CLUSTAL 2.1 multiple sequence alignment

KC470218.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470214.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470215.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470216.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470217.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470219.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470220.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470221.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470222.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470223.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470225.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470226.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470227.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470228.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470230.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470229.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470224.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KX514433.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KU298886.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
KC470213.1   ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCT
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KC470218.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470214.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470215.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470216.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470217.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470219.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470220.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470221.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470222.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470223.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470225.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470226.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470227.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470228.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470230.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470229.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470224.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KX514433.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KU298886.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
KC470213.1   GTGCACGGAACTGAACACTTCACTGCAAGACATAGAAATAACCTGTGTAT
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KC470218.1   ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA

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KC470214.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470215.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470216.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470217.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470219.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470220.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470221.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470222.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470223.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470225.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470226.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470227.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470228.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470230.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470229.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KC470224.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTCAAA
KX514433.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
KU298886.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
KC470213.1          ATTGCAAGACAGTATTGGAACTTACAGAGGTATTTGAATTTGCATTTAAA
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KC470218.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470214.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470215.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470216.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470217.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470219.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470220.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470221.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470222.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470223.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470225.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470226.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470227.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470228.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470230.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470229.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470224.1          GATTTATTTGTAGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KX514433.1          GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KU298886.1          GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
KC470213.1          GATTTATTTGTGGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAA
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KC470218.1          ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470214.1          ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470215.1          ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470216.1          ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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CLUSTAL 2.1 multiple sequence alignment

KC470217.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470219.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470220.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470221.1                    ATGTATAGATTTCTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470222.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470223.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470225.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470226.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470227.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470228.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470230.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470229.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470224.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KX514433.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KU298886.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
KC470213.1                    ATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATTATTCAGACT
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KC470218.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470214.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470215.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470216.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470217.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470219.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470220.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470221.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470222.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470223.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470225.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470226.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470227.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470228.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470230.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470229.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KC470224.1                    CTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAAT
KX514433.1                    CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
KU298886.1                    CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
KC470213.1                    CTGTGTATGGAGACACATTGGAAAAACTAACTAACACTGGGTTATACAAT
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KC470218.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470214.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470215.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470216.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470217.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470219.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470220.1                    TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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CLUSTAL 2.1 multiple sequence alignment
KC470221.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470222.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470223.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470225.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470226.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470227.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470228.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470230.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTGAATCCAGCAGAAAA
KC470229.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCATTGAATCCAGCAGAAAA
KC470224.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KX514433.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KU298886.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
KC470213.1                          TTATTAATAAGGTGCCTGCGGTGCCAGAAACCGTTGAATCCAGCAGAAAA
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KC470218.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470214.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470215.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470216.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
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KC470220.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
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KC470223.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470225.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470226.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470227.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470228.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACT
KC470230.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KC470229.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KC470224.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KX514433.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
KU298886.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACNNNGCTGGGCACT
KC470213.1                          ACTTAGACACCTTAATGAAAAACGACGATTCCACAACATAGCTGGGCACT
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KC470218.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCAAGCACGACAGGAGAGACTC
KC470214.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470215.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470216.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470217.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470219.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470220.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470221.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470222.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470223.1                          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
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CLUSTAL 2.1 multiple sequence alignment
KC470225.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470226.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470227.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470228.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470230.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470229.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KC470224.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAGAGACTC
KX514433.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
KU298886.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
KC470213.1          ATAGAGGCCAGTGCCATTCGTGCTGCAACCGAGCACGACAGGAAAGACTC
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KC470218.1          CAACGACGCAGAGAAACACAAGTATAA
KC470214.1          CAACGACGCAGAGAAACACAAGTATAA
KC470215.1          CAACGACGCAGAGAAACACAAGTATAA
KC470216.1          CAACGACGCAGAGAAACACAAGTATAA
KC470217.1          CAACGACGCAGAGAAACACAAGTATAA
KC470219.1          CAACGACGCAGAGAAACACAAGTATAA
KC470220.1          CAACGACGCAGAGAAACACAAGTATAA
KC470221.1          CAACGACGCAGAGAAACACAAGTATAA
KC470222.1          CAACGACGCAGAGAAACACAAGTATAA
KC470223.1          CAACGACGCAGAGAAACACAAGTATAA
KC470225.1          CAACGACGCAGAGAAACACAAGTATAA
KC470226.1          CAACGACGCAGAGAAACACAAGTATAA
KC470227.1          CAACGACGCAGAGAAACACAAGTATAA
KC470228.1          CAACGACGCAGAGAAACACAAGTATAA
KC470230.1          CAACGACGCAGAGAAACACAAGTATAA
KC470229.1          CAACGACGCAGAGAAACACAAGTATAA
KC470224.1          CAACGACGCAGAGAAACACAAGTATAA
KX514433.1          CAACGACGCAGAGAAACACAAGTATAA
KU298886.1          CAACGACGCAGAGAAACACAAGTATAA
KC470213.1          CAACGACGCAGAGAAACACAAGTATAA
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Multiple Sequence Alignment tree
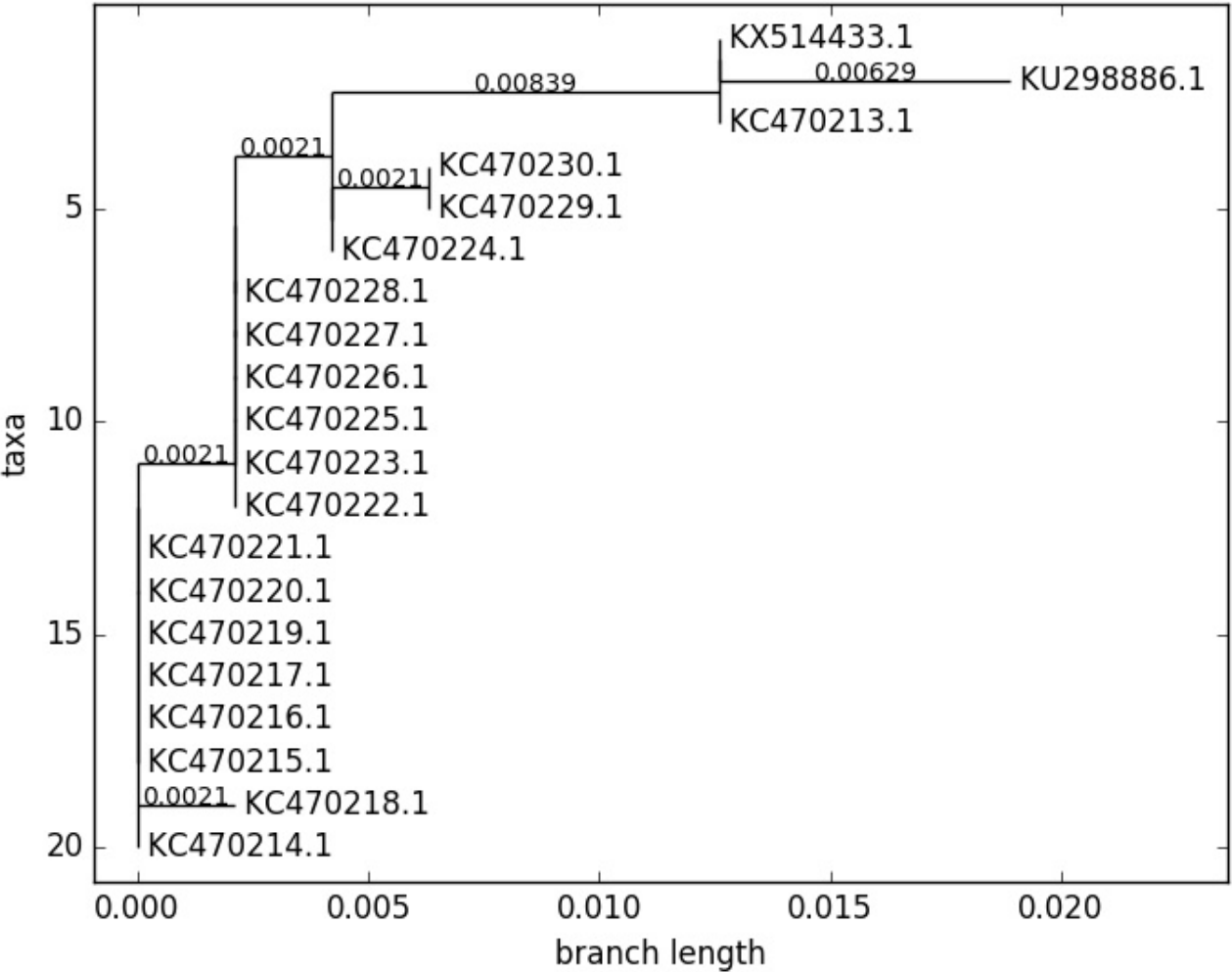
Consensus sequence

ATGGCGCGCTTTGAGGATCCAACACGGCGACCCTACAAGCTACCTGATCTGTGCACGGAACTGAACACTTCACTGCAAGAC
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AGTGTATAGAGACAGTATACCGCATGCTGCATGCCATAAATGTATAGATTTTTATTCTAGAATTAGAGAATTAAGACATT
ATTCAGACTCTGTGTATGGAGACACATTAGAAAAACTAACTAACACTGGGTTATACAATTTATTAATAAGGTGCCTGCGG
TGCCAGAAACCGTTGAATCCAGCAGAAAAACTTAGACACCTTAATGAAAAACGACGATTCCACAAAATAGCTGGGCACTA

Primers data

ACCEPTABLE LEFT PRIMERS

0-based # sequence	start	ln	N	GC%	Tm	self any_th	self end_th	hair-pin	qual-lity
0 GCGCTTTGAGGATCCAACAC	5	20	0	55.00	59.831	13.26	2.92	0.00	0.169
1 CGCTTTGAGGATCCAACACG	6	20	0	55.00	59.556	8.43	5.26	0.00	0.444
2 CTTTGAGGATCCAACACGGC	8	20	0	55.00	59.195	6.97	0.00	33.14	0.805
3 GCTTTGAGGATCCAACACGG	7	20	0	55.00	59.195	10.97	7.33	0.00	0.805
4 TTTGAGGATCCAACACGGCG	9	20	0	55.00	60.953	13.26	4.80	33.14	0.953
5 CGCGCTTTGAGGATCCAACA	4	20	0	55.00	61.298	13.26	9.79	0.00	1.298
6 TTGAGGATCCAACACGGCG	10	19	0	57.89	60.375	13.26	4.80	33.14	1.375
7 CGCGCTTTGAGGATCCAAC	4	19	0	57.89	59.575	8.27	2.56	0.00	1.425
8 GAGGATCCAACACGGCGAC	12	19	0	63.16	60.810	9.28	0.00	33.14	1.810
9 TTGAGGATCCAACACGGCGA	10	20	0	55.00	61.822	16.62	0.00	33.14	1.822
10 GATCCAACACGGCGACCCTA	15	20	0	60.00	61.952	0.00	0.00	33.14	1.952
11 ATCCAACACGGCGACCCTA	16	19	0	57.89	60.986	16.62	0.00	33.14	1.986
12 ATGGCGCGCTTTGAGGAT	0	18	0	55.56	60.125	14.45	0.00	0.00	2.125
13 ATGGCGCGCTTTGAGGATC	0	19	0	57.89	61.183	14.45	0.00	0.00	2.183
14 ATCCAACACGGCGACCCTAC	16	20	0	60.00	62.235	16.62	0.00	33.14	2.235
15 TGAGGATCCAACACGGCG	11	18	0	61.11	59.736	13.26	4.80	33.14	2.264
16 AGGATCCAACACGGCGAC	13	18	0	61.11	59.735	15.82	0.00	33.14	2.265
17 TGAGGATCCAACACGGCGA	11	19	0	57.89	61.280	16.62	0.00	33.14	2.280
18 CAACACGGCGACCCTACA	19	18	0	61.11	59.659	16.62	0.00	0.00	2.341
19 GCGCGCTTTGAGGATCCAA	3	19	0	57.89	61.399	26.67	0.00	0.00	2.399
20 CCAACACGGCGACCCTAC	18	18	0	66.67	60.434	16.62	0.00	0.00	2.434
21 TGAGGATCCAACACGGCGAC	11	20	0	60.00	62.501	13.26	0.00	33.14	2.501
22 GCGCTTTGAGGATCCAACA	5	19	0	52.63	58.445	13.26	9.79	0.00	2.555
23 GAGGATCCAACACGGCGA	12	18	0	61.11	59.423	16.62	0.00	33.14	2.577
24 GCGCGCTTTGAGGATCCAAC	3	20	0	60.00	62.584	26.67	2.56	0.00	2.584
25 TCCAACACGGCGACCCTA	17	18	0	61.11	60.601	16.62	0.00	33.14	2.601
26 GATCCAACACGGCGACCC	15	18	0	66.67	60.818	0.00	0.00	33.14	2.818
27 GGATCCAACACGGCGACC	14	18	0	66.67	60.818	6.95	0.00	33.14	2.818
28 GCGCGCTTTGAGGATCCA	3	18	0	61.11	60.820	26.67	0.00	0.00	2.820
29 TGGCGCGCTTTGAGGATC	1	18	0	61.11	60.820	32.29	11.34	0.00	2.820
30 CTTTGAGGATCCAACACGGCG	8	21	0	57.14	61.862	6.97	4.80	33.14	2.862
31 CGCTTTGAGGATCCAACACGG	6	21	0	57.14	61.862	10.97	7.33	0.00	2.862
32 TCCAACACGGCGACCCTAC	17	19	0	63.16	61.935	16.62	0.00	33.14	2.935
33 TTTGAGGATCCAACACGGC	9	19	0	52.63	58.059	13.26	0.00	33.14	2.941
34 GCTTTGAGGATCCAACACGGC	7	21	0	57.14	62.138	14.76	14.22	33.14	3.138
35 CCAACACGGCGACCCTACA	18	19	0	63.16	62.229	16.62	0.00	0.00	3.229
36 GATCCAACACGGCGACCCT	15	19	0	63.16	62.311	0.00	0.00	33.14	3.311
37 AGGATCCAACACGGCGACC	13	19	0	63.16	62.311	15.82	0.00	33.14	3.311
38 TTTGAGGATCCAACACGGCGA	9	21	0	52.38	62.314	16.62	0.00	33.14	3.314
39 ATCCAACACGGCGACCCT	16	18	0	61.11	61.319	16.62	0.00	33.14	3.319
40 GCGCTTTGAGGATCCAACACG	5	21	0	57.14	62.439	13.68	12.53	0.00	3.439
41 CGCGCTTTGAGGATCCAACAC	4	21	0	57.14	62.439	13.26	2.92	0.00	3.439
42 GGCGCGCTTTGAGGATCC	2	18	0	66.67	61.577	32.29	5.91	0.00	3.577
43 CGCGCTTTGAGGATCCAA	4	18	0	55.56	58.111	15.82	0.00	0.00	3.889
44 TTGAGGATCCAACACGGCGAC	10	21	0	57.14	62.955	13.26	0.00	33.14	3.955

Primers data

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45 TTGAGGATCCAACACGGC                10 18  0 55.56 57.286 13.26  0.00 33.14  4.714
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ACCEPTABLE RIGHT PRIMERS

0-based # sequence	start	ln	N	GC%	Tm	self any_th	self end_th	hair-pin	qual-lity
0 ACTGGCCTCTATAGTGCCCA	411	20	0	55.00	60.031	15.67	7.83	37.93	0.031
1 TTCTCTGCGTCGTTGGAGTC	464	20	0	55.00	60.039	9.66	0.00	0.00	0.039
2 TGTTTCTCTGCGTCGTTGGA	467	20	0	50.00	59.897	0.00	0.00	0.00	0.103
3 GTGTTTCTCTGCGTCGTTGG	468	20	0	55.00	59.768	0.00	0.00	0.00	0.232
4 GCACTGGCCTCTATAGTGCC	413	20	0	60.00	60.250	26.85	21.72	38.72	0.250
5 TTTCTCTGCGTCGTTGGAGT	465	20	0	50.00	59.612	9.66	0.00	0.00	0.388
6 CACTGGCCTCTATAGTGCCC	412	20	0	60.00	59.605	24.00	12.62	37.93	0.395
7 GAGTCTCTCCTGTCGTGCTC	449	20	0	60.00	59.550	0.00	0.00	0.00	0.450
8 CTCTGCGTCGTTGGAGTCTC	462	20	0	60.00	60.455	4.08	0.00	0.00	0.455
9 CTGCGTCGTTGGAGTCTCTC	460	20	0	60.00	60.455	0.00	0.00	0.00	0.455
10 CTGGCCTCTATAGTGCCCAG	410	20	0	60.00	59.316	18.76	14.40	37.93	0.684
11 GTTTCTCTGCGTCGTTGGAG	466	20	0	55.00	59.215	5.37	5.37	0.00	0.785
12 GCAGCATGCGGTATACTGTC	190	20	0	55.00	59.138	14.57	0.71	37.60	0.862
13 TCTCTGCGTCGTTGGAGTCT	463	20	0	55.00	60.890	9.66	0.00	0.00	0.890
14 TCTGCGTCGTTGGAGTCTCT	461	20	0	55.00	60.890	0.00	0.00	0.00	0.890
15 TGTGTTTCTCTGCGTCGTTG	469	20	0	50.00	59.072	0.00	0.00	0.00	0.928
16 ATTCAACGGTTTCTGGCACC	338	20	0	50.00	59.041	0.00	0.00	0.00	0.959
17 GGAGTCTCTCCTGTCGTGCT	450	20	0	60.00	60.963	8.38	0.00	46.41	0.963
18 GGATTCAACGGTTTCTGGCAC	340	21	0	52.38	60.069	0.00	0.00	0.00	1.069
19 GATTCAACGGTTTCTGGCACC	339	21	0	52.38	60.069	0.00	0.00	0.00	1.069
20 AGTGCCCAGCTATTTTGTGGA	399	21	0	47.62	59.925	0.00	0.00	0.00	1.075
21 GGCCTCTATAGTGCCCAGCT	408	20	0	60.00	61.124	19.28	0.00	34.65	1.124
22 CTCGGTTGCAGCACGAATG	432	19	0	57.89	59.867	13.22	2.38	0.00	1.133
23 GTCTCTCCTGTCGTGCTCG	447	19	0	63.16	59.864	0.81	0.81	38.55	1.136
24 GCTGGATTCAACGGTTTCTGG	343	21	0	52.38	59.800	0.00	0.00	0.00	1.200
25 CTGGATTCAACGGTTTCTGGC	342	21	0	52.38	59.800	0.00	0.00	0.00	1.200
26 ACTTGTGTTTCTCTGCGTCG	472	20	0	50.00	58.791	0.00	0.00	0.00	1.209
27 CTTGTGTTTCTCTGCGTCGT	471	20	0	50.00	58.791	0.00	0.00	0.00	1.209
28 TGGATTCAACGGTTTCTGGC	341	20	0	50.00	58.756	0.00	0.00	0.00	1.244
29 GGATTCAACGGTTTCTGGCA	340	20	0	50.00	58.756	0.00	0.00	0.00	1.244
30 AGTCTCTCCTGTCGTGCTCG	448	20	0	60.00	61.302	0.81	0.81	38.55	1.302
31 TTGTGTTTCTCTGCGTCGTTG	470	21	0	47.62	59.674	0.00	0.00	0.00	1.326
32 GGCCTCTATAGTGCCCAGC	408	19	0	63.16	59.627	19.28	8.03	34.65	1.373
33 TGGCCTCTATAGTGCCCAGC	409	20	0	60.00	61.411	15.67	2.73	37.93	1.411
34 ACTTGTGTTTCTCTGCGTCGT	472	21	0	47.62	60.471	0.00	0.00	0.00	1.471
35 TGGATTCAACGGTTTCTGGCA	341	21	0	47.62	60.478	0.00	0.00	0.00	1.478
36 GGAGTCTCTCCTGTCGTGC	450	19	0	63.16	59.491	8.38	0.00	46.41	1.509
37 GCAGCATGCGGTATACTGTCT	190	21	0	52.38	60.539	14.57	1.67	37.60	1.539
38 GTGCCCAGCTATTTTGTGGA	398	20	0	50.00	58.455	0.00	0.00	0.00	1.545
39 AGTGCCCAGCTATTTTGTGG	399	20	0	50.00	58.451	0.00	0.00	0.00	1.549

Primers data

40	TCTCTGCGTCGTTGGAGTC	463	19	0	57.89	59.420	9.66	0.00	0.00	1.580
41	TCTGCGTCGTTGGAGTCTC	461	19	0	57.89	59.420	0.00	0.00	0.00	1.580
42	TGCGTCGTTGGAGTCTCTC	459	19	0	57.89	59.420	0.00	0.00	0.00	1.580
43	CTCTGCGTCGTTGGAGTCT	462	19	0	57.89	59.418	4.08	0.00	0.00	1.582
44	CTGCGTCGTTGGAGTCTCT	460	19	0	57.89	59.418	0.00	0.00	0.00	1.582
45	CTTGTGTTTCTCTGCGTCGTT	471	21	0	47.62	59.407	0.00	0.00	0.00	1.593
46	TTTCTCTGCGTCGTTGGAGTC	465	21	0	52.38	60.602	9.66	0.00	0.00	1.602
47	GCCTCTATAGTGCCCAGCTA	407	20	0	55.00	58.366	5.93	0.00	0.00	1.634
48	TTGTGTTTCTCTGCGTCGTT	470	20	0	45.00	58.353	0.00	0.00	0.00	1.647
49	GTTGCAGCACGAATGGCAC	428	19	0	57.89	60.731	0.00	0.00	0.00	1.731
50	CTCCTGTCGTGCTCGGTTG	443	19	0	63.16	60.734	0.00	0.00	37.69	1.734
51	GGCCTCTATAGTGCCCAGCTA	408	21	0	57.14	60.828	19.28	0.00	34.65	1.828
52	CTCTCCTGTCGTGCTCGGTT	445	20	0	60.00	61.868	0.00	0.00	37.69	1.868
53	TGTTTCTCTGCGTCGTTGGAG	467	21	0	52.38	60.868	5.37	5.37	0.00	1.868
54	GTTTCTCTGCGTCGTTGGAGT	466	21	0	52.38	60.869	9.66	0.00	0.00	1.869
55	TGCTGGATTCAACGGTTTCTG	344	21	0	47.62	59.121	0.00	0.00	0.00	1.879
56	GTGCCCAGCTATTTTGTGGAA	398	21	0	47.62	59.108	0.00	0.00	0.00	1.892
57	TTGCAGCACGAATGGCACT	427	19	0	52.63	60.898	0.00	0.00	0.00	1.898
58	TCTCCTGTCGTGCTCGGTT	444	19	0	57.89	60.902	0.00	0.00	37.69	1.902
59	CAGCATGCGGTATACTGTCTCT	189	22	0	50.00	59.965	6.85	0.00	0.00	2.035
60	ACTGGCCTCTATAGTGCCCAG	411	21	0	57.14	61.037	21.88	20.23	37.93	2.037
61	TTCTCTGCGTCGTTGGAGT	464	19	0	52.63	58.961	9.66	0.00	0.00	2.039
62	TCTCCTGTCGTGCTCGG	446	19	0	63.16	61.041	8.49	0.00	37.69	2.041
63	CTGCTGGATTCAACGGTTTCTG	345	22	0	50.00	60.096	0.00	0.00	0.00	2.096
64	GGTTGCAGCACGAATGGC	429	18	0	61.11	60.126	2.05	0.00	0.00	2.126
65	GTGTTTCTCTGCGTCGTTGGA	468	21	0	52.38	61.132	0.00	0.00	0.00	2.132
66	TTGCAGCACGAATGGCACTG	427	20	0	55.00	62.133	0.00	0.00	0.00	2.133
67	GTTGCAGCACGAATGGCACT	428	20	0	55.00	62.134	0.00	0.00	0.00	2.134
68	TCTCCTGTCGTGCTCGGTTG	444	20	0	60.00	62.142	0.00	0.00	37.69	2.142
69	TCTGCTGGATTCAACGGTTTC	346	21	0	47.62	58.849	0.00	0.00	0.00	2.151
70	CTGCTGGATTCAACGGTTTCT	345	21	0	47.62	58.846	0.00	0.00	0.00	2.154
71	CGGTTGCAGCACGAATGG	430	18	0	61.11	59.823	5.71	0.00	0.00	2.177
72	GCAGCACGAATGGCACTG	425	18	0	61.11	59.822	0.00	0.00	0.00	2.178
73	GCCTCTATAGTGCCCAGCTAT	407	21	0	52.38	58.816	5.93	0.00	0.00	2.184
74	GCCCAGCTATTTTGTGGAATCG	396	22	0	50.00	60.224	0.00	0.00	0.00	2.224
75	TACTTGTGTTTCTCTGCGTCGT	473	22	0	45.45	60.224	0.00	0.00	0.00	2.224
76	TCTGCTGGATTCAACGGTTTCT	346	22	0	45.45	60.225	0.00	0.00	0.00	2.225
77	CTCGGTTGCAGCACGAATGG	432	20	0	60.00	62.244	0.00	0.00	0.00	2.244
78	GTCTCTCCTGTCGTGCTCGG	447	20	0	65.00	62.260	8.49	0.00	37.69	2.260
79	TTTCTGCTGGATTCAACGGT	348	20	0	45.00	57.730	0.00	0.00	0.00	2.270
80	TTCTGCTGGATTCAACGGTT	347	20	0	45.00	57.730	0.00	0.00	0.00	2.270
81	TCTGCTGGATTCAACGGTTT	346	20	0	45.00	57.730	0.00	0.00	0.00	2.270
82	TGCTGGATTCAACGGTTTCT	344	20	0	45.00	57.730	0.00	0.00	0.00	2.270
83	TGCAGCACGAATGGCACT	426	18	0	55.56	60.282	0.00	0.00	0.00	2.282
84	TCTCCTGTCGTGCTCGGT	444	18	0	61.11	60.282	0.00	0.00	37.69	2.282
85	TGCCCAGCTATTTTGTGGAA	397	20	0	45.00	57.699	0.00	0.00	0.00	2.301
86	TAGTGCCCAGCTATTTTGTGGA	400	22	0	45.45	59.693	0.00	0.00	0.00	2.307

