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BLAST Results

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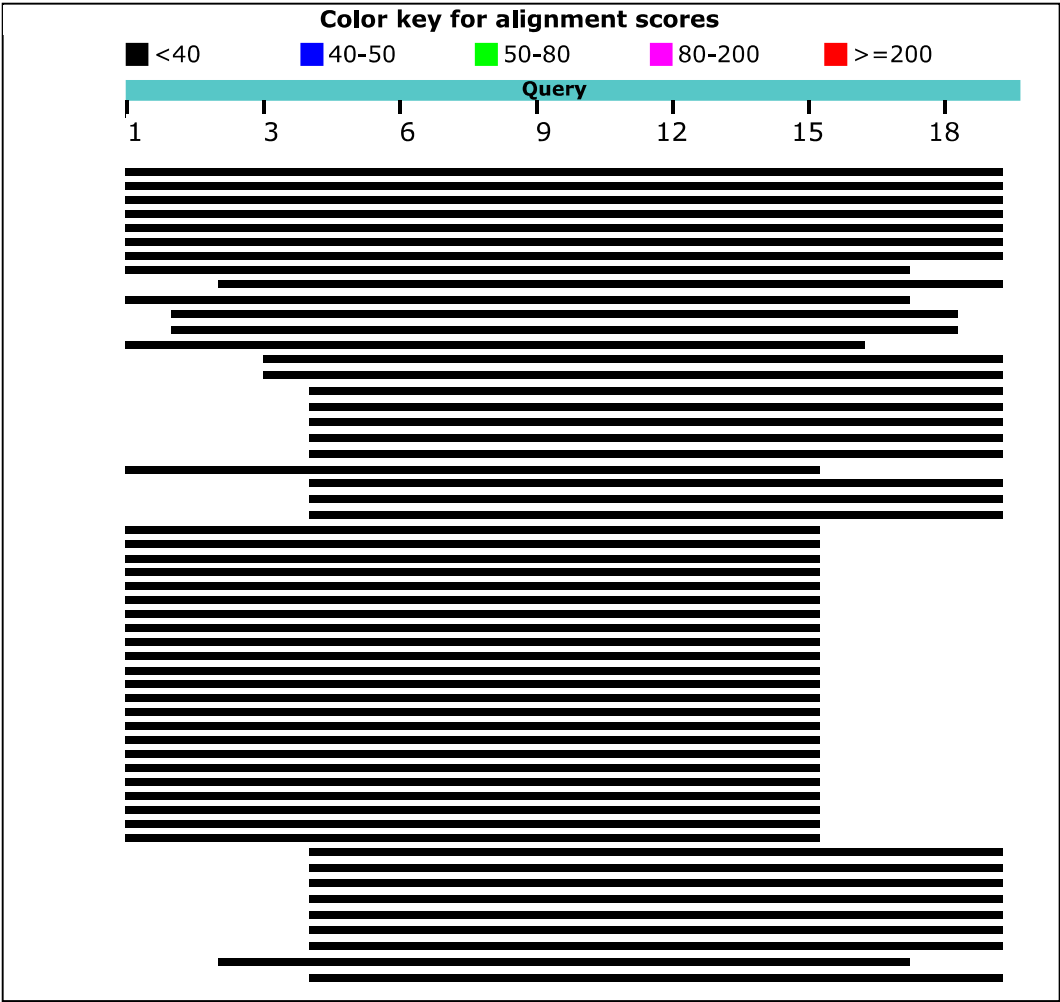
Job title: Nucleotide Sequence (19 letters)

RID [K1XRNUA2015](#) (Expires on 06-26 22:06 pm)

Query ID	Icl Query_178901	Database Name	Human G+T (2 databases)
Description	None	Description	ProgramBLASTN 2.8.0+
Molecule type	nucleic acid		
Query Length	19		

 [Graphic Summary](#)

