

BLAST®

Basic Local Alignment Search Tool

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Nucleotide Sequence (52 letters)

RID [54PMN01E015](#) (Expires on 10-31 23:34 pm)

Query ID |cl|26763

Description None

Molecule type nucleic acid

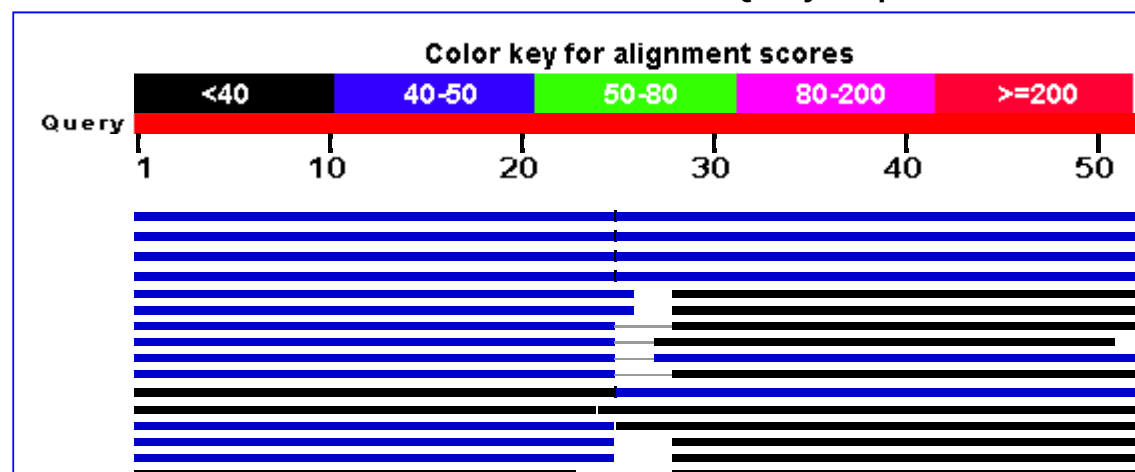
Query Length 52

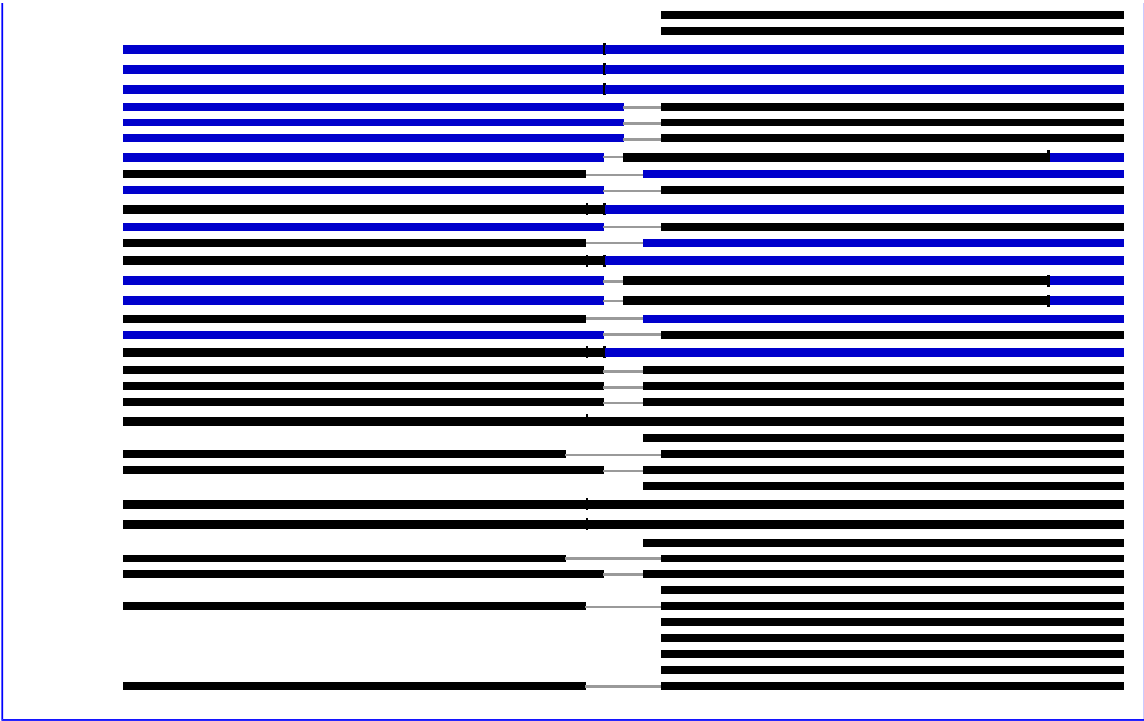
Database Name Human G+T (2 databases)