Primers data

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87  CACTGGCCTCTATAGTGCCCA      412 21  0 57.14 61.311 15.67  7.83 37.93  2.311
88  AGCATGCGGTATACTGTCTCT      188 21  0 47.62 58.689 13.01  0.00  0.00  2.311
89  TCGGTTGCAGCACGAATGG        431 19  0 57.89 61.324  0.00  0.00  0.00  2.324
90  GATTCAACGGTTTCTGGCAC       339 20  0 50.00 57.668  0.00  0.00  0.00  2.332
91  CTCTCCTGTCGTGCTCGGT        445 19  0 63.16 61.336  0.00  0.00 37.69  2.336
92  TCCTGTCGTGCTCGGTTG         442 18  0 61.11 59.661  0.00  0.00 37.69  2.339
93  TACTTGTGTTTCTCTGCGTCG      473 21  0 47.62 58.609  0.00  0.00  0.00  2.391
94  TGTGTTTCTCTGCGTCGTTGG      469 21  0 52.38 61.396  0.00  0.00  0.00  2.396
95  CAGCATGCGGTATACTGTCTC      189 21  0 52.38 58.602  6.85  0.00  0.00  2.398
96  TTCAACGGTTTCTGGCACC        337 19  0 52.63 58.590  0.00  0.00  0.00  2.410
97  TTCTCTGCGTCGTTGGAGTCT      464 21  0 52.38 61.422  9.66  0.00  0.00  2.422
98  GCCTCTATAGTGCCCAGCT        407 19  0 57.89 58.553  5.93  0.00  0.00  2.447
99  CTCTCCTGTCGTGCTCGG         445 18  0 66.67 59.513  8.49  0.00 37.69  2.487
100 AGTGCCCAGCTATTTTGTGGAA     399 22  0 45.45 60.491  0.00  0.00  0.00  2.491
101 GTGCCCAGCTATTTTGTGGAAT     398 22  0 45.45 59.503  0.00  0.00  0.00  2.497
102 CAGCATGCGGTATACTGTCT       189 20  0 50.00 57.484  9.90  1.67  0.00  2.516
103 TTCTGCTGGATTCAACGGTTTC     347 22  0 45.45 59.448  0.00  0.00  0.00  2.552
104 GAGTCTCTCCTGTCGTGCT        449 19  0 57.89 58.438  0.00  0.00  0.00  2.562
105 AGTCTCTCCTGTCGTGCTC        448 19  0 57.89 58.438  0.00  0.00  0.00  2.562
106 GCCTCTATAGTGCCCAGCTATT     407 22  0 50.00 59.431  5.93  0.00  0.00  2.569
107 TTTTCTGCTGGATTCAACGGT      349 21  0 42.86 58.418  0.00  0.00  0.00  2.582
108 TTTCTGCTGGATTCAACGGTT      348 21  0 42.86 58.418  0.00  0.00  0.00  2.582
109 TTCTGCTGGATTCAACGGTTT      347 21  0 42.86 58.418  0.00  0.00  0.00  2.582
110 CTTGTGTTTCTCTGCGTCGTTG     471 22  0 50.00 60.598  0.00  0.00  0.00  2.598
111 TGTTTCTCTGCGTCGTTGG        467 19  0 52.63 58.400  0.00  0.00  0.00  2.600
112 CTGCTGGATTCAACGGTTTC       345 20  0 50.00 57.381  0.00  0.00  0.00  2.619
113 GCTGGATTCAACGGTTTCTG       343 20  0 50.00 57.381  0.00  0.00  0.00  2.619
114 TGCAGCACGAATGGCACTG        426 19  0 57.89 61.619  0.00  0.00  0.00  2.619
115 GTTGCAGCACGAATGGCA         428 18  0 55.56 59.356  0.00  0.00  0.00  2.644
116 TTGCAGCACGAATGGCAC         427 18  0 55.56 59.356  0.00  0.00  0.00  2.644
117 CTCCTGTCGTGCTCGGTT         443 18  0 61.11 59.349  0.00  0.00 37.69  2.651
118 CTGTCGTGCTCGGTTGCA         440 18  0 61.11 60.662  3.16  0.00 41.05  2.662
119 TGTCGTGCTCGGTTGCAG         439 18  0 61.11 60.662  3.16  0.00 44.20  2.662
120 CTGTCGTGCTCGGTTGCAG        440 19  0 63.16 61.662  7.90  7.90 44.20  2.662
121 GCTCGGTTGCAGCACGAAT        433 19  0 57.89 61.681 13.22  0.00  0.00  2.681
122 TAGTGCCCAGCTATTTTGTGG      400 21  0 47.62 58.278  0.00  0.00  0.00  2.722
123 TCTCTCCTGTCGTGCTCGGT       446 20  0 60.00 62.750  0.00  0.00 37.69  2.750
124 TGCCCAGCTATTTTGTGGAATC     397 22  0 45.45 59.240  0.00  0.00  0.00  2.760
125 AGCATGCGGTATACTGTCTC       188 20  0 50.00 57.197 13.01  0.00  0.00  2.803
126 GCATGCGGTATACTGTCTCT       187 20  0 50.00 57.197  3.72  0.00  0.00  2.803
127 TCTCTGCGTCGTTGGAGTCTC      463 21  0 57.14 61.806  9.66  0.00  0.00  2.806
128 TCTGCGTCGTTGGAGTCTCTC      461 21  0 57.14 61.806  0.00  0.00  0.00  2.806
129 CTCTGCGTCGTTGGAGTCTCT      462 21  0 57.14 61.810  4.08  0.00  0.00  2.810
130 TGCCCAGCTATTTTGTGGAAT      397 21  0 42.86 58.181  0.00  0.00  0.00  2.819
131 GCTCGGTTGCAGCACGAATG       433 20  0 60.00 62.839  0.00  0.00  0.00  2.839
132 CTGGCCTCTATAGTGCCCA        410 19  0 57.89 58.160 15.67  7.83 37.93  2.840
133 TGGCCTCTATAGTGCCCAG        409 19  0 57.89 58.160 15.67  0.00 37.93  2.840
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Primers data

134	ACTGGCCTCTATAGTGCCC	411	19	0	57.89	58.158	24.00	12.62	37.93	2.842
135	CAGCACGAATGGCACTGG	424	18	0	61.11	59.127	0.00	0.00	0.00	2.873
136	GGAGTCTCTCCTGTCGTGCTC	450	21	0	61.90	61.878	8.38	0.00	46.41	2.878
137	GTTTCTCTGCGTCGTTGGA	466	19	0	52.63	58.105	0.00	0.00	0.00	2.895
138	GGTTGCAGCACGAATGGCA	429	19	0	57.89	61.918	2.05	0.00	0.00	2.918
139	TTTTTCTGCTGGATTCAACGGT	350	22	0	40.91	59.044	0.00	0.00	0.00	2.956
140	TTTTCTGCTGGATTCAACGGTT	349	22	0	40.91	59.044	0.00	0.00	0.00	2.956
141	TTTCTGCTGGATTCAACGGTTT	348	22	0	40.91	59.044	0.00	0.00	0.00	2.956
142	ATACTTGTGTTTCTCTGCGTCG	474	22	0	45.45	59.013	0.00	0.00	0.00	2.987
143	GCAGCATGCGGTATACTGT	190	19	0	52.63	58.008	14.57	0.00	37.60	2.992
144	ACTTGTGTTTCTCTGCGTCGTT	472	22	0	45.45	60.994	0.00	0.00	0.00	2.994
145	TTTCTGCTGGATTCAACGGTTTC	348	23	0	43.48	59.996	0.00	0.00	0.00	3.004
146	AGTTTTCTGCTGGATTCAACGG	352	23	0	43.48	59.995	0.00	0.00	0.00	3.005
147	GCCTCTATAGTGCCCAGCTATTT	407	23	0	47.83	59.992	5.93	0.00	0.00	3.008
148	CCCAGCTATTTTGTGGAATCGT	395	22	0	45.45	58.983	0.00	0.00	0.00	3.017
149	ATAGTGCCCAGCTATTTTGTGGA	401	23	0	43.48	60.054	0.00	0.00	0.00	3.054
150	AGCACGAATGGCACTGGC	423	18	0	61.11	61.058	0.00	0.00	40.13	3.058
151	CCCAGCTATTTTGTGGAATCGTC	395	23	0	47.83	59.935	0.00	0.00	0.00	3.065
152	GGCCTCTATAGTGCCCAGCTAT	408	22	0	54.55	61.156	19.28	0.00	34.65	3.156
153	GAGTCTCTCCTGTCGTGCTCG	449	21	0	61.90	62.184	0.81	0.81	38.55	3.184
154	TTTCTCTGCGTCGTTGGAG	465	19	0	52.63	57.805	5.37	5.37	0.00	3.195
155	CCAGCTATTTTGTGGAATCGTCG	394	23	0	47.83	60.242	0.00	0.00	0.00	3.242
156	GTTTTTCTGCTGGATTCAACGGT	351	23	0	43.48	60.243	0.00	0.00	0.00	3.243
157	TAGTGCCCAGCTATTTTGTGGAA	400	23	0	43.48	60.245	0.00	0.00	0.00	3.245
158	TCGGTTGCAGCACGAATG	431	18	0	55.56	58.747	0.00	0.00	0.00	3.253
159	CAGCATGCGGTATACTGTCTCTA	189	23	0	47.83	59.747	6.85	0.00	0.00	3.253
160	ATAGTGCCCAGCTATTTTGTGG	401	22	0	45.45	58.709	0.00	0.00	0.00	3.291
161	GCACTGGCCTCTATAGTGC	413	19	0	57.89	57.703	24.35	24.35	32.60	3.297
162	GTTTTTCTGCTGGATTCAACGG	351	22	0	45.45	58.691	0.00	0.00	0.00	3.309
163	CTGGCCTCTATAGTGCCCAGC	410	21	0	61.90	62.318	19.19	7.12	37.93	3.318
164	GCAGCACGAATGGCACTGG	425	19	0	63.16	62.332	3.18	0.00	0.00	3.332
165	CAGCACGAATGGCACTGGC	424	19	0	63.16	62.332	0.00	0.00	40.13	3.332
166	GCTCGGTTGCAGCACGAA	433	18	0	61.11	61.346	13.22	1.56	0.00	3.346
167	TTGTGTTTCTCTGCGTCGT	470	19	0	47.37	57.644	0.00	0.00	0.00	3.356
168	TGTGTTTCTCTGCGTCGTT	469	19	0	47.37	57.644	0.00	0.00	0.00	3.356
169	CAGCTATTTTGTGGAATCGTCGT	393	23	0	43.48	59.629	0.00	0.00	0.00	3.371
170	TTTTTCTGCTGGATTCAACGGTT	350	23	0	39.13	59.617	0.00	0.00	0.00	3.383
171	TTTTCTGCTGGATTCAACGGTTT	349	23	0	39.13	59.617	0.00	0.00	0.00	3.383
172	TGCTGGATTCAACGGTTTCTGG	344	22	0	50.00	61.392	0.00	0.00	0.00	3.392
173	CTGGATTCAACGGTTTCTGGCA	342	22	0	50.00	61.392	0.00	0.00	0.00	3.392
174	CCTGTCGTGCTCGGTTGC	441	18	0	66.67	61.415	0.00	0.00	37.69	3.415
175	GTGCCCAGCTATTTTGTGGAATC	398	23	0	47.83	60.429	0.00	0.00	0.00	3.429
176	GCAGCATGCGGTATACTGTCTC	190	22	0	54.55	61.430	14.57	0.00	37.60	3.430
177	GCCCAGCTATTTTGTGGAATC	396	21	0	47.62	57.557	0.00	0.00	0.00	3.443
178	AGCATGCGGTATACTGTCTCTA	188	22	0	45.45	58.513	13.01	0.00	0.00	3.487
179	ATACTTGTGTTTCTCTGCGTCGT	474	23	0	43.48	60.552	0.00	0.00	0.00	3.552
180	CTCGGTTGCAGCACGAAT	432	18	0	55.56	58.434	13.22	0.00	0.00	3.566

Primers data

181	TCTCTCCTGTCGTGCTCG	446	18	0	61.11	58.420	0.81	0.81	38.55	3.580
182	GCACTGGCCTCTATAGTGCCC	413	21	0	61.90	62.584	26.85	12.62	37.93	3.584
183	AGCTATTTTGTGGAATCGTCGT	392	22	0	40.91	58.404	0.00	0.00	0.00	3.596
184	TTTTTCTGCTGGATTCAACGG	350	21	0	42.86	57.359	0.00	0.00	0.00	3.641
185	TGGATTCAACGGTTTCTGGCAC	341	22	0	50.00	61.648	0.00	0.00	0.00	3.648
186	CCCAGCTATTTTGTGGAATCG	395	21	0	47.62	57.302	0.00	0.00	0.00	3.698
187	GTGTTTCTCTGCGTCGTTG	468	19	0	52.63	57.290	0.00	0.00	0.00	3.710
188	GTTTCTCTGCGTCGTTGGAGTC	466	22	0	54.55	61.732	2.30	0.00	0.00	3.732
189	TACTTGTGTTTCTCTGCGTCGTT	473	23	0	43.48	60.736	0.00	0.00	0.00	3.736
190	TTCTGCTGGATTCAACGGTTTCT	347	23	0	43.48	60.747	0.00	0.00	0.00	3.747
191	TCTCTGCGTCGTTGGAGT	463	18	0	55.56	58.240	9.66	0.00	0.00	3.760
192	TCTGCGTCGTTGGAGTCT	461	18	0	55.56	58.240	0.00	0.00	0.00	3.760
193	TGCGTCGTTGGAGTCTCT	459	18	0	55.56	58.240	0.00	0.00	0.00	3.760
194	TGGCCTCTATAGTGCCCAGCT	409	21	0	57.14	62.801	15.67	0.00	37.93	3.801
195	AGTGCCCAGCTATTTTGTGGAAT	399	23	0	43.48	60.819	0.00	0.00	0.00	3.819
196	TCCTGTCGTGCTCGGTTGC	442	19	0	63.16	62.859	0.00	0.00	37.69	3.859
197	TTGTGTTTCTCTGCGTCGTTGG	470	22	0	50.00	61.873	0.00	0.00	0.00	3.873
198	TTTCTCTGCGTCGTTGGAGTCT	465	22	0	50.00	61.907	9.66	0.00	0.00	3.907
199	GCATGCGGTATACTGTCTCTA	187	21	0	47.62	57.083	3.72	0.00	0.00	3.917
200	CAGCTATTTTGTGGAATCGTCG	393	22	0	45.45	58.072	0.00	0.00	0.00	3.928
201	CGGTTGCAGCACGAATGGC	430	19	0	63.16	62.952	5.71	0.00	0.00	3.952
202	CTCTCCTGTCGTGCTCGGTTG	445	21	0	61.90	62.980	0.00	0.00	37.69	3.980
203	GTGTTTCTCTGCGTCGTTGGAG	468	22	0	54.55	61.982	5.37	5.37	0.00	3.982
204	CACTGGCCTCTATAGTGCC	412	19	0	57.89	57.002	21.72	21.72	38.72	3.998
205	AGCTATTTTGTGGAATCGTCGTT	392	23	0	39.13	58.999	0.00	0.00	0.00	4.001
206	TGTCTCCATACACAGAGTCTGA	264	22	0	45.45	57.966	26.86	4.71	35.18	4.034
207	GTCGTGCTCGGTTGCAGC	438	18	0	66.67	62.077	0.00	0.00	44.20	4.077
208	CAGCATGCGGTATACTGTCTCTAT	189	24	0	45.83	60.083	6.85	0.00	0.00	4.083
209	AGCATGCGGTATACTGTCTCTAT	188	23	0	43.48	58.917	13.01	0.00	0.00	4.083
210	GGTGTCTAAGTTTTTCTGCTGGA	360	23	0	43.48	58.865	0.00	0.00	0.00	4.135
211	AGGTGTCTAAGTTTTTCTGCTGG	361	23	0	43.48	58.862	0.00	0.00	0.00	4.138
212	AGGTGTCTAAGTTTTTCTGCTGGA	361	24	0	41.67	60.141	0.00	0.00	0.00	4.141
213	TTTTTCTGCTGGATTCAACGGTTT	350	24	0	37.50	60.142	0.00	0.00	0.00	4.142
214	CAGCTATTTTGTGGAATCGTCGTT	393	24	0	41.67	60.143	0.00	0.00	0.00	4.143
215	TCAACGGTTTCTGGCACC	336	18	0	55.56	57.849	0.00	0.00	0.00	4.151
216	CTCTGCGTCGTTGGAGTC	462	18	0	61.11	57.845	4.08	0.00	0.00	4.155
217	CTGCGTCGTTGGAGTCTC	460	18	0	61.11	57.845	0.00	0.00	0.00	4.155
218	TATACTTGTGTTTCTCTGCGTCG	475	23	0	43.48	58.836	0.00	0.00	0.00	4.164
219	TATAGTGCCCAGCTATTTTGTGGA	402	24	0	41.67	59.835	0.00	0.00	0.00	4.165
220	CACTGGCCTCTATAGTGCCCAG	412	22	0	59.09	62.185	21.88	20.23	37.93	4.185
221	AGTTTTTCTGCTGGATTCAACG	352	22	0	40.91	57.771	0.00	0.00	0.00	4.229
222	TTCTCTGCGTCGTTGGAGTCTC	464	22	0	54.55	62.268	9.66	0.00	0.00	4.268
223	GGATTCAACGGTTTCTGGCACC	340	22	0	54.55	62.279	0.00	0.00	0.00	4.279
224	CCAGCTATTTTGTGGAATCGTC	394	22	0	45.45	57.721	0.00	0.00	0.00	4.279
225	TATACTTGTGTTTCTCTGCGTCGT	475	24	0	41.67	60.321	0.00	0.00	0.00	4.321
226	GCTATTTTGTGGAATCGTCGTT	391	22	0	40.91	57.663	0.00	0.00	0.00	4.337
227	TCTGCTGGATTCAACGGTTTCTG	346	23	0	47.83	61.360	0.00	0.00	0.00	4.360

Primers data

228	CGTGCTCGGTTGCAGCAC	436	18	0	66.67	62.375	15.86	15.86	44.20	4.375
229	GTGCTCGGTTGCAGCACG	435	18	0	66.67	62.375	13.30	9.35	44.20	4.375
230	TGTCTCCATACACAGAGTCTGAA	264	23	0	43.48	58.593	26.86	11.56	35.18	4.407
231	TGTTTCTCTGCGTCGTTGGAGT	467	22	0	50.00	62.417	9.66	0.00	0.00	4.417
232	TGGCCTCTATAGTGCCCAGCTA	409	22	0	54.55	62.440	15.67	1.80	37.93	4.440
233	GCATGCGGTATACTGTCTCTAT	187	22	0	45.45	57.558	3.72	0.00	0.00	4.442
234	AGCTATTTTGTGGAATCGTCGTTT	392	24	0	37.50	59.545	0.00	0.00	0.00	4.455
235	TATAGTGCCCAGCTATTTTGTGG	402	23	0	43.48	58.540	0.00	0.00	0.00	4.460
236	GCGTCGTTGGAGTCTCTC	458	18	0	61.11	57.538	0.00	0.00	0.00	4.462
237	GGTGTCTAAGTTTTTCTGCTGG	360	22	0	45.45	57.510	0.00	0.00	0.00	4.490
238	TTTTCTGCTGGATTCAACGGTTTC	349	24	0	41.67	60.499	0.00	0.00	0.00	4.499
239	AAGTTTTTCTGCTGGATTCAACGG	353	24	0	41.67	60.500	0.00	0.00	0.00	4.500
240	GCCTCTATAGTGCCCAGCTATTTT	407	24	0	45.83	60.506	5.93	0.00	0.00	4.506
241	CTATAGTGCCCAGCTATTTTGTGG	403	24	0	45.83	59.483	0.00	0.00	0.00	4.517
242	ATAGTGCCCAGCTATTTTGTGGAA	401	24	0	41.67	60.570	0.00	0.00	0.00	4.570
243	TAGTGCCCAGCTATTTTGTGGAAT	400	24	0	41.67	60.570	0.00	0.00	0.00	4.570
244	AAGGTGTCTAAGTTTTTCTGCTGG	362	24	0	41.67	59.419	0.00	0.00	0.00	4.581
245	GCTGGATTCAACGGTTTCTGGC	343	22	0	54.55	62.585	0.00	0.00	0.00	4.585
246	TCGTGCTCGGTTGCAGCA	437	18	0	61.11	62.601	8.49	0.00	44.20	4.601
247	TGCTCGGTTGCAGCACGA	434	18	0	61.11	62.601	12.06	12.06	38.12	4.601
248	AAGTTTTTCTGCTGGATTCAACG	353	23	0	39.13	58.389	0.00	0.00	0.00	4.611
249	TTTGTGGAATCGTCGTTTTTCA	386	22	0	36.36	57.382	7.33	0.88	0.00	4.618
250	TTATACTTGTGTTTCTCTGCGTCG	476	24	0	41.67	59.380	0.00	0.00	0.00	4.620
251	CTCTGCGTCGTTGGAGTCTCTC	462	22	0	59.09	62.624	4.08	0.00	0.00	4.624
252	GGCCTCTATAGTGCCCAGCTATT	408	23	0	52.17	61.644	19.28	0.00	34.65	4.644
253	TGTGTTTCTCTGCGTCGTTGGA	469	22	0	50.00	62.667	0.00	0.00	0.00	4.667
254	GCTATTTTGTGGAATCGTCGTTT	391	23	0	39.13	58.281	0.00	0.00	0.00	4.719
255	GTTTTTCTGCTGGATTCAACGGTT	351	24	0	41.67	60.736	0.00	0.00	0.00	4.736
256	TGCCCAGCTATTTTGTGGAATCG	397	23	0	47.83	61.737	0.00	0.00	0.00	4.737
257	GCCCAGCTATTTTGTGGAATCGT	396	23	0	47.83	61.738	0.00	0.00	0.00	4.738
258	GGTGTCTAAGTTTTTCTGCTGGAT	360	24	0	41.67	59.238	0.00	0.00	0.00	4.762
259	TTGTGGAATCGTCGTTTTTCAT	385	22	0	36.36	57.178	1.86	0.00	0.00	4.822
260	TGTGGAATCGTCGTTTTTCATT	384	22	0	36.36	57.178	1.86	0.00	0.00	4.822
261	AGTCTCTCCTGTCGTGCT	448	18	0	55.56	57.167	0.00	0.00	0.00	4.833
262	CCTCTATAGTGCCCAGCTATTT	406	22	0	45.45	57.101	0.00	0.00	0.00	4.899
263	TTCTCTGCGTCGTTGGAG	464	18	0	55.56	57.034	5.37	5.37	0.00	4.966
264	TTTTGTGGAATCGTCGTTTTTCA	387	23	0	34.78	58.017	7.33	0.88	0.00	4.983
265	CCTCTATAGTGCCCAGCTATTTTG	406	24	0	45.83	59.000	0.00	0.00	0.00	5.000
266	TGTCTCCATACACAGAGTCTGAAT	264	24	0	41.67	58.981	13.25	4.49	35.18	5.019
267	ATACTTGTGTTTCTCTGCGTCGTT	474	24	0	41.67	61.032	0.00	0.00	0.00	5.032
268	AGCTATTTTGTGGAATCGTCGTTTT	392	25	0	36.00	60.049	0.00	0.00	0.00	5.049
269	TCGTCGTTTTTCATTAAGGTGTCT	377	24	0	37.50	58.948	0.00	0.00	0.00	5.052
270	ACTTGTGTTTCTCTGCGTCGTTG	472	23	0	47.83	62.062	0.00	0.00	0.00	5.062
271	GCATGCGGTATACTGTCTCTATACA	187	25	0	44.00	60.106	3.72	0.00	31.23	5.106
272	CAGCATGCGGTATACTGTCTCTATA	189	25	0	44.00	59.876	6.85	0.00	0.00	5.124
273	AGCATGCGGTATACTGTCTCTATAC	188	25	0	44.00	59.876	13.01	0.00	0.00	5.124
274	GCTATTTTGTGGAATCGTCGTTTT	391	24	0	37.50	58.849	0.00	0.00	0.00	5.151

Primers data

275	ACTGTCTTGCAATATACACAGGT	112	23	0	39.13	57.834	18.84	9.32	0.00	5.166
276	TTTGTGGAATCGTCGTTTTTCAT	386	23	0	34.78	57.824	1.86	0.00	0.00	5.176
277	TTGTGGAATCGTCGTTTTTCATT	385	23	0	34.78	57.824	1.86	0.00	0.00	5.176
278	CTGCTGGATTCAACGGTTTCTGG	345	23	0	52.17	62.211	0.00	0.00	0.00	5.211
279	TTTCTGCTGGATTCAACGGTTTCT	348	24	0	41.67	61.227	0.00	0.00	0.00	5.227
280	CCTCTATAGTGCCCAGCTATTTT	406	23	0	43.48	57.766	0.00	0.00	0.00	5.234
281	GGTGTCTAAGTTTTTCTGCTGGATT	360	25	0	40.00	59.758	0.00	0.00	0.00	5.242
282	AGCATGCGGTATACTGTCTCTATA	188	24	0	41.67	58.746	13.01	0.00	0.00	5.254
283	TAAGTTTTTCTGCTGGATTCAACGG	354	25	0	40.00	60.278	0.00	0.00	0.00	5.278
284	TCGTCGTTTTTCATTAAGGTGTC	377	23	0	39.13	57.667	0.00	0.00	0.00	5.333
285	GCATGCGGTATACTGTCTCTATAC	187	24	0	45.83	58.666	3.72	0.00	0.00	5.334
286	CGTCGTTTTTCATTAAGGTGTCT	376	23	0	39.13	57.661	0.00	0.00	0.00	5.339
287	TATAGTGCCCAGCTATTTTGTGGAA	402	25	0	40.00	60.340	0.00	0.00	0.00	5.340
288	TCTATAGTGCCCAGCTATTTTGTG	404	24	0	41.67	58.632	0.00	0.00	0.00	5.368
289	CTGGATTCAACGGTTTCTGGCAC	342	23	0	52.17	62.451	0.00	0.00	0.00	5.451
290	CCTCTATAGTGCCCAGCTATTTTGT	406	25	0	44.00	60.455	0.00	0.00	0.00	5.455
291	AGGTGTCTAAGTTTTTCTGCTGGAT	361	25	0	40.00	60.457	0.00	0.00	0.00	5.457
292	AGTTTTTCTGCTGGATTCAACGGT	352	24	0	41.67	61.468	0.00	0.00	0.00	5.468
293	CTCTATAGTGCCCAGCTATTTTGTG	405	25	0	44.00	59.532	0.00	0.00	0.00	5.468
294	TGGAATCGTCGTTTTTCATTAAGGT	382	25	0	36.00	59.529	7.33	0.00	0.00	5.471
295	ACTGTCTTGCAATATACACAGGTT	112	24	0	37.50	58.439	18.84	4.80	0.00	5.561
296	GCATGCGGTATACTGTCTCTATA	187	23	0	43.48	57.437	3.72	0.00	0.00	5.563
297	ATTTTGTGGAATCGTCGTTTTTCA	388	24	0	33.33	58.417	7.33	0.88	0.00	5.583
298	TTTTGTGGAATCGTCGTTTTTCAT	387	24	0	33.33	58.417	1.86	0.00	0.00	5.583
299	TTTGTGGAATCGTCGTTTTTCATT	386	24	0	33.33	58.417	1.86	0.00	0.00	5.583
300	GTCTCCATACACAGAGTCTGAAT	263	23	0	43.48	57.409	13.25	4.49	35.18	5.591
301	CTCTATAGTGCCCAGCTATTTTGT	405	24	0	41.67	58.385	0.00	0.00	0.00	5.615
302	TGTAAGTTCCAATACTGTCTTGCA	125	24	0	37.50	58.384	0.00	0.00	0.00	5.616
303	CAGCTATTTTGTGGAATCGTCGTTT	393	25	0	40.00	60.617	0.00	0.00	0.00	5.617
304	TGCGGTATACTGTCTCTATACACT	184	24	0	41.67	58.382	9.90	0.00	31.23	5.618
305	GCTATTTTGTGGAATCGTCGTTTTT	391	25	0	36.00	59.372	0.00	0.00	0.00	5.628
306	TCTATAGTGCCCAGCTATTTTGT	404	23	0	39.13	57.370	0.00	0.00	0.00	5.630
307	AAGGTGTCTAAGTTTTTCTGCTGGA	362	25	0	40.00	60.631	0.00	0.00	0.00	5.631
308	CTTGTGTTTCTCTGCGTCGTTGG	471	23	0	52.17	62.649	0.00	0.00	0.00	5.649
309	AGTGCCCAGCTATTTTGTGGAATC	399	24	0	45.83	61.650	0.00	0.00	0.00	5.650
310	GCAGCATGCGGTATACTGTCTCT	190	23	0	52.17	62.652	14.57	0.00	37.60	5.652
311	CTATAGTGCCCAGCTATTTTGTG	403	23	0	43.48	57.320	0.00	0.00	0.00	5.680
312	CCAGCTATTTTGTGGAATCGTCGT	394	24	0	45.83	61.681	0.00	0.00	0.00	5.681
313	TCTATAGTGCCCAGCTATTTTGTGG	404	25	0	44.00	60.687	0.00	0.00	0.00	5.687
314	CTATAGTGCCCAGCTATTTTGTGGA	403	25	0	44.00	60.687	0.00	0.00	0.00	5.687
315	TTTCTCTGCGTCGTTGGAGTCTC	465	23	0	52.17	62.691	9.66	0.00	0.00	5.691
316	TGGCCTCTATAGTGCCCAGCTAT	409	23	0	52.17	62.692	15.67	0.00	37.93	5.692
317	ATCGTCGTTTTTCATTAAGGTGTCT	378	25	0	36.00	59.301	0.00	0.00	0.00	5.699
318	CTGTAAGTTCCAATACTGTCTTGCA	126	25	0	40.00	59.299	0.00	0.00	0.00	5.701
319	CCGCAGGCACCTTATTAATAAAT	320	23	0	39.13	57.294	9.15	0.00	46.14	5.706
320	AAGGTGTCTAAGTTTTTCTGCTG	362	23	0	39.13	57.242	0.00	0.00	0.00	5.758
321	TAAGTTTTTCTGCTGGATTCAACG	354	24	0	37.50	58.242	0.00	0.00	0.00	5.758