Distribution of the top 200 Blast Hits on 100 subject sequences



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
Transcripts						
Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA	38.2	38.2	100%	0.025	100%	NM_001304717.2
Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA	38.2	38.2	100%	0.025	100%	NM_000314.6
Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 2, mRNA	38.2	38.2	100%	0.025	100%	NM_001304718.1
Homo sapiens phosphatase and tensin homolog pseudogene 1 (PTENP1), non-coding RNA	38.2	38.2	100%	0.025	100%	NR_023917.1
Homo sapiens translocase of inner mitochondrial membrane 21 (TIMM21), mRNA	34.2	34.2	89%	0.39	100%	NM_014177.2
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X23, mRNA	32.2	32.2	84%	1.5	100%	XM_011541142.2
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X8, mRNA	30.2	30.2	78%	6.1	100%	XM_011515529.3
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X7, mRNA	30.2	30.2	78%	6.1	100%	XM_011515528.3
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X6, mRNA	30.2	30.2	78%	6.1	100%	XM_017012622.2
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X5, mRNA	30.2	30.2	78%	6.1	100%	XM_011515527.3
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X1, mRNA	30.2	30.2	78%	6.1	100%	XM_011515525.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X28, mRNA	30.2	30.2	78%	6.1	100%	XM_024446114.1
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X4, mRNA	30.2	30.2	78%	6.1	100%	XM_017012621.1
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X3, mRNA	30.2	30.2	78%	6.1	100%	XM_011515526.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant X2, mRNA	30.2	30.2	78%	6.1	100%	XM_006715775.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X27, mRNA	30.2	30.2	78%	6.1	100%	XM_006710538.2
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X22, mRNA	30.2	30.2	78%	6.1	100%	XM_017000879.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X21, mRNA	30.2	30.2	78%	6.1	100%	XM_017000878.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X20, mRNA	30.2	30.2	78%	6.1	100%	XM_017000877.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X19, mRNA	30.2	30.2	78%	6.1	100%	XM_006710531.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X18, mRNA	30.2	30.2	78%	6.1	100%	XM_006710530.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X17, mRNA	30.2	30.2	78%	6.1	100%	XM_006710529.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X16, mRNA	30.2	30.2	78%	6.1	100%	XM_006710535.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X15, mRNA	30.2	30.2	78%	6.1	100%	XM_006710528.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X14, mRNA	30.2	30.2	78%	6.1	100%	XM_006710526.3
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X13, mRNA	30.2	30.2	78%	6.1	100%	XM_017000875.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X12, mRNA	30.2	30.2	78%	6.1	100%	XM_017000874.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X10, mRNA	30.2	30.2	78%	6.1	100%	XM_017000873.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X5, mRNA	30.2	30.2	78%	6.1	100%	XM_006710520.2