Description **Program**BLASTN 2.2.30+

 [Graphic Summary](#)

Distribution of 151 Blast Hits on the Query Sequence





Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Transcripts						
PREDICTED: Homo sapiens actin, gamma 1 (ACTG1), transcript variant X1, mRNA	44.6	85.5	100%	0.008	94%	XM_006722048.1
Homo sapiens actin, gamma 1 (ACTG1), transcript variant 3, non-coding RNA	44.6	85.5	100%	0.008	94%	NR_037688.1
Homo sapiens actin, gamma 1 (ACTG1), transcript variant 1, mRNA	44.6	85.5	100%	0.008	94%	NM_001199954.1
Homo sapiens actin, gamma 1 (ACTG1), transcript variant 2, mRNA	44.6	85.5	100%	0.008	94%	NM_001614.3
Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), transcript variant 2, mRNA	42.8	42.8	50%	0.028	96%	NM_001199893.1
Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), transcript variant 1, mRNA	42.8	42.8	50%	0.028	96%	NM_001615.3
PREDICTED: Homo sapiens actin, beta (ACTB), transcript variant X1, mRNA	41.0	80.1	94%	0.096	96%	XM_006715764.1
Homo sapiens actin, gamma 1 pseudogene (LOC644961), non-coding RNA	41.0	80.1	94%	0.096	96%	NR_033926.1
Homo sapiens actin, gamma 1 pseudogene 4 (ACTG1P4), non-coding RNA	41.0	81.9	96%	0.096	96%	NR_024438.2
Homo sapiens actin, beta (ACTB), mRNA	41.0	80.1	94%	0.096	96%	NM_001101.3
Homo sapiens actin, alpha, cardiac muscle 1 (ACTC1), mRNA	41.0	78.3	100%	0.096	93%	NM_005159.4
Homo sapiens actin, beta pseudogene (LOC644936), non-coding RNA	39.2	39.2	46%	0.34	96%	NR_004845.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens actin, alpha 1, skeletal muscle (ACTA1), mRNA	39.2	39.2	46%	0.34	96%	NM_001100.3
Homo sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), transcript variant 2, mRNA	37.4	37.4	53%	1.2	89%	NM_001613.2
Homo sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), transcript variant 1, mRNA	37.4	37.4	53%	1.2	89%	NM_001141945.1
PREDICTED: Homo sapiens POTE ankyrin domain family, member E (POTEE), transcript variant X1, mRNA	35.6	35.6	46%	4.1	92%	XM_006712538.1
Homo sapiens POTE ankyrin domain family, member I (POTEI), mRNA	35.6	35.6	46%	4.1	92%	NM_001277406.1
Homo sapiens POTE ankyrin domain family, member J (POTEJ), mRNA	35.6	35.6	46%	4.1	92%	NM_001277083.1
Homo sapiens actin-related protein T1 (ACTRT1), mRNA	35.6	35.6	46%	4.1	92%	NM_138289.3
Homo sapiens POTE ankyrin domain family, member M (POTEM), mRNA	35.6	35.6	46%	4.1	92%	NM_001145442.1
Homo sapiens POTE ankyrin domain family, member E (POTEE), mRNA	35.6	35.6	46%	4.1	92%	NM_001083538.1
Genomic sequences[show first]						
Homo sapiens chromosome 17, alternate assembly CHM1_1.1	44.6	85.5	100%	0.008	94%	NC_018928.2
Homo sapiens chromosome 17, alternate assembly HuRef	44.6	85.5	100%	0.008	94%	AC_000149.1
Homo sapiens chromosome 17, GRCh38 Primary Assembly	44.6	85.5	100%	0.008	94%	NC_000017.11
Homo sapiens chromosome 2, alternate assembly CHM1_1.1	42.8	184	96%	0.028	96%	NC_018913.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 2, alternate assembly HuRef	42.8	113	96%	0.028	96%	AC_000134.1
Homo sapiens chromosome 2, GRCh38 Primary Assembly	42.8	184	96%	0.028	96%	NC_000002.12
Homo sapiens chromosome 1, alternate assembly CHM1_1.1	41.0	236	98%	0.096	96%	NC_018912.2
Homo sapiens chromosome 3, alternate assembly CHM1_1.1	41.0	76.5	94%	0.096	96%	NC_018914.2
Homo sapiens chromosome 7, alternate assembly CHM1_1.1	41.0	80.1	94%	0.096	96%	NC_018918.2
Homo sapiens chromosome 15, alternate assembly CHM1_1.1	41.0	153	100%	0.096	93%	NC_018926.2
Homo sapiens chromosome X, alternate assembly CHM1_1.1	41.0	76.5	48%	0.096	96%	NC_018934.2
Homo sapiens chromosome X, alternate assembly HuRef	41.0	76.5	48%	0.096	96%	AC_000155.1
Homo sapiens chromosome 7, alternate assembly HuRef	41.0	80.1	94%	0.096	96%	AC_000139.1
Homo sapiens chromosome 3, alternate assembly HuRef	41.0	76.5	94%	0.096	96%	AC_000135.1
Homo sapiens chromosome 15, alternate assembly HuRef	41.0	153	100%	0.096	93%	AC_000147.1
Homo sapiens chromosome 1, alternate assembly HuRef	41.0	236	98%	0.096	96%	AC_000133.1
Homo sapiens chromosome 1, GRCh38 Primary Assembly	41.0	236	98%	0.096	96%	NC_000001.11
Homo sapiens chromosome 3, GRCh38 Primary Assembly	41.0	76.5	94%	0.096	96%	NC_000003.12
Homo sapiens chromosome 7, GRCh38 Primary Assembly	41.0	80.1	94%	0.096	96%	NC_000007.14