Primers data

322	TAAGGTGTCTAAGTTTTTCTGCTGG	363	25	0	40.00	59.237	0.00	0.00	0.00	5.763
323	TACTTGTGTTTCTCTGCGTCGTTG	473	24	0	45.83	61.777	0.00	0.00	0.00	5.777
324	ACCTCTGTAAGTTCCAATACTGTCT	130	25	0	40.00	59.219	0.00	0.00	0.00	5.781
325	TTATACTTGTGTTTCTCTGCGTCGT	476	25	0	40.00	60.791	0.00	0.00	0.00	5.791
326	TATACTTGTGTTTCTCTGCGTCGTT	475	25	0	40.00	60.791	0.00	0.00	0.00	5.791
327	GTGGAATCGTCGTTTTTCATTAAGG	383	25	0	40.00	59.207	1.86	0.00	0.00	5.793
328	GGAATCGTCGTTTTTCATTAAGGTG	381	25	0	40.00	59.207	7.33	0.00	0.00	5.793
329	TTCTGCTGGATTCAACGGTTTCTG	347	24	0	45.83	61.808	0.00	0.00	0.00	5.808
330	CTAAGTTTTTCTGCTGGATTCAACG	355	25	0	40.00	59.147	0.00	0.00	0.00	5.853
331	ATAGTGCCCAGCTATTTTGTGGAAT	401	25	0	40.00	60.870	0.00	0.00	0.00	5.870
332	TCTATACATTTATGGCATGCAGC	208	23	0	39.13	57.115	7.99	0.11	44.65	5.885
333	CCGCAGGCACCTTATTAATAAATTG	320	25	0	40.00	59.080	9.79	9.79	46.14	5.920
334	ATCGTCGTTTTTCATTAAGGTGTC	378	24	0	37.50	58.076	0.00	0.00	0.00	5.924
335	TGTGGAATCGTCGTTTTTCATTA	384	23	0	34.78	57.074	1.86	0.00	0.00	5.926
336	TCTGTAAGTTCCAATACTGTCTTGC	127	25	0	40.00	59.068	0.75	0.00	0.00	5.932
337	TGGAATCGTCGTTTTTCATTAAGG	382	24	0	37.50	58.066	7.33	0.00	0.00	5.934
338	GTTTCTCTGCGTCGTTGGAGTCT	466	23	0	52.17	62.935	4.98	0.00	0.00	5.935
339	GGAATCGTCGTTTTTCATTAAGGT	381	24	0	37.50	58.065	7.33	0.00	0.00	5.935
340	ATCGTCGTTTTTCATTAAGGTGT	378	23	0	34.78	57.065	0.00	0.00	0.00	5.935
341	TGCGGTATACTGTCTCTATACAC	184	23	0	43.48	57.063	9.90	0.00	31.23	5.937
342	GTGTCTAAGTTTTTCTGCTGGAT	359	23	0	39.13	57.051	0.00	0.00	0.00	5.949
343	TTTTTCTGCTGGATTCAACGGTTTC	350	25	0	40.00	60.963	0.00	0.00	0.00	5.963
344	GTGTCTAAGTTTTTCTGCTGGATTCA	359	26	0	38.46	60.017	0.00	0.00	0.00	6.017
345	TTTTGTGGAATCGTCGTTTTTCATT	387	25	0	32.00	58.963	1.86	0.00	0.00	6.037
346	ACCTCTGTAAGTTCCAATACTGTC	130	24	0	41.67	57.961	0.00	0.00	0.00	6.039
347	TGTAAGTTCCAATACTGTCTTGCAA	125	25	0	36.00	58.941	0.00	0.00	0.00	6.059
348	TGTCTAAGTTTTTCTGCTGGATTCA	358	25	0	36.00	58.939	0.00	0.00	0.00	6.061
349	CCGCAGGCACCTTATTAATAAATT	320	24	0	37.50	57.916	9.15	0.00	46.14	6.084
350	GGCCTCTATAGTGCCCAGCTATTT	408	24	0	50.00	62.091	19.28	0.00	34.65	6.091
351	CTCTGTAAGTTCCAATACTGTCTTGC	128	26	0	42.31	59.909	0.75	0.00	0.00	6.091
352	CATGCGGTATACTGTCTCTATACACT	186	26	0	42.31	59.850	9.90	0.00	31.23	6.150
353	CTGTAAGTTCCAATACTGTCTTGC	126	24	0	41.67	57.829	0.75	0.00	0.00	6.171
354	GCTATTTTGTGGAATCGTCGTTTTTC	391	26	0	38.46	60.183	0.00	0.00	0.00	6.183
355	TGTCTCCATACACAGAGTCTGAATA	264	25	0	40.00	58.812	16.96	9.54	35.18	6.188
356	GTTTTTCTGCTGGATTCAACGGTTT	351	25	0	40.00	61.191	0.00	0.00	0.00	6.191
357	AATCGTCGTTTTTCATTAAGGTGTCT	379	26	0	34.62	59.796	0.00	0.00	0.00	6.204
358	CTGTAAGTTCCAATACTGTCTTGCAA	126	26	0	38.46	59.795	0.00	0.00	0.00	6.205
359	ATTTTGTGGAATCGTCGTTTTTCAT	388	25	0	32.00	58.787	1.86	0.00	0.00	6.213
360	TCGTCGTTTTTCATTAAGGTGTCTA	377	25	0	36.00	58.785	0.00	0.00	0.00	6.215
361	ATGCGGTATACTGTCTCTATACACT	185	25	0	40.00	58.761	9.90	0.00	31.23	6.239
362	CCCAGCTATTTTGTGGAATCGTCG	395	24	0	50.00	62.256	0.00	0.00	0.00	6.256
363	TTAAGGTGTCTAAGTTTTTCTGCTGG	364	26	0	38.46	59.738	0.00	0.00	0.00	6.262
364	ACCTCTGTAAGTTCCAATACTGTCTT	130	26	0	38.46	59.730	0.00	0.00	0.00	6.270
365	CCTCTGTAAGTTCCAATACTGTCT	129	24	0	41.67	57.712	0.00	0.00	0.00	6.288
366	TCTAAGTTTTTCTGCTGGATTCAACG	356	26	0	38.46	60.293	0.00	0.00	0.00	6.293
367	TACTGTCTTGCAATATACACAGGT	113	24	0	37.50	57.706	11.41	5.21	0.00	6.294
368	TTGTGGAATCGTCGTTTTTCATTA	385	24	0	33.33	57.698	1.86	0.00	0.00	6.302

369	TGTGGAATCGTCGTTTTTCATTAA	384	24	0	33.33	57.698	1.86	0.00	0.00	6.302
370	AATCGTCGTTTTTCATTAAGGTGT	379	24	0	33.33	57.692	0.00	0.00	0.00	6.308
371	CATGCGGTATACTGTCTCTATACAC	186	25	0	44.00	58.684	9.90	0.00	31.23	6.316
372	GTGTCTAAGTTTTTCTGCTGGATT	359	24	0	37.50	57.681	0.00	0.00	0.00	6.319
373	GCAGCATGCGGTATACTGTCTCTA	190	24	0	50.00	62.339	14.57	0.00	37.60	6.339
374	TGTGGAATCGTCGTTTTTCATTAAG	384	25	0	36.00	58.633	0.15	0.00	0.00	6.367
375	GAATCGTCGTTTTTCATTAAGGTGT	380	25	0	36.00	58.632	2.12	0.00	0.00	6.368
376	AATCGTCGTTTTTCATTAAGGTGTC	379	25	0	36.00	58.632	0.00	0.00	0.00	6.368
377	GTGTCTAAGTTTTTCTGCTGGATTC	359	25	0	40.00	58.625	0.00	0.00	0.00	6.375
378	TAGTGCCCAGCTATTTTGTGGAATC	400	25	0	44.00	61.382	0.00	0.00	0.00	6.382
379	TAAGGTGTCTAAGTTTTTCTGCTGGA	363	26	0	38.46	60.409	0.00	0.00	0.00	6.409
380	ATCTATACATTTATGGCATGCAGC	209	24	0	37.50	57.553	7.99	0.11	44.65	6.447
381	CGTCGTTTTTCATTAAGGTGTCTA	376	24	0	37.50	57.544	0.00	0.00	0.00	6.456
382	CCGCAGGCACCTTATTAATAAATTGT	320	26	0	38.46	60.461	13.46	7.70	46.14	6.461
383	TCTGTAAGTTCCAATACTGTCTTGCA	127	26	0	38.46	60.464	0.00	0.00	0.00	6.464
384	CATGCGGTATACTGTCTCTATACA	186	24	0	41.67	57.504	9.90	0.00	31.23	6.496
385	ATGCGGTATACTGTCTCTATACAC	185	24	0	41.67	57.502	9.90	0.00	31.23	6.498
386	GCCCAGCTATTTTGTGGAATCGTC	396	24	0	50.00	62.502	0.00	0.00	0.00	6.502
387	CGCAGGCACCTTATTAATAAATTGT	319	25	0	36.00	58.496	13.46	7.70	0.00	6.504
388	AGCTATTTTGTGGAATCGTCGTTTTT	392	26	0	34.62	60.514	0.00	0.00	0.00	6.514
389	GAATCGTCGTTTTTCATTAAGGTGTC	380	26	0	38.46	59.481	2.12	0.00	0.00	6.519
390	GCCTCTATAGTGCCCAGCTATTTTG	407	25	0	48.00	61.544	5.93	0.00	0.00	6.544
391	TGTCTAAGTTTTTCTGCTGGATTCAA	358	26	0	34.62	59.454	0.00	0.00	0.00	6.546
392	GTAAGTTCCAATACTGTCTTGCAA	124	24	0	37.50	57.446	0.00	0.00	0.00	6.554
393	TGTCTAAGTTTTTCTGCTGGATTC	358	24	0	37.50	57.440	0.00	0.00	0.00	6.560
394	GTCTAAGTTTTTCTGCTGGATTCA	357	24	0	37.50	57.440	0.00	0.00	0.00	6.560
395	TGTGGAATCGTCGTTTTTCATTAAGG	384	26	0	38.46	60.567	0.15	0.00	0.00	6.567
396	TGGAATCGTCGTTTTTCATTAAGGTG	382	26	0	38.46	60.567	7.33	0.00	0.00	6.567
397	GTGGAATCGTCGTTTTTCATTAAGGT	383	26	0	38.46	60.567	1.86	0.00	0.00	6.567
398	GGAATCGTCGTTTTTCATTAAGGTGT	381	26	0	38.46	60.567	7.33	0.00	0.00	6.567
399	GGTGTCTAAGTTTTTCTGCTGGATTC	360	26	0	42.31	60.569	0.00	0.00	0.00	6.569
400	CCTCTGTAAGTTCCAATACTGTCTTG	129	26	0	42.31	59.408	0.00	0.00	0.00	6.592
401	TATAGTGCCCAGCTATTTTGTGGAAT	402	26	0	38.46	60.637	0.00	0.00	0.00	6.637
402	TGCGGTATACTGTCTCTATACACTAC	184	26	0	42.31	59.352	9.90	0.00	31.23	6.648
403	GCGGTATACTGTCTCTATACACTACA	183	26	0	42.31	59.352	6.27	0.00	31.23	6.648
404	TGTCTCCATACACAGAGTCTGAATAA	264	26	0	38.46	59.336	7.70	0.00	35.18	6.664
405	TTTTCTGCTGGATTCAACGGTTTCT	349	25	0	40.00	61.669	0.00	0.00	0.00	6.669
406	ATTTTGTGGAATCGTCGTTTTTCATT	388	26	0	30.77	59.300	1.86	0.00	0.00	6.700
407	TCGTCGTTTTTCATTAAGGTGTCTAA	377	26	0	34.62	59.299	0.00	0.00	0.00	6.701
408	GTCTCCATACACAGAGTCTGAATA	263	24	0	41.67	57.299	16.96	9.54	35.18	6.701
409	CCTCTGTAAGTTCCAATACTGTCTT	129	25	0	40.00	58.298	0.00	0.00	0.00	6.702
410	TACTGTCTTGCAATATACACAGGTT	113	25	0	36.00	58.293	18.84	8.21	0.00	6.707
411	ACTGTCTTGCAATATACACAGGTTA	112	25	0	36.00	58.293	18.84	0.00	0.00	6.707
412	TGTAAGTTCCAATACTGTCTTGCAAT	125	26	0	34.62	59.285	0.00	0.00	0.00	6.715
413	TATTTTGTGGAATCGTCGTTTTTCA	389	25	0	32.00	58.274	7.33	0.88	0.00	6.726
414	TTTGTGGAATCGTCGTTTTTCATTA	386	25	0	32.00	58.274	1.86	0.00	0.00	6.726
415	TTGTGGAATCGTCGTTTTTCATTAA	385	25	0	32.00	58.274	1.45	0.00	0.00	6.726

Primers data

416	GTGCCCAGCTATTTTGTGGAATCG	398	24	0	50.00	62.736	0.00	0.00	0.00	6.736
417	TGCGGTATACTGTCTCTATACACTA	184	25	0	40.00	58.238	9.90	0.00	31.23	6.762
418	GTGGAATCGTCGTTTTTCATTAAG	383	24	0	37.50	57.167	1.86	0.00	0.00	6.833
419	GAATCGTCGTTTTTCATTAAGGTG	380	24	0	37.50	57.167	2.12	0.00	0.00	6.833
420	CTATTTTGTGGAATCGTCGTTTTTCA	390	26	0	34.62	59.146	7.33	0.88	0.00	6.854
421	TTGTGGAATCGTCGTTTTTCATTAAG	385	26	0	34.62	59.146	2.73	0.00	0.00	6.854
422	GTCTAAGTTTTTCTGCTGGATTCAAC	357	26	0	38.46	59.142	0.00	0.00	0.00	6.858
423	AATCTATACATTTATGGCATGCAGC	210	25	0	36.00	58.140	7.99	0.11	44.65	6.860
424	TAAGGTGTCTAAGTTTTTCTGCTG	363	24	0	37.50	57.139	0.00	0.00	0.00	6.861
425	ATCGTCGTTTTTCATTAAGGTGTCTA	378	26	0	34.62	59.130	0.00	0.00	0.00	6.870
426	CGTCGTTTTTCATTAAGGTGTCTAA	376	25	0	36.00	58.120	0.00	0.00	0.00	6.880
427	ATACTGTCTTGCAATATACACAGGT	114	25	0	36.00	58.111	11.41	5.21	0.00	6.889
428	CAGCATGCGGTATACTGTCTCTATAC	189	26	0	46.15	60.894	6.85	0.00	0.00	6.894
429	AAGTTTTTCTGCTGGATTCAACGGT	353	25	0	40.00	61.899	0.00	0.00	0.00	6.899
430	AGTTTTTCTGCTGGATTCAACGGTT	352	25	0	40.00	61.899	0.00	0.00	0.00	6.899
431	AAGGTGTCTAAGTTTTTCTGCTGGAT	362	26	0	38.46	60.917	0.00	0.00	0.00	6.917
432	AGGTGTCTAAGTTTTTCTGCTGGATT	361	26	0	38.46	60.917	0.00	0.00	0.00	6.917
433	TACCTCTGTAAGTTCCAATACTGTCT	131	26	0	38.46	59.048	0.00	0.00	0.00	6.952
434	GTCTAAGTTTTTCTGCTGGATTCAA	357	25	0	36.00	58.030	0.00	0.00	0.00	6.970
435	TCTAAGTTTTTCTGCTGGATTCAAC	356	25	0	36.00	58.030	0.00	0.00	0.00	6.970
436	CGCAGGCACCTTATTAATAAATTG	319	24	0	37.50	57.009	9.79	9.79	0.00	6.991
437	CGTCGTTTTTCATTAAGGTGTCTAAG	376	26	0	38.46	58.992	0.00	0.00	0.00	7.008
438	ATACTTGTGTTTCTCTGCGTCGTTG	474	25	0	44.00	62.020	0.00	0.00	0.00	7.020
439	ATTAAGGTGTCTAAGTTTTTCTGCTGG	365	27	0	37.04	60.040	0.00	0.00	0.00	7.040
440	CAGCTATTTTGTGGAATCGTCGTTTT	393	26	0	38.46	61.055	0.00	0.00	0.00	7.055
441	CTAAGTTTTTCTGCTGGATTCAACGG	355	26	0	42.31	61.057	0.00	0.00	0.00	7.057
442	GCGGTATACTGTCTCTATACACTAC	183	25	0	44.00	57.941	6.27	0.00	31.23	7.059
443	CTGTAAGTTCCAATACTGTCTTGCAAT	126	27	0	37.04	60.095	0.00	0.00	0.00	7.095
444	TCGTCGTTTTTCATTAAGGTGTCTAAG	377	27	0	37.04	60.096	0.00	0.00	0.00	7.096
445	CCAGCTATTTTGTGGAATCGTCGTT	394	25	0	44.00	62.096	0.00	0.00	0.00	7.096
446	GTCTCCATACACAGAGTCTGAATAA	263	25	0	40.00	57.898	7.70	0.00	35.18	7.102
447	GCATGCGGTATACTGTCTCTATACAC	187	26	0	46.15	61.111	3.72	0.00	31.23	7.111
448	CTATAGTGCCCAGCTATTTTGTGGAA	403	26	0	42.31	61.135	0.00	0.00	0.00	7.135
449	GTAAGTTCCAATACTGTCTTGCAAT	124	25	0	36.00	57.854	0.24	0.00	0.00	7.146
450	TACCTCTGTAAGTTCCAATACTGTC	131	25	0	40.00	57.833	0.00	0.00	0.00	7.167
451	GCGGTATACTGTCTCTATACACTACAA	183	27	0	40.74	59.828	6.27	0.00	31.23	7.172
452	TTTTGTGGAATCGTCGTTTTTCATTA	387	26	0	30.77	58.806	1.86	0.00	0.00	7.194
453	TTTGTGGAATCGTCGTTTTTCATTAA	386	26	0	30.77	58.806	1.62	0.00	0.00	7.194
454	TTTCTGCTGGATTCAACGGTTTCTG	348	25	0	44.00	62.221	0.00	0.00	0.00	7.221
455	TTATACTTGTGTTTCTCTGCGTCGTT	476	26	0	38.46	61.227	0.00	0.00	0.00	7.227
456	TGAATGCAAATTCAAATACCTCTGT	147	25	0	32.00	57.769	2.83	0.00	37.59	7.231
457	AGCATGCGGTATACTGTCTCTATACA	188	26	0	42.31	61.247	13.01	0.00	31.23	7.247
458	CTATTTTGTGGAATCGTCGTTTTTC	390	25	0	36.00	57.752	0.00	0.00	0.00	7.248
459	CCAATACTGTCTTGCAATATACACAGG	117	27	0	40.74	60.255	18.84	8.97	0.00	7.255
460	CCGCAGGCACCTTATTAATAAATTGTA	320	27	0	37.04	60.255	13.46	0.00	46.14	7.255
461	TTAAGGTGTCTAAGTTTTTCTGCTG	364	25	0	36.00	57.741	0.00	0.00	0.00	7.259
462	CAATACTGTCTTGCAATATACACAGGT	116	27	0	37.04	59.719	11.41	5.21	0.00	7.281

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463	CGTCGTTTTTCATTAAGGTGTCTAAGT	376	27	0	37.04	60.307	0.00	0.00	0.00	7.307
464	AAATCTATACATTTATGGCATGCAGC	211	26	0	34.62	58.682	7.99	0.11	44.65	7.318
465	CATGCGGTATACTGTCTCTATACACTA	186	27	0	40.74	59.666	9.90	0.00	31.23	7.334
466	ATGCGGTATACTGTCTCTATACACTAC	185	27	0	40.74	59.666	9.90	0.00	31.23	7.334
467	TCCAATACTGTCTTGCAATATACACA	118	26	0	34.62	58.665	9.08	3.86	0.00	7.335
468	AATACTGTCTTGCAATATACACAGGT	115	26	0	34.62	58.661	11.41	5.21	0.00	7.339
469	ATACTGTCTTGCAATATACACAGGTT	114	26	0	34.62	58.661	18.84	9.01	0.00	7.339
470	ACTGTCTTGCAATATACACAGGTTAT	112	26	0	34.62	58.661	18.84	4.09	0.00	7.339
471	TGTCTCCATACACAGAGTCTGAATAAT	264	27	0	37.04	59.657	8.51	0.00	35.18	7.343
472	TCTCCATACACAGAGTCTGAATAATGT	262	27	0	37.04	59.657	16.73	13.16	35.18	7.343
473	TCCATACACAGAGTCTGAATAATGTCT	260	27	0	37.04	59.657	16.73	5.64	35.18	7.343
474	TATTTTGTGGAATCGTCGTTTTTCAT	389	26	0	30.77	58.636	1.86	0.00	0.00	7.364
475	TTTGTGGAATCGTCGTTTTTCATTAAG	386	27	0	33.33	59.623	2.89	0.00	0.00	7.377
476	AATCGTCGTTTTTCATTAAGGTGTCTA	379	27	0	33.33	59.614	0.00	0.00	0.00	7.386
477	ATCGTCGTTTTTCATTAAGGTGTCTAA	378	27	0	33.33	59.614	0.00	0.00	0.00	7.386
478	ATGCGGTATACTGTCTCTATACACTA	185	26	0	38.46	58.608	9.90	0.00	31.23	7.392
479	TCCATACACAGAGTCTGAATAATGT	260	25	0	36.00	57.576	16.73	13.16	35.18	7.424
480	TACCTCTGTAAGTTCCAATACTGTCTT	131	27	0	37.04	59.546	0.00	0.00	0.00	7.454
481	CCTCTATAGTGCCCAGCTATTTTGTG	406	26	0	46.15	61.459	0.00	0.00	0.00	7.459
482	CTCTATAGTGCCCAGCTATTTTGTGG	405	26	0	46.15	61.459	0.00	0.00	0.00	7.459
483	GTGTCTAAGTTTTTCTGCTGGATTCAA	359	27	0	37.04	60.469	0.00	0.00	0.00	7.469
484	TGTCTAAGTTTTTCTGCTGGATTCAAC	358	27	0	37.04	60.469	0.00	0.00	0.00	7.469
485	TCCATACACAGAGTCTGAATAATGTC	260	26	0	38.46	58.507	16.73	0.00	35.18	7.493
486	TCCAATACTGTCTTGCAATATACACAG	118	27	0	37.04	59.504	15.54	15.54	0.00	7.496
487	CTCCATACACAGAGTCTGAATAATGT	261	26	0	38.46	58.504	16.73	13.16	35.18	7.496
488	CCATACACAGAGTCTGAATAATGTCT	259	26	0	38.46	58.504	16.73	5.64	35.18	7.496
489	GGCCTCTATAGTGCCCAGCTATTTT	408	25	0	48.00	62.503	19.28	0.00	34.65	7.503
490	CTATTTTGTGGAATCGTCGTTTTTCAT	390	27	0	33.33	59.463	1.86	0.00	0.00	7.537
491	CCAATACTGTCTTGCAATATACACA	117	25	0	36.00	57.448	9.08	3.86	0.00	7.552
492	GCAGCATGCGGTATACTGTCTCTAT	190	25	0	48.00	62.567	14.57	0.00	37.60	7.567
493	GAATCGTCGTTTTTCATTAAGGTGTCT	380	27	0	37.04	60.571	2.12	0.00	0.00	7.571
494	CTCTGTAAGTTCCAATACTGTCTTG	128	25	0	40.00	57.412	0.00	0.00	0.00	7.588
495	ATACCTCTGTAAGTTCCAATACTGTCT	132	27	0	37.04	59.380	0.00	0.00	0.00	7.620
496	TAAGTTTTTCTGCTGGATTCAACGGT	354	26	0	38.46	61.633	0.00	0.00	0.00	7.633
497	CCAATACTGTCTTGCAATATACACAG	117	26	0	38.46	58.366	15.54	15.54	0.00	7.634
498	CAATACTGTCTTGCAATATACACAGG	116	26	0	38.46	58.366	18.84	8.89	0.00	7.634
499	ATAGTGCCCAGCTATTTTGTGGAATC	401	26	0	42.31	61.638	0.00	0.00	0.00	7.638
500	CGCAGGCACCTTATTAATAAATTGTA	319	26	0	34.62	58.356	13.46	0.00	0.00	7.644
501	GTCTCCATACACAGAGTCTGAATAATG	263	27	0	40.74	59.349	15.00	12.15	35.18	7.651
502	CTCCATACACAGAGTCTGAATAATGTC	261	27	0	40.74	59.349	16.73	0.00	35.18	7.651
503	TTGAATGCAAATTCAAATACCTCTGT	148	26	0	30.77	58.331	0.00	0.00	44.64	7.669
504	TGCGGTATACTGTCTCTATACACTACA	184	27	0	40.74	60.688	9.90	0.00	31.23	7.688
505	TAAGGTGTCTAAGTTTTTCTGCTGGAT	363	27	0	37.04	60.692	0.00	0.00	0.00	7.692
506	TTTTGTGGAATCGTCGTTTTTCATTAA	387	27	0	29.63	59.299	1.62	0.00	0.00	7.701
507	CCATACACAGAGTCTGAATAATGTC	259	25	0	40.00	57.294	16.73	0.00	35.18	7.706
508	TCATTAAGGTGTCTAAGTTTTTCTGCT	367	27	0	33.33	59.280	0.00	0.00	0.00	7.720
509	TCTCCATACACAGAGTCTGAATAATG	262	26	0	38.46	58.280	15.00	12.15	35.18	7.720

