Descriptions

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Li
Genomic sequences							
NT_167190.1	Homo sapiens chromosome 11 genomic contig, GRCh37.p2 r	446	446	71%	4e-123	100%	
NW_001838028.2	Homo sapiens chromosome 11 genomic contig, alternate as	446	446	71%	4e-123	100%	

Alignments

Select All Get selected sequences Distance tree of results

>ref|NT_167190.1| Homo sapiens chromosome 11 genomic contig, GRCh37.p2 reference primary assembly
Length=41593379

Features in this part of subject sequence:
  teneurin-4

Score = 446 bits (241), Expect = 4e-123
Identities = 241/241 (100%), Gaps = 0/241 (0%)
Strand=Plus/Minus

```
Query  96        TCTCCCTCACCATAGTCGATGGGCTCAGTTCCCTGGAAGCATAGTATGGTGGACAAGTCA  155
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23763477  TCTCCCTCACCATAGTCGATGGGCTCAGTTCCCTGGAAGCATAGTATGGTGGACAAGTCA  23763418

Query  156       AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCCAGAAGATTCCTA  215
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23763417  AGGGCTCTGGTCTTGTGTACACTTTTATCAGCCAGCAGAAAATATTCCAGAAGATTCCTA  23763358

Query  216       TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCCACAGCCTTGAC  275
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23763357  TGGGAGAGGACTCAGCCTGAAGCATCAGCATTGAGCAGCCAGGCTGCCCACAGCCTTGAC  23763298

Query  276       AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC  335
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  23763297  AGATTGATTCTGCAGCCTGGGAGCTCACGCTCCCTTGGTGTCTGAAGGAGCTCAACAGCC  23763238

Query  336       A  336
                  |
Sbjct  23763237  A  23763237
```

>ref|NW_001838028.2| Homo sapiens chromosome 11 genomic contig, alternate assembly HuRef SCAF_1103279187758, whole genome shotgun sequence
Length=169I2879

Features in this part of subject sequence:
  teneurin-4

Score = 446 bits (241), Expect = 4e-123
Identities = 241/241 (100%), Gaps = 0/241 (0%)
Strand=Plus/Plus