA library, testis Homo sapiens cDNA clone H04D131C20, mRNA sequence. Length=467

Score = 144 bits (363), Expect = 2e-41, Method: Compositional matrix adjust.
Identities = 69/79 (87%), Positives = 73/79 (92%), Gaps = 0/79 (0%)
Frame = +1

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA**GNND** 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPA GN D
Sbjct 229 QGTVGVI FNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 408
Query 61 **NERLAIARQRIPYRLGRVV** 79
NERLAIARQRIPYRLGRVV
Sbjct 409 NERLAIARQRIPYRLGRVV 465

>dbj|DB465352.1| DB465352 RIKEN full-length enriched human cDNA library, hippocampus Homo sapiens cDNA clone H023016C09 5', mRNA sequence. Length=429

Score = 139 bits (351), Expect = 8e-40, Method: Compositional matrix adjust.
Identities = 69/70 (99%), Positives = 69/70 (99%), Gaps = 0/70 (0%)
Frame = +1

Query 79 **VDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIAIV 138
VDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDA IAIV
Sbjct 1 VDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDAKIAIV 180
Query 139 GNVRLVGEVP 148
GNVRLVGEVP
Sbjct 181 GNVRLVGEVP 210

>gb|BF529228.1| 602041680F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4179690 5', mRNA sequence. Length=627

Score = 94.7 bits (234), Expect(2) = 1e-37, Method: Compositional matrix adjust.
Identities = 51/102 (50%), Positives = 61/102 (60%), Gaps = 30/102 (29%)
Frame = +1

Query 47 SWPVIERYPA**GNNDNERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQ 106
+WPV ERYPAG RQLTIFNSQA I IGG++Q
Sbjct 193 AWPVNERYPAG-----RQLTIFNSQAAIKIGGRDQ 282
Query 107 GQPFQGLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
G+PFQGLSGLYYNGLKVL + AE++ N+ G +RLVGE P
Sbjct 283 GRPFQGLSGLYYNGLKVLALDAESEPNVRTEGQLRLVGEVP 408

>dbj|HY044110.1| HY044110 RIKEN full-length enriched human cDNA library, testis
Homo sapiens cDNA clone H04D155A10, mRNA sequence. Length=462

Score = 134 bits (336), Expect = 2e-37, Method: Compositional matrix adjust.
Identities = 63/73 (86%), Positives = 67/73 (92%), Gaps = 0/73 (0%)
Frame = +3

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPAGNND 60
      QG +GV FNVGTDDI I+E NAI++DGKYHVVRFTSRGGNATLQVDSWPV ERYPAGN D
Sbjct 243 QGTVGVIFNVGTDDITIDEPNAIVSDGKYHVVRFTSRGGNATLQVDSWPVNERYPAGNFD 422

Query 61 NERLAIARQRIPY 73
      NERLAIARQRIPY
Sbjct 423 NERLAIARQRIPY 461
```

>gb|BQ723058.1| AGENCOURT_8109177 Lupski_sympathetic_trunk Homo sapiens cDNA
clone IMAGE:6189515 5', mRNA sequence. Length=921

Score = 127 bits (319), Expect = 2e-33, Method: Compositional matrix adjust.
Identities = 67/115 (58%), Positives = 76/115 (66%), Gaps = 30/115 (26%)
Frame = +1

```
Query 34 FTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIF 93
      FTRSGGNATLQVDSWPV ERYPA GRQLTIF
Sbjct 1 FTRSGGNATLQVDSWPVNERYP-----GRQLTIF 90

Query 94 NSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
      NSQA I IGG++QG+PFQGG+SGLYYNGLKVL +AAE+D N+ G++RLVGE P
Sbjct 91 NSQAAIKIGGRDQGRPFQGVVSGLYYNGKVLALAAESDPNVRTEGHLRLVGEVP 255
```

>gb|BG913108.1| 602811713F1 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943715
5', mRNA sequence. Length=1007

Score = 120 bits (302), Expect = 9e-31, Method: Compositional matrix adjust.
Identities = 55/72 (76%), Positives = 64/72 (89%), Gaps = 0/72 (0%)
Frame = +1

```
Query 77 RVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIA 136
      RVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYNGLKVL +AAE+D N+
Sbjct 1 RVVDEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYNGKVLALAAESDPNVR 180

Query 137 IVGNVRLVGEVP 148
      G++RLVGE P
Sbjct 181 TEGHLRLVGEVP 216
```

>dbj|HY135994.1| HY135994 RIKEN full-length enriched human cDNA library, brain
Homo sapiens cDNA clone H06D115F11, mRNA sequence. Length=480

Score = 116 bits (290), Expect = 2e-30, Method: Compositional matrix adjust.
Identities = 54/71 (76%), Positives = 63/71 (89%), Gaps = 0/71 (0%)
Frame = +1

```
Query 78 VVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIAI 137
      VVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYNGLKVL +AAE+D N+
Sbjct 1 VVDEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYNGKVLALAAESDPNVRT 180