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510	GTCTCCATACACAGAGTCTGAATAAT	263	26	0	38.46	58.279	8.51	0.00	35.18	7.721
511	ATACCTCTGTAAGTTCCAATACTGT	132	25	0	36.00	57.265	0.00	0.00	0.00	7.735
512	ACCTCTGTAAGTTCCAATACTGTCTTG	130	27	0	40.74	60.741	0.00	0.00	0.00	7.741
513	GCAAATTCAAATACCTCTGTAAGTTCC	142	27	0	37.04	59.245	0.00	0.00	0.00	7.755
514	TATACTTGTGTTTCTCTGCGTCGTTG	475	26	0	42.31	61.756	0.00	0.00	0.00	7.756
515	TGCAAATTCAAATACCTCTGTAAGT	143	25	0	32.00	57.241	0.00	0.00	0.00	7.759
516	ATACCTCTGTAAGTTCCAATACTGTC	132	26	0	38.46	58.217	0.00	0.00	0.00	7.783
517	TCCAATACTGTCTTGCAATATACAC	118	25	0	36.00	57.214	9.08	0.02	0.00	7.786
518	AATACTGTCTTGCAATATACACAGG	115	25	0	36.00	57.208	18.84	8.89	0.00	7.792
519	CTGTCTTGCAATATACACAGGTTAT	111	25	0	36.00	57.208	11.78	0.00	0.00	7.792
520	CATTAAGGTGTCTAAGTTTTTCTGCTG	366	27	0	37.04	59.195	0.00	0.00	0.00	7.805
521	AAAATCTATACATTTATGGCATGCAGC	212	27	0	33.33	59.184	7.99	0.11	44.65	7.816
522	TCTATAGTGCCCAGCTATTTTGTGGA	404	26	0	42.31	61.826	0.00	0.00	0.00	7.826
523	TTCCAATACTGTCTTGCAATATACACA	119	27	0	33.33	59.173	9.08	3.86	0.00	7.827
524	AATACTGTCTTGCAATATACACAGGTT	115	27	0	33.33	59.171	13.29	8.25	0.00	7.829
525	ACTGTCTTGCAATATACACAGGTTATT	112	27	0	33.33	59.171	18.84	3.84	0.00	7.829
526	TACTGTCTTGCAATATACACAGGTTA	113	26	0	34.62	58.157	18.84	7.57	0.00	7.843
527	TTAAGGTGTCTAAGTTTTTCTGCTGGA	364	27	0	37.04	60.853	0.00	0.00	0.00	7.853
528	GTCGTTTTTCATTAAGGTGTCTAAGT	375	26	0	34.62	58.141	0.00	0.00	0.00	7.859
529	TATTTTGTGGAATCGTCGTTTTTCATT	389	27	0	29.63	59.137	0.00	0.00	0.00	7.863
530	ATTTTGTGGAATCGTCGTTTTTCATTA	388	27	0	29.63	59.137	0.00	0.00	0.00	7.863
531	TCATTAAGGTGTCTAAGTTTTTCTGC	367	26	0	34.62	58.128	0.00	0.00	0.00	7.872
532	CATTAAGGTGTCTAAGTTTTTCTGCT	366	26	0	34.62	58.124	0.00	0.00	0.00	7.876
533	ATTAAGGTGTCTAAGTTTTTCTGCTG	365	26	0	34.62	58.124	0.00	0.00	0.00	7.876
534	TGTAAGTTCCAATACTGTCTTGCAATA	125	27	0	33.33	59.119	0.00	0.00	0.00	7.881
535	TCTGTAAGTTCCAATACTGTCTTGCAA	127	27	0	37.04	60.904	0.00	0.00	0.00	7.904
536	TCTCCATACACAGAGTCTGAATAAT	262	25	0	36.00	57.095	8.51	0.00	35.18	7.905
537	GTTTTTCTGCTGGATTCAACGGTTTC	351	26	0	42.31	61.921	0.00	0.00	0.00	7.921
538	CTCCATACACAGAGTCTGAATAATG	261	25	0	40.00	57.057	15.00	12.15	35.18	7.943
539	AAGTTCCAATACTGTCTTGCAATAT	122	25	0	32.00	57.055	0.00	0.00	0.00	7.945
540	CCATACACAGAGTCTGAATAATGTCTT	259	27	0	37.04	59.016	16.73	4.96	35.18	7.984
541	TTGTGGAATCGTCGTTTTTCATTAAGG	385	27	0	37.04	60.994	2.73	0.00	0.00	7.994
542	AGTTCCAATACTGTCTTGCAATATACA	121	27	0	33.33	58.953	9.08	9.08	0.00	8.047
543	ATACACAGGTTATTTCTATGTCTTGCA	99	27	0	33.33	58.953	0.00	0.00	0.00	8.047
544	TTTTTCTGCTGGATTCAACGGTTTCT	350	26	0	38.46	62.076	0.00	0.00	0.00	8.076
545	GTTCCAATACTGTCTTGCAATATACAC	120	27	0	37.04	58.877	9.08	0.02	0.00	8.123
546	AATACCTCTGTAAGTTCCAATACTGT	133	26	0	34.62	57.853	0.00	0.00	0.00	8.147
547	TGCAAATTCAAATACCTCTGTAAGTT	143	26	0	30.77	57.823	0.00	0.00	0.00	8.177
548	GTTCCAATACTGTCTTGCAATATACA	120	26	0	34.62	57.791	9.08	9.08	0.00	8.209
549	TTCCAATACTGTCTTGCAATATACAC	119	26	0	34.62	57.791	9.08	0.02	0.00	8.209
550	CTGTCTTGCAATATACACAGGTTATT	111	26	0	34.62	57.786	11.78	0.00	0.00	8.214
551	CTCTGTAAGTTCCAATACTGTCTTGCA	128	27	0	40.74	61.218	0.00	0.00	0.00	8.218
552	GTCTAAGTTTTTCTGCTGGATTCAACG	357	27	0	40.74	61.250	0.00	0.00	0.00	8.250
553	AGCTATTTTGTGGAATCGTCGTTTTTC	392	27	0	37.04	61.253	0.00	0.00	0.00	8.253
554	AATACCTCTGTAAGTTCCAATACTGTC	133	27	0	37.04	58.741	0.00	0.00	0.00	8.259
555	GTAAGTTCCAATACTGTCTTGCAATA	124	26	0	34.62	57.736	0.00	0.00	0.00	8.264
556	GCAGCATGCGGTATACTGTCTCTATA	190	26	0	46.15	62.278	14.57	0.00	37.60	8.278

Primers data

557	CGCAGGCACCTTATTAATAAATTGTAT	319	27	0	33.33	58.703	13.46	4.54	0.00	8.297
558	TGCAAATTCAAATACCTCTGTAAGTTC	143	27	0	33.33	58.703	0.00	0.00	0.00	8.297
559	AAGTTTTTCTGCTGGATTCAACGGTT	353	26	0	38.46	62.298	0.00	0.00	0.00	8.298
560	AGTTTTTCTGCTGGATTCAACGGTTT	352	26	0	38.46	62.298	0.00	0.00	0.00	8.298
561	GGAATCGTCGTTTTTCATTAAGGTGTC	381	27	0	40.74	61.299	7.33	0.00	0.00	8.299
562	GTCGTTTTTCATTAAGGTGTCTAAGTT	375	27	0	33.33	58.660	0.00	0.00	0.00	8.340
563	AAGGTGTCTAAGTTTTTCTGCTGGATT	362	27	0	37.04	61.343	0.00	0.00	0.00	8.343
564	TGAATGCAAATTCAAATACCTCTGTA	147	26	0	30.77	57.653	2.83	0.00	37.59	8.347
565	TTCATTAAGGTGTCTAAGTTTTTCTGC	368	27	0	33.33	58.650	0.00	0.00	0.00	8.350
566	ATGCAAATTCAAATACCTCTGTAAGT	144	26	0	30.77	57.647	0.00	0.00	0.00	8.353
567	TATAGTGCCCAGCTATTTTGTGGAATC	402	27	0	40.74	61.389	0.00	0.00	0.00	8.389
568	CTATAGTGCCCAGCTATTTTGTGGAAT	403	27	0	40.74	61.392	0.00	0.00	0.00	8.392
569	AGTTCCAATACTGTCTTGCAATATAC	121	26	0	34.62	57.561	0.98	0.98	0.00	8.439
570	ATACACAGGTTATTTCTATGTCTTGC	99	26	0	34.62	57.561	0.00	0.00	0.00	8.439
571	TCGTTTTTCATTAAGGTGTCTAAGTT	374	26	0	30.77	57.559	0.00	0.00	0.00	8.441
572	GCTATTTTGTGGAATCGTCGTTTTTCA	391	27	0	37.04	61.460	7.33	0.88	0.00	8.460
573	CAGCTATTTTGTGGAATCGTCGTTTTT	393	27	0	37.04	61.462	0.00	0.00	0.00	8.462
574	CCAGCTATTTTGTGGAATCGTCGTTT	394	26	0	42.31	62.481	0.00	0.00	0.00	8.481
575	ATACTGTCTTGCAATATACACAGGTTA	114	27	0	33.33	58.517	4.29	0.00	0.00	8.483
576	TACTGTCTTGCAATATACACAGGTTAT	113	27	0	33.33	58.517	3.21	0.00	0.00	8.483
577	GTGGAATCGTCGTTTTTCATTAAGGTG	383	27	0	40.74	61.507	1.86	0.00	0.00	8.507
578	TGTCTTGCAATATACACAGGTTATTT	110	26	0	30.77	57.426	9.60	0.00	0.00	8.574
579	CGGTATACTGTCTCTATACACTACAA	182	26	0	38.46	57.401	3.31	0.00	31.23	8.599
580	TTTTCTGCTGGATTCAACGGTTTCTG	349	26	0	42.31	62.603	0.00	0.00	0.00	8.603
581	AAATACCTCTGTAAGTTCCAATACTGT	134	27	0	33.33	58.397	0.00	0.00	0.00	8.603
582	AGGTGTCTAAGTTTTTCTGCTGGATTC	361	27	0	40.74	61.653	0.00	0.00	0.00	8.653
583	TGTCTTGCAATATACACAGGTTATTTC	110	27	0	33.33	58.326	9.60	0.00	0.00	8.674
584	GCAAATTCAAATACCTCTGTAAGTTC	142	26	0	34.62	57.325	0.00	0.00	0.00	8.675
585	CTGTCTTGCAATATACACAGGTTATTT	111	27	0	33.33	58.323	11.78	0.00	0.00	8.677
586	CCTCTGTAAGTTCCAATACTGTCTTGC	129	27	0	44.44	61.743	0.75	0.00	0.00	8.743
587	CAAATTCAAATACCTCTGTAAGTTCCA	141	27	0	33.33	58.207	0.00	0.00	0.00	8.793
588	TTGAATGCAAATTCAAATACCTCTGTA	148	27	0	29.63	58.199	0.00	0.00	44.64	8.801
589	TGAATGCAAATTCAAATACCTCTGTAA	147	27	0	29.63	58.199	2.83	0.00	37.59	8.801
590	AATGCAAATTCAAATACCTCTGTAAGT	145	27	0	29.63	58.194	0.00	0.00	0.00	8.806
591	ATGCAAATTCAAATACCTCTGTAAGTT	144	27	0	29.63	58.194	0.00	0.00	0.00	8.806
592	TCAAATACCTCTGTAAGTTCCAATACT	136	27	0	33.33	58.177	0.00	0.00	0.00	8.823
593	TGTGGAATCGTCGTTTTTCATTAAGGT	384	27	0	37.04	61.856	0.15	0.00	0.00	8.856
594	TGGAATCGTCGTTTTTCATTAAGGTGT	382	27	0	37.04	61.856	7.33	0.00	0.00	8.856
595	GGTGTCTAAGTTTTTCTGCTGGATTCA	360	27	0	40.74	61.863	0.00	0.00	0.00	8.863
596	GCCTCTATAGTGCCCAGCTATTTTGT	407	26	0	46.15	62.869	5.93	0.00	0.00	8.869
597	CAAATACCTCTGTAAGTTCCAATACTG	135	27	0	37.04	58.116	0.00	0.00	0.00	8.884
598	GTAAGTTCCAATACTGTCTTGCAATAT	124	27	0	33.33	58.106	0.00	0.00	0.00	8.894
599	AAGTTCCAATACTGTCTTGCAATATAC	122	27	0	33.33	58.106	0.98	0.98	0.00	8.894
600	GTCTTGCAATATACACAGGTTATTTCT	109	27	0	33.33	58.106	2.76	0.00	0.00	8.894
601	TCGTTTTTCATTAAGGTGTCTAAGTTT	374	27	0	29.63	58.104	0.00	0.00	0.00	8.896
602	AAATTCAAATACCTCTGTAAGTTCCA	140	26	0	30.77	57.066	0.00	0.00	0.00	8.934
603	AATTCAAATACCTCTGTAAGTTCCAA	139	26	0	30.77	57.066	0.00	0.00	0.00	8.934

Primers data

604	CATACACAGAGTCTGAATAATGTCTT	258	26	0	34.62	57.061	14.59	2.70	35.18	8.939
605	TAAGTTTTTCTGCTGGATTCAACGGTT	354	27	0	37.04	62.027	0.00	0.00	0.00	9.027
606	CGGTATACTGTCTCTATACACTACAAA	182	27	0	37.04	57.950	3.31	0.00	31.23	9.050
607	ACCCAGTGTTAGTTAGTTTTTCTAATG	291	27	0	33.33	57.936	0.00	0.00	40.23	9.064
608	CCCAGTGTTAGTTAGTTTTTCTAATGT	290	27	0	33.33	57.936	0.00	0.00	40.23	9.064
609	TCTAAGTTTTTCTGCTGGATTCAACGG	356	27	0	40.74	62.117	0.00	0.00	0.00	9.117
610	TTATACTTGTGTTTCTCTGCGTCGTTG	476	27	0	40.74	62.136	0.00	0.00	0.00	9.136
611	CAGCATGCGGTATACTGTCTCTATACA	189	27	0	44.44	62.172	6.85	0.00	31.23	9.172
612	AGCATGCGGTATACTGTCTCTATACAC	188	27	0	44.44	62.173	13.01	0.00	31.23	9.173
613	GCATGCGGTATACTGTCTCTATACACT	187	27	0	44.44	62.173	3.72	0.00	31.23	9.173
614	TCTATAGTGCCCAGCTATTTTGTGGAA	404	27	0	40.74	62.220	0.00	0.00	0.00	9.220
615	GAATGCAAATTCAAATACCTCTGTAAG	146	27	0	33.33	57.706	0.00	0.00	0.00	9.294
616	CTAAGTTTTTCTGCTGGATTCAACGGT	355	27	0	40.74	62.330	0.00	0.00	0.00	9.330
617	AAATTCAAATACCTCTGTAAGTTCCAA	140	27	0	29.63	57.638	0.00	0.00	0.00	9.362
618	TTCAAATACCTCTGTAAGTTCCAATAC	137	27	0	33.33	57.555	0.00	0.00	0.00	9.445
619	CGTTTTTCATTAAGGTGTCTAAGTTTT	373	27	0	29.63	57.489	0.00	0.00	0.00	9.511
620	CTCTATAGTGCCCAGCTATTTTGTGGA	405	27	0	44.44	62.525	0.00	0.00	0.00	9.525
621	AATTCAAATACCTCTGTAAGTTCCAAT	139	27	0	29.63	57.466	0.00	0.00	0.00	9.534
622	TATACACAGGTTATTTCTATGTCTTGC	100	27	0	33.33	57.458	0.00	0.00	0.00	9.542
623	AACCCAGTGTTAGTTAGTTTTTCTAAT	292	27	0	29.63	57.363	0.00	0.00	36.90	9.637
624	AAGTTTTTCTGCTGGATTCAACGGTTT	353	27	0	37.04	62.668	0.00	0.00	0.00	9.668
625	AAAAATCTATACATTTATGGCATGCAG	213	27	0	29.63	57.299	7.99	0.00	0.00	9.701
626	CCAGCTATTTTGTGGAATCGTCGTTTT	394	27	0	40.74	62.838	0.00	0.00	0.00	9.838
627	TGCAATATACACAGGTTATTTCTATGT	105	27	0	29.63	57.154	0.00	0.00	0.00	9.846
628	TTGTATAACCCAGTGTTAGTTAGTTTT	298	27	0	29.63	57.150	0.00	0.00	42.50	9.850
629	TGTATAACCCAGTGTTAGTTAGTTTTT	297	27	0	29.63	57.150	0.00	0.00	42.50	9.850
630	CCAGTGTTAGTTAGTTTTTCTAATGTG	289	27	0	33.33	57.121	0.00	0.00	40.23	9.879
631	ACACAGAGTCTGAATAATGTCTTAATT	255	27	0	29.63	57.050	17.85	0.00	35.18	9.950
632	TTTTTCTGCTGGATTCAACGGTTTCTG	350	27	0	40.74	62.957	0.00	0.00	0.00	9.957
633	AGTTTTTCTGCTGGATTCAACGGTTTC	352	27	0	40.74	62.959	0.00	0.00	0.00	9.959
634	GTTTTTCTGCTGGATTCAACGGTTTCT	351	27	0	40.74	62.959	0.00	0.00	0.00	9.959
635	ACACTACAAATAAATCTTTGAATGCAA	165	27	0	25.93	57.020	2.43	0.00	38.17	9.980

BLAST INFORMATION

```
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<html xmlns="http://www.w3.org/1999/xhtml">
<head>

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<meta http-equiv="X-UA-Compatible" content="IE=edge,chrome=1">
<meta name="jig" content="ncbitoggler ncbiautocomplete"/>
<meta name="ncbitoggler" content="animation:'none'"/>


<meta name="referrer" content="origin-when-cross-origin" />
<meta name="ncbi_app" content="blast" />
<meta name="ncbi_pdid" content="oldblastresults" />

<meta name="ncbi_db" content="nt" />
<meta name="ncbi_program" content="blastn" />
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<meta name="ncbi_phid" content="5AAB9F5C963F4ED10000000000000001" />
<script type="text/javascript"> var ncbi_startTime = new Date(); </script>
<title>NCBI Blast:Nucleotide Sequence (20 letters)</title>
<script type="text/javascript" src="/core/jig/1.14.8/js/jig.min.js          "></script>
<script type="text/javascript">     jQuery.getScript("/core/alerts/alerts.js", function() {
                                    galert(['div#header', 'body > *:nth-child(1)'])
});</script>
<link rel="stylesheet" type="text/css" href="css/header.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/google-fonts.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/footer.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/main.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/blastRes.css" media="screen" />
<!--[if IE]>
<link rel="stylesheet" type="text/css" href="css/descriptionsIE.css" media="screen" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/print.css" media="print" />
<!--[if lte IE 6]>
<link rel="stylesheet" type="text/css" href="css/ie6_or_less.css" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/blastReq.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/results.css" media="screen" />


</head>

<body id="type-a" class="noToggleCheck " >
<div id="wrap">
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BLAST INFORMATION

```html
<header id="page_header" role="banner">
<ul class="skip_nav">
<li><a accesskey="1" title="NCBI Homepage" href="https://www.ncbi.nlm.nih.gov/">NCBI Home</a><
<li><a accesskey="2" title="MyNCBI" href="https://www.ncbi.nlm.nih.gov/myncbi">Sign in to NCBI<
<li><a accesskey="3" title="Skip to main content" href="#content">Skip to Main Content</a></li
<li><a accesskey="4" title="Skip to navigation" href="#navcontent">Skip to Navigation</a></li>
<li><a accesskey="0" title="About NCBI Accesskeys" href="https://www.ncbi.nlm.nih.gov/guide/bro
</ul>
<nav class="blue_nav_bar">
<div class="nih">
<a id="page_header_6" href="https://www.nih.gov/" class="left norm_height">
<img src="images/nih_logo.svg" alt="NIH logo" class="left"/></a>
<a id="page_header_7" href="https://www.nlm.nih.gov/" class="left header_link">U.S. National L
</div>


<div class="left">
<img src="images/arrow.svg" class="left norm_height" alt=""/>
</div>



<div class="ncbi">
<a id="page_header_8" href="https://www.ncbi.nlm.nih.gov/" class="header_link">
<span class="ncbi_name">NCBI</span>
<span class="med_hidden">National Center for Biotechnology Information</span></a>

<div class="right sign-in">
<ul class="myncbi2">
<li id="myncbiusername">
<span id="mnu">
<a id="mnu_0" href="https://www.ncbi.nlm.nih.gov/account/settings/" title="Edit account setting
</span>
</li>
<li id="myncbi"><a id="myncbi_0"  href="https://www.ncbi.nlm.nih.gov/myncbi/">My NCBI</a></li>
<li id="myncbi_sign_in"><a id="myncbi_sign_in_0" href="https://www.ncbi.nlm.nih.gov/account/?ba
<li id="myncbi_register"><a id="myncbi_register_0" href="https://www.ncbi.nlm.nih.gov/account/
<li id="myncbi_sign_out"><a id="myncbi_sign_out_0" href="https://www.ncbi.nlm.nih.gov/account/
</ul>
</div>
</div>
</nav>


<div class="bg-gray header-div">
<nav class="top-nav" id="navcontent" role="navigation">
<a class="lf" href="Blast.cgi">BLAST <sup>&reg;</sup></a> <span id="brc"><span class="brcrmbsig
<span class="rf">
<ul id="blnav">
<li  class="first "><a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastHome" title="BLAST Home">Home
```

BLAST INFORMATION
```html
<li  class="recent "><a href="Blast.cgi?CMD=GetSaved&amp;RECENT_RESULTS=on" title="Unexpired B
<li  class="saved "><a href="Blast.cgi?CMD=GetSaved" title="Saved sets of BLAST search paramet
<li  class= "last documentation "> <a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs" title="
</ul>
</span>
</nav>
</div>
</header>

<div id="content-wrap">

<div class="pageTitle">
BLAST Results
</div>
<div class="inlineDiv resHeader resPage">

</div>
<ul class="print-log-res"><li></li></ul>

<!-- CDD info for old design -->




<div id="content">

<!--<ul id="msg" class="msg"><li class=""><p class=""></p><p class=""></p><p class=""></p></li
<ul id="msg" class="msg"><li class=""></li></ul>
<a  href="#" class="resLink resPage" id="searchOptions" submitForm="setSavedOptions">Edit and I
<a  href="#" class="resLink resPage hidden" id="saveSearchOptions" submitForm="saveOptions">Sav
<span class="reslink  resPage" >[Sign in above to save your search strategy]</span>
<a  id="showFormat" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggler
<span class="ui-ncbitoggler-master-text">Formatting options </span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<a  id="showDownload" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggle
<span class="ui-ncbitoggler-master-text">Download</span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<span id="hnr">
<a id="ytb" class="ytb " title="External link to YouTube" href="https://www.youtube.com/playli
<a id="brFtp" class="" title="Blast report description" href="ftp://ftp.ncbi.nlm.nih.gov/pub/fa
</span>
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BLAST INFORMATION

```html
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<input name="QUERY_INDEX" type="hidden" value="0">
<input name="_PGR" type="hidden" value="" >
<input id="seqViewUrl" type="hidden" value="https://www.ncbi.nlm.nih.gov" >
<input id="userAgent" type="hidden" value="">
<input name="CMD" type="hidden" value="Get">
</form>
<!-- Reformat and downlaod for new design -->
<div class="ui-helper-reset" aria-live="assertive" >
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="Format
<table class="options blastn ">
<tr>
<td class="frh" colspan=2>
<div class="fi">
<div class="tb">Formatting options</div>
<input type="image"  border="0" id="onPageReformat" src="css/images/reformat.jpg" class="blast
</div>
</tr>
<tr class="paramSet xgl">
<td class="hd"><label for="FORMAT_OBJECT">Show</label></td>
<td>
<div class="fi">
<input type="hidden" id="FORMAT_OBJECT" value="Alignment" name="FORMAT_OBJECT" />
<label for="FORMAT_TYPE" id="nft">Alignment as</label>
<select name="FORMAT_TYPE" id="FORMAT_TYPE" class="reset" defVal="HTML">
<option value="HTML"  >HTML</option>
<option value="Text"  >Plain text</option>

</select>

<span id="advView" class="">
<span class=""><input name="OLD_VIEW" id="OLD_VIEW" type="checkbox" class="cb reset" defVal="u
<label for="OLD_VIEW">Old View</label></span>
</span>
<a class="resetAll" id="resetAll" >Reset form to defaults</a>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments object formatting
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp1">
These options control formatting of alignments in results pages. The
default is HTML, but other formats (including plain text) are available.
PSSM and PssmWithParameters are representations of Position Specific Scoring Matrices and are
The Advanced view option allows the database descriptions to be sorted by various indices in a
</p>
</div><!-- ARIA -->
</div>
```

BLAST INFORMATION
```
</td>
</tr>

<tr class="odd paramSet">
<td class="hd"><label for="ALIGNMENT_VIEW">Alignment View</label></td>
<td>
<div class="fi">
<select name="ALIGNMENT_VIEW" id="ALIGNMENT_VIEW" defVal="Pairwise" class="reset">
<option value="Pairwise" selected="selected" >Pairwise</option>
<option value="PairwiseWithIdentities"  >Pairwise with dots for identities</option>
<option value="QueryAnchored"  >Query-anchored with dots for identities</option>
<option value="QueryAnchoredNoIdentities"  >Query-anchored with letters for identities</option>
<option value="FlatQueryAnchored"  >Flat query-anchored with dots for identities</option>
<option value="FlatQueryAnchoredNoIdentities"  >Flat query-anchored with letters for identities

</select>


<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments view options help
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp2">
Choose how to view alignments.
The default "pairwise" view shows how each subject sequence aligns
individually to the query sequence. The "query-anchored" view shows how
all subject sequences align to the query sequence. For each view type,
you can choose to show "identities" (matching residues) as letters or
dots.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#alignment_view" targe
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet">
<td class="hd"><label>Display</label></td>
<td class="cb">
<div class="fi">
<input name="SHOW_OVERVIEW" id="SHOW_OVERVIEW" type="checkbox" class="cb reset" defVal="checke
<label class="rb" for="SHOW_OVERVIEW">Graphical Overview</label>

<span id="shl" >
<input name="SHOW_LINKOUT" id="SHOW_LINKOUT" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="SHOW_LINKOUT">Linkout</label>
</span>
<span id="gts" >
```