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 15, GRCh38 Primary Assembly	41.0	153	100%	0.096	93%	NC_000015.10
Homo sapiens chromosome X, GRCh38 Primary Assembly	41.0	76.5	48%	0.096	96%	NC_000023.11
Homo sapiens chromosome 5, alternate assembly CHM1_1.1	39.2	225	96%	0.34	96%	NC_018916.2
Homo sapiens chromosome 5, alternate assembly HuRef	39.2	225	96%	0.34	96%	AC_000137.1
Homo sapiens chromosome 5, GRCh38 Primary Assembly	39.2	225	96%	0.34	96%	NC_000005.10
Homo sapiens chromosome 10, alternate assembly CHM1_1.1	37.4	72.9	100%	1.2	89%	NC_018921.2
Homo sapiens chromosome 16, alternate assembly CHM1_1.1	37.4	37.4	48%	1.2	92%	NC_018927.2
Homo sapiens chromosome 22, alternate assembly CHM1_1.1	37.4	72.9	90%	1.2	96%	NC_018933.2
Homo sapiens chromosome Y, alternate assembly HuRef	37.4	74.7	96%	1.2	92%	AC_000156.1
Homo sapiens chromosome 22, alternate assembly HuRef	37.4	37.4	44%	1.2	96%	AC_000154.1
Homo sapiens chromosome 16, alternate assembly HuRef	37.4	37.4	48%	1.2	92%	AC_000148.1
Homo sapiens chromosome 10, alternate assembly HuRef	37.4	72.9	100%	1.2	89%	AC_000142.1
Homo sapiens chromosome 10, GRCh38 Primary Assembly	37.4	72.9	100%	1.2	89%	NC_000010.11
Homo sapiens chromosome 16, GRCh38 Primary Assembly	37.4	37.4	48%	1.2	92%	NC_000016.10
Homo sapiens chromosome 22, GRCh38 Primary Assembly	37.4	72.9	90%	1.2	96%	NC_000022.11