Query 138 VGNVRLVGEVP 148
      G++RLVGE P
Sbjct 181 EGHLRLVGEVP 213
```

>gb|AW894889.1| CM1-NN0033-110400-181-e04 NN0033 Homo sapiens cDNA, mRNA sequence. Length=437

Score = 100 bits (248), Expect = 2e-24, Method: Compositional matrix adjust. Identities = 46/67 (69%), Positives = 58/67 (87%), Gaps = 0/67 (0%)
Frame = +1

Query 66 IARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVL 125
+ Q+IP++ R V+EWL +KGRQLTIFN+QA I IGGK++G+ FQGQLSGLYY+GLKVL
Sbjct 118 MVEQKIPFKYNRPVVEEWLQEKGRQLTIFNTQAQIAIGGKDKGRLFQGLSGLYYDGLKVL 297
Query 126 NMAAEND 132
NMAAEN+
Sbjct 298 NMAAENN 318

>gb|BQ879316.1| AGENCOURT_8113386 Lupski_dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6178941 5', mRNA sequence. Length=940

Score = 99.8 bits (247), Expect = 3e-23, Method: Compositional matrix adjust. Identities = 51/76 (67%), Positives = 57/76 (75%), Gaps = 3/76 (4%)
Frame = +1

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPA GNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFTSRGGNATLQ DSW V ERY P G
Sbjct 334 QGTVGVI FNVGTDDITIDEPNAI VSDGKYHVVRFTSRGGNATLQADSWTVNERYP-GQPP 510
Query 61 NERLAIARQRIPYRLG 76
E L + R+P R G
Sbjct 511 AEHL--QQPRLPSRSG 552

>dbj|DA745012.1| DA745012 NT2RP7 Homo sapiens cDNA clone NT2RP7009828 5', mRNA sequence. Length=564

Score = 94.4 bits (233), Expect = 8e-22, Method: Compositional matrix adjust. Identities = 51/97 (53%), Positives = 58/97 (60%), Gaps = 30/97 (31%)
Frame = +2

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPA GNND 60
QGKIGV FN+GT DI+I+E +NDGKYHVVRFTSR+GGNATLQVD+WPV E YP
Sbjct 362 QGKIGVFNIGTVDISIKEERTPVNDGKYHVVRFTSRNGGNATLQVDNWPVNEHYPT---- 529
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA 97
GRQLTIFN+QA
Sbjct 530 -----GRQLTIFNTQA 562

>gb|AA984057.1| am76b03.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1616333 3' similar to TR:Q63376 Q63376 NEUREXIN II-BETA-A PRECURSOR. ;, mRNA sequence. Length=728

Score = 63.9 bits (154), Expect(2) = 4e-21, Method: Compositional matrix adjust. Identities = 42/109 (39%), Positives = 51/109 (47%), Gaps = 31/109 (28%)
Frame = -2

Query 40 NATLQVDSWPVIERYPA GNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATI 99
N TLQVDSWPV ERY AG RQLTIFNSQA I
Sbjct 508 NRTLQVDSWPVNERAAG-----RQLTIFNSQA AI 419
Query 100 IIGGKEQGQPFQGLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
I G++QG+P + G + AE+D N+ ++RLVGE P
Sbjct 418 KIVGRDQGRPSRVPVCPASTTMGSRCC-AGAESDPNVRTECHLRLVGE GP 275

Mus Musculus (4/27 splice variants)

Sequences producing significant alignments:			Score (Bits)	E Value
gb	CF553803.1	AGENCOURT_15611286 Organ of Corti Mus musculus...	283	7e-94
gb	CB249743.1	UI-M-EX0-by1-b-10-0-UI.r1 NIH_BMAP_EX0 Mus mus...	253	1e-82
gb	BM944179.1	UI-M-EH0p-bvq-g-21-0-UI.r1 NIH_BMAP_EH0p Mus m...	249	8e-82
gb	BM950483.1	UI-M-EH0p-buu-o-21-0-UI.r1 NIH_BMAP_EH0p Mus m...	244	1e-80
gb	DT927517.1	PCRS30340 Hematopoietic stem cells Mus musculu...	241	1e-78
gb	CX208193.1	MNS13294 Mouse Neurosphere Normalized cDNA lib...	239	4e-78
gb	CX217204.1	MNS31265 Mouse Neurosphere Normalized cDNA lib...	236	5e-77
gb	DT924042.1	PCRS10316 Hematopoietic stem cells Mus musculu...	233	4e-76
gb	DT925356.1	PCRS50408 Hematopoietic stem cells Mus musculu...	233	7e-76
gb	BU056634.1	UI-M-FO0-cac-b-20-0-UI.r1 NIH_BMAP_FO0 Mus mus...	229	7e-74
gb	CX206076.1	MNS10169 Mouse Neurosphere Normalized cDNA lib...	226	3e-73
gb	CF743000.1	UI-M-GV0-cln-a-15-0-UI.r1 NIH_BMAP_GV0 Mus mus...	226	9e-73
gb	CF743053.1	UI-M-GV0-cln-k-17-0-UI.r1 NIH_BMAP_GV0 Mus mus...	226	3e-72
gb	CX202063.1	MNS03719 Mouse Neurosphere Normalized cDNA lib...	221	3e-71
gb	CF743182.1	UI-M-GV0-clo-c-19-0-UI.r1 NIH_BMAP_GV0 Mus mus...	199	2e-61
gb	CX217588.1	MNS31680 Mouse Neurosphere Normalized cDNA lib...	153	2e-60
gb	CA328232.1	UI-M-FY0-cdb-m-23-0-UI.r1 NIH_BMAP_FY0 Mus mus...	195	3e-60
gb	CX215555.1	MNS25539 Mouse Neurosphere Normalized cDNA lib...	187	1e-58
gb	CX223578.1	MNS41923 Mouse Neurosphere Normalized cDNA lib...	184	3e-57
gb	CX199726.1	MNS08623 Mouse Neurosphere Normalized cDNA lib...	184	3e-56
gb	CX216431.1	MNS29780 Mouse Neurosphere Normalized cDNA lib...	182	5e-56
gb	DN173237.1	NMB07261 Mus Musculus Lateral Ventricle Wall C...	182	6e-56
gb	CA327544.1	UI-M-FY0-ccz-i-02-0-UI.r1 NIH_BMAP_FY0 Mus mus...	178	7e-54
dbj	BB858994.1	BB858994 RIKEN full-length enriched, brain CR...	145	5e-42
gb	DT904887.1	BMSB13606 Hematopoietic stem cells Mus musculu...	144	8e-41
gb	CX220555.1	MNS36241 Mouse Neurosphere Normalized cDNA lib...	100	2e-37
gb	CX212965.1	MNS18219 Mouse Neurosphere Normalized cDNA lib...	129	2e-35
gb	CX203319.1	MNS05584 Mouse Neurosphere Normalized cDNA lib...	125	1e-33
dbj	BP427400.1	BP427400 Mus musculus cerebellum E18-P56 Mus ...	120	2e-32
dbj	BB692115.1	BB692115 RIKEN full-length enriched, 2 days n...	119	7e-32
dbj	BB695296.1	BB695296 RIKEN full-length enriched, 2 days n...	115	2e-30
dbj	BB130803.1	BB130803 RIKEN full-length enriched, 16 days ...	109	4e-29
gb	DT915246.1	BMSB12312 Hematopoietic stem cells Mus musculu...	111	9e-28
dbj	BY632421.1	BY632421 RIKEN full-length enriched, visual c...	105	1e-26
gb	DT906469.1	PCRS50341 Hematopoietic stem cells Mus musculu...	100	5e-25

ALIGNMENTS

>gb|CF553803.1| AGENCOURT_15611286 Organ of Corti Mus musculus cDNA clone
 IMAGE:30519294 5', mRNA sequence. Length=925

Score = 283 bits (723), Expect = 7e-94, Method: Compositional matrix adjust.
 Identities = 135/136 (99%), Positives = 136/136 (100%), Gaps = 0/136 (0%)
 Frame = +2

Query	13	DDIAIEESNAIINDGKYHVFRFTRSGGNATLQVDSWPVIERYPA GNNNDNERLAIARQRIP	72
Sbjct	8	DDIAIEESNAIINDGKYHVFRFTRSGGNATLQVDSWPVIERYPAGNNNDNERLAIARQRIP	187
Query	73	YRLGRVVDEWLLDKG RQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAEND	132
Sbjct	188	YRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYNGLKVLNMAAEND	367
Query	133	ANIAIVGNVRLVGEVP 148	
Sbjct	368	ANIAIVGNV+LVGEVP 415	

>gb|CB249743.1| UI-M-EX0-by1-b-10-0-UI.r1 NIH_BMAP_EX0 Mus musculus cDNA clone
IMAGE:5719593 5', mRNA sequence. Length=881

Score = 253 bits (647), Expect = 1e-82, Method: Compositional matrix adjust.
Identities = 121/148 (82%), Positives = 134/148 (91%), Gaps = 0/148 (0%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA**GNND** 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 69 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 248
Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYN 120
NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN
Sbjct 249 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGGVSGLYYN 428
Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
GLKVL +AAE+D N+ G++RLVGE P
Sbjct 429 GLKVLALAAESDPNVRTEGHLRLVGEVP 512

>gb|BM944179.1| UI-M-EH0p-bvq-g-21-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
IMAGE:5695532 5', mRNA sequence. Length=711

Score = 249 bits (636), Expect = 8e-82, Method: Compositional matrix adjust.
Identities = 119/145 (82%), Positives = 132/145 (91%), Gaps = 0/145 (0%)
Frame = +2

Query 4 IGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA**GNNDNER** 63
+GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN DNER
Sbjct 8 VGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFDNER 187
Query 64 **LAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYNGLK 123
LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYNGLK
Sbjct 188 LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGGVSGLYYNGLK 367
Query 124 VLNMAAENDANIAIVGNVRLVGEVP 148
VL +AAE+D N+ G++RLVGE P
Sbjct 368 VLALAAESDPNVRTEGHLRLVGEVP 442

>gb|BM950483.1| UI-M-EH0p-buu-o-21-0-UI.r1 NIH_BMAP_EH0p Mus musculus cDNA clone
IMAGE:5687276 5', mRNA sequence. Length=590

Score = 244 bits (624), Expect = 1e-80, Method: Compositional matrix adjust.
Identities = 118/145 (81%), Positives = 131/145 (90%), Gaps = 0/145 (0%)
Frame = +1

Query 4 IGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPA**GNNDNER** 63
+GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN DNER
Sbjct 46 LGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFDNER 225
Query 64 **LAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYNGLK 123
LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYNGLK
Sbjct 226 LAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGGVSGLYYNGLK 405
Query 124 VLNMAAENDANIAIVGNVRLVGEVP 148
VL +AAE+D N+ ++RLVGE P
Sbjct 406 VLALAAESDPNVRTECHLRLVGEVP 480

>gb|DT927517.1| PCRS30340 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
Length=699

Score = 241 bits (615), Expect = 1e-78, Method: Compositional matrix adjust.
Identities = 116/116 (100%), Positives = 116/116 (100%), Gaps = 0/116 (0%)
Frame = +2