BLAST INFORMATION

```
<input name="GET_SEQUENCE" id="GET_SEQUENCE" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="GET_SEQUENCE">Sequence Retrieval</label>
</span>

<input name="NCBI_GI" id="NCBI_GI" type="checkbox" class="cb reset" defVal="unchecked" false /
<label class="rb" for="NCBI_GI">NCBI-gi</label>
<span id="scf" >
<input name="SHOW_CDS_FEATURE" id="SHOW_CDS_FEATURE" type="checkbox" class="cb reset blastn" d
<label for="SHOW_CDS_FEATURE" class="blastn">CDS feature</label>
</span>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments display options he
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp3">
<li>Graphical Overview: Graphical Overview: Show graph of similar sequence regions aligned to
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_overview" targe
</li>
<li>NCBI-gi: Show NCBI gi identifiers.
</li>
<li>CDS feature: Show annotated coding region and translation.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_cds_feature" ti
</li></ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"><label>Masking</label></td>
<td>
<div class="fi">
<label for="MASK_CHAR"> Character: </label>
<select name="MASK_CHAR" id="MASK_CHAR"  class="reset" defVal="2">
<option value="0"  >X for protein, n for nucleotide</option>
<option value="2" selected="selected" >Lower Case</option>
</select>
<label for="MASK_COLOR"> Color:</label>
<select name="MASK_COLOR" id="MASK_COLOR" class="reset" defVal="1">
<option value="0"  >Black
</option>

<option value="1" selected="selected" >Grey
</option>

<option value="2"  >Red
</option>
```

```
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments masking help" id=
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp4">
<li>Masking Character: Display masked (filtered) sequence regions as lower-case or as specific
</li>
<li>Masking Color: Display masked sequence regions in the given color.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr id="lr" class="paramSet xgl">
<td class="hd"><label>Limit results</label></td>
<td>
<div class="fi">
<label for="FRM_DESCRIPTIONS">Descriptions:</label>
<select name="DESCRIPTIONS" id="FRM_DESCRIPTIONS" class="reset" defVal="100">
<option value="0"      >0</option>
<option value="10"     >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"    >100</option>
<option value="250"    >250</option>
<option value="500"    >500</option>
<option value="1000"   >1000</option>
<option value="5000"   >5000</option>
<option value="10000"  >10000</option>
<option value="20000"  >20000</option>
</select>

<label for="FRM_NUM_OVERVIEW">Graphical overview:</label>
<select name="NUM_OVERVIEW" id="FRM_NUM_OVERVIEW" class="reset" defVal="100">
<option value="0"      >0</option>
<option value="10"     >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"    >100</option>
<option value="250"    >250</option>
<option value="500"   >500</option>
<option value="1000"  >1000</option>
</select>
<span id="frmAln">
<label for="FRM_ALIGNMENTS">Alignments:</label>
<select name="ALIGNMENTS" id="FRM_ALIGNMENTS" class="reset" defVal="100">
```

BLAST INFORMATION

```html
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"    >1000</option>
<option value="5000"    >5000</option>
<option value="10000"  >10000</option>
<option value="20000"  >20000</option>
</select>
</span>
<label for="FRM_LINE_LENGTH">Line length:</label>
<select name="LINE_LENGTH" id="FRM_LINE_LENGTH" class="reset" defVal="60">
<option value="60"    selected="selected" >60</option>
<option value="90"      >90</option>
<option value="120"      >120</option>
<option value="150"       >150</option>
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit number of descriptions
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp5">
<li>Descriptions: Show short descriptions for up to the given number of  sequences.</li>
<li>Alignments:  Show alignments for up to the given number of sequences, in order of statisti
<li>Line lenghth:  Number of letters to show on one line in an alignment.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl ">
<td class="hd"></td>
<td>
<div class="">
<label for="qorganism">Organism</label>
<span class="instr">Type common name, binomial, taxid, or group name. Only 20 top taxa will be
<input name="FORMAT_ORGANISM" size="55"  type="text" id=qorganism" value="" data-jigconfig="d
<input type="checkbox" name="FORMAT_ORG_EXCLUDE"  class="oExclR cb" id="orgExcl"/>
<input type="hidden" value = "1" name="FORMAT_NUM_ORG" id="numOrg" />
<label for="orgExcl" class="right">Exclude</label>
<a href="#" title="Add organism" id="addOrg"><img border="0" src="css/images/addOrg.jpg" id="a
<div id="orgs">

</div>
<div class="fi">
```

BLAST INFORMATION

```
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by organism he
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp6">
Show only sequences from the given organism.
</p>
</div><!-- ARIA -->
</div>
</div>
</td>
</tr>

<tr class="paramSet xgl ">
<td class="hd"></td>
<td>
<div class="fi">
<label for="FORMAT_EQ_TEXT">Entrez query:</label>
<input name="FORMAT_EQ_TEXT" id="FORMAT_EQ_TEXT" size="60" type="text" value="" class="reset"
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by Entrez query
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp7">
Show only those sequences that match the given Entrez query.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#limit_result" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="EXPECT_LOW">Expect Min:</label> <input name="EXPECT_LOW" id="EXPECT_LOW" size="10"
<label for="EXPECT_HIGH">Expect Max:</label> <input name="EXPECT_HIGH" id="EXPECT_HIGH" size="1
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by expect value
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp8">
Show only sequences with expect values in the given range.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#expect_range" target=
</p>
</div><!-- ARIA -->
</div>
</td>
```

BLAST INFORMATION

```html
</tr>
<tr class="paramSet xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="PERC_IDENT_LOW">Percent Identity Min:</label> <input name="PERC_IDENT_LOW" id="PERC
<label for="PERC_IDENT_HIGH">Percent Identity Max:</label> <input name="PERC_IDENT_HIGH" id="PI
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by percent iden
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp10">
Show only sequences with percent identity values in the given range.
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="psiBlast odd paramSet xgl">
<td class="hd"><label>Format for</label></td>
<td>
<div class="fi">
<input name="RUN_PSIBLAST_FORM" id="RUN_PSIBLAST" type="checkbox" class="cb psiBlast"  />
<label class="rb psiBlast" for="RUN_PSIBLAST">PSI-BLAST</label>
<label for="I_THRESH">with inclusion threshold:</label>
<input name="I_THRESH" id="I_THRESH" size="10" type="text" value="" defVal="0.005" />
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="PSI BLAST formatting help" i
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp9">
<li>Format for PSI-BLAST: The Position-Specific Iterated BLAST (PSI-BLAST) program performs it
in which sequences found in one round of search are used to build a custom score model for the
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#psiblast" target="he
</li>
<li>Inclusion Threshold: This sets the statistical significance threshold for including a seque
by PSI-BLAST to create the PSSM on the next iteration.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>
</table>



<input name="ViewReport" value="ViewReport" type="hidden" />
<input name="REFORMAT_REPORT" value="shown" type="hidden" />
<input name="RID" value="P7X5BEZP015" type="hidden" />
<input name="CDD_RID" value="" type="hidden" />
```

BLAST INFORMATION

```html
<input name="CDD_SEARCH_STATE" type="hidden" value="" />


<input name="STEP_NUMBER" value="" id="stepNumber" type="hidden" />
<input name="CMD" value="Get" type="hidden" />
<input name="FORMAT_EQ_OP" value="AND" type="hidden" />
<input name="RESULTS_PAGE_TARGET" type="hidden" id="resPageTarget" value="" />
<!-- <input name="QUERY_INFO" type="hidden" value="" /> -->
<!-- <input name="ENTREZ_QUERY" type="hidden" value="" /> -->
<input name="QUERY_INDEX" type="hidden" value="0"/>
<input name="NUM_QUERIES" type="hidden" value="1"/>


<!-- Those params are set in the template (blastn.dat, blastp.dat etc. -->
<input name="BLAST_PROGRAMS" type="hidden" value="blastn"/>
<input name="PAGE" type="hidden" value="Nucleotides"/>
<input name="PROGRAM" type="hidden" value="blastn"/>
<input name="MEGABLAST" type="hidden" value="" />
<input name="RUN_PSIBLAST" type="hidden" value="" />
<input name="BLAST_SPEC" id="blastSpec" type="hidden" value=""/>


<input name="QUERY" type="hidden" value="GCGCTTTGAGGATCCAACAC"/>
<input name="JOB_TITLE" type="hidden" value="Nucleotide Sequence (20 letters)"/>
<input name="QUERY_TO" type="hidden" value=""/>
<input name="QUERY_FROM" type="hidden" value=""/>
<input name="SUBJECTS_FROM" type="hidden" value=""/>
<input name="SUBJECTS_TO" type="hidden" value=""/>
<input name="EQ_TEXT" type="hidden" value=""/>
<input name="ORGN" type="hidden" value=""/>
<input name="EQ_MENU" type="hidden" value=""/>
<input name="ORG_EXCLUDE" type="hidden" value=""/>
<input name="PHI_PATTERN" type="hidden" value=""/>
<input name="EXPECT" type="hidden" value="10"/>
<input name="DATABASE" type="hidden" value="nt"/>
<input name="DB_GROUP" type="hidden" value=""/>
<input name="SUBGROUP_NAME" type="hidden" value=""/>


<input name="GENETIC_CODE" type="hidden" value=""/>
<input name="WORD_SIZE" type="hidden" value="11"/>
<input name="MATCH_SCORES" type="hidden" value="2,-3"/>
<input name="MATRIX_NAME" type="hidden" value=""/>
<input name="GAPCOSTS" type="hidden" value="5 2"/>
<input name="MAX_NUM_SEQ" id="maxNumSeq" type="hidden" value="50"/>
<input name="COMPOSITION_BASED_STATISTICS" type="hidden" value=""/>
<input name="NEWWIN" type="hidden" value=""/>
<input name="SHORT_QUERY_ADJUST" type="hidden" value=""/>
<input name="FILTER" type="hidden" value="L;m;"/>
<input name="REPEATS" type="hidden" value=""/>
```

BLAST INFORMATION

```html
<input name="ID_FOR_PSSM" type="hidden" value=""/>
<input name="EXCLUDE_MODELS" type="hidden" value=""/>
<input name="EXCLUDE_SEQ_UNCULT" type="hidden" value=""/>
<input name="WP_PROTEINS" type="hidden" value=""/>
<input name="SEQ_FROM_TYPE" type="hidden" value=""/>
<input name="ENTREZ_QUERY" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET_EXCL" type="hidden" value=""/>
<input name="NUM_ORG" type="hidden" value = "1" />


<!-- PSSM -->
<input name="LCASE_MASK" type="hidden" value=""/>
<input name="TEMPLATE_TYPE" type="hidden" value=""/>
<input name="TEMPLATE_LENGTH" type="hidden" value=""/>
<input name="I_THRESH" type="hidden" value=""/>
<input name="PSI_PSEUDOCOUNT" type="hidden" value=""/>
<input name="DI_THRESH" type="hidden" id="diThresh" value=""/>
<input name="HSP_RANGE_MAX" type="hidden" value="0"/>




<input name="ADJUSTED_FOR_SHORT_QUERY" type="hidden" value=""/>
<input name="MIXED_QUERIES" type="hidden" value=""/>
<input name="MIXED_DATABASE" id="mixedDb" type="hidden" value=""/>
<input name="BUILD_NAME"  type="hidden" value=""/>
<input name="ORG_DBS"  type="hidden" value=""/>
<input name="WWW_BLAST_TYPE" type="hidden" value="newblast"/>

</form>
</div> <!-- aria -->
<div class="ui-helper-reset" aria-live="assertive" >
<form  name="FormatDownload" id="FormatDownload" class="resbox ui-ncbitoggler-slave">
<table class="options dwnl blastn ">
<tr><td class="frh" colspan=6><div class="tb">Download</div></td></tr>
<tr>
<td id="tdal">
<div class="dnHeader">Alignment</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=Text&FORMAT_OBJECT=Alignment&D
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=XML&FORMAT_OBJECT=
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=Alignment&
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=JSONSA&FORMAT_OBJECT=Alignment
<a  id="hitText" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=Text&FORMAT_OBJEC
<a  id="hitCvs" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=CSV&FORMAT_OBJECT=
<a  class="xgl" href="Blast.cgi?RID=P7X5BEZP015&FORMAT_TYPE=XML2&FORMAT_OBJECT=Alignment&CMD=G
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=XML2_S&FORMAT_OBJE
<a  class="xgl" href="Blast.cgi?RID=P7X5BEZP015&FORMAT_TYPE=JSON2&FORMAT_OBJECT=Alignment&CMD=
```

BLAST INFORMATION

```
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=JSON2_S&FORMAT_OBJI
<a  class="xgl blastn" href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=SAM_SQ&FORM
</div>
</td>
<td class="dnl xgl">
<div class="dnHeader">Search Strategies</div>
<div class="dnLinks">
<a  href="Blast.cgi?CMD=GetSaved&RECENT_RESULTS=on&RID=P7X5BEZP015&DOWNLOAD_OPTIONS=true">ASN.
</div>
</td>
<td class="dnl" id="dnPSSMPar">
<div class="dnHeader">PSSM to restart search</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X5BEZP015&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=PSSM_Score
</div>
</td>
<td>
<a class="helplink ui-ncbitoggler" data-jig="ncbitoggler" title="Download help" data-ncbitoggle
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
</td>
</tr>
</table>
<div class="ui-helper-reset" aria-live="assertive" >
<div class="helpbox ui-ncbitoggler-slave" id="hlp11">
The Download link provides BLAST output that may be used as input to another program.
This includes parseable formats such as the tabular report or XML as well as the Search Strate
More details on the parseable (XML, tabular, and ASN.1) reports can be found at
<a href="https://www.ncbi.nlm.nih.gov/books/NBK153387/" target="helpWin" >https://www.ncbi.nlm
<br/>
<p>
The following formats are offered under the Alignment section:<br/>
1). "Text". Non-HTML standard BLAST report.<br/>
2). "XML". XML report based upon the DTD at <a href="https://www.ncbi.nlm.nih.gov/data_specs/d
3). "ASN.1". Alignment written out in Abstract Syntax Notation 1.<br/>
4). "JSON Seq-align". Alignment written out in JSON.<br/>
4). "Hit Table(text)". The tabular report as text.<br/>
5). "Hit Table(csv)". The tabular report ready for import into spread-sheet programs like Excel
6). "XML2". New XML format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NE
7). "JSON". New JSON format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/N
8). "SAM". Sequence Alignment Map format.<br/>
</p>
<p>
XML2 and JSON can be downloaded either as one file per query (multiple-file) or one file for a
</p>
<p>
The following report is offered under the Search Strategy section:<br/>
1). "ASN.1" Search Strategy. A record of the parameters, query, and database used in the searc
```

BLASTN 2.6.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

RID: P7X5BEZP015

Database: Nucleotide collection (nt)
43,324,577 sequences; 150,093,331,920 total letters
Query=
Length=20

Score   E
Sequences producing significant alignments: (Bits) Value

KY457840.1 Human papillomavirus type 18 strain 18CNTZ36 E6 (E... 37.4   2.6
KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E... 37.4   2.6
KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E... 37.4   2.6
KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E... 37.4   2.6
KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E... 37.4   2.6
KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E... 37.4   2.6
KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E... 37.4   2.6
KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E... 37.4   2.6
KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E... 37.4   2.6
KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E... 37.4   2.6
KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E... 37.4   2.6
KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E... 37.4   2.6

```
KY457828.1  Human papillomavirus type 18 strain 18CNTZ24 E6 (E...   37.4    2.6
KY457827.1  Human papillomavirus type 18 strain 18CNTZ23 E6 (E...   37.4    2.6
KY457826.1  Human papillomavirus type 18 strain 18CNTZ22 E6 (E...   37.4    2.6
KY457825.1  Human papillomavirus type 18 strain 18CNTZ21 E6 (E...   37.4    2.6
KY457824.1  Human papillomavirus type 18 strain 18CNTZ20 E6 (E...   37.4    2.6
KY457823.1  Human papillomavirus type 18 strain 18CNTZ19 E6 (E...   37.4    2.6
KY457822.1  Human papillomavirus type 18 strain 18CNTZ18 E6 (E...   37.4    2.6
KY457821.1  Human papillomavirus type 18 strain 18CNTZ17 E6 (E...   37.4    2.6
KY457820.1  Human papillomavirus type 18 strain 18CNTZ16 E6 (E...   37.4    2.6
KY457819.1  Human papillomavirus type 18 strain 18CNTZ15 E6 (E...   37.4    2.6
KY457818.1  Human papillomavirus type 18 strain 18CNTZ14 E6 (E...   37.4    2.6
KY457817.1  Human papillomavirus type 18 strain 18CNTZ13 E6 (E...   37.4    2.6
KY457816.1  Human papillomavirus type 18 strain 18CNTZ12 E6 (E...   37.4    2.6
KY457815.1  Human papillomavirus type 18 strain 18CNTZ11 E6 (E...   37.4    2.6
KY457814.1  Human papillomavirus type 18 strain 18CNTZ10 E6 (E...   37.4    2.6
KY457813.1  Human papillomavirus type 18 strain 18CNTZ09 E6 (E...   37.4    2.6
KY457812.1  Human papillomavirus type 18 strain 18CNTZ08 E6 (E...   37.4    2.6
KY457811.1  Human papillomavirus type 18 strain 18CNTZ07 E6 (E...   37.4    2.6
KY457810.1  Human papillomavirus type 18 strain 18CNTZ06 E6 (E...   37.4    2.6
KY457809.1  Human papillomavirus type 18 strain 18CNTZ05 E6 (E...   37.4    2.6
KY457808.1  Human papillomavirus type 18 strain 18CNTZ04 E6 (E...   37.4    2.6
KY457807.1  Human papillomavirus type 18 strain 18CNTZ03 E6 (E...   37.4    2.6
KY457806.1  Human papillomavirus type 18 strain 18CNTZ02 E6 (E...   37.4    2.6
KY457805.1  Human papillomavirus type 18 strain 18CNTZ01 E6 (E...   37.4    2.6
KX514433.1  Human papillomavirus type 18 isolate pam9, complet...   37.4    2.6
KY502096.1  Human papillomavirus isolate HPV18 P2-50 transform...   37.4    2.6
KY502095.1  Human papillomavirus isolate HPV18 P2-40 transform...   37.4    2.6
KY502094.1  Human papillomavirus isolate HPV18 P2-30 transform...   37.4    2.6
KY502093.1  Human papillomavirus isolate HPV18 P2-20 transform...   37.4    2.6
KY502092.1  Human papillomavirus isolate HPV18 P2-10 transform...   37.4    2.6
KY502091.1  Human papillomavirus isolate HPV18 P2 transforming...   37.4    2.6
KY502090.1  Human papillomavirus isolate HPV18 P1-50 transform...   37.4    2.6
KY502089.1  Human papillomavirus isolate HPV18 P1-40 transform...   37.4    2.6
KY502088.1  Human papillomavirus isolate HPV18 P1-30 transform...   37.4    2.6
KY502086.1  Human papillomavirus isolate HPV18 P1-10 transform...   37.4    2.6
KY502085.1  Human papillomavirus isolate HPV18 P1 transforming...   37.4    2.6
KX545359.1  Human papillomavirus type 18 isolate NGSk274-18 E6...   37.4    2.6
KX545354.1  Human papillomavirus type 18 isolate NGSk256-18 E6...   37.4    2.6


ALIGNMENTS
>KY457840.1 Human papillomavirus type 18 strain 18CNTZ36 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502


Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus
```

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

BLAST INFORMATION

Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||

BLAST INFORMATION

```
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
```

BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

           ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457828.1 Human papillomavirus type 18 strain 18CNTZ24 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

           ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457827.1 Human papillomavirus type 18 strain 18CNTZ23 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

           ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457826.1 Human papillomavirus type 18 strain 18CNTZ22 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

           ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

BLAST INFORMATION

>KY457825.1 Human papillomavirus type 18 strain 18CNTZ21 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457824.1 Human papillomavirus type 18 strain 18CNTZ20 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457823.1 Human papillomavirus type 18 strain 18CNTZ19 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457822.1 Human papillomavirus type 18 strain 18CNTZ18 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query  1    GCGCTTTGAGGATCCAACAC  20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC  25
```

>KY457821.1 Human papillomavirus type 18 strain 18CNTZ17 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC  20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC  25
```

>KY457820.1 Human papillomavirus type 18 strain 18CNTZ16 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC  20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC  25
```

>KY457819.1 Human papillomavirus type 18 strain 18CNTZ15 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC  20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC  25
```

>KY457818.1 Human papillomavirus type 18 strain 18CNTZ14 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457817.1 Human papillomavirus type 18 strain 18CNTZ13 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457816.1 Human papillomavirus type 18 strain 18CNTZ12 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457815.1 Human papillomavirus type 18 strain 18CNTZ11 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KY457814.1 Human papillomavirus type 18 strain 18CNTZ10 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457813.1 Human papillomavirus type 18 strain 18CNTZ09 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457812.1 Human papillomavirus type 18 strain 18CNTZ08 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY457811.1 Human papillomavirus type 18 strain 18CNTZ07 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)

BLAST INFORMATION

Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457810.1 Human papillomavirus type 18 strain 18CNTZ06 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457809.1 Human papillomavirus type 18 strain 18CNTZ05 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457808.1 Human papillomavirus type 18 strain 18CNTZ04 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCGCTTTGAGGATCCAACAC   20
            ||||||||||||||||||||
Sbjct  6    GCGCTTTGAGGATCCAACAC   25
```

>KY457807.1 Human papillomavirus type 18 strain 18CNTZ03 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20

        ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY457806.1 Human papillomavirus type 18 strain 18CNTZ02 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20

        ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY457805.1 Human papillomavirus type 18 strain 18CNTZ01 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20

        ||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KX514433.1 Human papillomavirus type 18 isolate pam9, complete genome

Length=7857

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20

        ||||||||||||||||||||

Sbjct 110 GCGCTTTGAGGATCCAACAC 129

>KY502096.1 Human papillomavirus isolate HPV18 P2-50 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502095.1 Human papillomavirus isolate HPV18 P2-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502094.1 Human papillomavirus isolate HPV18 P2-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
           ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502093.1 Human papillomavirus isolate HPV18 P2-20 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6

BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY502092.1 Human papillomavirus isolate HPV18 P2-10 transforming protein
E6 (E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY502091.1 Human papillomavirus isolate HPV18 P2 transforming protein E6
(E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

>KY502090.1 Human papillomavirus isolate HPV18 P1-50 transforming protein
E6 (E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC   20

||||||||||||||||||||

Sbjct 6   GCGCTTTGAGGATCCAACAC   25

BLAST INFORMATION

>KY502089.1 Human papillomavirus isolate HPV18 P1-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502088.1 Human papillomavirus isolate HPV18 P1-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502086.1 Human papillomavirus isolate HPV18 P1-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCGCTTTGAGGATCCAACAC 20
            ||||||||||||||||||||
Sbjct 6   GCGCTTTGAGGATCCAACAC 25

>KY502085.1 Human papillomavirus isolate HPV18 P1 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KX545359.1 Human papillomavirus type 18 isolate NGSk274-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=516

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

>KX545354.1 Human papillomavirus type 18 isolate NGSk256-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=579

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   GCGCTTTGAGGATCCAACAC  20
           ||||||||||||||||||||
Sbjct  6   GCGCTTTGAGGATCCAACAC  25
```

Database: Nucleotide collection (nt)
Posted date: Jul 8, 2017 5:09 AM
Number of letters in database: 150,093,331,920
Number of sequences in database: 43,324,577

Lambda   K   H
0.634   0.408   0.912
Gapped
Lambda   K   H
0.625   0.410   0.780
Matrix: blastn matrix:2 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 43324577
Number of Hits to DB: 805788
Number of extensions: 268
Number of successful extensions: 268

BLAST INFORMATION

Number of sequences better than 10: 30

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 268

Number of HSP's successfully gapped: 30

Length of query: 20

Length of database: 150093331920

Length adjustment: 17

Effective length of query: 3

Effective length of database: 149356814111

Effective search space: 448070442333

Effective search space used: 448070442333

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 28 (26.5 bits)

S2: 38 (35.6 bits)

```
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</div><!-- /#content -->
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<input name="QUERY_INFO" type="hidden" value="" />
<input name="ENTREZ_QUERY" type="hidden" value="" />
<input name="CDD_RID" type="hidden" value="" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />
<input name="RID" type="hidden" value="P7X5BEZP015" />
<input name="STEP_NUMBER" type="hidden" value="" />
<input name="CMD" type="hidden" value="Web"/>
<input NAME="PAGE_TYPE" type="hidden"  value="BlastFormatting"/>

<!-- TO DO: test all of those changes -->
<!-- Psi blast params  PSI_BLAST_PARAMS - commented- using forms[0] from fromatter> -->
<!-- Current Formatting options FORMATTING_OPTIONS- commented- using forms[0] from fromatter> 
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="setSa
<input name="PAGE_TYPE" type="hidden" value="BlastSearch" />
<input name="VIEW_SEARCH" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="Web" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="save
<input name="SAVE" type="hidden" value="true"/>
```

BLAST INFORMATION

```html
<input name="CMD" type="hidden" value="GetSaved" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from formatter> -->
</form>
</div><!-- /#content-wrap -->


<footer id="page_footer">
<div class="foot_wrap">
<div class="left col two_col">
BLAST is a registered trademark of the National Library of Medicine
</div>
<div class="right">
<a class="help_desk jig-ncbihelpwindow" target="_blank" href="https://support.ncbi.nlm.nih.gov
Ncbi_App=blast&amp;Page=oldblastresults&Time=2017-07-10T17:43:09&amp;Host=blast359&amp;ncbi_ph
</a>
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=MailList">Mailing list</a>
<a href="https://www.youtube.com/ncbinlm" target="_blank" id="page_footer_54">
<img class="icon-medium gray-medium" src="images/youtube.svg" alt="">
<span class="icon-fallback-text">YouTube</span>
</a>
</div>


</div>


<!-- bottom section of footer -->
<div class="col" id="contentinfo">
<ul class="right inline_list logos">
<li>
<a href="https://www.nlm.nih.gov" id="page_footer_60">
<img class="gray-medium" src="images/nlm-logo.svg" alt="">
<span class="icon-fallback-text">National Library Of Medicine</span>
</a>
</li>
<li>
<a href="https://www.nih.gov" id="page_footer_61">
<img class="gray-medium" src="images/nih-logo.svg" alt="">
<span class="icon-fallback-text">National Institutes Of Health</span>
</a>
</li>
<li>
<a href="https://www.hhs.gov" id="page_footer_62">
<img class="gray-medium" src="images/hhs-logo.svg" alt="">
<span class="icon-fallback-text">U.S. Department of Health &amp; Human Services</span>
</a>
</li>
<li>
<a href="https://www.usa.gov" id="page_footer_63">
<img class="icon-large-wide gray-medium" src="images/usagov-logo.svg" alt="">
```

BLAST INFORMATION

```html
<span class="icon-fallback-text">USA.gov</span>
</a>
</li>
</ul>

<div class="footer_padding">

<div class="footer_border h-card">

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url" id="page_footer_64">
<h3 role="heading" aria-level="3" class="ncbi_blue p-org">NCBI</h3>
</a>

<address>

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url p-org" id="page_footer_65">National Center
<a href="https://www.nlm.nih.gov/" id="page_footer_66"> U.S. National Library of Medicine</a>

<span class="h-adr">
<span class="p-street-address">8600 Rockville Pike</span>,
<span class="p-locality">Bethesda</span>
<span class="p-region"> MD</span>,
<span class="p-postal-code">20894</span>
<span class="p-country-name">USA</span>
</span>

</address>

</div>
<div class="inline_list about_list">
<a href="https://www.ncbi.nlm.nih.gov/home/about/policies.shtml" id="page_footer_67">Policies
|
<a href="https://www.ncbi.nlm.nih.gov/home/about/contact.shtml" id="page_footer_68">Contact</a
</div>
</div>
</div>
</footer>
<script type="text/javascript" src="js/header.js"> </script>
</div><!--/#wrap-->

<script type="text/javascript" src="js/utils.js"></script>
<script type="text/javascript" src="js/toggle.js"></script>
<script type="text/javascript" src="js/remote_data_provider.js"></script>
<script type="text/javascript" src="js/results.js"></script>
<script type="text/javascript" src="js/blast.js"></script>
<script type="text/javascript" src="js/format.js"></script>
```