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome Y, GRCh38 Primary Assembly	37.4	149	96%	1.2	92%	NC_000024.10
Homo sapiens chromosome 6, alternate assembly CHM1_1.1	35.6	35.6	46%	4.1	92%	NC_018917.2
Homo sapiens chromosome 11, alternate assembly CHM1_1.1	35.6	71.1	92%	4.1	92%	NC_018922.2
Homo sapiens chromosome 14, alternate assembly CHM1_1.1	35.6	35.6	46%	4.1	92%	NC_018925.2
Homo sapiens chromosome 18, alternate assembly CHM1_1.1	35.6	35.6	46%	4.1	92%	NC_018929.2
Homo sapiens chromosome 6, alternate assembly HuRef	35.6	35.6	46%	4.1	92%	AC_000138.1
Homo sapiens chromosome 18, alternate assembly HuRef	35.6	35.6	46%	4.1	92%	AC_000150.1
Homo sapiens chromosome 11, alternate assembly HuRef	35.6	71.1	92%	4.1	92%	AC_000143.1
Homo sapiens unplaced genomic scaffold, alternate assembly HuRef DEGEN_1103279047854	35.6	35.6	46%	4.1	92%	NW_001841363.1
Homo sapiens chromosome 6, GRCh38 Primary Assembly	35.6	35.6	46%	4.1	92%	NC_000006.12
Homo sapiens chromosome 11, GRCh38 Primary Assembly	35.6	71.1	92%	4.1	92%	NC_000011.10
Homo sapiens chromosome 14, GRCh38 Primary Assembly	35.6	71.1	46%	4.1	92%	NC_000014.9
Homo sapiens chromosome 18, GRCh38 Primary Assembly	35.6	35.6	46%	4.1	92%	NC_000018.10

[Alignments](#)

PREDICTED: Homo sapiens actin, gamma 1 (ACTG1), transcript variant X1, mRNA

Sequence ID: **ref|XM_006722048.1|** Length: 2129 Number of Matches: 2

Range 1: 1386 to 1415

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

```

Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   1415    TCCGT- TTAGAAGCATTTCGCGGTGGACGATG   1386

```

Range 2: 1127 to 1151

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query    1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct   1127    TCATGAAGTGTGACGTGGACATCCG   1151

```

Homo sapiens actin, gamma 1 (ACTG1), transcript variant 3, non-coding RNA

Sequence ID: **ref|NR_037688.1|** Length: 1855 Number of Matches: 2

Range 1: 1243 to 1272

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

```

Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   1272    TCCGT- TTAGAAGCATTTCGCGGTGGACGATG   1243

```

Range 2: 984 to 1008

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct  984      TCATGAAGTGTGACGTGGACATCCG  1008

```

Homo sapiens actin, gamma 1 (ACTG1), transcript variant 1, mRNA

Sequence ID: **ref[NM_001199954.1]** Length: 2123 Number of Matches: 2

Range 1: 1362 to 1391

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

```

Query  22      TCCGTCTTAGAAGCATTGCGGTGCACGATG   52
          |||||
Sbjct  1391      TCCGT-TTAGAAGCATTGCGGTGGACGATG  1362

```

Range 2: 1103 to 1127

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct  1103      TCATGAAGTGTGACGTGGACATCCG  1127

```

Homo sapiens actin, gamma 1 (ACTG1), transcript variant 2, mRNA

Sequence ID: **ref[NM_001614.3]** Length: 2004 Number of Matches: 2

Range 1: 1243 to 1272

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Minus	

Features:

```

Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct  1272    TCCGT- TTAGAAGCATTTCGCGGTGGACGATG   1243

```

Range 2: 984 to 1008

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query    1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct   984    TCATGAAGTGTGACGTGGACATCCG   1008

```

Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), transcript variant 2, mRNA

Sequence ID: **ref|NM_001199893.1|** Length: 1216 Number of Matches: 1

Range 1: 841 to 866

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.028()	25/26(96%)	0/26(0%)	Plus/Plus	

Features:

```

Query    1      TCATGAAGTGTGACGTTGACATCCGT   26
          |||||
Sbjct   841    TCATGAAGTGTGACATTGACATCCGT   866

```

Homo sapiens actin, gamma 2, smooth muscle, enteric (ACTG2), transcript variant 1, mRNA

