

BLAST ®

Basic Local Alignment Search Tool

NCBI/ [BLAST](#)/ [blastn suite](#)/ **Formatting Results - Y0RUB6SJ014**

► [Formatting options](#)

► [Download](#)

[Blast report description](#)

ACGT

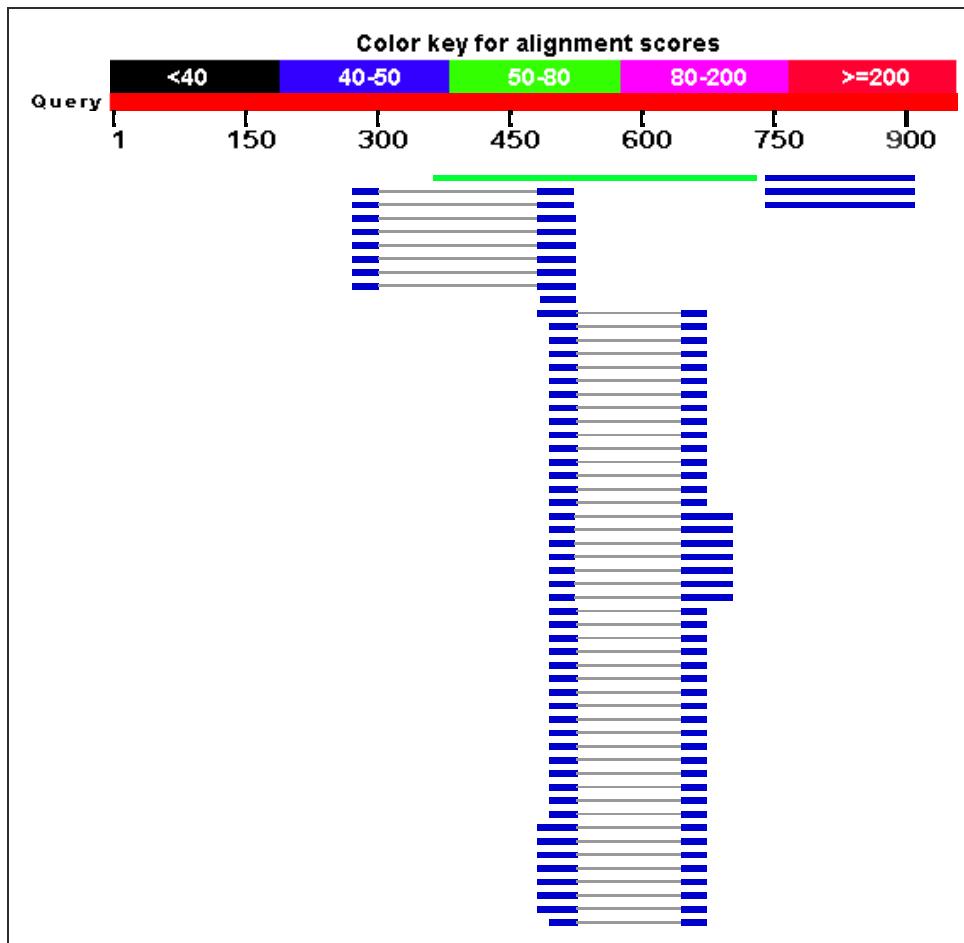
RID [Y0RUB6SJ014](#) (Expires on 08-06 12:36 pm)

Query ID Icl|56407
Description None
Molecule type nucleic acid
Query Length 952

Database Name nr
Description Nucleotide collection (nt)
Program BLASTN 2.2.29+

[Graphic Summary](#)

Distribution of 223 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Mus musculus BAC clone RP24-299I4 from chromosome 14, complete sequence	57.2	207	38%	3e-04	66%	AC154677.2
PREDICTED: Panthera tigris altaica factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA	46.4	90.9	7%	0.62	84%	XM_007075922.1
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	46.4	90.9	7%	0.62	84%	XM_003985384.2
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA	46.4	90.9	7%	0.62	84%	XM_006931126.1
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA	46.4	90.9	7%	0.62	84%	XM_006931125.1
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA	46.4	90.9	7%	0.62	84%	XM_006931124.1
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	46.4	90.9	7%	0.62	84%	XM_003985383.2
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	46.4	90.9	7%	0.62	84%	XM_003985382.2
PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	46.4	90.9	7%	0.62	84%	XM_006931123.1
Homo sapiens BAC clone RP11-704A15 from chromosome x, complete sequence	46.4	46.4	17%	0.62	70%	AC239601.2
Branchiostoma floridae hypothetical protein, mRNA	46.4	46.4	3%	0.62	87%	XM_002593504.1
Human DNA sequence from clone RP1-279N11 on chromosome Xq11.2-13.3 Contain the 3' end of a novel gene, complete sequence	46.4	46.4	17%	0.62	70%	Z98255.2
Human Chromosome X clone bWXD531, complete sequence	46.4	46.4	17%	0.62	70%	AC004384.1
PREDICTED: Equus przewalskii factor interacting with PAPOLA and CPSF1 (FIP1L1), partial mRNA	44.6	131	7%	2.2	93%	XM_008522213.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X14, mRNA	44.6	89.1	6%	2.2	93%	XM_007613853.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X13, mRNA	44.6	89.1	6%	2.2	93%	XM_007613852.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X12, mRNA	44.6	89.1	6%	2.2	93%	XM_007613851.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X11, mRNA	44.6	89.1	6%	2.2	93%	XM_007613850.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X10, mRNA	44.6	89.1	6%	2.2	93%	XM_007613849.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X9, mRNA	44.6	89.1	6%	2.2	93%	XM_007613848.1
PREDICTED: Cricetulus griseus factor						

interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X8, mRNA	44.6	89.1	6%	2.2	93%	XM_007613847.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X7, mRNA	44.6	89.1	6%	2.2	93%	XM_007651670.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X6, mRNA	44.6	89.1	6%	2.2	93%	XM_007651669.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X5, mRNA	44.6	89.1	6%	2.2	93%	XM_007651668.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X4, mRNA	44.6	89.1	6%	2.2	93%	XM_007651667.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X3, mRNA	44.6	89.1	6%	2.2	93%	XM_007651666.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X2, mRNA	44.6	89.1	6%	2.2	93%	XM_007651664.1
PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X1, mRNA	44.6	89.1	6%	2.2	93%	XM_007651663.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA	44.6	87.3	8%	2.2	79%	XM_007539714.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA	44.6	87.3	8%	2.2	79%	XM_007539713.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA	44.6	87.3	8%	2.2	79%	XM_007539712.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	44.6	87.3	8%	2.2	79%	XM_007539711.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	87.3	8%	2.2	79%	XM_007539710.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	87.3	8%	2.2	79%	XM_007539709.1
PREDICTED: Erinaceus europaeus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	87.3	8%	2.2	79%	XM_007539708.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA	44.6	89.1	6%	2.2	93%	XM_007456085.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA	44.6	89.1	6%	2.2	93%	XM_007456084.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	44.6	89.1	6%	2.2	93%	XM_007456083.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	89.1	6%	2.2	93%	XM_007456082.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	89.1	6%	2.2	93%	XM_007456081.1
PREDICTED: Lipotes vexillifer factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	89.1	6%	2.2	93%	XM_007456080.1
PREDICTED: Bubalus bubalis factor						

interacting with PAPOLA and CPSF1 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_006047768.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X9, mRNA	44.6	89.1	6%	2.2	93%	XM_007119431.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X8, mRNA	44.6	89.1	6%	2.2	93%	XM_007119430.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA	44.6	89.1	6%	2.2	93%	XM_007119429.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA	44.6	89.1	6%	2.2	93%	XM_007119428.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA	44.6	89.1	6%	2.2	93%	XM_007119427.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	44.6	89.1	6%	2.2	93%	XM_007119426.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	89.1	6%	2.2	93%	XM_007119425.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	89.1	6%	2.2	93%	XM_007119424.1
PREDICTED: Physeter catodon factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	89.1	6%	2.2	93%	XM_007119423.1
PREDICTED: Leptonychotes weddellii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	44.6	131	7%	2.2	93%	XM_006734383.1
PREDICTED: Leptonychotes weddellii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	131	7%	2.2	93%	XM_006734382.1
PREDICTED: Leptonychotes weddellii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	131	7%	2.2	93%	XM_006734381.1
PREDICTED: Leptonychotes weddellii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	131	7%	2.2	93%	XM_006734380.1
PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	131	7%	2.2	93%	XM_005961478.1
PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	131	7%	2.2	93%	XM_005961477.1
PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	131	7%	2.2	93%	XM_005961476.1
PREDICTED: Bos mutus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	89.1	6%	2.2	93%	XM_005899823.1
PREDICTED: Bos mutus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	89.1	6%	2.2	93%	XM_005899822.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X10, mRNA	44.6	89.1	6%	2.2	93%	XM_005681625.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X9, mRNA	44.6	89.1	6%	2.2	93%	XM_005681624.1
PREDICTED: Capra hircus factor						

interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X8, mRNA	44.6	89.1	6%	2.2	93%	XM_005681623.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA	44.6	89.1	6%	2.2	93%	XM_005681622.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA	44.6	89.1	6%	2.2	93%	XM_005681621.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA	44.6	89.1	6%	2.2	93%	XM_005681620.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA	44.6	89.1	6%	2.2	93%	XM_005681619.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA	44.6	89.1	6%	2.2	93%	XM_005681618.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA	44.6	89.1	6%	2.2	93%	XM_005681617.1
PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA	44.6	89.1	6%	2.2	93%	XM_005681616.1
PREDICTED: Sus scrofa factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_005666647.1
PREDICTED: Canis lupus familiaris factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA	44.6	131	7%	2.2	93%	XM_848862.3
PREDICTED: Equus caballus factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA	44.6	131	7%	2.2	93%	XM_001492511.4
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X7, mRNA	44.6	131	7%	2.2	93%	XM_005320008.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X6, mRNA	44.6	131	7%	2.2	93%	XM_005320007.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X5, mRNA	44.6	131	7%	2.2	93%	XM_005320006.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X4, mRNA	44.6	131	7%	2.2	93%	XM_005320005.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X3, mRNA	44.6	131	7%	2.2	93%	XM_005320004.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X2, mRNA	44.6	131	7%	2.2	93%	XM_005320003.1
PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X1, mRNA	44.6	131	7%	2.2	93%	XM_005320002.1
PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X3, mRNA	44.6	131	7%	2.2	93%	XM_004764963.1
PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X2, mRNA	44.6	131	7%	2.2	93%	XM_004764962.1
PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X1, mRNA	44.6	131	7%	2.2	93%	XM_004764961.1

PREDICTED: Ceratotherium simum simum FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 3 (FIP1L1), mRNA	44.6	131	7%	2.2	93%	XM_004419065.1
PREDICTED: Ceratotherium simum simum FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 2 (FIP1L1), mRNA	44.6	131	7%	2.2	93%	XM_004419064.1
PREDICTED: Ceratotherium simum simum FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 1 (FIP1L1), mRNA	44.6	131	7%	2.2	93%	XM_004419063.1
PREDICTED: Tursiops truncatus FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 4 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004323424.1
PREDICTED: Tursiops truncatus FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 3 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004323423.1
PREDICTED: Tursiops truncatus FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 2 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004323422.1
PREDICTED: Tursiops truncatus FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 1 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004323421.1
PREDICTED: Orcinus orca FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 4 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004268273.1
PREDICTED: Orcinus orca FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 3 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004268272.1
PREDICTED: Orcinus orca FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 2 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004268271.1
PREDICTED: Orcinus orca FIP1 like 1 (<i>S. cerevisiae</i>), transcript variant 1 (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004268270.1
PREDICTED: Ovis aries FIP1 like 1 (<i>S. cerevisiae</i>) (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	XM_004010068.1
Sus scrofa mRNA, clone: OVRT10042C05, expressed in ovary	44.6	89.1	6%	2.2	93%	AK395642.1
Bos taurus FIP1 like 1 (<i>S. cerevisiae</i>) (FIP1L1), mRNA	44.6	89.1	6%	2.2	93%	NM_001206690.1
Caenorhabditis remanei hypothetical protein (CRE_09068) mRNA, complete cds	44.6	87.3	4%	2.2	83%	XM_003115900.1
PREDICTED: Ailuropoda melanoleuca pre-mRNA 3'-end-processing factor FIP1-like, transcript variant 3 (LOC100474965), mRNA	44.6	131	7%	2.2	93%	XM_002919404.1
PREDICTED: Ailuropoda melanoleuca pre-mRNA 3'-end-processing factor FIP1-like, transcript variant 2 (LOC100474965), mRNA	44.6	131	7%	2.2	93%	XM_002919403.1