BLAST INFORMATION

```
<script type="text/javascript" src="/portal/portal3rc.fcgi/rlib/js/InstrumentOmnitureBaseJS/In
<!--
<script type="text/javascript" src="://www.ncbi.nlm.nih.gov/portal/portal3rc.fcgi/supportedbrow
<script type="text/javascript">$("#browsers_ajax").browserCheck();</script>
-->
</body>
</html>


<!DOCTYPE html PUBLIC "-//W3C//DTD XHTML 1.0 Transitional//EN" "http://www.w3.org/TR/xhtml1/DT
<html xmlns="http://www.w3.org/1999/xhtml">
<head>

<meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
<meta http-equiv="X-UA-Compatible" content="IE=edge,chrome=1">
<meta name="jig" content="ncbitoggler ncbiautocomplete"/>
<meta name="ncbitoggler" content="animation:'none'"/>



<meta name="referrer" content="origin-when-cross-origin" />
<meta name="ncbi_app" content="blast" />
<meta name="ncbi_pdid" content="oldblastresults" />

<meta name="ncbi_db" content="nt" />
<meta name="ncbi_program" content="blastn" />
<meta name="ncbi_algorithm" content="blastn" />


<meta name="ncbi_stat" content="false" />
<meta name="ncbi_sessionid" content="55BA4691963F51A1_0000SID" />
<meta name="ncbi_phid" content="55BA4691963F51A10000000000000001" />
<script type="text/javascript"> var ncbi_startTime = new Date(); </script>
<title>NCBI Blast:Nucleotide Sequence (20 letters)</title>
<script type="text/javascript" src="/core/jig/1.14.8/js/jig.min.js          "></script>
<script type="text/javascript">    jQuery.getScript("/core/alerts/alerts.js", function() {
                                galert(['div#header', 'body > *:nth-child(1)'])
});</script>
<link rel="stylesheet" type="text/css" href="css/header.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/google-fonts.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/footer.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/main.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/blastRes.css" media="screen" />
<!--[if IE]>
<link rel="stylesheet" type="text/css" href="css/descriptionsIE.css" media="screen" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/print.css" media="print" />
<!--[if lte IE 6]>
<link rel="stylesheet" type="text/css" href="css/ie6_or_less.css" />
<![endif]-->
```

BLAST INFORMATION

```html
<link rel="stylesheet" type="text/css" href="css/blastReq.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/results.css" media="screen" />


</head>

<body id="type-a" class="noToggleCheck " >
<div id="wrap">

<header id="page_header" role="banner">
<ul class="skip_nav">
<li><a accesskey="1" title="NCBI Homepage" href="https://www.ncbi.nlm.nih.gov/">NCBI Home</a><
<li><a accesskey="2" title="MyNCBI" href="https://www.ncbi.nlm.nih.gov/myncbi">Sign in to NCBI
<li><a accesskey="3" title="Skip to main content" href="#content">Skip to Main Content</a></li
<li><a accesskey="4" title="Skip to navigation" href="#navcontent">Skip to Navigation</a></li
<li><a accesskey="0" title="About NCBI Accesskeys" href="https://www.ncbi.nlm.nih.gov/guide/br
</ul>
<nav class="blue_nav_bar">
<div class="nih">
<a id="page_header_6" href="https://www.nih.gov/" class="left norm_height">
<img src="images/nih_logo.svg" alt="NIH logo" class="left"/></a>
<a id="page_header_7" href="https://www.nlm.nih.gov/" class="left header_link">U.S. National L
</div>

<div class="left">
<img src="images/arrow.svg" class="left norm_height" alt=""/>
</div>



<div class="ncbi">
<a id="page_header_8" href="https://www.ncbi.nlm.nih.gov/" class="header_link">
<span class="ncbi_name">NCBI</span>
<span class="med_hidden">National Center for Biotechnology Information</span></a>

<div class="right sign-in">
<ul class="myncbi2">
<li id="myncbiusername">
<span id="mnu">
<a id="mnu_0" href="https://www.ncbi.nlm.nih.gov/account/settings/" title="Edit account setting
</span>
</li>
<li id="myncbi"><a id="myncbi_0"  href="https://www.ncbi.nlm.nih.gov/myncbi/">My NCBI</a></li>
<li id="myncbi_sign_in"><a id="myncbi_sign_in_0" href="https://www.ncbi.nlm.nih.gov/account/?ba
<li id="myncbi_register"><a id="myncbi_register_0" href="https://www.ncbi.nlm.nih.gov/account/
<li id="myncbi_sign_out"><a id="myncbi_sign_out_0" href="https://www.ncbi.nlm.nih.gov/account/
</ul>
</div>
```

BLAST INFORMATION

```
</div>
</nav>

<div class="bg-gray header-div">
<nav class="top-nav" id="navcontent" role="navigation">
<a class="lf" href="Blast.cgi">BLAST <sup>&reg;</sup></a> <span id="brc"><span class="brcrmbsig
<span class="rf">
<ul id="blnav">
<li  class="first "><a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastHome" title="BLAST Home">Home
<li  class="recent "><a href="Blast.cgi?CMD=GetSaved&amp;RECENT_RESULTS=on" title="Unexpired Bl
<li  class="saved "><a href="Blast.cgi?CMD=GetSaved" title="Saved sets of BLAST search paramete
<li  class= "last documentation "> <a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs" title="I
</ul>
</span>
</nav>
</div>
</header>

<div id="content-wrap">

<div class="pageTitle">
BLAST Results
</div>
<div class="inlineDiv resHeader resPage">

</div>
<ul class="print-log-res"><li></li></ul>

<!-- CDD info for old design -->




<div id="content">

<!--<ul id="msg" class="msg"><li class=""><p class=""></p><p class=""></p><p class=""></p></li
<ul id="msg" class="msg"><li class=""></li></ul>
<a  href="#" class="resLink resPage" id="searchOptions" submitForm="setSavedOptions">Edit and I
<a  href="#" class="resLink resPage hidden" id="saveSearchOptions" submitForm="saveOptions">Sav
<span class="reslink  resPage" >[Sign in above to save your search strategy]</span>
<a  id="showFormat" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggler
<span class="ui-ncbitoggler-master-text">Formatting options </span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
```

BLAST INFORMATION
```
</a>
<a  id="showDownload" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggle
<span class="ui-ncbitoggler-master-text">Download</span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<span id="hnr">
<a id="ytb" class="ytb " title="External link to YouTube" href="https://www.youtube.com/playli
<a id="brFtp" class="" title="Blast report description" href="ftp://ftp.ncbi.nlm.nih.gov/pub/fa
</span>
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST" id="results

<input name="QUERY_INDEX" type="hidden" value="0">
<input name="_PGR" type="hidden" value="" >
<input id="seqViewUrl" type="hidden" value="https://www.ncbi.nlm.nih.gov" >
<input id="userAgent" type="hidden" value="">
<input name="CMD" type="hidden" value="Get">
</form>
<!-- Reformat and downlaod for new design -->
<div class="ui-helper-reset" aria-live="assertive" >
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="Format
<table class="options blastn ">
<tr>
<td class="frh" colspan=2>
<div class="fi">
<div class="tb">Formatting options</div>
<input type="image"  border="0" id="onPageReformat" src="css/images/reformat.jpg" class="blastb
</div>
</tr>
<tr class="paramSet xgl">
<td class="hd"><label for="FORMAT_OBJECT">Show</label></td>
<td>
<div class="fi">
<input type="hidden" id="FORMAT_OBJECT" value="Alignment" name="FORMAT_OBJECT" />
<label for="FORMAT_TYPE" id="nft">Alignment as</label>
<select name="FORMAT_TYPE" id="FORMAT_TYPE" class="reset" defVal="HTML">
<option value="HTML"  >HTML</option>
<option value="Text"  >Plain text</option>

</select>

<span id="advView" class="">
<span class=""><input name="OLD_VIEW" id="OLD_VIEW" type="checkbox" class="cb reset" defVal="un
<label for="OLD_VIEW">Old View</label></span>
</span>
<a class="resetAll" id="resetAll" >Reset form to defaults</a>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments object formatting
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
```

BLAST INFORMATION

```
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp1">
These options control formatting of alignments in results pages. The
default is HTML, but other formats (including plain text) are available.
PSSM and PssmWithParameters are representations of Position Specific Scoring Matrices and are
The Advanced view option allows the database descriptions to be sorted by various indices in a
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="odd paramSet">
<td class="hd"><label for="ALIGNMENT_VIEW">Alignment View</label></td>
<td>
<div class="fi">
<select name="ALIGNMENT_VIEW" id="ALIGNMENT_VIEW" defVal="Pairwise" class="reset">
<option value="Pairwise" selected="selected" >Pairwise</option>
<option value="PairwiseWithIdentities"  >Pairwise with dots for identities</option>
<option value="QueryAnchored"  >Query-anchored with dots for identities</option>
<option value="QueryAnchoredNoIdentities"  >Query-anchored with letters for identities</option>
<option value="FlatQueryAnchored"  >Flat query-anchored with dots for identities</option>
<option value="FlatQueryAnchoredNoIdentities"  >Flat query-anchored with letters for identitie

</select>


<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments view options help
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp2">
Choose how to view alignments.
The default "pairwise" view shows how each subject sequence aligns
individually to the query sequence. The "query-anchored" view shows how
all subject sequences align to the query sequence. For each view type,
you can choose to show "identities" (matching residues) as letters or
dots.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#alignment_view" targe
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet">
<td class="hd"><label>Display</label></td>
<td class="cb">
```

BLAST INFORMATION

```
<div class="fi">
<input name="SHOW_OVERVIEW" id="SHOW_OVERVIEW" type="checkbox" class="cb reset" defVal="checked
<label class="rb" for="SHOW_OVERVIEW">Graphical Overview</label>

<span id="shl" >
<input name="SHOW_LINKOUT" id="SHOW_LINKOUT" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="SHOW_LINKOUT">Linkout</label>
</span>
<span id="gts" >
<input name="GET_SEQUENCE" id="GET_SEQUENCE" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="GET_SEQUENCE">Sequence Retrieval</label>
</span>

<input name="NCBI_GI" id="NCBI_GI" type="checkbox" class="cb reset" defVal="unchecked" false /
<label class="rb" for="NCBI_GI">NCBI-gi</label>
<span id="scf" >
<input name="SHOW_CDS_FEATURE" id="SHOW_CDS_FEATURE" type="checkbox" class="cb reset blastn" d
<label for="SHOW_CDS_FEATURE" class="blastn">CDS feature</label>
</span>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments display options h
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp3">
<li>Graphical Overview: Graphical Overview: Show graph of similar sequence regions aligned to
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_overview" targe
</li>
<li>NCBI-gi: Show NCBI gi identifiers.
</li>
<li>CDS feature: Show annotated coding region and translation.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_cds_feature" ti
</li></ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"><label>Masking</label></td>
<td>
<div class="fi">
<label for="MASK_CHAR"> Character: </label>
<select name="MASK_CHAR" id="MASK_CHAR"  class="reset" defVal="2">
<option value="0"  >X for protein, n for nucleotide</option>
<option value="2" selected="selected" >Lower Case</option>
</select>
<label for="MASK_COLOR"> Color:</label>
```

```
<select name="MASK_COLOR" id="MASK_COLOR" class="reset" defVal="1">
<option value="0"  >Black
</option>

<option value="1" selected="selected" >Grey
</option>

<option value="2"  >Red
</option>

</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments masking help" id=
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp4">
<li>Masking Character: Display masked (filtered) sequence regions as lower-case or as specific
</li>
<li>Masking Color: Display masked sequence regions in the given color.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr id="lr" class="paramSet xgl">
<td class="hd"><label>Limit results</label></td>
<td>
<div class="fi">
<label for="FRM_DESCRIPTIONS">Descriptions:</label>
<select name="DESCRIPTIONS" id="FRM_DESCRIPTIONS" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"    >1000</option>
<option value="5000"    >5000</option>
<option value="10000"  >10000</option>
<option value="20000"  >20000</option>
</select>

<label for="FRM_NUM_OVERVIEW">Graphical overview:</label>
<select name="NUM_OVERVIEW" id="FRM_NUM_OVERVIEW" class="reset" defVal="100">
<option value="0"      >0</option>
<option value="10"     >10</option>
```

```
<option value="50"   selected="selected" >50</option>
<option value="100"    >100</option>
<option value="250"    >250</option>
<option value="500"   >500</option>
<option value="1000"  >1000</option>
</select>
<span id="frmAln">
<label for="FRM_ALIGNMENTS">Alignments:</label>
<select name="ALIGNMENTS" id="FRM_ALIGNMENTS" class="reset" defVal="100">
<option value="0"      >0</option>
<option value="10"      >10</option>
<option value="50"     selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"   >1000</option>
<option value="5000"    >5000</option>
<option value="10000"  >10000</option>
<option value="20000"   >20000</option>
</select>
</span>
<label for="FRM_LINE_LENGTH">Line length:</label>
<select name="LINE_LENGTH" id="FRM_LINE_LENGTH" class="reset" defVal="60">
<option value="60"     selected="selected" >60</option>
<option value="90"      >90</option>
<option value="120"      >120</option>
<option value="150"       >150</option>
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit number of descriptions
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp5">
<li>Descriptions: Show short descriptions for up to the given number of  sequences.</li>
<li>Alignments:  Show alignments for up to the given number of sequences, in order of statistic
<li>Line lenghth:  Number of letters to show on one line in an alignment.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl ">
<td class="hd"></td>
<td>
<div class="">
<label for="qorganism">Organism</label>
<span class="instr">Type common name, binomial, taxid, or group name. Only 20 top taxa will be
```

BLAST INFORMATION

```
<input name="FORMAT_ORGANISM" size="55"  type="text" id="qorganism" value="" data-jigconfig="d
<input type="checkbox" name="FORMAT_ORG_EXCLUDE"   class="oExclR cb" id="orgExcl"/>
<input type="hidden" value = "1" name="FORMAT_NUM_ORG" id="numOrg" />
<label for="orgExcl" class="right">Exclude</label>
<a href="#" title="Add organism" id="addOrg"><img border="0" src="css/images/addOrg.jpg" id="ac
<div id="orgs">

</div>
<div class="fi">
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by organism hel
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp6">
Show only sequences from the given organism.
</p>
</div><!-- ARIA -->
</div>
</div>
</td>
</tr>


<tr class="paramSet xgl ">
<td class="hd"></td>
<td>
<div class="fi">
<label for="FORMAT_EQ_TEXT">Entrez query:</label>
<input name="FORMAT_EQ_TEXT" id="FORMAT_EQ_TEXT" size="60" type="text" value="" class="reset"
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by Entrez query
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp7">
Show only those sequences that match the given Entrez query.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#limit_result" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="EXPECT_LOW">Expect Min:</label> <input name="EXPECT_LOW" id="EXPECT_LOW" size="10"
<label for="EXPECT_HIGH">Expect Max:</label> <input name="EXPECT_HIGH" id="EXPECT_HIGH" size="1
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by expect value
```

BLAST INFORMATION

```
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp8">
Show only sequences with expect values in the given range.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#expect_range" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="paramSet xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="PERC_IDENT_LOW">Percent Identity Min:</label> <input name="PERC_IDENT_LOW" id="PERC
<label for="PERC_IDENT_HIGH">Percent Identity Max:</label> <input name="PERC_IDENT_HIGH" id="PI
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by percent ider
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp10">
Show only sequences with percent identity values in the given range.
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="psiBlast odd paramSet xgl">
<td class="hd"><label>Format for</label></td>
<td>
<div class="fi">
<input name="RUN_PSIBLAST_FORM" id="RUN_PSIBLAST" type="checkbox" class="cb psiBlast"  />
<label class="rb psiBlast" for="RUN_PSIBLAST">PSI-BLAST</label>
<label for="I_THRESH">with inclusion threshold:</label>
<input name="I_THRESH" id="I_THRESH" size="10" type="text" value="" defVal="0.005" />
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="PSI BLAST formatting help" id
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp9">
<li>Format for PSI-BLAST: The Position-Specific Iterated BLAST (PSI-BLAST) program performs ite
in which sequences found in one round of search are used to build a custom score model for the
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#psiblast" target="hel
</li>
<li>Inclusion Threshold: This sets the statistical significance threshold for including a seque
by PSI-BLAST to create the PSSM on the next iteration.</li>
</ul>
</div><!-- ARIA -->
</div>
```

BLAST INFORMATION
```
</td>
</tr>
</table>


<input name="ViewReport" value="ViewReport" type="hidden" />
<input name="REFORMAT_REPORT" value="shown" type="hidden" />
<input name="RID" value="P7X7F2GR014" type="hidden" />
<input name="CDD_RID" value="" type="hidden" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />

<input name="STEP_NUMBER" value="" id="stepNumber" type="hidden" />
<input name="CMD" value="Get" type="hidden" />
<input name="FORMAT_EQ_OP" value="AND" type="hidden" />
<input name="RESULTS_PAGE_TARGET" type="hidden" id="resPageTarget" value="" />
<!-- <input name="QUERY_INFO" type="hidden" value="" /> -->
<!-- <input name="ENTREZ_QUERY" type="hidden" value="" /> -->
<input name="QUERY_INDEX" type="hidden" value="0"/>
<input name="NUM_QUERIES" type="hidden" value="1"/>

<!-- Those params are set in the template (blastn.dat, blastp.dat etc. -->
<input name="BLAST_PROGRAMS" type="hidden" value="blastn"/>
<input name="PAGE" type="hidden" value="Nucleotides"/>
<input name="PROGRAM" type="hidden" value="blastn"/>
<input name="MEGABLAST" type="hidden" value="" />
<input name="RUN_PSIBLAST" type="hidden" value="" />
<input name="BLAST_SPEC" id="blastSpec" type="hidden" value=""/>


<input name="QUERY" type="hidden" value="CGCTTTGAGGATCCAACACG"/>
<input name="JOB_TITLE" type="hidden" value="Nucleotide Sequence (20 letters)"/>
<input name="QUERY_TO" type="hidden" value=""/>
<input name="QUERY_FROM" type="hidden" value=""/>
<input name="SUBJECTS_FROM" type="hidden" value=""/>
<input name="SUBJECTS_TO" type="hidden" value=""/>
<input name="EQ_TEXT" type="hidden" value=""/>
<input name="ORGN" type="hidden" value=""/>
<input name="EQ_MENU" type="hidden" value=""/>
<input name="ORG_EXCLUDE" type="hidden" value=""/>
<input name="PHI_PATTERN" type="hidden" value=""/>
<input name="EXPECT" type="hidden" value="10"/>
<input name="DATABASE" type="hidden" value="nt"/>
<input name="DB_GROUP" type="hidden" value=""/>
<input name="SUBGROUP_NAME" type="hidden" value=""/>

<input name="GENETIC_CODE" type="hidden" value=""/>
<input name="WORD_SIZE" type="hidden" value="11"/>
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BLAST INFORMATION

```
<input name="MATCH_SCORES" type="hidden" value="2,-3"/>
<input name="MATRIX_NAME" type="hidden" value=""/>
<input name="GAPCOSTS" type="hidden" value="5 2"/>
<input name="MAX_NUM_SEQ" id="maxNumSeq" type="hidden" value="50"/>
<input name="COMPOSITION_BASED_STATISTICS" type="hidden" value=""/>
<input name="NEWWIN" type="hidden" value=""/>
<input name="SHORT_QUERY_ADJUST" type="hidden" value=""/>
<input name="FILTER" type="hidden" value="L;m;"/>
<input name="REPEATS" type="hidden" value=""/>
<input name="ID_FOR_PSSM" type="hidden" value=""/>
<input name="EXCLUDE_MODELS" type="hidden" value=""/>
<input name="EXCLUDE_SEQ_UNCULT" type="hidden" value=""/>
<input name="WP_PROTEINS" type="hidden" value=""/>
<input name="SEQ_FROM_TYPE" type="hidden" value=""/>
<input name="ENTREZ_QUERY" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET_EXCL" type="hidden" value=""/>
<input name="NUM_ORG" type="hidden" value = "1" />


<!-- PSSM -->
<input name="LCASE_MASK" type="hidden" value=""/>
<input name="TEMPLATE_TYPE" type="hidden" value=""/>
<input name="TEMPLATE_LENGTH" type="hidden" value=""/>
<input name="I_THRESH" type="hidden" value=""/>
<input name="PSI_PSEUDOCOUNT" type="hidden" value=""/>
<input name="DI_THRESH" type="hidden" id="diThresh" value=""/>
<input name="HSP_RANGE_MAX" type="hidden" value="0"/>




<input name="ADJUSTED_FOR_SHORT_QUERY" type="hidden" value=""/>
<input name="MIXED_QUERIES" type="hidden" value=""/>
<input name="MIXED_DATABASE" id="mixedDb" type="hidden" value=""/>
<input name="BUILD_NAME"  type="hidden" value=""/>
<input name="ORG_DBS"  type="hidden" value=""/>
<input name="WWW_BLAST_TYPE" type="hidden" value="newblast"/>

</form>
</div> <!-- aria -->
<div class="ui-helper-reset" aria-live="assertive" >
<form  name="FormatDownload" id="FormatDownload" class="resbox ui-ncbitoggler-slave">
<table class="options dwnl blastn ">
<tr><td class="frh" colspan=6><div class="tb">Download</div></td></tr>
<tr>
<td id="tdal">
<div class="dnHeader">Alignment</div>
<div class="dnLinks">
```

BLAST INFORMATION

```
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=Text&FORMAT_OBJECT=Alignment&DI
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=XML&FORMAT_OBJECT=A
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=Alignment&Q
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=JSONSA&FORMAT_OBJECT=Alignment&
<a  id="hitText" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=Text&FORMAT_OBJECT
<a  id="hitCvs" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=CSV&FORMAT_OBJECT=A
<a  class="xgl" href="Blast.cgi?RID=P7X7F2GR014&FORMAT_TYPE=XML2&FORMAT_OBJECT=Alignment&CMD=Ge
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=XML2_S&FORMAT_OBJEC
<a  class="xgl" href="Blast.cgi?RID=P7X7F2GR014&FORMAT_TYPE=JSON2&FORMAT_OBJECT=Alignment&CMD=G
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=JSON2_S&FORMAT_OBJ
<a  class="xgl blastn" href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=SAM_SQ&FORM
</div>
</td>
<td class="dnl xgl">
<div class="dnHeader">Search Strategies</div>
<div class="dnLinks">
<a  href="Blast.cgi?CMD=GetSaved&RECENT_RESULTS=on&RID=P7X7F2GR014&DOWNLOAD_OPTIONS=true">ASN.
</div>
</td>
<td class="dnl" id="dnPSSMPar">
<div class="dnHeader">PSSM to restart search</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X7F2GR014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=PSSM_Scorer
</div>
</td>
<td>
<a class="helplink ui-ncbitoggler" data-jig="ncbitoggler" title="Download help" data-ncbitoggle
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
</td>
</tr>
</table>
<div class="ui-helper-reset" aria-live="assertive" >
<div class="helpbox ui-ncbitoggler-slave" id="hlp11">
The Download link provides BLAST output that may be used as input to another program.
This includes parseable formats such as the tabular report or XML as well as the Search Strateg
More details on the parseable (XML, tabular, and ASN.1) reports can be found at
<a href="https://www.ncbi.nlm.nih.gov/books/NBK153387/" target="helpWin" >https://www.ncbi.nlm
<br/>
<p>
The following formats are offered under the Alignment section:<br/>
1). "Text". Non-HTML standard BLAST report.<br/>
2). "XML". XML report based upon the DTD at <a href="https://www.ncbi.nlm.nih.gov/data_specs/dt
3). "ASN.1". Alignment written out in Abstract Syntax Notation 1.<br/>
4). "JSON Seq-align". Alignment written out in JSON.<br/>
4). "Hit Table(text)". The tabular report as text.<br/>
5). "Hit Table(csv)". The tabular report ready for import into spread-sheet programs like Excel
6). "XML2". New XML format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NEW
```

BLAST INFORMATION

7). "JSON". New JSON format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/N
8). "SAM". Sequence Alignment Map format.
</p>
<p>
XML2 and JSON can be downloaded either as one file per query (multiple-file) or one file for a
</p>
<p>
The following report is offered under the Search Strategy section:
1). "ASN.1" Search Strategy. A record of the parameters, query, and database used in the search
<a href="https://www.ncbi.nlm.nih.gov/books/NBK1763/#CmdLineAppsManual.I455_BLAST_search_stra"
</p>
</div>
</div><!-- ARIA -->
</form>
</div> <!-- aria -->
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST" name="over

<input name="CMD" type="hidden" value="">
<p><!--
QBlastInfoBegin
Status=READY
QBlastInfoEnd
--><p>
<PRE>
BLASTN 2.6.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

RID: P7X7F2GR014

Database: Nucleotide collection (nt)
43,324,577 sequences; 150,093,331,920 total letters
Query=
Length=20

                                                                 Score   E
Sequences producing significant alignments: (Bits) Value

KY457840.1 Human papillomavirus type 18 strain 18CNTZ36 E6 (E... 37.4   2.6
KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E... 37.4   2.6
KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E... 37.4   2.6

BLAST INFORMATION