Sequence ID: **ref|NM_001615.3|** Length: 1345 Number of Matches: 1

Range 1: 970 to 995

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.028()	25/26(96%)	0/26(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCGT   26
          |||||
Sbjct  970    TCATGAAGTGTGACATTGACATCCGT   995

```

PREDICTED: Homo sapiens actin, beta (ACTB), transcript variant X1, mRNA

Sequence ID: **ref|XM_006715764.1|** Length: 1816 Number of Matches: 2

Range 1: 933 to 957

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct  933    TCATGAAGTGTGACGTGGACATCCG   957

```

Range 2: 1192 to 1215

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	0.34()	23/24(96%)	0/24(0%)	Plus/Minus	

Features:

```

Query  29      TAGAAGCATTTGCGGTGCACGATG   52
          |||||
Sbjct 1215    TAGAAGCATTTGCGGTGGACGATG   1192

```

Homo sapiens actin, gamma 1 pseudogene (LOC644961), non-coding RNA

Sequence ID: **ref|NR_033926.1|** Length: 2652 Number of Matches: 2

Range 1: 1640 to 1664

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct  1640  TCATGAAGTGTGACGTAGACATCCG   1664

```

Range 2: 1900 to 1923

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	0.34()	23/24(96%)	0/24(0%)	Plus/Minus	

Features:

```

Query   28      TTAGAAGCATTGCGGTGCACGAT   51
          |||||
Sbjct  1923  TTAGAAGCATTGCGGTGGACGAT   1900

```

Homo sapiens actin, gamma 1 pseudogene 4 (ACTG1P4), non-coding RNA

Sequence ID: **ref|NR_024438.2|** Length: 1988 Number of Matches: 2

Range 1: 991 to 1015

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct   991  TCATGAAGTGTGACGTGGACATCCG  1015

```

Range 2: 1247 to 1271

Score	Expect	Identities	Gaps	Strand	Frame
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41.0 bits(44) 0.096() 24/25(96%) 0/25(0%) Plus/Minus

Features:

```
Query  28      TTAGAAGCATTTCGCGGTGCACGATG  52
          |||
Sbjct 1271    TTAGAAGCATTTCGCGGTGGACGATG 1247
```

Homo sapiens actin, beta (ACTB), mRNA

Sequence ID: **ref|NM_001101.3|** Length: 1852 Number of Matches: 2

Range 1: 929 to 953

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Plus	

Features:

```
Query  1      TCATGAAGTGTGACGTTGACATCCG  25
          |||
Sbjct  929    TCATGAAGTGTGACGTGGACATCCG  953
```

Range 2: 1188 to 1211

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	0.34()	23/24(96%)	0/24(0%)	Plus/Minus	

Features:

```
Query  29      TAGAAGCATTTCGCGGTGCACGATG  52
          |||
Sbjct 1211    TAGAAGCATTTCGCGGTGGACGATG 1188
```

Homo sapiens actin, alpha, cardiac muscle 1 (ACTC1), mRNA

Sequence ID: **ref|NM_005159.4|** Length: 3693 Number of Matches: 2

Range 1: 1353 to 1379

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

41.0 bits(44) 0.096() 25/27(93%) 0/27(0%) Plus/Minus

Features:

```
Query   26   TCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||
Sbjct   1379 TCTTAGAAGCATTTCGCGGTGGACAATG   1353
```

Range 2: 1094 to 1118

Score	Expect	Identities	Gaps	Strand	Frame
37.4 bits(40)	1.2()	23/25(92%)	0/25(0%)	Plus/Plus	

Features:

```
Query    1   TCATGAAGTGTGACGTTGACATCCG   25
          |||
Sbjct   1094 TCATGAAGTGTGACATTGATATCCG   1118
```

Homo sapiens actin, beta pseudogene (LOC644936), non-coding RNA

Sequence ID: **ref|NR_004845.1|** Length: 1456 Number of Matches: 1

Range 1: 777 to 800

Score	Expect	Identities	Gaps	Strand	Frame
39.2 bits(42)	0.34()	23/24(96%)	0/24(0%)	Plus/Minus	

Features:

```
Query   29   TAGAAGCATTTCGCGGTGCACGATG   52
          |||
Sbjct   800   TAGAAGCATTTCGCGGTGGACGATG   777
```