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X4, mRNA	30.2	30.2	78%	6.1	100%	XM_011541141.2
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X11, mRNA	30.2	30.2	78%	6.1	100%	XM_006710522.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X8, mRNA	30.2	30.2	78%	6.1	100%	XM_006710521.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X2, mRNA	30.2	30.2	78%	6.1	100%	XM_006710519.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X9, mRNA	30.2	30.2	78%	6.1	100%	XM_005270698.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X7, mRNA	30.2	30.2	78%	6.1	100%	XM_005270697.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X6, mRNA	30.2	30.2	78%	6.1	100%	XM_005270696.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X3, mRNA	30.2	30.2	78%	6.1	100%	XM_005270695.1
PREDICTED: Homo sapiens microtubule-actin crosslinking factor 1 (MACF1), transcript variant X1, mRNA	30.2	30.2	78%	6.1	100%	XM_005270694.1
Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant 3, mRNA	30.2	30.2	78%	6.1	100%	NM_001193313.1
Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant 2, mRNA	30.2	30.2	78%	6.1	100%	NM_001193312.1
Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant 1, mRNA	30.2	30.2	78%	6.1	100%	NM_001193311.1
Homo sapiens succinyl-CoA:glutarate-CoA transferase (SUGCT), transcript variant 4, mRNA	30.2	30.2	78%	6.1	100%	NM_024728.2
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X8, mRNA	28.2	28.2	73%	24	100%	XM_024447472.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X7, mRNA	28.2	28.2	73%	24	100%	XM_017014548.2
PREDICTED: Homo sapiens diaphanous related formin 1 (DIAPH1), transcript variant X4, mRNA	28.2	28.2	73%	24	100%	XM_024454387.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens diaphanous related formin 1 (DIAPH1), transcript variant X3, mRNA	28.2	28.2	73%	24	100%	XM_024454386.1
PREDICTED: Homo sapiens diaphanous related formin 1 (DIAPH1), transcript variant X2, mRNA	28.2	28.2	73%	24	100%	XM_024454385.1
PREDICTED: Homo sapiens diaphanous related formin 1 (DIAPH1), transcript variant X1, mRNA	28.2	28.2	73%	24	100%	XM_024454384.1
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X8, misc_RNA	28.2	28.2	73%	24	100%	XR_002957196.1
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X6, mRNA	28.2	28.2	73%	24	100%	XM_017018298.2
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X4, mRNA	28.2	28.2	73%	24	100%	XM_006718905.2
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X3, mRNA	28.2	28.2	73%	24	100%	XM_017018296.2
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 8, mRNA	28.2	28.2	73%	24	100%	NM_001352401.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 7, mRNA	28.2	28.2	73%	24	100%	NM_001352400.1
Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant 4, mRNA	28.2	28.2	73%	24	100%	NM_001330701.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X11, mRNA	28.2	28.2	73%	24	100%	XM_011518420.2
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X10, misc_RNA	28.2	28.2	73%	24	100%	XR_001746261.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X9, mRNA	28.2	28.2	73%	24	100%	XM_017014549.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X6, mRNA	28.2	28.2	73%	24	100%	XM_017014547.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X5, mRNA	28.2	28.2	73%	24	100%	XM_017014546.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X3, mRNA	28.2	28.2	73%	24	100%	XM_017014545.1
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X2, mRNA	28.2	28.2	73%	24	100%	XM_011518418.2
PREDICTED: Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), transcript variant X2, mRNA	28.2	28.2	73%	24	100%	XM_017011494.1
PREDICTED: Homo sapiens Rho GTPase activating protein 18 (ARHGAP18), transcript variant X1, mRNA	28.2	28.2	73%	24	100%	XM_005267212.2
PREDICTED: Homo sapiens pleckstrin homology domain containing M3 (PLEKHM3), transcript variant X2, mRNA	28.2	28.2	73%	24	100%	XM_017004071.1
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X7, mRNA	28.2	28.2	73%	24	100%	XM_006718906.3
PREDICTED: Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant X5, mRNA	28.2	28.2	73%	24	100%	XM_017018297.1
Homo sapiens diaphanous related formin 1 (DIAPH1), transcript variant 3, mRNA	28.2	28.2	73%	24	100%	NM_001314007.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 4, mRNA	28.2	28.2	73%	24	100%	NM_001312919.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 5, mRNA	28.2	28.2	73%	24	100%	NM_001312920.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 6, mRNA	28.2	28.2	73%	24	100%	NM_001312921.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 3, mRNA	28.2	28.2	73%	24	100%	NM_001308027.1
Homo sapiens Myb/SANT DNA binding domain containing 2 (MSANTD2), transcript variant 1, mRNA	28.2	28.2	73%	24	100%	NM_024631.3
PREDICTED: Homo sapiens ATP/GTP binding protein 1 (AGTPBP1), transcript variant X4, mRNA	28.2	28.2	73%	24	100%	XM_005251849.3
Homo sapiens long intergenic non-protein coding RNA, p53 induced transcript (LINC-PINT), transcript variant 7, long non-coding RNA	28.2	28.2	73%	24	100%	NR_109854.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens long intergenic non-protein coding RNA, p53 induced transcript (LINC-PINT), transcript variant 6, long non-coding RNA	28.2	28.2	73%	24	100%	NR_109853.1
Genomic sequences[show first]						
Homo sapiens chromosome 9, GRCh38.p12 Primary Assembly	38.2	7694	100%	0.025	100%	NC_000009.12
Homo sapiens chromosome 10 genomic patch of type FIX, GRCh38.p12 PATCHES HG2334_PATCH	38.2	88.7	100%	0.025	100%	NW_013171807.1
Homo sapiens chromosome 10, GRCh38.p12 Primary Assembly	38.2	8336	100%	0.025	100%	NC_000010.11
Homo sapiens chromosome 1, GRCh38.p12 Primary Assembly	34.2	15626	100%	0.39	100%	NC_000001.11
Homo sapiens chromosome 2, GRCh38.p12 Primary Assembly	34.2	18064	100%	0.39	100%	NC_000002.12
Homo sapiens chromosome 6, GRCh38.p12 Primary Assembly	34.2	12318	100%	0.39	100%	NC_000006.12
Homo sapiens chromosome 18, GRCh38.p12 Primary Assembly	34.2	5174	100%	0.39	100%	NC_000018.10
Homo sapiens chromosome 5, GRCh38.p12 Primary Assembly	32.2	12768	100%	1.5	100%	NC_000005.10
Homo sapiens chromosome X, GRCh38.p12 Primary Assembly	32.2	10759	100%	1.5	100%	NC_000023.11
Homo sapiens chromosome 3, GRCh38.p12 Primary Assembly	30.2	13816	100%	6.1	100%	NC_000003.12
Homo sapiens chromosome 4, GRCh38.p12 Primary Assembly	30.2	14864	100%	6.1	100%	NC_000004.12
Homo sapiens chromosome 7, GRCh38.p12 Primary Assembly	30.2	10708	100%	6.1	100%	NC_000007.14
Homo sapiens chromosome 11, GRCh38.p12 Primary Assembly	30.2	8382	100%	6.1	100%	NC_000011.10
Homo sapiens chromosome 12, GRCh38.p12 Primary Assembly	30.2	9020	100%	6.1	100%	NC_000012.12
Homo sapiens chromosome 13, GRCh38.p12 Primary Assembly	30.2	8396	100%	6.1	100%	NC_000013.11
Homo sapiens chromosome 14, GRCh38.p12 Primary Assembly	30.2	5743	100%	6.1	100%	NC_000014.9
Homo sapiens chromosome 16, GRCh38.p12 Primary Assembly	30.2	4632	100%	6.1	100%	NC_000016.10
Homo sapiens chromosome 20, GRCh38.p12 Primary Assembly	30.2	3094	100%	6.1	100%	NC_000020.11
Homo sapiens chromosome 21, GRCh38.p12 Primary Assembly	30.2	3057	100%	6.1	100%	NC_000021.9
Homo sapiens chromosome 22, GRCh38.p12 Primary Assembly	30.2	1264	100%	6.1	100%	NC_000022.11
Homo sapiens chromosome 8, GRCh38.p12 Primary Assembly	30.2	9772	100%	6.1	100%	NC_000008.11
Homo sapiens chromosome 17, GRCh38.p12 Primary Assembly	30.2	3622	100%	6.1	100%	NC_000017.11
Homo sapiens chromosome Y, GRCh38.p12 Primary Assembly	30.2	1753	100%	6.1	100%	NC_000024.10