```
KY457837.1  Human papillomavirus type 18 strain 18CNTZ33 E6 (E...   37.4   2.6
KY457836.1  Human papillomavirus type 18 strain 18CNTZ32 E6 (E...   37.4   2.6
KY457835.1  Human papillomavirus type 18 strain 18CNTZ31 E6 (E...   37.4   2.6
KY457834.1  Human papillomavirus type 18 strain 18CNTZ30 E6 (E...   37.4   2.6
KY457833.1  Human papillomavirus type 18 strain 18CNTZ29 E6 (E...   37.4   2.6
KY457832.1  Human papillomavirus type 18 strain 18CNTZ28 E6 (E...   37.4   2.6
KY457831.1  Human papillomavirus type 18 strain 18CNTZ27 E6 (E...   37.4   2.6
KY457830.1  Human papillomavirus type 18 strain 18CNTZ26 E6 (E...   37.4   2.6
KY457829.1  Human papillomavirus type 18 strain 18CNTZ25 E6 (E...   37.4   2.6
KY457828.1  Human papillomavirus type 18 strain 18CNTZ24 E6 (E...   37.4   2.6
KY457827.1  Human papillomavirus type 18 strain 18CNTZ23 E6 (E...   37.4   2.6
KY457826.1  Human papillomavirus type 18 strain 18CNTZ22 E6 (E...   37.4   2.6
KY457825.1  Human papillomavirus type 18 strain 18CNTZ21 E6 (E...   37.4   2.6
KY457824.1  Human papillomavirus type 18 strain 18CNTZ20 E6 (E...   37.4   2.6
KY457823.1  Human papillomavirus type 18 strain 18CNTZ19 E6 (E...   37.4   2.6
KY457822.1  Human papillomavirus type 18 strain 18CNTZ18 E6 (E...   37.4   2.6
KY457821.1  Human papillomavirus type 18 strain 18CNTZ17 E6 (E...   37.4   2.6
KY457820.1  Human papillomavirus type 18 strain 18CNTZ16 E6 (E...   37.4   2.6
KY457819.1  Human papillomavirus type 18 strain 18CNTZ15 E6 (E...   37.4   2.6
KY457818.1  Human papillomavirus type 18 strain 18CNTZ14 E6 (E...   37.4   2.6
KY457817.1  Human papillomavirus type 18 strain 18CNTZ13 E6 (E...   37.4   2.6
KY457816.1  Human papillomavirus type 18 strain 18CNTZ12 E6 (E...   37.4   2.6
KY457815.1  Human papillomavirus type 18 strain 18CNTZ11 E6 (E...   37.4   2.6
KY457814.1  Human papillomavirus type 18 strain 18CNTZ10 E6 (E...   37.4   2.6
KY457813.1  Human papillomavirus type 18 strain 18CNTZ09 E6 (E...   37.4   2.6
KY457812.1  Human papillomavirus type 18 strain 18CNTZ08 E6 (E...   37.4   2.6
KY457811.1  Human papillomavirus type 18 strain 18CNTZ07 E6 (E...   37.4   2.6
KY457810.1  Human papillomavirus type 18 strain 18CNTZ06 E6 (E...   37.4   2.6
KY457809.1  Human papillomavirus type 18 strain 18CNTZ05 E6 (E...   37.4   2.6
KY457808.1  Human papillomavirus type 18 strain 18CNTZ04 E6 (E...   37.4   2.6
KY457807.1  Human papillomavirus type 18 strain 18CNTZ03 E6 (E...   37.4   2.6
KY457806.1  Human papillomavirus type 18 strain 18CNTZ02 E6 (E...   37.4   2.6
KY457805.1  Human papillomavirus type 18 strain 18CNTZ01 E6 (E...   37.4   2.6
KX514433.1  Human papillomavirus type 18 isolate pam9, complet...   37.4   2.6
KY502096.1  Human papillomavirus isolate HPV18 P2-50 transform...   37.4   2.6
KY502095.1  Human papillomavirus isolate HPV18 P2-40 transform...   37.4   2.6
KY502094.1  Human papillomavirus isolate HPV18 P2-30 transform...   37.4   2.6
KY502093.1  Human papillomavirus isolate HPV18 P2-20 transform...   37.4   2.6
KY502092.1  Human papillomavirus isolate HPV18 P2-10 transform...   37.4   2.6
KY502091.1  Human papillomavirus isolate HPV18 P2 transforming...   37.4   2.6
KY502090.1  Human papillomavirus isolate HPV18 P1-50 transform...   37.4   2.6
KY502089.1  Human papillomavirus isolate HPV18 P1-40 transform...   37.4   2.6
KY502088.1  Human papillomavirus isolate HPV18 P1-30 transform...   37.4   2.6
KY502086.1  Human papillomavirus isolate HPV18 P1-10 transform...   37.4   2.6
KY502085.1  Human papillomavirus isolate HPV18 P1 transforming...   37.4   2.6
KX545359.1  Human papillomavirus type 18 isolate NGSk274-18 E6...   37.4   2.6
KX545354.1  Human papillomavirus type 18 isolate NGSk256-18 E6...   37.4   2.6
```

BLAST INFORMATION

ALIGNMENTS
>KY457840.1 Human papillomavirus type 18 strain 18CNTZ36 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
           ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
           ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
           ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)

BLAST INFORMATION

Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E6), E7 (E7),

BLAST INFORMATION

and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

BLAST INFORMATION

```
||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457828.1 Human papillomavirus type 18 strain 18CNTZ24 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457827.1 Human papillomavirus type 18 strain 18CNTZ23 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY457826.1 Human papillomavirus type 18 strain 18CNTZ22 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457825.1 Human papillomavirus type 18 strain 18CNTZ21 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457824.1 Human papillomavirus type 18 strain 18CNTZ20 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457823.1 Human papillomavirus type 18 strain 18CNTZ19 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

BLAST INFORMATION

>KY457822.1 Human papillomavirus type 18 strain 18CNTZ18 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457821.1 Human papillomavirus type 18 strain 18CNTZ17 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457820.1 Human papillomavirus type 18 strain 18CNTZ16 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY457819.1 Human papillomavirus type 18 strain 18CNTZ15 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457818.1 Human papillomavirus type 18 strain 18CNTZ14 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457817.1 Human papillomavirus type 18 strain 18CNTZ13 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457816.1 Human papillomavirus type 18 strain 18CNTZ12 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG  20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG  26
```

>KY457815.1 Human papillomavirus type 18 strain 18CNTZ11 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

BLAST INFORMATION

Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG   20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG   26
```

>KY457814.1 Human papillomavirus type 18 strain 18CNTZ10 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG   20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG   26
```

>KY457813.1 Human papillomavirus type 18 strain 18CNTZ09 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG   20
           ||||||||||||||||||||
Sbjct  7   CGCTTTGAGGATCCAACACG   26
```

>KY457812.1 Human papillomavirus type 18 strain 18CNTZ08 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CGCTTTGAGGATCCAACACG   20
           ||||||||||||||||||||
```

Sbjct   7   CGCTTTGAGGATCCAACACG   26

>KY457811.1 Human papillomavirus type 18 strain 18CNTZ07 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40),   Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query   1   CGCTTTGAGGATCCAACACG   20
             ||||||||||||||||||||
Sbjct   7   CGCTTTGAGGATCCAACACG   26

>KY457810.1 Human papillomavirus type 18 strain 18CNTZ06 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40),   Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query   1   CGCTTTGAGGATCCAACACG   20
             ||||||||||||||||||||
Sbjct   7   CGCTTTGAGGATCCAACACG   26

>KY457809.1 Human papillomavirus type 18 strain 18CNTZ05 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40),   Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query   1   CGCTTTGAGGATCCAACACG   20
             ||||||||||||||||||||
Sbjct   7   CGCTTTGAGGATCCAACACG   26

>KY457808.1 Human papillomavirus type 18 strain 18CNTZ04 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40),   Expect = 2.6

BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG   20

           ||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG   26

>KY457807.1 Human papillomavirus type 18 strain 18CNTZ03 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG   20

           ||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG   26

>KY457806.1 Human papillomavirus type 18 strain 18CNTZ02 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG   20

           ||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG   26

>KY457805.1 Human papillomavirus type 18 strain 18CNTZ01 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG   20

           ||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG   26

>KX514433.1 Human papillomavirus type 18 isolate pam9, complete genome
Length=7857

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
            ||||||||||||||||||||
Sbjct 111 CGCTTTGAGGATCCAACACG 130

>KY502096.1 Human papillomavirus isolate HPV18 P2-50 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
           ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY502095.1 Human papillomavirus isolate HPV18 P2-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20
           ||||||||||||||||||||
Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY502094.1 Human papillomavirus isolate HPV18 P2-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

```
||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY502093.1 Human papillomavirus isolate HPV18 P2-20 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY502092.1 Human papillomavirus isolate HPV18 P2-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY502091.1 Human papillomavirus isolate HPV18 P2 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KY502090.1 Human papillomavirus isolate HPV18 P1-50 transforming protein
E6 (E6) gene, partial cds
Length=474

BLAST INFORMATION

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

|||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY502089.1 Human papillomavirus isolate HPV18 P1-40 transforming protein
E6 (E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

|||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY502088.1 Human papillomavirus isolate HPV18 P1-30 transforming protein
E6 (E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

|||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG 26

>KY502086.1 Human papillomavirus isolate HPV18 P1-10 transforming protein
E6 (E6) gene, partial cds

Length=474

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CGCTTTGAGGATCCAACACG 20

|||||||||||||||||||||

Sbjct 7   CGCTTTGAGGATCCAACACG 26

BLAST INFORMATION

>KY502085.1 Human papillomavirus isolate HPV18 P1 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KX545359.1 Human papillomavirus type 18 isolate NGSk274-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=516

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
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            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

>KX545354.1 Human papillomavirus type 18 isolate NGSk256-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=579

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CGCTTTGAGGATCCAACACG  20
            ||||||||||||||||||||
Sbjct  7    CGCTTTGAGGATCCAACACG  26
```

Database: Nucleotide collection (nt)
Posted date: Jul 8, 2017 5:09 AM
Number of letters in database: 150,093,331,920
Number of sequences in database: 43,324,577

Lambda   K   H
0.634   0.408   0.912

BLAST INFORMATION

Gapped

Lambda   K   H

0.625   0.410   0.780

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 43324577

Number of Hits to DB: 798593

Number of extensions: 258

Number of successful extensions: 258

Number of sequences better than 10: 17

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 258

Number of HSP's successfully gapped: 17

Length of query: 20

Length of database: 150093331920

Length adjustment: 17

Effective length of query: 3

Effective length of database: 149356814111

Effective search space: 448070442333

Effective search space used: 448070442333

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 28 (26.5 bits)

S2: 38 (35.6 bits)


```
</form>
</div><!-- /#content -->
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="refo:
<input name="QUERY_INFO" type="hidden" value="" />
<input name="ENTREZ_QUERY" type="hidden" value="" />
<input name="CDD_RID" type="hidden" value="" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />
<input name="RID" type="hidden" value="P7X7F2GR014" />
<input name="STEP_NUMBER" type="hidden" value="" />
<input name="CMD" type="hidden" value="Web"/>
<input NAME="PAGE_TYPE" type="hidden"  value="BlastFormatting"/>

<!-- TO DO: test all of those changes -->
<!-- Psi blast params  PSI_BLAST_PARAMS - commented- using forms[0] from fromatter> -->
<!-- Current Formatting options FORMATTING_OPTIONS- commented- using forms[0] from fromatter> 
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>
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BLAST INFORMATION

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<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="setSa
<input name="PAGE_TYPE" type="hidden" value="BlastSearch" />
<input name="VIEW_SEARCH" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="Web" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>


<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="saveO
<input name="SAVE" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="GetSaved" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from formatter> -->
</form>
</div><!-- /#content-wrap -->

<footer id="page_footer">
<div class="foot_wrap">
<div class="left col two_col">
BLAST is a registered trademark of the National Library of Medicine
</div>
<div class="right">
<a class="help_desk jig-ncbihelpwindow" target="_blank" href="https://support.ncbi.nlm.nih.gov
Ncbi_App=blast&amp;Page=oldblastresults&Time=2017-07-10T17:43:54&amp;Host=blast349&amp;ncbi_ph
</a>
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=MailList">Mailing list</a>
<a href="https://www.youtube.com/ncbinlm" target="_blank" id="page_footer_54">
<img class="icon-medium gray-medium" src="images/youtube.svg" alt="">
<span class="icon-fallback-text">YouTube</span>
</a>
</div>

</div>

<!-- bottom section of footer -->
<div class="col" id="contentinfo">
<ul class="right inline_list logos">
<li>
<a href="https://www.nlm.nih.gov" id="page_footer_60">
<img class="gray-medium" src="images/nlm-logo.svg" alt="">
<span class="icon-fallback-text">National Library Of Medicine</span>
</a>
</li>
<li>
<a href="https://www.nih.gov" id="page_footer_61">
<img class="gray-medium" src="images/nih-logo.svg" alt="">
<span class="icon-fallback-text">National Institutes Of Health</span>
</a>
</li>
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```
<li>
<a href="https://www.hhs.gov" id="page_footer_62">
<img class="gray-medium" src="images/hhs-logo.svg" alt="">
<span class="icon-fallback-text">U.S. Department of Health &amp; Human Services</span>
</a>
</li>
<li>
<a href="https://www.usa.gov" id="page_footer_63">
<img class="icon-large-wide gray-medium" src="images/usagov-logo.svg" alt="">
<span class="icon-fallback-text">USA.gov</span>
</a>
</li>
</ul>

<div class="footer_padding">

<div class="footer_border h-card">

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url" id="page_footer_64">
<h3 role="heading" aria-level="3" class="ncbi_blue p-org">NCBI</h3>
</a>

<address>

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url p-org" id="page_footer_65">National Cente
<a href="https://www.nlm.nih.gov/" id="page_footer_66"> U.S. National Library of Medicine</a>

<span class="h-adr">
<span class="p-street-address">8600 Rockville Pike</span>,
<span class="p-locality">Bethesda</span>
<span class="p-region"> MD</span>,
<span class="p-postal-code">20894</span>
<span class="p-country-name">USA</span>
</span>

</address>

</div>
<div class="inline_list about_list">
<a href="https://www.ncbi.nlm.nih.gov/home/about/policies.shtml" id="page_footer_67">Policies a
|
<a href="https://www.ncbi.nlm.nih.gov/home/about/contact.shtml" id="page_footer_68">Contact</a
</div>
</div>
</div>
</footer>
<script type="text/javascript" src="js/header.js"> </script>
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BLAST INFORMATION

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</div><!--/#wrap-->

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<script type="text/javascript" src="js/toggle.js"></script>
<script type="text/javascript" src="js/remote_data_provider.js"></script>
<script type="text/javascript" src="js/results.js"></script>
<script type="text/javascript" src="js/blast.js"></script>
<script type="text/javascript" src="js/format.js"></script>

<script type="text/javascript" src="/portal/portal3rc.fcgi/rlib/js/InstrumentOmnitureBaseJS/In
<!--
<script type="text/javascript" src="://www.ncbi.nlm.nih.gov/portal/portal3rc.fcgi/supportedbrow
<script type="text/javascript">$("#browsers_ajax").browserCheck();</script>
-->
</body>
</html>

<!DOCTYPE html PUBLIC "-//W3C//DTD XHTML 1.0 Transitional//EN" "http://www.w3.org/TR/xhtml1/DTI
<html xmlns="http://www.w3.org/1999/xhtml">
<head>

<meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
<meta http-equiv="X-UA-Compatible" content="IE=edge,chrome=1">
<meta name="jig" content="ncbitoggler ncbiautocomplete"/>
<meta name="ncbitoggler" content="animation:'none'"/>

<meta name="referrer" content="origin-when-cross-origin" />
<meta name="ncbi_app" content="blast" />
<meta name="ncbi_pdid" content="oldblastresults" />

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<meta name="ncbi_stat" content="false" />
<meta name="ncbi_sessionid" content="55BA7B14963F55D1_0000SID" />
<meta name="ncbi_phid" content="55BA7B14963F55D10000000000000001" />
<script type="text/javascript"> var ncbi_startTime = new Date(); </script>
<title>NCBI Blast:Nucleotide Sequence (20 letters)</title>
<script type="text/javascript" src="/core/jig/1.14.8/js/jig.min.js          "></script>
<script type="text/javascript">    jQuery.getScript("/core/alerts/alerts.js", function() {
                              galert(['div#header', 'body > *:nth-child(1)'])
});</script>
<link rel="stylesheet" type="text/css" href="css/header.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/google-fonts.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/footer.css" media="screen" />
```

BLAST INFORMATION

```html
<link rel="stylesheet" type="text/css" href="css/main.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/blastRes.css" media="screen" />
<!--[if IE]>
<link rel="stylesheet" type="text/css" href="css/descriptionsIE.css" media="screen" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/print.css" media="print" />
<!--[if lte IE 6]>
<link rel="stylesheet" type="text/css" href="css/ie6_or_less.css" />
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</head>

<body id="type-a" class="noToggleCheck " >
<div id="wrap">

<header id="page_header" role="banner">
<ul class="skip_nav">
<li><a accesskey="1" title="NCBI Homepage" href="https://www.ncbi.nlm.nih.gov/">NCBI Home</a><
<li><a accesskey="2" title="MyNCBI" href="https://www.ncbi.nlm.nih.gov/myncbi">Sign in to NCBI
<li><a accesskey="3" title="Skip to main content" href="#content">Skip to Main Content</a></li
<li><a accesskey="4" title="Skip to navigation" href="#navcontent">Skip to Navigation</a></li
<li><a accesskey="0" title="About NCBI Accesskeys" href="https://www.ncbi.nlm.nih.gov/guide/br
</ul>
<nav class="blue_nav_bar">
<div class="nih">
<a id="page_header_6" href="https://www.nih.gov/" class="left norm_height">
<img src="images/nih_logo.svg" alt="NIH logo" class="left"/></a>
<a id="page_header_7" href="https://www.nlm.nih.gov/" class="left header_link">U.S. National L
</div>

<div class="left">
<img src="images/arrow.svg" class="left norm_height" alt=""/>
</div>


<div class="ncbi">
<a id="page_header_8" href="https://www.ncbi.nlm.nih.gov/" class="header_link">
<span class="ncbi_name">NCBI</span>
<span class="med_hidden">National Center for Biotechnology Information</span></a>

<div class="right sign-in">
<ul class="myncbi2">
<li id="myncbiusername">
<span id="mnu">
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BLAST INFORMATION

```html
<a id="mnu_0" href="https://www.ncbi.nlm.nih.gov/account/settings/" title="Edit account setting
</span>
</li>
<li id="myncbi"><a id="myncbi_0"  href="https://www.ncbi.nlm.nih.gov/myncbi/">My NCBI</a></li>
<li id="myncbi_sign_in"><a id="myncbi_sign_in_0" href="https://www.ncbi.nlm.nih.gov/account/?ba
<li id="myncbi_register"><a id="myncbi_register_0" href="https://www.ncbi.nlm.nih.gov/account/
<li id="myncbi_sign_out"><a id="myncbi_sign_out_0" href="https://www.ncbi.nlm.nih.gov/account/
</ul>
</div>
</div>
</nav>


<div class="bg-gray header-div">
<nav class="top-nav" id="navcontent" role="navigation">
<a class="lf" href="Blast.cgi">BLAST <sup>&reg;</sup></a> <span id="brc"><span class="brcrmbsig
<span class="rf">
<ul id="blnav">
<li  class="first "><a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastHome" title="BLAST Home">Home
<li  class="recent "><a href="Blast.cgi?CMD=GetSaved&amp;RECENT_RESULTS=on" title="Unexpired Bl
<li  class="saved "><a href="Blast.cgi?CMD=GetSaved" title="Saved sets of BLAST search paramete
<li  class= "last documentation "> <a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs" title="
</ul>
</span>
</nav>
</div>
</header>


<div id="content-wrap">

<div class="pageTitle">
BLAST Results
</div>
<div class="inlineDiv resHeader resPage">

</div>
<ul class="print-log-res"><li></li></ul>


<!-- CDD info for old design -->








<div id="content">
```

BLAST INFORMATION

```
<!--<ul id="msg" class="msg"><li class=""><p class=""></p><p class=""></p><p class=""></p></li
<ul id="msg" class="msg"><li class=""></li></ul>
<a  href="#" class="resLink resPage" id="searchOptions" submitForm="setSavedOptions">Edit and
<a  href="#" class="resLink resPage hidden" id="saveSearchOptions" submitForm="saveOptions">Sav
<span class="reslink  resPage" >[Sign in above to save your search strategy]</span>
<a  id="showFormat" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggler
<span class="ui-ncbitoggler-master-text">Formatting options </span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<a  id="showDownload" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggle
<span class="ui-ncbitoggler-master-text">Download</span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<span id="hnr">
<a id="ytb" class="ytb " title="External link to YouTube" href="https://www.youtube.com/playli
<a id="brFtp" class="" title="Blast report description" href="ftp://ftp.ncbi.nlm.nih.gov/pub/fa
</span>
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST" id="results

<input name="QUERY_INDEX" type="hidden" value="0">
<input name="_PGR" type="hidden" value="" >
<input id="seqViewUrl" type="hidden" value="https://www.ncbi.nlm.nih.gov" >
<input id="userAgent" type="hidden" value="">
<input name="CMD" type="hidden" value="Get">
</form>
<!-- Reformat and downlaod for new design -->
<div class="ui-helper-reset" aria-live="assertive" >
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="Format
<table class="options blastn ">
<tr>
<td class="frh" colspan=2>
<div class="fi">
<div class="tb">Formatting options</div>
<input type="image"  border="0" id="onPageReformat" src="css/images/reformat.jpg" class="blastl
</div>
</tr>
<tr class="paramSet xgl">
<td class="hd"><label for="FORMAT_OBJECT">Show</label></td>
<td>
<div class="fi">
<input type="hidden" id="FORMAT_OBJECT" value="Alignment" name="FORMAT_OBJECT" />
<label for="FORMAT_TYPE" id="nft">Alignment as</label>
<select name="FORMAT_TYPE" id="FORMAT_TYPE" class="reset" defVal="HTML">
<option value="HTML"  >HTML</option>
<option value="Text"  >Plain text</option>
```

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</select>

<span id="advView" class="">
<span class=""><input name="OLD_VIEW" id="OLD_VIEW" type="checkbox" class="cb reset" defVal="u
<label for="OLD_VIEW">Old View</label></span>
</span>
<a class="resetAll" id="resetAll" >Reset form to defaults</a>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments object formatting
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp1">
These options control formatting of alignments in results pages. The
default is HTML, but other formats (including plain text) are available.
PSSM and PssmWithParameters are representations of Position Specific Scoring Matrices and are
The Advanced view option allows the database descriptions to be sorted by various indices in a
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="odd paramSet">
<td class="hd"><label for="ALIGNMENT_VIEW">Alignment View</label></td>
<td>
<div class="fi">
<select name="ALIGNMENT_VIEW" id="ALIGNMENT_VIEW" defVal="Pairwise" class="reset">
<option value="Pairwise" selected="selected" >Pairwise</option>
<option value="PairwiseWithIdentities"  >Pairwise with dots for identities</option>
<option value="QueryAnchored"  >Query-anchored with dots for identities</option>
<option value="QueryAnchoredNoIdentities"  >Query-anchored with letters for identities</option
<option value="FlatQueryAnchored"  >Flat query-anchored with dots for identities</option>
<option value="FlatQueryAnchoredNoIdentities"  >Flat query-anchored with letters for identitie

</select>


<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments view options help
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp2">
Choose how to view alignments.
The default "pairwise" view shows how each subject sequence aligns
individually to the query sequence. The "query-anchored" view shows how
all subject sequences align to the query sequence. For each view type,
you can choose to show "identities" (matching residues) as letters or
dots.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#alignment_view" targe
```

BLAST INFORMATION
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</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet">
<td class="hd"><label>Display</label></td>
<td class="cb">
<div class="fi">
<input name="SHOW_OVERVIEW" id="SHOW_OVERVIEW" type="checkbox" class="cb reset" defVal="checke
<label class="rb" for="SHOW_OVERVIEW">Graphical Overview</label>

<span id="shl" >
<input name="SHOW_LINKOUT" id="SHOW_LINKOUT" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="SHOW_LINKOUT">Linkout</label>
</span>
<span id="gts" >
<input name="GET_SEQUENCE" id="GET_SEQUENCE" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="GET_SEQUENCE">Sequence Retrieval</label>
</span>

<input name="NCBI_GI" id="NCBI_GI" type="checkbox" class="cb reset" defVal="unchecked" false /
<label class="rb" for="NCBI_GI">NCBI-gi</label>
<span id="scf" >
<input name="SHOW_CDS_FEATURE" id="SHOW_CDS_FEATURE" type="checkbox" class="cb reset blastn" d
<label for="SHOW_CDS_FEATURE" class="blastn">CDS feature</label>
</span>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments display options h
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp3">
<li>Graphical Overview: Graphical Overview: Show graph of similar sequence regions aligned to
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_overview" targe
</li>
<li>NCBI-gi: Show NCBI gi identifiers.
</li>
<li>CDS feature: Show annotated coding region and translation.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_cds_feature" ti
</li></ul>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl">
```

BLAST INFORMATION

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<td class="hd"><label>Masking</label></td>
<td>
<div class="fi">
<label for="MASK_CHAR"> Character: </label>
<select name="MASK_CHAR" id="MASK_CHAR"  class="reset" defVal="2">
<option value="0"  >X for protein, n for nucleotide</option>
<option value="2" selected="selected" >Lower Case</option>
</select>
<label for="MASK_COLOR"> Color:</label>
<select name="MASK_COLOR" id="MASK_COLOR" class="reset" defVal="1">
<option value="0"  >Black
</option>

<option value="1" selected="selected" >Grey
</option>

<option value="2"  >Red
</option>

</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments masking help" id=
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp4">
<li>Masking Character: Display masked (filtered) sequence regions as lower-case or as specific
</li>
<li>Masking Color: Display masked sequence regions in the given color.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr id="lr" class="paramSet xgl">
<td class="hd"><label>Limit results</label></td>
<td>
<div class="fi">
<label for="FRM_DESCRIPTIONS">Descriptions:</label>
<select name="DESCRIPTIONS" id="FRM_DESCRIPTIONS" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"    >100</option>
<option value="250"    >250</option>
<option value="500"    >500</option>
<option value="1000"   >1000</option>
```

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<option value="5000"   >5000</option>
<option value="10000"  >10000</option>
<option value="20000"  >20000</option>
</select>

<label for="FRM_NUM_OVERVIEW">Graphical overview:</label>
<select name="NUM_OVERVIEW" id="FRM_NUM_OVERVIEW" class="reset" defVal="100">
<option value="0"      >0</option>
<option value="10"     >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"    >100</option>
<option value="250"    >250</option>
<option value="500"   >500</option>
<option value="1000"   >1000</option>
</select>
<span id="frmAln">
<label for="FRM_ALIGNMENTS">Alignments:</label>
<select name="ALIGNMENTS" id="FRM_ALIGNMENTS" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"    >1000</option>
<option value="5000"    >5000</option>
<option value="10000"   >10000</option>
<option value="20000"   >20000</option>
</select>
</span>
<label for="FRM_LINE_LENGTH">Line length:</label>
<select name="LINE_LENGTH" id="FRM_LINE_LENGTH" class="reset" defVal="60">
<option value="60"    selected="selected" >60</option>
<option value="90"      >90</option>
<option value="120"      >120</option>
<option value="150"      >150</option>
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit number of descriptions
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp5">
<li>Descriptions: Show short descriptions for up to the given number of  sequences.</li>
<li>Alignments:  Show alignments for up to the given number of sequences, in order of statisti
<li>Line lenghth:  Number of letters to show on one line in an alignment.</li>
</ul>
</div><!-- ARIA -->
</div>
```

BLAST INFORMATION

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</td>
</tr>

<tr class="paramSet odd xgl ">
<td class="hd"></td>
<td>
<div class="">
<label for="qorganism">Organism</label>
<span class="instr">Type common name, binomial, taxid, or group name. Only 20 top taxa will be
<input name="FORMAT_ORGANISM" size="55"  type="text" id="qorganism" value="" data-jigconfig="d:
<input type="checkbox" name="FORMAT_ORG_EXCLUDE"  class="oExclR cb" id="orgExcl"/>
<input type="hidden" value = "1" name="FORMAT_NUM_ORG" id="numOrg" />
<label for="orgExcl" class="right">Exclude</label>
<a href="#" title="Add organism" id="addOrg"><img border="0" src="css/images/addOrg.jpg" id="ac
<div id="orgs">

</div>
<div class="fi">
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by organism he:
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp6">
Show only sequences from the given organism.
</p>
</div><!-- ARIA -->
</div>
</div>
</td>
</tr>