```
Query 33 RFTRSGGNATLQVDSWPVIERYPAGNNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTI 92
Sbjct 2 RFTRSGGNATLQVDSWPVIERYPAGNNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTI 181

Query 93 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
Sbjct 182 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 349
```

>gb|CX208193.1| MNS13294 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=670

Score = 239 bits (611), Expect = 4e-78, Method: Compositional matrix adjust.
Identities = 114/135 (84%), Positives = 125/135 (93%), Gaps = 0/135 (0%)
Frame = +2

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNNND 60
Sbjct 257 QGTVGIVFNVGTDDITIDEPNNAIVSDGKYHVVRFTRSGGNATLQVDSWPVNERYPAGNFD 436

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
Sbjct 437 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN 616

Query 121 GLKVLNMAAENDANI 135
Sbjct 617 GLKVLALAAESDPNV 661
```

>gb|CX217204.1| MNS31265 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=642

Score = 236 bits (602), Expect = 5e-77, Method: Compositional matrix adjust.
Identities = 112/135 (83%), Positives = 123/135 (91%), Gaps = 0/135 (0%)
Frame = +1

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGNNND 60
Sbjct 220 HGTVGIVFNVGTDDITIDEPNNAIVSDGKYHVVRFTRSGGNATLQVDSWPVNERYPAGNFD 399

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
Sbjct 400 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I IGG++ G+PFQGG+SGLYYN 579