Alignments

Mus musculus BAC clone RP24-299I4 from chromosome 14, complete sequence

Sequence ID: **gb|AC154677.2** | Length: 149259 Number of Matches: 4

Range 1: 69181 to 69536

Sbjct	69296	GACTCTCTGTGTC---TCTCTCTGTGTC--TCTCTCTGTGTCCTCTCTATGA-CTC	69348
Query	537	TCTCTGTGTCGTAGTCTACGATCAAATCTCTCTGTGTCGTATATG---CTCGATATG--	591
Sbjct	69349	TCTCTGTGTCCTCTCTGTG-TC---TCTCTCTGTGTCCTCTCTGTGTCCTCTGTG	69404
Query	592	-ATCTCTGTGTCGTAGTGCCTGATATATGATTATATGCTCGATATGA-TCTCTCT	649
Sbjct	69405	TCTCTCTGTGTCCTCTCTGTGTCCTCTGTGTCCTCTGTGTC	69461
Query	650	GTGTCGTAGTTCTGTGTCGTAGTCTACGATCAAATCTCTGTGTCGTATATG----	705
Sbjct	69462	GTGTC---TCTCTGTGTC---TCT-CTAT-GACTCTCTGTGTCCTCTGTGTC	69512
Query	706	-CTCGATATGA-TCTCTGTGTC 727	
Sbjct	69513	TCTCTATGACTCTCTGTGTC 69536	

Range 2: 69419 to 69604

Score	Expect	Identities	Gaps	Strand	Frame
53.6 bits(58)	0.004()	135/197(69%)	19/197(9%)	Plus/Plus	

Features:

Query	416	TCTCTGTGTCGTATATG----CTCGATATGA-TCTCTGTGTCGTAGTGCCTGTA	469
Sbjct	69419	TCTCTGTGTCCTCTCTGTGTCCTCTGTGACTCTCTGTGTCCTCTGTGTC	69478
Query	470	TATATATGAATCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCGTAGTCTA	529
Sbjct	69479	TCTCTATGACTCTCTGTGTC---TCTCTGTGTC---TCTCTATGACTCTCTG	69532
Query	530	CGATCAATCTCTGTGTCGTAGTCTACGATCAAATCTCTGTGTCGTATAT-GCTCGAT	588
Sbjct	69533	TG-TCTCTCTGTGTCCTCTGTG-TC---TCTCTGTGTCCTGTGTCCTCTCT	69587
Query	589	ATGA-TCTCTGTGTC 604	
Sbjct	69588	ATGACTCTCTGTGTC 69604	

Range 3: 69173 to 69260

Score	Expect	Identities	Gaps	Strand	Frame
50.0 bits(54)	0.051()	73/99(74%)	11/99(11%)	Plus/Plus	

Features:

Query	474	TATGAATCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCGTAGTCTACGAT	533
Sbjct	69173	TATGACTCTCTGTGTC---TCTCTGTGTC---TCTCTGTGTCCTCTATGA-	69225
Query	534	CAATCTCTGTGTCGTAGTCTACGATCAAATCTCTGTGTCGTATATG-----CTCGAT	572
Sbjct	69226	CTCTCTCTGTGTCCTCTGTG-TC---TCTCTGTGTC 69260	

Range 4: 69341 to 69466

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	96/137(70%)	17/137(12%)	Plus/Plus	

Features:

Query	474	TATGAATCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCGTAGTCTACGAT	533
Sbjct	69341	TATGACTCTCTGTGTC---TCTCTGTGTC---TCTCTGTGTCCTCTGTG-	69393
Query	534	CAATCTCTGTGTCGTAGTCTACGATCAAATCTCTGTGTCGTATATG-----CTCGAT	588
Sbjct	69394	CTCTCTCTGTGTCCTCTGTG-TC---TCTCTGTGTCCTCTGTGTCCTCT	69449
Query	589	ATGA-TCTCTGTGTC 604	
Sbjct	69450	GTGACTCTCTGTGTC 69466	

PREDICTED: Panthera tigris altaica factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA

Sequence ID: **refXM_007075922.1** | Length: 2004 Number of Matches: 2

Range 1: 1618 to 1660

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCG 522	
Sbjct	1660	TCTCTCTGTGTCGTCTCTGTGTCGTGTCGTTCTCTCT 1618	

Range 2: 1632 to 1660

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 273 TCTCTCTGTGTCGGATCTCTGTGTCGT 301
Sbjct 1660 ||||||| ||||| ||||| ||||| ||||| 1632

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA

Sequence ID: [ref|XM_003985384.2|](#) Length: 1939 Number of Matches: 2

Range 1: 1561 to 1603

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1603 ||||||| ||||| ||||| ||||| ||||| 1561

Range 2: 1575 to 1603

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 273 TCTCTCTGTGTCGGATCTCTGTGTCGT 301
Sbjct 1603 ||||||| ||||| ||||| ||||| 1575

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA

Sequence ID: [ref|XM_006931126.1|](#) Length: 2012 Number of Matches: 2

Range 1: 1634 to 1676

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1676 ||||||| ||||| ||||| ||||| ||||| 1634

Range 2: 1648 to 1676

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 273 TCTCTCTGTGTCGGATCTCTGTGTCGT 301
Sbjct 1676 ||||||| ||||| ||||| ||||| 1648