Homo sapiens actin, alpha 1, skeletal muscle (ACTA1), mRNA

Sequence ID: **ref|NM_001100.3|** Length: 1509 Number of Matches: 1

Range 1: 1215 to 1238

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

39.2 bits(42) 0.34() 23/24(96%) 0/24(0%) Plus/Minus

Features:

```

Query   29      TAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   1238    TAGAAGCATTTCGCGGTGGACGATG   1215

```

Homo sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), transcript variant 2, mRNA

Sequence ID: **ref|NM_001613.2|** Length: 1415 Number of Matches: 1

Range 1: 1226 to 1253

Score	Expect	Identities	Gaps	Strand	Frame
37.4 bits(40)	1.2()	25/28(89%)	0/28(0%)	Plus/Minus	

Features:

```

Query   25      GTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   1253    GTTTTAGAAGCATTTCGCGGTGGACAATG   1226

```

Homo sapiens actin, alpha 2, smooth muscle, aorta (ACTA2), transcript variant 1, mRNA

Sequence ID: **ref|NM_001141945.1|** Length: 1798 Number of Matches: 1

Range 1: 1585 to 1612

Score	Expect	Identities	Gaps	Strand	Frame
37.4 bits(40)	1.2()	25/28(89%)	0/28(0%)	Plus/Minus	

Features:

```

Query   25      GTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   1612    GTTTTAGAAGCATTTCGCGGTGGACAATG   1585

```

PREDICTED: Homo sapiens POTE ankyrin domain family, member E (POTEE), transcript variant X1, mRNA

Sequence ID: **ref|XM_006712538.1|** Length: 2816 Number of Matches: 1
 Range 1: 2027 to 2050

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

```

Query   29      TAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   2050    TAGAAGCATTTCGCGGTGGACAATG   2027
  
```

Homo sapiens POTE ankyrin domain family, member I (POTEI), mRNA

Sequence ID: **ref|NM_001277406.1|** Length: 3228 Number of Matches: 1
 Range 1: 3204 to 3227

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

```

Query   29      TAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   3227    TAGAAGCATTTCGCGGTGGACAATG   3204
  
```

Homo sapiens POTE ankyrin domain family, member J (POTEJ), mRNA

Sequence ID: **ref|NM_001277083.1|** Length: 3277 Number of Matches: 1
 Range 1: 3093 to 3116

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

```

Query   29      TAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   3116    TAGAAGCATTTCGCGGTGGACAATG   3093
  
```

Homo sapiens actin-related protein T1 (ACTRT1), mRNA

Sequence ID: **ref|NM_138289.3|** Length: 1452 Number of Matches: 1

Range 1: 1045 to 1068

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Plus	

Features:

```

Query   1      TCATGAAGTGTGACGTTGACATCC  24
          |||||
Sbjct  1045  TCATGAAGTGTGACACTGACATCC  1068

```

Homo sapiens POTE ankyrin domain family, member M (POTEM), mRNA

Sequence ID: **ref|NM_001145442.1|** Length: 6666 Number of Matches: 1

Range 1: 2885 to 2908

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

```

Query   29      TAGAAGCATTTCGCGTGCACGATG  52
          |||||
Sbjct  2908  TAGAAGCATTTCGCGTGGACAATG  2885

```

Homo sapiens POTE ankyrin domain family, member E (POTEE), mRNA

Sequence ID: **ref|NM_001083538.1|** Length: 3440 Number of Matches: 1

Range 1: 3256 to 3279

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

```

Query   29      TAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   3279    TAGAAGCATTTCGCGGTGGACAATG   3256

```

Homo sapiens chromosome 17, alternate assembly CHM1_1.1

Sequence ID: **ref|NC_018928.2|** Length: 81289577 Number of Matches: 2

Range 1: 79563992 to 79564021

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Plus	

Features:

actin, cytoplasmic 2**actin, cytoplasmic 2**

```

Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||
Sbjct   79563992 TCCGT-TTAGAAGCATTTCGCGGTGGACGATG   79564021

```

Range 2: 79564349 to 79564373

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Minus	

Features:

actin, cytoplasmic 2**actin, cytoplasmic 2**

```

Query   1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct   79564373 TCATGAAGTGTGACGTGGACATCCG   79564349