Query 121 GLKVLNMAAENDANI 135
Sbjct 580 GLKVLALAAESDPNV 624
```

>gb|DT924042.1| PCRS10316 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
Length=563

Score = 233 bits (594), Expect = 4e-76, Method: Compositional matrix adjust.
Identities = 113/116 (97%), Positives = 113/116 (97%), Gaps = 0/116 (0%)
Frame = +2

Query 33 RFTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTI 92
Sbjct 2 RFTRSGGNATLQVDSWPVIERYPAGNNDNE AIARQR PYRLGRVVDEWLLDKGRQLTI 181

Query 93 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
Sbjct 182 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 349

>gb|DT925356.1| PCRS50408 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
Length=635

Score = 233 bits (595), Expect = 7e-76, Method: Compositional matrix adjust.
Identities = 113/116 (97%), Positives = 115/116 (99%), Gaps = 0/116 (0%)
Frame = +2

Query 33 RFTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTI 92
Sbjct 2 RFTRSGGNATLQVDSWP IERYPAGNNDNERLA+ARQRIPYRLGRVVDEWLLD+GRQLTI 181

Query 93 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
Sbjct 182 FNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 349

>gb|BU056634.1| UI-M-FO0-cac-b-20-0-UI.r1 NIH_BMAP_F00 Mus musculus cDNA clone
IMAGE:6409267 5', mRNA sequence. Length=710

Score = 229 bits (584), Expect = 7e-74, Method: Compositional matrix adjust.
Identities = 109/132 (83%), Positives = 119/132 (90%), Gaps = 0/132 (0%)
Frame = +2

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
Sbjct 314 QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D 493

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
Sbjct 494 NERLAIARQRI YRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PF GQ+SGLYY 673

Query 121 GLKVLNMAAEND 132
Sbjct 674 GLTVLALAAESD 709

>gb|CX206076.1| MNS10169 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=621

Score = 226 bits (577), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 109/125 (87%), Positives = 117/125 (94%), Gaps = 0/125 (0%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
Sbjct 222 QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D 401

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
Sbjct 402 NERLAIARQRI YRLGRVVDEWLLDKGRQLTIFNSQA I IGG++QG+PFQGQ+SGLYYN 581

Query 121 GLKVL 125

Sbjct 582 GLKVL 596

>gb|CF743000.1| UI-M-GV0-cln-a-15-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30616238 5', mRNA sequence. Length=734

Score = 226 bits (577), Expect = 9e-73, Method: Compositional matrix adjust.
Identities = 118/148 (80%), Positives = 118/148 (80%), Gaps = 30/148 (20%)
Frame = +2

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPA**GNND** 60
QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAG
Sbjct 296 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAG--- 466
Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
RQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN
Sbjct 467 -----RQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 565
Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
GLKVLNMAAENDANIAIVGNVRLVGEVP
Sbjct 566 GLKVLNMAAENDANIAIVGNVRLVGEVP 649

>gb|CF743053.1| UI-M-GV0-cln-k-17-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30616480 5', mRNA sequence. Length=751

Score = 226 bits (575), Expect = 3e-72, Method: Compositional matrix adjust.
Identities = 118/148 (80%), Positives = 118/148 (80%), Gaps = 30/148 (20%)
Frame = +2

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPA**GNND** 60
QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAG
Sbjct 296 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAG--- 466
Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
RQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN
Sbjct 467 -----RQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 565
Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
GLKVLNMAAENDANIAIVGNVRLVGEVP
Sbjct 566 GLKVLNMAAENDANIAIVGNVRLVGEVP 649

>gb|CX202063.1| MNS03719 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=627

Score = 221 bits (564), Expect = 3e-71, Method: Compositional matrix adjust.
Identities = 106/123 (86%), Positives = 115/123 (93%), Gaps = 0/123 (0%)
Frame = +2

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPA**GNND** 60
QG +GV FNVGTDDI I+E NAI++DGKYHVRFTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 227 QGTVGVIFNVGTDDITIDEPNAIIVSDGKYHVRFTRSGGNATLQVDSWPVNERYPAGNFD 406
Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
NERLAIARQRIPYRLGRVV+EWLLDKGRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN
Sbjct 407 NERLAIARQRIPYRLGRVVNEWLLDKGRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYN 586
Query 121 GLK 123
GLK
Sbjct 587 GLK 595

>gb|CF743182.1| UI-M-GV0-clo-c-19-0-UI.r1 NIH_BMAP_GV0 Mus musculus cDNA clone
IMAGE:30621282 5', mRNA sequence. Length=833

Score = 199 bits (505), Expect = 2e-61, Method: Compositional matrix adjust.
Identities = 93/130 (72%), Positives = 111/130 (85%), Gaps = 0/130 (0%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QGKIGV FN+GT DI+I+E +NDGKYHVVRFRTR+GGNATLQVD+WPV E YP GN D
Sbjct 300 QGKIGVVFNIGTVDISIKEERTPVNDGKYHVVRFRTRNGGNATLQVDNWPVNEHYPTGNTD 479

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
NERL + +Q+IP++ R V+EWL +KGRQLTIFN+QA I IGGK++G+ FQGQLSGLYY+
Sbjct 480 NERLQMVKQKIPFKYNRPVVEEWLQEKGRQLTIFNTQAQIAIGGKDKGRLFQGLSGLYYD 659

Query 121 GLKVLNMAAE 130
GLKVLNMAAE
Sbjct 660 GLKVLNMAAE 689

>gb|CX217588.1| MNS31680 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=765

Score = 153 bits (386), Expect(2) = 2e-60, Method: Compositional matrix adjust.
Identities = 72/82 (88%), Positives = 76/82 (93%), Gaps = 0/82 (0%)
Frame = +3

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 42 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 221

Query 61 NERLAIARQRIPYRLGRVVDEW 82
NERLAIARQRIPYRLGRVVDEW
Sbjct 222 NERLAIARQRIPYRLGRVVDEW 287

>gb|CA328232.1| UI-M-FY0-cdb-m-23-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE:6827424 5', mRNA sequence. Length=790

Score = 195 bits (496), Expect = 3e-60, Method: Compositional matrix adjust.
Identities = 93/109 (85%), Positives = 100/109 (92%), Gaps = 0/109 (0%)
Frame = +1

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 382 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 561

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQP 109
NERLAIARQRIPYRLGRVV EWLLDKGRQLTIFNSQA I IGG++QG+P
Sbjct 562 NERLAIARQRIPYRLGRVVXEWLLDKGRQLTIFNSQAAIKIGGRDQGRP 708

>gb|CX215555.1| MNS25539 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=401

Score = 187 bits (474), Expect = 1e-58, Method: Compositional matrix adjust.
Identities = 90/90 (100%), Positives = 90/90 (100%), Gaps = 0/90 (0%)
Frame = +1

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60

```
Sbjct 130 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 309
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQL 90
NERLAIARQRIPYRLGRVVDEWLLDKGRQL
Sbjct 310 NERLAIARQRIPYRLGRVVDEWLLDKGRQL 399
```

>gb|CX223578.1| MNS41923 Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence. Length=503

Score = 184 bits (467), Expect = 3e-57, Method: Compositional matrix adjust.
Identities = 89/101 (88%), Positives = 93/101 (92%), Gaps = 0/101 (0%)
Frame = +1

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 151 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 330
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII 101
NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I I
Sbjct 331 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIKI 453
```

>gb|CX199726.1| MNS08623 Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence. Length=747

Score = 184 bits (467), Expect = 3e-56, Method: Compositional matrix adjust.
Identities = 89/101 (88%), Positives = 93/101 (92%), Gaps = 0/101 (0%)
Frame = +3

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 348 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 527
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII 101
NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I I
Sbjct 528 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIRI 650
```

>gb|CX216431.1| MNS29780 Mouse Neurosphere Normalized cDNA library Mus musculus cDNA 5', mRNA sequence. Length=588

Score = 182 bits (462), Expect = 5e-56, Method: Compositional matrix adjust.
Identities = 88/101 (87%), Positives = 92/101 (91%), Gaps = 0/101 (0%)
Frame = +3

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
QG +GV FNVGTDDI I+E NAI++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGN D
Sbjct 240 QGTVGVIFNVGTDDITIDEPNNAIVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNFD 419
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIII 101
NERLAIARQRIPYRLGRVV EWLLDKGRQLTIFNSQA I I
Sbjct 420 NERLAIARQRIPYRLGRVVHEWLLDKGRQLTIFNSQAAIKI 542
```

>gb|DN173237.1| NMB07261 Mus Musculus Lateral Ventricle Wall C57BL/6 adult Mus musculus cDNA 5', mRNA sequence. Length=631

Score = 182 bits (462), Expect = 6e-56, Method: Compositional matrix adjust.
Identities = 88/106 (83%), Positives = 97/106 (92%), Gaps = 0/106 (0%)
Frame = +3

Query 41 ATLOVDSWPVIERYPA**GNNDNERLAIARQRIPYRLGRVVDEWLLDKG**RQLTIFNSQATII 100
 ATLOVDSWPV ERYPAGN DNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I
 Sbjct 3 ATLOVDSWPVNERYPAGNFDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAAIK 182

Query 101 IGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGE 146
 IGG++QG+PFQGG+SGLYYNGLKVL +AAE+D N+ G++RLVGE
 Sbjct 183 IGGRDQGRPFQGVVSGLYYNGKVLALAAESDPNVRTEGHLRLVGE 320

>gb|CA327544.1| UI-M-FY0-ccz-i-02-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
 IMAGE:6826539 5', mRNA sequence. Length=766

Score = 178 bits (452), Expect = 7e-54, Method: Compositional matrix adjust.
 Identities = 92/148 (62%), Positives = 105/148 (71%), Gaps = 30/148 (20%)
 Frame = +1