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA

Sequence ID: [ref|XM_006931125.1|](#) Length: 2081 Number of Matches: 2

Range 1: 1703 to 1745

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1745 ||||||| ||||| ||||| ||||| ||||| 1703

Range 2: 1717 to 1745

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	273	TCTCTCTGTGTCGGATCTCTCTGTGTCGT	301
Sbjct	1745	TCTCTCTGTGTCGTCTCTCTGTGTCGT	1717

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA

Sequence ID: [ref|XM_006931124.1|](#) Length: 2120 Number of Matches: 2

Range 1: 1742 to 1784

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1784	TCTCTCTGTGTCGTCTCTCTGTGTCGTTCTTCTCTCG	1742

Range 2: 1756 to 1784

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	273	TCTCTCTGTGTCGGATCTCTCTGTGTCGT	301
Sbjct	1784	TCTCTCTGTGTCGTCTCTCTGTGTCGT	1756

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA

Sequence ID: [ref|XM_003985383.2|](#) Length: 2144 Number of Matches: 2

Range 1: 1766 to 1808

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1808	TCTCTCTGTGTCGTCTCTCTGTGTCGTTCTTCTCTCG	1766

Range 2: 1780 to 1808

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	273	TCTCTCTGTGTCGGATCTCTCTGTGTCGT	301
Sbjct	1808	TCTCTCTGTGTCGTCTCTCTGTGTCGT	1780

PREDICTED: Felis catus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA

Sequence ID: [ref|XM_003985382.2|](#) Length: 2161 Number of Matches: 2

Range 1: 1783 to 1825

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1825	TCTCTCTGTGTCGTCTCTCTGTGTCGTTCTTCTCTCG	1783

Range 2: 1797 to 1825

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	273	TCTCTCTGTGTCGGATCTCTCTGTGTCGT	301
		: : : : : :	
Sbjct	1825	TCTCTCTGTGTCGTCTCTCTGTGTCGT	17997

PREDICTED: *Felis catus* factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA
Sequence ID: **ref|XM_006931123.1|** Length: 2189 Number of Matches: 2
Range 1: 1811 to 1853

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	36/43(84%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG	522
Sbjct	1853	TCTCTCTGTGTCGTCTCTCTGTGTCGTGTTCTTCTCTCTCG	1811

Range 2: 1825 to 1853

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

```

Query 273 TCTCTCTGTGTCGGATCTCTCTGTGTCGT 301
||||||||||||||| ||||||||||||||||||||| |
Sbjct 1853 TCTCTCTGTGTCGTCTCTCTGTGTCGT 1825

```

Homo sapiens BAC clone RP11-704A15 from chromosome x, complete sequence

Sequence ID: **gb|AC239601.2** | Length: 182334 Number of Matches: 1
Range 1: 137956 to 138121

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	123/175(70%)	16/175(9%)	Plus/Plus	

Features:

Query	738	TATATATATGATTATATGCTCGATATTCTCTGTGTCGTTAGTCTACGATCAATTATATGCT	797
Sbjct	137956	TATATATATGATCATAT-----ATATGATCTATGT-GATCTATATGATCATATATGTGAT	138009
Query	798	CGATATGATC-TCTCTGTGTCGTTAGTGCGCGTATATATATGAT-TATATGCTCGATATGA	855
Sbjct	138010	CTATATGATCATATATGTGATCTA-TATGATCATATATGTGATCTATATGATCTATATGA	138068
Query	856	TC-TCTCTGTG-TC-GTAGTATC-TCTCTGTG-TCGTTATATGCTCGATATGATC	905
Sbjct	138069	TCATATATGTGATCTATATGATCATATATGTGATC--TATATGATCTATATGATC	138121

Branchiostoma floridae hypothetical protein, mRNA

Sequence ID: ref|XM_002593504.1| Length: 1770 Number of Matches: 1
Range 1: 1426 to 1463

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	33/38(87%)	0/38(0%)	Plus/Minus	

Features:

Query	484	TCTGTGTCGGATCTCTCTGTGTCGTAGTTCTGTGTC	521
Sbjct	1463	TCTGTGTCGTAGTTCTCTGTGTCGTCCGAGTTCTGTGTC	1426

Human DNA sequence from clone RP1-279N11 on chromosome Xq11.2-13.3 Contain the 3' end of a novel gene, complete sequence
Sequence ID: **emb|Z98255.2** Length: 169998 Number of Matches: 1
Range 1: 152653 to 152818

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	123/175(70%)	16/175(9%)	Plus/Plus	

Features:

```

Query 738 TATATATATGATTATATGCTCGATATTCTCTGTGTCGTAGTCTACGATCAATTATATGCT 797
Sbjct 152653 TATATATATGATCATT-----ATATGATCTATGCTCATCTATGATCTATGATCTATGAT 152706

```

Query	798	CGATATGATC-TCTCTGTGTCGTAGTGC CGTATATATGAT-TATATGCTCGATATGA	855
Sbjct	152707	CTATATGATCATATATGATCTA-TATGATCATATATGATCTATATGATCTATATGA	152765
Query	856	TC-TCTCTGTG-TC-GTAGTATC-TCTCTGTG-TCGTTATATGCTCGATATGATC	905
Sbjct	152766	TCATATATGTGATCTATATGATCATATATGATGATC-TATATGATCTATATGATC	152818

Human Chromosome X clone bWXD531, complete sequence

Sequence ID: **gb|AC004384.1|AC004384** Length: 164675 Number of Matches: 1
Range 1: 135219 to 135384

Score	Expect	Identities	Gaps	Strand	Frame
46.4 bits(50)	0.62()	123/175(70%)	16/175(9%)	Plus/Minus	

Features:

Query	738	TATATATATGATTATATGCTCGATATTCTCTGTGTCGTAGTCTACGATCAATTATATGCT	797
Sbjct	135384	TATATATATGATCATAT-----ATATGATCTATGT-GATCTATATGATCATATATGAT	135331
Query	798	CGATATGATC-TCTCTGTGTCGTAGTGC CGTATATATGAT-TATATGCTCGATATGA	855
Sbjct	135330	CTATATGATCATATATGATCTA-TATGATCATATATGATCTATATGATCTATATGAT	135272
Query	856	TC-TCTCTGTG-TC-GTAGTATC-TCTCTGTG-TCGTTATATGCTCGATATGATC	905
Sbjct	135271	TCATATATGTGATCTATATGATCATATATGATGATC-TATATGATCTATATGATC	135219