```

Homo sapiens chromosome 17, alternate assembly HuRef

Sequence ID: **ref|AC_000149.1|** Length: 76567021 Number of Matches: 2

Range 1: 74926527 to 74926556

Score	Expect	Identities	Gaps	Strand	Frame
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44.6 bits(48) 0.008() 29/31(94%) 1/31(3%) Plus/Plus

Features:

actin, cytoplasmic 2actin, cytoplasmic 2

```
Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||  |||
Sbjct   74926527 TCCGT-TTAGAAGCATTTCGCGGTGGACGATG   74926556
```

Range 2: 74926884 to 74926908

Score	Expect	Identities	Gaps	Strand	Frame
41.0 bits(44)	0.096()	24/25(96%)	0/25(0%)	Plus/Minus	

Features:

actin, cytoplasmic 2actin, cytoplasmic 2

```
Query    1      TCATGAAGTGTGACGTTGACATCCG   25
          |||||  |||
Sbjct   74926908 TCATGAAGTGTGACGTGGACATCCG   74926884
```

Homo sapiens chromosome 17, GRCh38 Primary Assembly

Sequence ID: **ref|NC_000017.11|** Length: 83257441 Number of Matches: 2

Range 1: 81510685 to 81510714

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	0.008()	29/31(94%)	1/31(3%)	Plus/Plus	

Features:

actin, cytoplasmic 2actin, cytoplasmic 2

```
Query   22      TCCGTCTTAGAAGCATTTCGCGGTGCACGATG   52
          |||||  |||
Sbjct   81510685 TCCGT-TTAGAAGCATTTCGCGGTGGACGATG   81510714
```

Range 2: 81511042 to 81511066

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

41.0 bits(44) 0.096() 24/25(96%) 0/25(0%) Plus/Minus

Features:

actin, cytoplasmic 2actin, cytoplasmic 2

```
Query   1          TCATGAAGTGTGACGTTGACATCCG   25
          |||||
Sbjct   81511066   TCATGAAGTGTGACGTGGACATCCG   81511042
```

Homo sapiens chromosome 2, alternate assembly CHM1_1.1

Sequence ID: **ref|NC_018913.2|** Length: 243205335 Number of Matches: 5

Range 1: 74073013 to 74073038

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	0.028()	25/26(96%)	0/26(0%)	Plus/Plus	

Features:

actin, gamma-enteric smooth muscle isoform 1 precursoractin, gamma-enteric smooth muscle isoform 2 precursor

```
Query   1          TCATGAAGTGTGACGTTGACATCCGT   26
          |||||
Sbjct   74073013   TCATGAAGTGTGACATTGACATCCGT   74073038
```

Range 2: 131224266 to 131224289

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Plus	

Features:

POTE ankyrin domain family member I

```
Query   29          TAGAAGCATTGCGGTGCACGATG   52
          |||||
Sbjct   131224266   TAGAAGCATTGCGGTGGACAATG   131224289
```

Range 3: 131419073 to 131419096

Score	Expect	Identities	Gaps	Strand	Frame
-------	--------	------------	------	--------	-------

35.6 bits(38) 4.1() 22/24(92%) 0/24(0%) Plus/Minus

Features:

POTE ankyrin domain family member J

```
Query   29          TAGAAGCATTTCGCGTGCACGATG   52
          |||||
Sbjct   131419096  TAGAAGCATTTCGCGTGGACAATG   131419073
```

Range 4: 132025795 to 132025818

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

POTE ankyrin domain family member E

```
Query   29          TAGAAGCATTTCGCGTGCACGATG   52
          |||||
Sbjct   132025818  TAGAAGCATTTCGCGTGGACAATG   132025795
```

Range 5: 132388335 to 132388358

Score	Expect	Identities	Gaps	Strand	Frame
35.6 bits(38)	4.1()	22/24(92%)	0/24(0%)	Plus/Minus	

Features:

93742 bp at 5' side: coiled-coil domain-containing protein 74A isoform 2124222 bp at 3' side: uncharacterized protein C2orf27

```
Query   29          TAGAAGCATTTCGCGTGCACGATG   52
          |||||
Sbjct   132388358  TAGAAGCATTTCGCGTGGACAATG   132388335
```