Query 1 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPVIERYPA**GNND** 60
 QG +GV FNVGTDDI I+E NAI++DGKYHVVRFTSRGGNATLOVDSWPV ERYPA
 Sbjct 244 QGTVGVIFNVGTDDITIDEPNAIIVSDGKYHVVRFTSRGGNATLOVDSWPVNERYPAAAA 411

Query 61 **NERLAIARQRIPYRLGRVVDEWLLDKG**RQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
 GRQLTIFNSQA I IGG++QG+PFQGG+SGLYYN
 Sbjct 412 -----GRQLTIFNSQAAIKIGGRDQGRPFQGVVSGLYYN 513

Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
 GLKVL +AAE+D N+ G++RLVGE P
 Sbjct 514 GLKVLALAAESDPNVRTEGHLRLVGEVP 597

>dbj|BB858994.1| BB858994 RIKEN full-length enriched, brain CRL-1443 BC3H1 cDNA
 Mus musculus cDNA clone G430003L02 5', mRNA sequence. Length=460

Score = 145 bits (365), Expect = 5e-42, Method: Compositional matrix adjust.
 Identities = 84/142 (59%), Positives = 94/142 (66%), Gaps = 25/142 (18%)
 Frame = +1

Query 1 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPVIERYPA**GNND** 60
 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWP P
 Sbjct 70 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPAYRTLPC---- 237

Query 61 **NERLAIARQ--RIPYRLGRVVDEWLLD-----KGR**QLTIFNSQATII-----IGGKEQG 107
 +Q R P+RL + E+ +D G +SQ++I + GK +
 Sbjct 238 -----RKQ**RAPWRL--LDSEFHIDLVE*LMNGYSTKGVSSQSSIAKQP**LAGKSRA 393

Query 108 QPFQQLSGLYYNGLKVLNMAA 129
 PFQQLSGLYYNGLKVLNMAA
 Sbjct 394 SPFQQLSGLYYNGLKVLNMAA 459

>gb|DT904887.1| BMSB13606 Hematopoietic stem cells Mus musculus cDNA, mRNA sequence.
 Length=721

Score = 144 bits (364), Expect = 8e-41, Method: Compositional matrix adjust.
 Identities = 69/69 (100%), Positives = 69/69 (100%), Gaps = 0/69 (0%)
 Frame = +3

Query 4 IGKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPVIERYPA**GNNDNER** 63
 IGKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPVIERYPAGNNDNER
 Sbjct 513 IGKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLOVDSWPVIERYPAGNNDNER 692

Query 64 **LAIARQRIP** 72

LAIARQRIP
Sbjct 693 LAIARQRIP 719

>gb|CX220555.1| MNS36241 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=854

Score = 100 bits (250), Expect(2) = 2e-37, Method: Compositional matrix adjust.
Identities = 60/108 (56%), Positives = 64/108 (59%), Gaps = 31/108 (29%)
Frame = +1

Query 37 SGGNATLQVDSWPVIERYPAGNNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQ 96
SGGNATLQVDSWPVIERYPAG RQLTIFNSQ
Sbjct 454 SGGNATLQVDSWPVIERYPAG-----RQLTIFNSQ 543
Query 97 ATIIIIGGKEQGQPFQGLSGLYYNGLKVLNMAA-ENDANIAIVGNVRL 143
ATIIIIGGKEQGQPFQGLSGLYYNG + + E + GNV+L
Sbjct 544 ATIIIIGGKEQGQPFQGLSGLYYNGFESSEYGSRERCQHRHSGGNVKL 687

>gb|CX203319.1| MNS05584 Mouse Neurosphere Normalized cDNA library Mus musculus
cDNA 5', mRNA sequence. Length=645

Score = 125 bits (313), Expect = 1e-33, Method: Compositional matrix adjust.
Identities = 60/66 (91%), Positives = 62/66 (94%), Gaps = 0/66 (0%)
Frame = +2

Query 34 FTRSGGNATLQVDSWPVIERYPAGNNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIF 93
+RSGGNATLQVDSWPV ERYPAGN DNERLAIARQRIPYRLGRVV+EWLLDKGRQLTIF
Sbjct 446 LSRSGGNATLQVDSWPVNERYPAGNFDNERLAIARQRIPYRLGRVVNEWLLDKGRQLTIF 625
Query 94 NSQATI 99
NSQA I
Sbjct 626 NSQAAI 643

Xenopus (1/9 splice variants)

Sequences producing significant alignments:			Score	E
			(Bits)	Value
gb	CX806523.1	JGI_CAAJ17809.fwd NIH_XGC_tropBrn2 Xenopus (Si...	258	1e-84
gb	CX390033.2	JGI_XZT38012.fwd NIH_XGC_tropTad5 Xenopus (Sil...	254	1e-83
gb	CX842791.2	JGI_CAAK10710.rev NIH_XGC_tropBrn3 Xenopus (Si...	228	3e-73
gb	CX849796.2	JGI_CAAL6519.rev NIH_XGC_tropBrn4 Xenopus (Sil...	210	5e-66
gb	EL657246.1	AGENCOURT_103340710 NICHD_XGC_tropInt_62 Xenop...	210	6e-66
gb	CX875450.1	JGI_CAAL11566.fwd NIH_XGC_tropBrn4 Xenopus (Si...	203	9e-64
gb	CX802944.2	JGI_CAAJ15807.rev NIH_XGC_tropBrn2 Xenopus (Si...	200	2e-62
gb	CX849797.1	JGI_CAAL6519.fwd NIH_XGC_tropBrn4 Xenopus (Sil...	198	3e-61
gb	CX881742.2	JGI_CAAL20915.rev NIH_XGC_tropBrn4 Xenopus (Si...	137	5e-38
gb	CX806710.2	JGI_CAAJ17915.rev NIH_XGC_tropBrn2 Xenopus (Si...	111	4e-28
gb	CN079641.1	EC2BBA16DC06.b1 Xenopus tropicalis xtbs plasmid...	109	2e-27
gb	EL638922.1	CBTC435.fwd NICHD_XGC_tropBonel Xenopus (Silur...	101	1e-24
gb	CX879987.2	JGI_CAAL19921.rev NIH_XGC_tropBrn4 Xenopus (Si...	99.0	6e-24
gb	CX814841.2	JGI_CAAK651.rev NIH_XGC_tropBrn3 Xenopus (Silu...	99.0	6e-24
gb	CX879988.1	JGI_CAAL19921.fwd NIH_XGC_tropBrn4 Xenopus (Si...	97.4	5e-23
gb	CX799128.1	JGI_CAAJ13677.fwd NIH_XGC_tropBrn2 Xenopus (Si...	88.2	9e-20

ALIGNMENTS

>gb|CX806523.1| JGI_CAAJ17809.fwd NIH_XGC_tropBrn2 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7647663 5', mRNA sequence. Length=839