PREDICTED: Equus przewalskii factor interacting with PAPOLA and CPSF1 (FIP1L1), partial mRNA

Sequence ID: **ref|XM_008522213.1|** Length: 1891 Number of Matches: 3
Range 1: 1461 to 1489

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1489	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1461

Range 2: 1461 to 1489

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	1489	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1461

Range 3: 1447 to 1489

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG	522
Sbjct	1489	TCTCTCTGTGTCGTCTTCTCTGTGTCGTCTTCTCTCG	1447

PREDICTED: Cricetus griseus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X14, mRNA

Sequence ID: **ref|XM_007613853.1|** Length: 2023 Number of Matches: 2
Range 1: 1651 to 1679

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1679	TCTCTCTGTGACGTCGTTCTCTGTGTCGT	1651

Range 2: 1651 to 1679

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1679 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1651

PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X13, mRNA

Sequence ID: [ref|XM_007613852.1|](#) Length: 2050 Number of Matches: 2

Range 1: 1678 to 1706

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1706 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1678

Range 2: 1678 to 1706

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1706 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1678

PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X12, mRNA

Sequence ID: [ref|XM_007613851.1|](#) Length: 2092 Number of Matches: 2

Range 1: 1720 to 1748

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1748 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1720

Range 2: 1720 to 1748

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1748 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1720

PREDICTED: Cricetulus griseus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X11, mRNA

Sequence ID: [ref|XM_007613850.1|](#) Length: 2119 Number of Matches: 2

Range 1: 1747 to 1775

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1775 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1747

Range 2: 1747 to 1775

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| ||||| |||||
Sbjct 1775 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1747

PREDICTED: Cricetus griseus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X10, mRNA
Sequence ID: **refXM_007613849.1** Length: 2158 Number of Matches: 2
Range 1: 1786 to 1814

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1814 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1786

Range 2: 1786 to 1814

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1814 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1786

PREDICTED: Cricetus griseus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X9, mRNA
Sequence ID: **refXM_007613848.1** Length: 2200 Number of Matches: 2
Range 1: 1828 to 1856

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1856 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1828

Range 2: 1828 to 1856

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1856 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1828

PREDICTED: Leptonychotes weddellii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA
Sequence ID: **refXM_006734381.1** Length: 2439 Number of Matches: 3
Range 1: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1791 TCTCTCTGTGACGTCGTTCTCTGTGTCGT 1763

Range 2: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
 Sbjct 1791 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1763

Range 3: 1749 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCGT 522
 Sbjct 1791 TCTCTCTGTGTCGTCTTCTCTGTGTCGTCTTCTCTCG 1749

PREDICTED: Leptonychotes weddelli factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA

Sequence ID: [refXM_006734380.1](#) Length: 2188 Number of Matches: 3

Range 1: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
 Sbjct 1796 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1768

Range 2: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
 Sbjct 1796 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1768

Range 3: 1754 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCGT 522
 Sbjct 1796 TCTCTCTGTGTCGTCTTCTCTGTGTCGTCTTCTCTCG 1754

PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA

Sequence ID: [refXM_005961478.1](#) Length: 1991 Number of Matches: 3

Range 1: 1566 to 1594

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
 Sbjct 1594 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1566

Range 2: 1566 to 1594

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
 Sbjct 1594 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1566

Range 3: 1552 to 1594

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1594		1552

PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA
Sequence ID: [ref|XM_005961477.1|](#) Length: 1964 Number of Matches: 3
Range 1: 1596 to 1624

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1624		1596

Range 2: 1596 to 1624

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1624		1596

Range 3: 1582 to 1624

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1624		1582

PREDICTED: Pantholops hodgsonii factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA
Sequence ID: [ref|XM_005961476.1|](#) Length: 2239 Number of Matches: 3
Range 1: 1638 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1666		1638

Range 2: 1638 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1666		1638

Range 3: 1624 to 1666

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG	522
Sbjct	1666	TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCTCG	1624

PREDICTED: Bos mutus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA
Sequence ID: **refXM_005899823.1|** Length: 1919 Number of Matches: 2
Range 1: 1497 to 1525

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1525	TCTCTCTGTGTCGTCTTCTGTGTCGT	1497

Range 2: 1497 to 1525

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1525	TCTCTCTGTGTCGTCTTCTGTGTCGT	1497

PREDICTED: Bos mutus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA
Sequence ID: **refXM_005899822.1|** Length: 1946 Number of Matches: 2
Range 1: 1581 to 1609

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1609	TCTCTCTGTGTCGTCTTCTGTGTCGT	1581

Range 2: 1581 to 1609

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1609	TCTCTCTGTGTCGTCTTCTGTGTCGT	1581

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X10, mRNA
Sequence ID: **refXM_005681625.1|** Length: 2136 Number of Matches: 2
Range 1: 1711 to 1739

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1739	TCTCTCTGTGTCGTCTTCTGTGTCGT	1711

Range 2: 1711 to 1739

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1739	TCTCTCTGTGTCGTCTTCTGTGTCGT	1711

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X9, mRNA
Sequence ID: **refXM_005681624.1** | Length: 2022 Number of Matches: 2
Range 1: 1597 to 1625

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| ||||| |||||
Sbjct 1625 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1597

Range 2: 1597 to 1625

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1625 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1597

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X8, mRNA
Sequence ID: **refXM_005681623.1** | Length: 1995 Number of Matches: 2
Range 1: 1627 to 1655

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1655 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1627

Range 2: 1627 to 1655

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1655 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1627

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X7, mRNA
Sequence ID: **refXM_005681622.1** | Length: 2039 Number of Matches: 2
Range 1: 1669 to 1697

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1697 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1669

Range 2: 1669 to 1697

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1697 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1669