Description	Max score	Total score	Query cover	E value	Ident	Accession
Homo sapiens chromosome 15, GRCh38.p12 Primary Assembly	28.2	5256	100%	24	100%	NC_000015.10

Alignments

Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA

Sequence ID: **NM_001304717.2** Length: 8718 Number of Matches: 1

Range 1: 1852 to 1870

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	0.025()	19/19(100%)	0/19(0%)	Plus/Plus	

Features:

```

Query  1      GGGTAAATACATTCTTCAT  19
          |||||
Sbjct 1852 GGGTAAATACATTCTTCAT 1870

```

Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 1, mRNA

Sequence ID: **NM_000314.6** Length: 8718 Number of Matches: 1

Range 1: 1852 to 1870

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	0.025()	19/19(100%)	0/19(0%)	Plus/Plus	

Features:

```

Query  1      GGGTAAATACATTCTTCAT  19
          |||||
Sbjct 1852 GGGTAAATACATTCTTCAT 1870

```

Homo sapiens phosphatase and tensin homolog (PTEN), transcript variant 2, mRNA

Sequence ID: **NM_001304718.1** Length: 8833 Number of Matches: 1

Range 1: 1966 to 1984

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	0.025()	19/19(100%)	0/19(0%)	Plus/Plus	

Features:

```

Query  1      GGGTAAATACATTCTTCAT  19
          |||||
Sbjct 1966 GGGTAAATACATTCTTCAT 1984

```

Homo sapiens phosphatase and tensin homolog pseudogene 1 (PTENP1), non-coding RNA

Sequence ID: **NR_023917.1** Length: 3932 Number of Matches: 1

Range 1: 1590 to 1608

Score	Expect	Identities	Gaps	Strand	Frame
38.2 bits(19)	0.025()	19/19(100%)	0/19(0%)	Plus/Plus	

Features:

```

Query  1      GGGTAAATACATTCTTCAT  19
          |||||
Sbjct 1590 GGGTAAATACATTCTTCAT 1608

```

Homo sapiens translocase of inner mitochondrial membrane 21 (TIMM21), mRNA

Sequence ID: **NM_014177.2** Length: 1562 Number of Matches: 1

Range 1: 1505 to 1521

Score	Expect	Identities	Gaps	Strand	Frame
34.2 bits(17)	0.39()	17/17(100%)	0/17(0%)	Plus/Plus	

Features:

Query	2	GGTAAATACATTCTTCA	18
Sbjct	1505	GGTAAATACATTCTTCA	1521

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