Score = 258 bits (658), Expect = 1e-84, Method: Compositional matrix adjust.
Identities = 120/148 (81%), Positives = 135/148 (91%), Gaps = 0/148 (0%)
Frame = +1

```

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
      QG +GV FNVGTDDI IEE A+++DGKYHVVRFRTRSGGNATLQVDSWPV ERYPAGNND D
Sbjct 118 QGTVGIVFNVGTDDITIEEPGALVSDGKYHVVRFRTRSGGNATLQVDSWPVNERYPAGNPD 297

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYN 120
      +ERLA+ARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I +GGK+QG+PFQGGQ+SGLYYN
Sbjct 298 SERLALARQRIPYRLGRVVDEWLLDKGRQLTIFNSQAEIKVGGKDQGRPFQGGQISGLYYN 477

Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
      GLKVL++AAEND N+ GN+RL+GEVP
Sbjct 478 GLKVLSLAAENDPNVKTEGNLRLIGEVP 561

```

>gb|CX390033.2| JGI_XZT38012.fwd NIH_XGC_tropTad5 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7614026 5', mRNA sequence. Length=818

Score = 254 bits (650), Expect = 1e-83, Method: Compositional matrix adjust.
Identities = 121/135 (90%), Positives = 128/135 (95%), Gaps = 0/135 (0%)
Frame = +2

```

Query 14 DIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPY 73
      DI+IEE NAIINDGKYH VRFRTRSGGNATL VD+WPVIERYPAGNNDNERLAIARQRIPY
Sbjct 2 DISIEEVNAIINDGKYHTVFRTRSGGNATLHVDNWPVIERYPAGNNDNERLAIARQRIPY 181

Query 74 RLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGGQLSGLYYNGLKVLNMAAENDA 133
      RLGRVVD+WLLDKGRQLTIFNSQATI IGGK+QGQPFQGGQLSGLYYNGLKVLNMAAEN+
Sbjct 182 RLGRVVDWLLDKGRQLTIFNSQATIKIGGKDQGGQPFQGGQLSGLYYNGLKVLNMAAENNP 361

Query 134 NIAIVGNVRLVGEVP 148
      +I I GNVRLVG+VP
Sbjct 362 DIVIEGNVRLVGDVP 406

```

>gb|CX842791.2| JGI_CAAK10710.rev NIH_XGC_tropBrn3 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7661344 3', mRNA sequence. Length=831

Score = 228 bits (581), Expect = 3e-73, Method: Compositional matrix adjust.
Identities = 107/119 (90%), Positives = 113/119 (95%), Gaps = 0/119 (0%)
Frame = -1

Query 30 HVVRFTRSGGNATLQVDSWPVIERYPA**GNNDNERLAIARQRIPYRLGRVVDEWLLDKGR**Q 89
H VRFTRSGGNATL VD+WPVIERYYPAGNNDNERLAIARQRIPYRLGRVVD+WLLDKGRQ
Sbjct 831 HTVRFTRSGGNATLHVDNWPVIERYYPAGNNDNERLAIARQRIPYRLGRVVDDWLLDKGRQ 652

Query 90 LTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
LTIFNSQATI IGGK+QGQPFQQLSGLYYNGLKVLNMAAEN+ +I I GNVRLVG+VP
Sbjct 651 LTIFNSQATIKIGGKDQGQPFQQLSGLYYNGLKVLNMAAENNPDIIVIEGNVRLVGDVP 475

>gb|CX849796.2| JGI_CAAL6519.rev NIH_XGC_tropBrn4 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7664856 3', mRNA sequence. Length=852

Score = 210 bits (534), Expect = 5e-66, Method: Compositional matrix adjust.
Identities = 100/115 (87%), Positives = 106/115 (92%), Gaps = 0/115 (0%)
Frame = -1

Query 34 FTRSGGNATLQVDSWPVIERYPA**GNNDNERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIF 93
F GNATL VD+WPVIERYYPAGNNDNERLAIARQRIPYRLGRVVD+WLLDKGRQLTIF
Sbjct 810 FYAKWGNATLHVDNWPVIERYYPAGNNDNERLAIARQRIPYRLGRVVDDWLLDKGRQLTIF 631

Query 94 NSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
NSQATI IGGK+QGQPFQQLSGLYYNGLKVLNMAAEN+ +I I GNVRLVG+VP
Sbjct 630 NSQATIKIGGKDQGQPFQQLSGLYYNGLKVLNMAAENNPDIIVIEGNVRLVGDVP 466

Score = 36.6 bits (83), Expect = 0.16, Method: Compositional matrix adjust.
Identities = 16/18 (89%), Positives = 16/18 (89%), Gaps = 0/18 (0%)
Frame = -2

Query 21 NAIINDGKYHVRFTRSG 38
NAIINDGK H VRFTRSG
Sbjct 848 NAIINDGKSHTVRFTRSG 795

>gb|EL657246.1| AGENCOURT_103340710 NICHD_XGC_tropInt_62 Xenopus (Silurana)
tropicalis cDNA clone IMAGE:8956924 5', mRNA sequence. Length=879

Score = 210 bits (534), Expect = 6e-66, Method: Compositional matrix adjust.
Identities = 100/115 (87%), Positives = 107/115 (93%), Gaps = 0/115 (0%)
Frame = +1

Query 34 FTRSGGNATLQVDSWPVIERYPA**GNNDNERLAIARQRIPYRLGRVVDEWLLDKGR**QLTIF 93
+ GGNATL VD+WPVIERYYPAGNNDNERLAIARQRIPYRLGRVVD+WLLDKGRQLTIF
Sbjct 7 YCEVGGNATLHVDNWPVIERYYPAGNNDNERLAIARQRIPYRLGRVVDDWLLDKGRQLTIF 186

Query 94 NSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
NSQATI IGGK+QGQPFQQLSGLYYNGLKVLNMAAEN+ +I I GNVRLVG+VP
Sbjct 187 NSQATIKIGGKDQGQPFQQLSGLYYNGLKVLNMAAENNPDIIVIEGNVRLVGDVP 351

>gb|CX875450.1| JGI_CAAL11566.fwd NIH_XGC_tropBrn4 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7669381 5', mRNA sequence. Length=766

Score = 203 bits (517), Expect = 9e-64, Method: Compositional matrix adjust.