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X6, mRNA

Sequence ID: [ref|XM_005681621.1|](#) Length: 2042 Number of Matches: 2

Range 1: 1672 to 1700

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1700 TCTCTCTGTGTCGTCTTCTGTGTCGT 1672

Range 2: 1672 to 1700

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1700 TCTCTCTGTGTCGTCTTCTGTGTCGT 1672

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X5, mRNA

Sequence ID: [ref|XM_005681620.1|](#) Length: 2063 Number of Matches: 2

Range 1: 1693 to 1721

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1721 TCTCTCTGTGTCGTCTTCTGTGTCGT 1693

Range 2: 1693 to 1721

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1721 TCTCTCTGTGTCGTCTTCTGTGTCGT 1693

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X4, mRNA

Sequence ID: [ref|XM_005681619.1|](#) Length: 2066 Number of Matches: 2

Range 1: 1696 to 1724

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1724 TCTCTCTGTGTCGTCTTCTGTGTCGT 1696

Range 2: 1696 to 1724

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1724 TCTCTCTGTGTCGTCTTCTGTGTCGT 1696

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X3, mRNA

Sequence ID: ref|XM_005681618.1| Length: 2139 Number of Matches: 2
Range 1: 1714 to 1742

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1742 TCTCTCTGTGTCGTCTTCTGTGTCGT 1714

Range 2: 1714 to 1742

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1742 TCTCTCTGTGTCGTCTTCTGTGTCGT 1714

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X2, mRNA
Sequence ID: ref|XM_005681617.1| Length: 2108 Number of Matches: 2
Range 1: 1738 to 1766

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1766 TCTCTCTGTGTCGTCTTCTGTGTCGT 1738

Range 2: 1738 to 1766

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1766 TCTCTCTGTGTCGTCTTCTGTGTCGT 1738

PREDICTED: Capra hircus factor interacting with PAPOLA and CPSF1 (FIP1L1), transcript variant X1, mRNA
Sequence ID: ref|XM_005681616.1| Length: 2111 Number of Matches: 2
Range 1: 1741 to 1769

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1769 TCTCTCTGTGTCGTCTTCTGTGTCGT 1741

Range 2: 1741 to 1769

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1769 TCTCTCTGTGTCGTCTTCTGTGTCGT 1741

PREDICTED: Sus scrofa factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA
Sequence ID: ref|XM_005666647.1| Length: 1190 Number of Matches: 2
Range 1: 816 to 844

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	844	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	816

Range 2: 816 to 844

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	844	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	816

PREDICTED: Canis lupus familiaris factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA

Sequence ID: [ref|XM_848862.3|](#) Length: 2527 Number of Matches: 3

Range 1: 2154 to 2182

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	2182	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	2154

Range 2: 2154 to 2182

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	2182	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	2154

Range 3: 2140 to 2182

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	2182	TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCTCG	2140

PREDICTED: Equus caballus factor interacting with PAPOLA and CPSF1 (FIP1L1), mRNA

Sequence ID: [ref|XM_001492511.4|](#) Length: 2104 Number of Matches: 3

Range 1: 1761 to 1789

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1789	TCTCTCTGTGTCGTCTTCTGTGTCGT	1761

Range 2: 1761 to 1789

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
-------	-----	-----------------------------	-----

Sbjct 1789 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1761

Range 3: 1747 to 1789

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1789 TCTCTCTGTGTCGTCTTCTCTGTGTCGTTCTCTCTCG 1747

PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X7, mRNA

Sequence ID: [ref|XM_005320008.1|](#) Length: 1968 Number of Matches: 3

Range 1: 1542 to 1570

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1570 TCTCTCTGTGTCGTCTTCTGTGTCGT 1542

Range 2: 1542 to 1570

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1570 TCTCTCTGTGTCGTCTTCTGTGTCGT 1542

Range 3: 1528 to 1570

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1570 TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCTCG 1528

PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X6, mRNA

Sequence ID: [ref|XM_005320007.1|](#) Length: 2093 Number of Matches: 3

Range 1: 1667 to 1695

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1695 TCTCTCTGTGTCGTCTTCTGTGTCGT 1667

Range 2: 1667 to 1695

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1695 TCTCTCTGTGTCGTCTTCTGTGTCGT 1667

Range 3: 1653 to 1695

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG	522
Sbjct	1695	TCTCTCTGTGTCGTCTTCTCTGTGTCGTCTTCTTCTCTCG	1653

PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X5, mRNA
Sequence ID: ref|XM_005320006.1| Length: 3049 Number of Matches: 3
Range 1: 1694 to 1722

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

```

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
       ||||||| | | | | | | | | | | | | | | |
Sbjct 1722 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1694

```

Range 2: 1694 to 1722

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

```

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
       ||||||| | | | | | | | | | | | | | | | |
Sbjct 1722 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1694

```

Range 3: 1680 to 1722

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG	522
Sbjct	1722	TCTCTCTGTGTCGTCTTCTCTGTGTCGTCTTCTTCTCTCG	1680

PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X4, mRNA
Sequence ID: **refXM_005320005.1** | Length: 3292 Number of Matches: 3
Range 1: 2866 to 2894

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	2894	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	2866

Range 2: 2866 to 2894

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	2894	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	2866

Range 3: 2852 to 2894

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTCTGTGTCGTAGTTCTCTGTGTCG 522

Sbjct 2894 TCTCTCTGTCGTCTTCTCTGTGCGTTCTCTCTCG 2852

PREDICTED: *Spermophilus tridecemlineatus* factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X3, mRNA
Sequence ID: **ref|XM_005320004.1|** Length: 3157 Number of Matches: 3
Range 1: 1802 to 1830

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTCGTAGTTCTCTGTGCGT 671
Sbjct 1830 TCTCTCTGTCGTCTTCTCTGTGCGT 1802

Range 2: 1802 to 1830

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTCGTAGTTCTCTGTGCGT 523
Sbjct 1830 TCTCTCTGTCGTCTTCTCTGTGCGT 1802