Identities = 105/148 (71%), Positives = 111/148 (75%), Gaps = 30/148 (20%)
Frame = +3

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAGNND 60
          QGKIGVKFNVGTDDI+IEE NAIINDGKYH VRFTRSGGNATL VD+WPVIERYPA
Sbjct 3 QGKIGVKFNVGTDDISIEEVNAIINDGKYHTVRFTRSGGNATLHVDNWPVIERYPA---- 170

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYN 120
          GRQLTIFNSQATI IGGK+QGQPFQQLSGLYYN
Sbjct 171 -----GRQLTIFNSQATIKIGGKDQGQPFQQLSGLYYN 272

Query 121 GLKVLNMAAENDANIAIVGNVRLVGEVP 148
          GLKVLNMAAEN+ +I I GNVRLVG+VP
Sbjct 273 GLKVLNMAAENNPDIVIEGNVRLVGDVP 356
```

>gb|CX802944.2| JGI_CAAJ15807.rev NIH_XGC_tropBrn2 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7646009 3', mRNA sequence. Length=791

Score = 200 bits (509), Expect = 2e-62, Method: Compositional matrix adjust.
Identities = 94/105 (90%), Positives = 100/105 (95%), Gaps = 0/105 (0%)
Frame = -3

```
Query 44 QVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGG 103
          VD+WPVIERYPAGNNDNERLAIARQRIPYRLGRVVD+WLLDKGRQLTIFNSQATI IGG
Sbjct 789 HVDNWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDWLLDKGRQLTIFNSQATIKIGG 610

Query 104 KEQGQPFQQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEVP 148
          K+QGQPFQQLSGLYYNGLKVLNMAAEN+ +I I GNVRLVG+VP
Sbjct 609 KDQGQPFQQLSGLYYNGLKVLNMAAENNPDIVIEGNVRLVGDVP 475
```

>gb|CX849797.1| JGI_CAAL6519.fwd NIH_XGC_tropBrn4 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7664856 5', mRNA sequence. Length=922

Score = 198 bits (504), Expect = 3e-61, Method: Compositional matrix adjust.
Identities = 95/107 (89%), Positives = 101/107 (94%), Gaps = 0/107 (0%)
Frame = +1

```
Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVRFTRSGGNATLQVDSWPVIERYPAGNND 60
          QGKIGVKFNVGTDDI+IEE NAIINDGKYH VRFTRSGGNATL VD+WPVIERYPAG ND
Sbjct 565 QGKIGVKFNVGTDDISIEEVNAIINDGKYHTVRFTRSGGNATLHVDNWPVIERYPAGXND 744

Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQG 107
          NERLAIARQRIPYRLGRVVD+WLLDKGRQLTIF+SQ+TI IGG+ QG
Sbjct 745 NERLAIARQRIPYRLGRVVDWLLDKGRQLTIFHSQSTIKIGGEGQG 885
```

>gb|CX881742.2| JGI_CAAL20915.rev NIH_XGC_tropBrn4 Xenopus (Silurana) tropicalis
cDNA clone IMAGE:7672727 3', mRNA sequence. Length=846

Score = 137 bits (346), Expect = 5e-38, Method: Compositional matrix adjust.
Identities = 65/75 (87%), Positives = 70/75 (93%), Gaps = 0/75 (0%)
Frame = -1

```
Query 74 RLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAENDA 133
          RLGRVVD+WLLDKGRQLTIFN QATI IGGK+QGQPFQQLSGLYYNGLKVLNMAAEN+
Sbjct 846 RLGRVVDWLLDKGRQLTIFNXQATIKIGGKDQGQPFQQLSGLYYNGLKVLNMAAENNP 667

Query 134 NIAIVGNVRLVGEVP 148
          +I I GNVRLVG+VP
Sbjct 666 DIVIEGNVRLVGDVP 622
```

Danio rerio (1/6 splice variants)

Sequences producing significant alignments:			Score	E
			(Bits)	Value
gb CN505896.1	AGENCOURT_22422788 NIH_ZGC_9	Danio rerio cDNA ...	230	9e-74
gb EB940169.1	9541915 ZF34	Danio rerio cDNA clone 3410906, m...	205	2e-65
gb DN896482.1	nap10b06.y1	Zebrafish anterior segment (minus ...	169	8e-51
gb EG574210.1	AGENCOURT_88150324 NIH_ZGC_26	Danio rerio cDNA...	152	5e-44
gb EB962033.1	14363019 ZF35XL	Danio rerio cDNA clone 3866436...	128	8e-37
gb EB961180.1	14363301 ZF35XL	Danio rerio cDNA clone 3866772...	111	6e-30
gb EB923101.1	12401429 ZF31	Danio rerio cDNA clone 3275619, ...	59.3	4e-10
emb AL914040.1	AL914040 PJR-Z1+Z2	Danio rerio cDNA clone 088...	34.7	0.34

ALIGNMENTS

>gb|CN505896.1| AGENCOURT_22422788 NIH_ZGC_9 Danio rerio cDNA clone IMAGE:7275113
5', mRNA sequence. Length=947

Score = 230 bits (587), Expect = 9e-74, Method: Compositional matrix adjust.
Identities = 110/148 (74%), Positives = 127/148 (86%), Gaps = 0/148 (0%)
Frame = +3

```

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
Sbjct 330 QGK+GV FNVGTDDI I+E +NDGKYHVVRFRTRSGGNATLQVD+ PVIER+P+GN D 509
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
Sbjct 510 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQA I +GG+++G+PF GQ+S LYYN 689
Query 121 GLKVLNMAAENDANIAIIVGNVRLVGEVP 148
Sbjct 690 GL+VL +AAE + N+ + G LVGE P 773

```

>gb|EB940169.1| 9541915 ZF34 Danio rerio cDNA clone 3410906, mRNA sequence.
Length=620

Score = 205 bits (522), Expect = 2e-65, Method: Compositional matrix adjust.
Identities = 94/141 (67%), Positives = 120/141 (85%), Gaps = 0/141 (0%)
Frame = +1