Range 3: 1788 to 1830

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTCGGATCTCTGTGCGTAGTTCTCTGTGCG 522
Sbjct 1830 TCTCTCTGTCGTCTTCTCTGTGCGTTCTCTCTCG 1788

PREDICTED: *Spermophilus tridecemlineatus* factor interacting with PAPOLA and CPSF1 (Fip1I1), transcript variant X2, mRNA
Sequence ID: **ref|XM_005320003.1|** Length: 3112 Number of Matches: 3
Range 1: 1757 to 1785

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTCGTAGTTCTCTGTGCGT 671
Sbjct 1785 TCTCTCTGTCGTCTTCTCTGTGCGT 1757

Range 2: 1757 to 1785

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTCGTAGTTCTCTGTGCGT 523
Sbjct 1785 TCTCTCTGTCGTCTTCTCTGTGCGT 1757

Range 3: 1743 to 1785

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTCGGATCTCTGTGCGTAGTTCTCTGTGCG 522
Sbjct 1785 TCTCTCTGTCGTCTTCTCTGTGCGTTCTCTCTCG 1743

PREDICTED: Spermophilus tridecemlineatus factor interacting with PAPOLA and CPSF1 (Fip1l1), transcript variant X1, mRNA

Sequence ID: **refXM_005320002.1|** Length: 2270 Number of Matches: 3

Range 1: 1844 to 1872

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1872 |||||||TGTGTCGTCTTCTGTGTCGT 1844

Range 2: 1844 to 1872

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1872 TCTCTCTGTGTCGTCTTCTGTGTCGT 1844

Range 3: 1830 to 1872

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1872 |||||||TGTGTCGTCTTCTGTGTCGTTCTCTCTCG 1830

PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X3, mRNA

Sequence ID: **refXM_004764963.1|** Length: 2226 Number of Matches: 3

► See 1 more title(s)

Range 1: 1913 to 1941

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1941 |||||||TGTGTCGTCTTCTGTGTCGT 1913

Range 2: 1913 to 1941

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1941 |||||||TGTGTCGTCTTCTGTGTCGT 1913

Range 3: 1899 to 1941

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1941 |||||||TGTGTCGTCTTCTGTGTCGTTCTCTCTCG 1899

PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X2, mRNA

Sequence ID: **refXM_004764962.1|** Length: 2451 Number of Matches: 3

▶ See 1 more title(s)

Range 1: 2138 to 2166

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| ||||| |||||
Sbjct 2166 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 2138

Range 2: 2138 to 2166

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 2166 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 2138

Range 3: 2124 to 2166

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCG 522
||||||| ||||| ||||| ||||| |||||
Sbjct 2166 TCTCTCTGTGTCGTCTTCTCTGTGTCGTTCTCTCTCG 2124

PREDICTED: Mustela putorius furo FIP1 like 1 (S. cerevisiae) (FIP1L1), transcript variant X1, mRNA
Sequence ID: **refXM_004764961.1** | Length: 2432 Number of Matches: 3

▶ See 1 more title(s)

Range 1: 2119 to 2147

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 2147 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 2119

Range 2: 2119 to 2147

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 2147 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 2119

Range 3: 2105 to 2147

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTCTGTGTCG 522
||||||| ||||| ||||| |||||
Sbjct 2147 TCTCTCTGTGTCGTCTTCTCTGTGTCGTTCTCTCTCG 2105

PREDICTED: Ceratotherium simum simum FIP1 like 1 (S. cerevisiae), transcript variant 3 (FIP1L1), mRNA
Sequence ID: **refXM_004419065.1** | Length: 2218 Number of Matches: 3
Range 1: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| ||||| |||||
Sbjct 1574 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1546

Range 2: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| |||||
Sbjct 1574 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1546

Range 3: 1532 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
||||||| ||||| |||||
Sbjct 1574 TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCTCG 1532

PREDICTED: Ceratotherium simum simum FIP1 like 1 (S. cerevisiae), transcript variant 2 (FIP1L1), mRNA

Sequence ID: [ref|XM_004419064.1|](#) Length: 2435 Number of Matches: 3

Range 1: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| |||||
Sbjct 1791 TCTCTCTGTGTCGTCTTCTGTGTCGT 1763

Range 2: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| |||||
Sbjct 1791 TCTCTCTGTGTCGTCTTCTGTGTCGT 1763

Range 3: 1749 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
||||||| ||||| |||||
Sbjct 1791 TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCTCG 1749

PREDICTED: Ceratotherium simum simum FIP1 like 1 (S. cerevisiae), transcript variant 1 (FIP1L1), mRNA

Sequence ID: [ref|XM_004419063.1|](#) Length: 2440 Number of Matches: 3

Range 1: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| |||||
Sbjct 1796 TCTCTCTGTGTCGTCTTCTGTGTCGT 1768

Range 2: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1796 TCTCTCTGTGTCGTCTTCTGTGTCGT 1768

Range 3: 1754 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1796 TCTCTCTGTGTCGTCTTCTGTGTCGTTCTTCTCTCG 1754

PREDICTED: Tursiops truncatus FIP1 like 1 (S. cerevisiae), transcript variant 4 (FIP1L1), mRNA

Sequence ID: [ref|XM_004323424.1|](#) Length: 2226 Number of Matches: 2

Range 1: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1574 TCTCTCTGTGTCGTCTTCTGTGTCGT 1546

Range 2: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1574 TCTCTCTGTGTCGTCTTCTGTGTCGT 1546

PREDICTED: Tursiops truncatus FIP1 like 1 (S. cerevisiae), transcript variant 3 (FIP1L1), mRNA

Sequence ID: [ref|XM_004323423.1|](#) Length: 1961 Number of Matches: 2

Range 1: 1587 to 1615

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTGTGTCGT 671
Sbjct 1615 TCTCTCTGTGTCGTCTTCTGTGTCGT 1587

Range 2: 1587 to 1615

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTGTGTCGT 523
Sbjct 1615 TCTCTCTGTGTCGTCTTCTGTGTCGT 1587

PREDICTED: Tursiops truncatus FIP1 like 1 (S. cerevisiae), transcript variant 2 (FIP1L1), mRNA