```

Query 1 QGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGNND 60
Sbjct 196 QGKIGV FN+GT DI ++ES+ +NDGKYHVVRFRTR+GGNATLQVD+W + E +P+GN+D 375
Query 61 NERLAIARQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGKEQGQPFQGLSGLYYN 120
Sbjct 376 NER+ +A ++IP++ R V+EWL +KGRQLTIFN+QATI IGG ++ +PFQGLSGLYYN 555
Query 121 GLKVLNMAAENDANIAIIVGNV 141
Sbjct 556 GLKVLNMAA+ + NI I G+V 618

```

>gb|DN896482.1| nap10b06.y1 Zebrafish anterior segment (minus lens). Unnormalized
(nap) Danio rerio cDNA clone nap10b06 5', mRNA sequence. Length=697

Score = 169 bits (427), Expect = 8e-51, Method: Compositional matrix adjust.
Identities = 89/149 (60%), Positives = 102/149 (68%), Gaps = 31/149 (21%)
Frame = +3

Query 1 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPA**GNND** 60
 +G I V FNVGTDDI IEE++ +NDGKYH+VRFTRSGGNATLQVD PVIERYP+
 Sbjct 120 RGNIKVVFNVGTDDINIEETS~~SKFVNDGKYHIVRFTRSGGNATLQVDDL~~PVIERYPS---- 287

Query 61 **NERLAIARQRIPYRLGRVVDEWLLDK**GRQLTIFNSQATIIIGGKEQG-QPFQQLSGLYY 119
 GRQLTIFNSQ TI IGG E+G +PFQQLSGLYY
 Sbjct 288 -----GRQLTIFNSQTTIKIGGWEKGSRPFQQLSGLYY 389

Query 120 NGLKVLNMAAENDANIAIVGNVRLVGEVP 148
 NGLKVLNMAAE D N+ + G+ RLVG++P
 Sbjct 390 NGLKVLNMAAEGDPNVRVEGSARLVGDMP 476

>gb|EG574210.1| AGENCOURT_88150324 NIH_ZGC_26 Danio rerio cDNA clone IMAGE:8766761
 5', mRNA sequence. Length=829

Score = 152 bits (385), Expect = 5e-44, Method: Compositional matrix adjust.
 Identities = 71/86 (83%), Positives = 80/86 (93%), Gaps = 0/86 (0%)
 Frame = +3

Query 1 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPA**GNND** 60
 +G++GV FNVGTDDI IEES +++DGKYHVVRFTSRGGNATLQVD+ PVIER+PAGN D
 Sbjct 420 RGRVGVIFNVGTDDIVIEESGVMVSDGKYHVVRFTSRGGNATLQVDNLPVIERFPAGNFD 599

Query 61 **NERLAIARQRIPYRLGRVVDEWLLDK** 86
 +ERLAIARQRIPYRLGRVVDEWLLDK
 Sbjct 600 SERLAIARQRIPYRLGRVVDEWLLDK 677

>gb|EB962033.1| 14363019 ZF35XL Danio rerio cDNA clone 3866436, mRNA sequence.
 Length=247

Score = 128 bits (322), Expect = 8e-37, Method: Compositional matrix adjust.
 Identities = 58/78 (74%), Positives = 70/78 (90%), Gaps = 0/78 (0%)
 Frame = +1

Query 71 **IPYRLGRVVDEWLLDK**GRQLTIFNSQATIIIGGKEQGQPFQQLSGLYYNGLKVLNMAAE 130
 IPYRLGRVVDEWLLDKGRQLTIFNSQA I +GG+++G+PFQGG+SGLYYNGL+VL +AAE
 Sbjct 1 IPYRLGRVVDEWLLDKGRQLTIFNSQAAIKVGGQDKRPFQGISGLYYNGLQVLKLAEE 180

Query 131 NDANIAIVGNVRLVGEVP 148
 D N+ + GN+RLVG+ P
 Sbjct 181 GDPNVQVAGNLRRLVGDAP 234

>gb|EB961180.1| 14363301 ZF35XL Danio rerio cDNA clone 3866772, mRNA sequence.
 Length=318

Score = 111 bits (277), Expect = 6e-30, Method: Compositional matrix adjust.
 Identities = 47/77 (61%), Positives = 64/77 (83%), Gaps = 0/77 (0%)
 Frame = +2

Query 1 QGKIGVKFNVTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPA**GNND** 60
 QGKIGV FN+GT DI ++ES+ +NDGKYHVVRFTSR+GGNATLQVD+W + E +P+ N+D
 Sbjct 83 QGKIGVTFNIGTADITVQESSTAVNDGKYHVVRFTSRNGGNATLQVDNWAINEHFPSXNSD 262

Query 61 **NERLAIARQRIPYRLGR** 77
 NER+ +A ++IP++ R
 Sbjct 263 NERIQMANKKIPFQYAR 313

CIONA (0/2 splice variants)

Sequences producing significant alignments: (Bits) Value

dbj	AV990413.1	AV990413 Nori Satoh unpublished cDNA library,...	102	3e-25
dbj	BW351510.1	BW351510 Yutaka Satou unpublished cDNA librar...	92.0	1e-21
dbj	AV854354.1	AV854354 Nori Satoh unpublished cDNA library,...	31.6	2.6
dbj	AV854371.1	AV854371 Nori Satoh unpublished cDNA library,...	31.6	3.7

>dbj|AV990413.1| AV990413 Nori Satoh unpublished cDNA library, larva Ciona intestinalis
cDNA clone cilv22i22 5', mRNA sequence. Length=692

Score = 102 bits (253), Expect = 3e-25, Method: Compositional matrix adjust.
Identities = 54/156 (35%), Positives = 88/156 (56%), Gaps = 19/156 (12%)
Frame = +1

Query	8	FNVGTDDIAIEESNAIINDGKYHVVRFTSRGGNATLQVDSWPVIERYPAGNNDNERLAIA	67
		FN+G D+ ++E ++ ++DG+YH VR R NATL+VD+WP G + +R A+A	
Sbjct	25	FNIGNSDVKLQE-HSPVSDGQYHTVRRKWMNATLRVDNWPERTATTTGGS-RDRFALA	198
Query	68	RQRIPYRLGRVVDEWLLDKGRQLTIFNSQATIIIGGK-EQGQP-----F	110
		+ IP + V+ WL K T+FNSQ+ I IGG +Q P F	
Sbjct	199	KPSIPTSVLSTVETWLRSEKEYSNTVFNSQSVIQIGLLDQSSPYLNSMRSKRSPGIRKAF	378
Query	111	QGQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGE	146
		GQ+ G ++N ++V +AA+ D ++ ++G+V ++GE	
Sbjct	379	HGQMMGFFFNDVRFQLAAQGDPSVQLIGDVEIIGE	486

>dbj|BW351510.1| BW351510 Yutaka Satou unpublished cDNA library, embryo whole animal Ciona intestinalis cDNA clone ciem848m04 5', mRNA sequence. Length=623

Score = 92.0 bits (227), Expect = 1e-21, Method: Compositional matrix adjust.
Identities = 49/139 (35%), Positives = 76/139 (55%), Gaps = 18/139 (13%)
Frame = +1

Query	25	NDGKYHVVRFTSRGGNATLQVDSWPVIERYPAGNNDNERLAIARQRIPYRLGRVVDEWLL	84
		+DG+YH VR R NATL+VD+WP G + +R A+A+ IP + V+ WL	
Sbjct	1	SDGQYHTVRRKWMNATLRVDNWPERTATTTGGS-RDRFALAKPSIPTSVLSTVETWLR	177
Query	85	DKGRQLTIFNSQATIIIGGK-EQGQP-----FQGQLSGLYYNGLKVLNM	127
		K T+FNSQ+ I IGG +Q P F GQ+ G ++N ++V +	
Sbjct	178	SKEYSNTVFNSQSVIQIGLLDQSSPYLNSMRSKRSPGIRKAFHGQMMGFFFNDVRFQL	357
Query	128	AAENDANIAIVGNVRLVGE	146
		AA+ D ++ ++G+V ++GE	
Sbjct	358	AAQGDPSVQLIGDVEIIGE	414