Sequence ID: [ref|XM_004323422.1|](#) Length: 2443 Number of Matches: 2

Range 1: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1791 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1763

Range 2: 1763 to 1791

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1791 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1763

PREDICTED: Tursiops truncatus FIP1 like 1 (S. cerevisiae), transcript variant 1 (FIP1L1), mRNA

Sequence ID: [ref|XM_004323421.1|](#) Length: 2448 Number of Matches: 2
Range 1: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1796 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1768

Range 2: 1768 to 1796

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1796 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1768

PREDICTED: Orcinus orca FIP1 like 1 (S. cerevisiae), transcript variant 4 (FIP1L1), mRNA

Sequence ID: [ref|XM_004268273.1|](#) Length: 2226 Number of Matches: 2
Range 1: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
Sbjct 1574 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1546

Range 2: 1546 to 1574

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
Sbjct 1574 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1546

PREDICTED: Orcinus orca FIP1 like 1 (S. cerevisiae), transcript variant 3 (FIP1L1), mRNA

Sequence ID: [ref|XM_004268272.1|](#) Length: 1961 Number of Matches: 2
Range 1: 1587 to 1615

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1615	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1587

Range 2: 1587 to 1615

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	1615	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1587

PREDICTED: Orcinus orca FIP1 like 1 (*S. cerevisiae*), transcript variant 2 (FIP1L1), mRNA

Sequence ID: **ref|XM_004268271.1|** Length: 2443 Number of Matches: 2

Range 1: 1763 to 1791

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1791	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1763

Range 2: 1763 to 1791

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	1791	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1763

PREDICTED: Orcinus orca FIP1 like 1 (*S. cerevisiae*), transcript variant 1 (FIP1L1), mRNA

Sequence ID: **ref|XM_004268270.1|** Length: 2448 Number of Matches: 2

Range 1: 1768 to 1796

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	671
Sbjct	1796	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1768

Range 2: 1768 to 1796

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTCTGTGTCGT	523
Sbjct	1796	TCTCTCTGTGTCGTCTTCTCTGTGTCGT	1768

PREDICTED: Ovis aries FIP1 like 1 (*S. cerevisiae*) (FIP1L1), mRNA

Sequence ID: **ref|XM_004010068.1|** Length: 1773 Number of Matches: 2

Range 1: 1404 to 1432

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

44.6 bits(48) 2.2() 27/29(93%) 0/29(0%) Plus/Minus

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| ||||| |||||
Sbjct 1432 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1404

Range 2: 1404 to 1432

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1432 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1404

Sus scrofa mRNA, clone: OVRT10042C05, expressed in ovary

Sequence ID: [dbj|AK395642.1|](#) Length: 1889 Number of Matches: 2

Range 1: 1491 to 1519

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1519 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1491

Range 2: 1491 to 1519

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1519 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1491

Bos taurus FIP1 like 1 (S. cerevisiae) (FIP1L1), mRNA

Sequence ID: [ref|NM_001206690.1|](#) Length: 1951 Number of Matches: 2

Range 1: 1572 to 1600

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 643 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 671
||||||| ||||| ||||| |||||
Sbjct 1600 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1572

Range 2: 1572 to 1600

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query 495 TCTCTCTGTGTCGTAGTTCTCTGTGTCGT 523
||||||| ||||| ||||| |||||
Sbjct 1600 TCTCTCTGTGTCGTCTTCTCTGTGTCGT 1572

Caenorhabditis remanei hypothetical protein (CRE_09068) mRNA, complete cds

Sequence ID: [ref|XM_003115900.1|](#) Length: 1410 Number of Matches: 2

Range 1: 1142 to 1183

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	35/42(83%)	0/42(0%)	Plus/Minus	

Features:

Query	484	TCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCGTAG	525
Sbjct	1183	TCTGTGTCGTAGATGTCTGCCTCGTAGATGTCTGTGTCGTAG	1142

Range 2: 1128 to 1168

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	34/41(83%)	0/41(0%)	Plus/Minus	

Features:

Query	484	TCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCGTAG	524
Sbjct	1168	TCTGCCTCGTAGATGTCTGTGTCGTAGATGTCTGTGTCGTAG	1128

PREDICTED: Ailuropoda melanoleuca pre-mRNA 3'-end-processing factor FIP1-like, transcript variant 3 (LOC100474965), mRNA

Sequence ID: **refXM_002919404.1** | Length: 1971 Number of Matches: 3

Range 1: 1367 to 1395

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1395	TCTCTCTGTGTCGTCTTCTGTGTCGT	1367

Range 2: 1367 to 1395

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1395	TCTCTCTGTGTCGTCTTCTGTGTCGT	1367

Range 3: 1353 to 1395

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query	480	TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG	522
Sbjct	1395	TCTCTCTGTGTCGTCTTCTGTGTCGTCTTCTGTGTCG	1353

PREDICTED: Ailuropoda melanoleuca pre-mRNA 3'-end-processing factor FIP1-like, transcript variant 2 (LOC100474965), mRNA

Sequence ID: **refXM_002919403.1** | Length: 2182 Number of Matches: 3

Range 1: 1578 to 1606

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	643	TCTCTCTGTGTCGTAGTTCTGTGTCGT	671
Sbjct	1606	TCTCTCTGTGTCGTCTTCTGTGTCGT	1578

Range 2: 1578 to 1606

Score	Expect	Identities	Gaps	Strand	Frame
44.6 bits(48)	2.2()	27/29(93%)	0/29(0%)	Plus/Minus	

Features:

Query	495	TCTCTCTGTGTCGTAGTTCTGTGTCGT	523
Sbjct	1606	TCTCTCTGTGTCGTCTTCTGTGTCGT	1578

Range 3: 1564 to 1606

Score	Expect	Identities	Gaps	Strand	Frame
42.8 bits(46)	7.6()	35/43(81%)	0/43(0%)	Plus/Minus	

Features:

Query 480 TCTCTCTGTGTCGGATCTCTGTGTCGTAGTTCTGTGTCG 522
Sbjct 1606 TCTCTCTGTGTCGTCTTCTGTGTCGTTCTCTCG 1564