<tr class="paramSet xgl ">
<td class="hd"></td>
<td>
<div class="fi">
<label for="FORMAT_EQ_TEXT">Entrez query:</label>
<input name="FORMAT_EQ_TEXT" id="FORMAT_EQ_TEXT" size="60" type="text" value="" class="reset"
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by Entrez query
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp7">
Show only those sequences that match the given Entrez query.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#limit_result" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
```

```
<tr class="paramSet odd xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="EXPECT_LOW">Expect Min:</label> <input name="EXPECT_LOW" id="EXPECT_LOW" size="10"
<label for="EXPECT_HIGH">Expect Max:</label> <input name="EXPECT_HIGH" id="EXPECT_HIGH" size="1
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by expect valu
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp8">
Show only sequences with expect values in the given range.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#expect_range" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="paramSet xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="PERC_IDENT_LOW">Percent Identity Min:</label> <input name="PERC_IDENT_LOW" id="PERC
<label for="PERC_IDENT_HIGH">Percent Identity Max:</label> <input name="PERC_IDENT_HIGH" id="PI
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by percent ider
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp10">
Show only sequences with percent identity values in the given range.
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="psiBlast odd paramSet xgl">
<td class="hd"><label>Format for</label></td>
<td>
<div class="fi">
<input name="RUN_PSIBLAST_FORM" id="RUN_PSIBLAST" type="checkbox" class="cb psiBlast"  />
<label class="rb psiBlast" for="RUN_PSIBLAST">PSI-BLAST</label>
<label for="I_THRESH">with inclusion threshold:</label>
<input name="I_THRESH" id="I_THRESH" size="10" type="text" value="" defVal="0.005" />
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="PSI BLAST formatting help" id
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp9">
```

BLAST INFORMATION

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<li>Format for PSI-BLAST: The Position-Specific Iterated BLAST (PSI-BLAST) program performs it
in which sequences found in one round of search are used to build a custom score model for the
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#psiblast" target="hel
</li>
<li>Inclusion Threshold: This sets the statistical significance threshold for including a sequ
by PSI-BLAST to create the PSSM on the next iteration.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>
</table>


<input name="ViewReport" value="ViewReport" type="hidden" />
<input name="REFORMAT_REPORT" value="shown" type="hidden" />
<input name="RID" value="P7X8V4EJ015" type="hidden" />
<input name="CDD_RID" value="" type="hidden" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />

<input name="STEP_NUMBER" value="" id="stepNumber" type="hidden" />
<input name="CMD" value="Get" type="hidden" />
<input name="FORMAT_EQ_OP" value="AND" type="hidden" />
<input name="RESULTS_PAGE_TARGET" type="hidden" id="resPageTarget" value="" />
<!-- <input name="QUERY_INFO" type="hidden" value="" /> -->
<!-- <input name="ENTREZ_QUERY" type="hidden" value="" /> -->
<input name="QUERY_INDEX" type="hidden" value="0"/>
<input name="NUM_QUERIES" type="hidden" value="1"/>

<!-- Those params are set in the template (blastn.dat, blastp.dat etc. -->
<input name="BLAST_PROGRAMS" type="hidden" value="blastn"/>
<input name="PAGE" type="hidden" value="Nucleotides"/>
<input name="PROGRAM" type="hidden" value="blastn"/>
<input name="MEGABLAST" type="hidden" value="" />
<input name="RUN_PSIBLAST" type="hidden" value="" />
<input name="BLAST_SPEC" id="blastSpec" type="hidden" value=""/>


<input name="QUERY" type="hidden" value="CTTTGAGGATCCAACACGGC"/>
<input name="JOB_TITLE" type="hidden" value="Nucleotide Sequence (20 letters)"/>
<input name="QUERY_TO" type="hidden" value=""/>
<input name="QUERY_FROM" type="hidden" value=""/>
<input name="SUBJECTS_FROM" type="hidden" value=""/>
<input name="SUBJECTS_TO" type="hidden" value=""/>
<input name="EQ_TEXT" type="hidden" value=""/>
<input name="ORGN" type="hidden" value=""/>
<input name="EQ_MENU" type="hidden" value=""/>
```

BLAST INFORMATION

```
<input name="ORG_EXCLUDE" type="hidden" value=""/>
<input name="PHI_PATTERN" type="hidden" value=""/>
<input name="EXPECT" type="hidden" value="10"/>
<input name="DATABASE" type="hidden" value="nt"/>
<input name="DB_GROUP" type="hidden" value=""/>
<input name="SUBGROUP_NAME" type="hidden" value=""/>

<input name="GENETIC_CODE" type="hidden" value=""/>
<input name="WORD_SIZE" type="hidden" value="11"/>
<input name="MATCH_SCORES" type="hidden" value="2,-3"/>
<input name="MATRIX_NAME" type="hidden" value=""/>
<input name="GAPCOSTS" type="hidden" value="5 2"/>
<input name="MAX_NUM_SEQ" id="maxNumSeq" type="hidden" value="50"/>
<input name="COMPOSITION_BASED_STATISTICS" type="hidden" value=""/>
<input name="NEWWIN" type="hidden" value=""/>
<input name="SHORT_QUERY_ADJUST" type="hidden" value=""/>
<input name="FILTER" type="hidden" value="L;m;"/>
<input name="REPEATS" type="hidden" value=""/>
<input name="ID_FOR_PSSM" type="hidden" value=""/>
<input name="EXCLUDE_MODELS" type="hidden" value=""/>
<input name="EXCLUDE_SEQ_UNCULT" type="hidden" value=""/>
<input name="WP_PROTEINS" type="hidden" value=""/>
<input name="SEQ_FROM_TYPE" type="hidden" value=""/>
<input name="ENTREZ_QUERY" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET_EXCL" type="hidden" value=""/>
<input name="NUM_ORG" type="hidden" value = "1" />

<!-- PSSM -->
<input name="LCASE_MASK" type="hidden" value=""/>
<input name="TEMPLATE_TYPE" type="hidden" value=""/>
<input name="TEMPLATE_LENGTH" type="hidden" value=""/>
<input name="I_THRESH" type="hidden" value=""/>
<input name="PSI_PSEUDOCOUNT" type="hidden" value=""/>
<input name="DI_THRESH" type="hidden" id="diThresh" value=""/>
<input name="HSP_RANGE_MAX" type="hidden" value="0"/>




<input name="ADJUSTED_FOR_SHORT_QUERY" type="hidden" value=""/>
<input name="MIXED_QUERIES" type="hidden" value=""/>
<input name="MIXED_DATABASE" id="mixedDb" type="hidden" value=""/>
<input name="BUILD_NAME"  type="hidden" value=""/>
<input name="ORG_DBS"  type="hidden" value=""/>
<input name="WWW_BLAST_TYPE" type="hidden" value="newblast"/>

</form>
```

```
</div> <!-- aria -->
<div class="ui-helper-reset" aria-live="assertive" >
<form  name="FormatDownload" id="FormatDownload" class="resbox ui-ncbitoggler-slave">
<table class="options dwnl blastn ">
<tr><td class="frh" colspan=6><div class="tb">Download</div></td></tr>
<tr>
<td id="tdal">
<div class="dnHeader">Alignment</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=Text&FORMAT_OBJECT=Alignment&D
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=XML&FORMAT_OBJECT=
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=Alignment&
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=JSONSA&FORMAT_OBJECT=Alignment
<a  id="hitText" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=Text&FORMAT_OBJEC
<a  id="hitCvs" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=CSV&FORMAT_OBJECT=
<a  class="xgl" href="Blast.cgi?RID=P7X8V4EJ015&FORMAT_TYPE=XML2&FORMAT_OBJECT=Alignment&CMD=G
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=XML2_S&FORMAT_OBJE
<a  class="xgl" href="Blast.cgi?RID=P7X8V4EJ015&FORMAT_TYPE=JSON2&FORMAT_OBJECT=Alignment&CMD=
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=JSON2_S&FORMAT_OBJ
<a  class="xgl blastn" href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=SAM_SQ&FORM
</div>
</td>
<td class="dnl xgl">
<div class="dnHeader">Search Strategies</div>
<div class="dnLinks">
<a  href="Blast.cgi?CMD=GetSaved&RECENT_RESULTS=on&RID=P7X8V4EJ015&DOWNLOAD_OPTIONS=true">ASN.
</div>
</td>
<td class="dnl" id="dnPSSMPar">
<div class="dnHeader">PSSM to restart search</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7X8V4EJ015&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=PSSM_Score
</div>
</td>
<td>
<a class="helplink ui-ncbitoggler" data-jig="ncbitoggler" title="Download help" data-ncbitoggl
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
</td>
</tr>
</table>
<div class="ui-helper-reset" aria-live="assertive" >
<div class="helpbox ui-ncbitoggler-slave" id="hlp11">
The Download link provides BLAST output that may be used as input to another program.
This includes parseable formats such as the tabular report or XML as well as the Search Strate
More details on the parseable (XML, tabular, and ASN.1) reports can be found at
<a href="https://www.ncbi.nlm.nih.gov/books/NBK153387/" target="helpWin" >https://www.ncbi.nlm
<br/>
```

BLAST INFORMATION

```
<p>
The following formats are offered under the Alignment section:<br/>
1). "Text". Non-HTML standard BLAST report.<br/>
2). "XML". XML report based upon the DTD at <a href="https://www.ncbi.nlm.nih.gov/data_specs/d
3). "ASN.1". Alignment written out in Abstract Syntax Notation 1.<br/>
4). "JSON Seq-align". Alignment written out in JSON.<br/>
4). "Hit Table(text)". The tabular report as text.<br/>
5). "Hit Table(csv)". The tabular report ready for import into spread-sheet programs like Exce
6). "XML2". New XML format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NEW
7). "JSON". New JSON format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NE
8). "SAM". Sequence Alignment Map format.<br/>
</p>
<p>
XML2 and JSON can be downloaded either as one file per query (multiple-file) or one file for al
</p>
<p>
The following report is offered under the Search Strategy section:<br/>
1). "ASN.1" Search Strategy. A record of the parameters, query, and database used in the searc
<a href="https://www.ncbi.nlm.nih.gov/books/NBK1763/#CmdLineAppsManual.I455_BLAST_search_stra"
</p>
</div>
</div><!-- ARIA -->
</form>
</div> <!-- aria -->
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<input name="CMD" type="hidden" value="">
<p><!--
QBlastInfoBegin
Status=READY
QBlastInfoEnd
--><p>
<PRE>
BLASTN 2.6.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.


RID: P7X8V4EJ015


Database: Nucleotide collection (nt)
43,324,577 sequences; 150,093,331,920 total letters
Query=
```

BLAST INFORMATION

Length=20

```
                                                                    Score     E
Sequences producing significant alignments:                         (Bits)  Value

KY457840.1  Human papillomavirus type 18 strain 18CNTZ36 E6 (E...   37.4    2.6
KY457839.1  Human papillomavirus type 18 strain 18CNTZ35 E6 (E...   37.4    2.6
KY457838.1  Human papillomavirus type 18 strain 18CNTZ34 E6 (E...   37.4    2.6
KY457837.1  Human papillomavirus type 18 strain 18CNTZ33 E6 (E...   37.4    2.6
KY457836.1  Human papillomavirus type 18 strain 18CNTZ32 E6 (E...   37.4    2.6
KY457835.1  Human papillomavirus type 18 strain 18CNTZ31 E6 (E...   37.4    2.6
KY457834.1  Human papillomavirus type 18 strain 18CNTZ30 E6 (E...   37.4    2.6
KY457833.1  Human papillomavirus type 18 strain 18CNTZ29 E6 (E...   37.4    2.6
KY457832.1  Human papillomavirus type 18 strain 18CNTZ28 E6 (E...   37.4    2.6
KY457831.1  Human papillomavirus type 18 strain 18CNTZ27 E6 (E...   37.4    2.6
KY457830.1  Human papillomavirus type 18 strain 18CNTZ26 E6 (E...   37.4    2.6
KY457829.1  Human papillomavirus type 18 strain 18CNTZ25 E6 (E...   37.4    2.6
KY457828.1  Human papillomavirus type 18 strain 18CNTZ24 E6 (E...   37.4    2.6
KY457827.1  Human papillomavirus type 18 strain 18CNTZ23 E6 (E...   37.4    2.6
KY457826.1  Human papillomavirus type 18 strain 18CNTZ22 E6 (E...   37.4    2.6
KY457825.1  Human papillomavirus type 18 strain 18CNTZ21 E6 (E...   37.4    2.6
KY457824.1  Human papillomavirus type 18 strain 18CNTZ20 E6 (E...   37.4    2.6
KY457823.1  Human papillomavirus type 18 strain 18CNTZ19 E6 (E...   37.4    2.6
KY457822.1  Human papillomavirus type 18 strain 18CNTZ18 E6 (E...   37.4    2.6
KY457821.1  Human papillomavirus type 18 strain 18CNTZ17 E6 (E...   37.4    2.6
KY457820.1  Human papillomavirus type 18 strain 18CNTZ16 E6 (E...   37.4    2.6
KY457819.1  Human papillomavirus type 18 strain 18CNTZ15 E6 (E...   37.4    2.6
KY457818.1  Human papillomavirus type 18 strain 18CNTZ14 E6 (E...   37.4    2.6
KY457817.1  Human papillomavirus type 18 strain 18CNTZ13 E6 (E...   37.4    2.6
KY457816.1  Human papillomavirus type 18 strain 18CNTZ12 E6 (E...   37.4    2.6
KY457815.1  Human papillomavirus type 18 strain 18CNTZ11 E6 (E...   37.4    2.6
KY457814.1  Human papillomavirus type 18 strain 18CNTZ10 E6 (E...   37.4    2.6
KY457813.1  Human papillomavirus type 18 strain 18CNTZ09 E6 (E...   37.4    2.6
KY457812.1  Human papillomavirus type 18 strain 18CNTZ08 E6 (E...   37.4    2.6
KY457811.1  Human papillomavirus type 18 strain 18CNTZ07 E6 (E...   37.4    2.6
KY457810.1  Human papillomavirus type 18 strain 18CNTZ06 E6 (E...   37.4    2.6
KY457809.1  Human papillomavirus type 18 strain 18CNTZ05 E6 (E...   37.4    2.6
KY457808.1  Human papillomavirus type 18 strain 18CNTZ04 E6 (E...   37.4    2.6
KY457807.1  Human papillomavirus type 18 strain 18CNTZ03 E6 (E...   37.4    2.6
KY457806.1  Human papillomavirus type 18 strain 18CNTZ02 E6 (E...   37.4    2.6
KY457805.1  Human papillomavirus type 18 strain 18CNTZ01 E6 (E...   37.4    2.6
KX514433.1  Human papillomavirus type 18 isolate pam9, complet...   37.4    2.6
KY502096.1  Human papillomavirus isolate HPV18 P2-50 transform...   37.4    2.6
KY502095.1  Human papillomavirus isolate HPV18 P2-40 transform...   37.4    2.6
KY502094.1  Human papillomavirus isolate HPV18 P2-30 transform...   37.4    2.6
KY502093.1  Human papillomavirus isolate HPV18 P2-20 transform...   37.4    2.6
```

BLAST INFORMATION

```
KY502092.1  Human papillomavirus isolate HPV18 P2-10 transform...   37.4    2.6
KY502091.1  Human papillomavirus isolate HPV18 P2 transforming...   37.4    2.6
KY502090.1  Human papillomavirus isolate HPV18 P1-50 transform...   37.4    2.6
KY502089.1  Human papillomavirus isolate HPV18 P1-40 transform...   37.4    2.6
KY502088.1  Human papillomavirus isolate HPV18 P1-30 transform...   37.4    2.6
KY502086.1  Human papillomavirus isolate HPV18 P1-10 transform...   37.4    2.6
KY502085.1  Human papillomavirus isolate HPV18 P1 transforming...   37.4    2.6
KX545359.1  Human papillomavirus type 18 isolate NGSk274-18 E6...   37.4    2.6
KX545354.1  Human papillomavirus type 18 isolate NGSk256-18 E6...   37.4    2.6
```

ALIGNMENTS
>KY457840.1 Human papillomavirus type 18 strain 18CNTZ36 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Query  1   CTTTGAGGATCCAACACGGC  20
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Sbjct  9   CTTTGAGGATCCAACACGGC  28
```


>KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CTTTGAGGATCCAACACGGC  20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC  28
```


>KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CTTTGAGGATCCAACACGGC  20
           ||||||||||||||||||||
```

BLAST INFORMATION

```
Sbjct  9   CTTTGAGGATCCAACACGGC  28
```

>KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CTTTGAGGATCCAACACGGC  20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC  28
```

>KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CTTTGAGGATCCAACACGGC  20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC  28
```

>KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   CTTTGAGGATCCAACACGGC  20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC  28
```

>KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
```

BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus


```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```


>KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E6), E7 (E7), and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus


```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```


>KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E6), E7 (E7), and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus


```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```


>KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E6), E7 (E7), and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus


```
Query  1    CTTTGAGGATCCAACACGGC   20
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Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

BLAST INFORMATION

>KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457828.1 Human papillomavirus type 18 strain 18CNTZ24 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457827.1 Human papillomavirus type 18 strain 18CNTZ23 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457826.1 Human papillomavirus type 18 strain 18CNTZ22 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457825.1 Human papillomavirus type 18 strain 18CNTZ21 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457824.1 Human papillomavirus type 18 strain 18CNTZ20 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457823.1 Human papillomavirus type 18 strain 18CNTZ19 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457822.1 Human papillomavirus type 18 strain 18CNTZ18 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457821.1 Human papillomavirus type 18 strain 18CNTZ17 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457820.1 Human papillomavirus type 18 strain 18CNTZ16 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457819.1 Human papillomavirus type 18 strain 18CNTZ15 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC   28
```

>KY457818.1 Human papillomavirus type 18 strain 18CNTZ14 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC   28
```

>KY457817.1 Human papillomavirus type 18 strain 18CNTZ13 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9   CTTTGAGGATCCAACACGGC   28
```

>KY457816.1 Human papillomavirus type 18 strain 18CNTZ12 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)

BLAST INFORMATION

Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457815.1 Human papillomavirus type 18 strain 18CNTZ11 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457814.1 Human papillomavirus type 18 strain 18CNTZ10 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457813.1 Human papillomavirus type 18 strain 18CNTZ09 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457812.1 Human papillomavirus type 18 strain 18CNTZ08 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

           ||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457811.1 Human papillomavirus type 18 strain 18CNTZ07 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

           ||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457810.1 Human papillomavirus type 18 strain 18CNTZ06 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

           ||||||||||||||||||||

Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY457809.1 Human papillomavirus type 18 strain 18CNTZ05 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20

BLAST INFORMATION

```
||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457808.1 Human papillomavirus type 18 strain 18CNTZ04 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457807.1 Human papillomavirus type 18 strain 18CNTZ03 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457806.1 Human papillomavirus type 18 strain 18CNTZ02 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY457805.1 Human papillomavirus type 18 strain 18CNTZ01 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KX514433.1 Human papillomavirus type 18 isolate pam9, complete genome
Length=7857

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  113  CTTTGAGGATCCAACACGGC   132
```

>KY502096.1 Human papillomavirus isolate HPV18 P2-50 transforming protein
E6 (E6) gene, partial cds
Length=474

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502095.1 Human papillomavirus isolate HPV18 P2-40 transforming protein
E6 (E6) gene, partial cds
Length=474

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502094.1 Human papillomavirus isolate HPV18 P2-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY502093.1 Human papillomavirus isolate HPV18 P2-20 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY502092.1 Human papillomavirus isolate HPV18 P2-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct 9   CTTTGAGGATCCAACACGGC   28

>KY502091.1 Human papillomavirus isolate HPV18 P2 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502090.1 Human papillomavirus isolate HPV18 P1-50 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502089.1 Human papillomavirus isolate HPV18 P1-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502088.1 Human papillomavirus isolate HPV18 P1-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    CTTTGAGGATCCAACACGGC   20
           ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502086.1 Human papillomavirus isolate HPV18 P1-10 transforming protein
E6 (E6) gene, partial cds
Length=474

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KY502085.1 Human papillomavirus isolate HPV18 P1 transforming protein E6
(E6) gene, partial cds
Length=474

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KX545359.1 Human papillomavirus type 18 isolate NGSk274-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=516

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

>KX545354.1 Human papillomavirus type 18 isolate NGSk256-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=579

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    CTTTGAGGATCCAACACGGC   20
            ||||||||||||||||||||
Sbjct  9    CTTTGAGGATCCAACACGGC   28
```

BLAST INFORMATION

Database: Nucleotide collection (nt)

Posted date: Jul 8, 2017 5:09 AM

Number of letters in database: 150,093,331,920

Number of sequences in database: 43,324,577

Lambda   K   H

0.634   0.408   0.912

Gapped

Lambda   K   H

0.625   0.410   0.780

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 43324577

Number of Hits to DB: 753851

Number of extensions: 207

Number of successful extensions: 207

Number of sequences better than 10: 9

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 207

Number of HSP's successfully gapped: 9

Length of query: 20

Length of database: 150093331920

Length adjustment: 17

Effective length of query: 3

Effective length of database: 149356814111

Effective search space: 448070442333

Effective search space used: 448070442333

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 28 (26.5 bits)

S2: 38 (35.6 bits)

</form>
</div><!-- /#content -->
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="refo
<input name="QUERY_INFO" type="hidden" value="" />
<input name="ENTREZ_QUERY" type="hidden" value="" />
<input name="CDD_RID" type="hidden" value="" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />
<input name="RID" type="hidden" value="P7X8V4EJ015" />
<input name="STEP_NUMBER" type="hidden" value="" />

BLAST INFORMATION

```
<input name="CMD" type="hidden" value="Web"/>
<input NAME="PAGE_TYPE" type="hidden"  value="BlastFormatting"/>


<!-- TO DO: test all of those changes -->
<!-- Psi blast params  PSI_BLAST_PARAMS - commented- using forms[0] from fromatter> -->
<!-- Current Formatting options FORMATTING_OPTIONS- commented- using forms[0] from fromatter> -
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="setS
<input name="PAGE_TYPE" type="hidden" value="BlastSearch" />
<input name="VIEW_SEARCH" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="Web" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="saveO
<input name="SAVE" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="GetSaved" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from formatter> -->
</form>
</div><!-- /#content-wrap -->

<footer id="page_footer">
<div class="foot_wrap">
<div class="left col two_col">
BLAST is a registered trademark of the National Library of Medicine
</div>
<div class="right">
<a class="help_desk jig-ncbihelpwindow" target="_blank" href="https://support.ncbi.nlm.nih.gov
Ncbi_App=blast&amp;Page=oldblastresults&Time=2017-07-10T17:45:01&amp;Host=blast349&amp;ncbi_ph
</a>
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=MailList">Mailing list</a>
<a href="https://www.youtube.com/ncbinlm" target="_blank" id="page_footer_54">
<img class="icon-medium gray-medium" src="images/youtube.svg" alt="">
<span class="icon-fallback-text">YouTube</span>
</a>
</div>

</div>


<!-- bottom section of footer -->
<div class="col" id="contentinfo">
<ul class="right inline_list logos">
<li>
<a href="https://www.nlm.nih.gov" id="page_footer_60">
<img class="gray-medium" src="images/nlm-logo.svg" alt="">
```

BLAST INFORMATION

```
<span class="icon-fallback-text">National Library Of Medicine</span>
</a>
</li>
<li>
<a href="https://www.nih.gov" id="page_footer_61">
<img class="gray-medium" src="images/nih-logo.svg" alt="">
<span class="icon-fallback-text">National Institutes Of Health</span>
</a>
</li>
<li>
<a href="https://www.hhs.gov" id="page_footer_62">
<img class="gray-medium" src="images/hhs-logo.svg" alt="">
<span class="icon-fallback-text">U.S. Department of Health &amp; Human Services</span>
</a>
</li>
<li>
<a href="https://www.usa.gov" id="page_footer_63">
<img class="icon-large-wide gray-medium" src="images/usagov-logo.svg" alt="">
<span class="icon-fallback-text">USA.gov</span>
</a>
</li>
</ul>

<div class="footer_padding">

<div class="footer_border h-card">

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url" id="page_footer_64">
<h3 role="heading" aria-level="3" class="ncbi_blue p-org">NCBI</h3>
</a>

<address>

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url p-org" id="page_footer_65">National Cente
<a href="https://www.nlm.nih.gov/" id="page_footer_66"> U.S. National Library of Medicine</a>

<span class="h-adr">
<span class="p-street-address">8600 Rockville Pike</span>,
<span class="p-locality">Bethesda</span>
<span class="p-region"> MD</span>,
<span class="p-postal-code">20894</span>
<span class="p-country-name">USA</span>
</span>

</address>

</div>
```

BLAST INFORMATION

```
<div class="inline_list about_list">
<a href="https://www.ncbi.nlm.nih.gov/home/about/policies.shtml" id="page_footer_67">Policies a
|
<a href="https://www.ncbi.nlm.nih.gov/home/about/contact.shtml" id="page_footer_68">Contact</a
</div>
</div>
</div>
</footer>
<script type="text/javascript" src="js/header.js"> </script>
</div><!--/#wrap-->

<script type="text/javascript" src="js/utils.js"></script>
<script type="text/javascript" src="js/toggle.js"></script>
<script type="text/javascript" src="js/remote_data_provider.js"></script>
<script type="text/javascript" src="js/results.js"></script>
<script type="text/javascript" src="js/blast.js"></script>
<script type="text/javascript" src="js/format.js"></script>

<script type="text/javascript" src="/portal/portal3rc.fcgi/rlib/js/InstrumentOmnitureBaseJS/Ins
<!--
<script type="text/javascript" src="://www.ncbi.nlm.nih.gov/portal/portal3rc.fcgi/supportedbrow
<script type="text/javascript">$("#browsers_ajax").browserCheck();</script>
-->
</body>
</html>


<!DOCTYPE html PUBLIC "-//W3C//DTD XHTML 1.0 Transitional//EN" "http://www.w3.org/TR/xhtml1/DTI
<html xmlns="http://www.w3.org/1999/xhtml">
<head>

<meta http-equiv="Content-Type" content="text/html; charset=UTF-8" />
<meta http-equiv="X-UA-Compatible" content="IE=edge,chrome=1">
<meta name="jig" content="ncbitoggler ncbiautocomplete"/>
<meta name="ncbitoggler" content="animation:'none'"/>


<meta name="referrer" content="origin-when-cross-origin" />
<meta name="ncbi_app" content="blast" />
<meta name="ncbi_pdid" content="oldblastresults" />

<meta name="ncbi_db" content="nt" />
<meta name="ncbi_program" content="blastn" />
<meta name="ncbi_algorithm" content="blastn" />

<meta name="ncbi_stat" content="false" />
<meta name="ncbi_sessionid" content="50C9C897963F5781_0000SID" />
<meta name="ncbi_phid" content="50C9C897963F57810000000000000001" />
```

BLAST INFORMATION

```html
<script type="text/javascript"> var ncbi_startTime = new Date(); </script>
<title>NCBI Blast:Nucleotide Sequence (20 letters)</title>
<script type="text/javascript" src="/core/jig/1.14.8/js/jig.min.js          "></script>
<script type="text/javascript">    jQuery.getScript("/core/alerts/alerts.js", function() {
                                galert(['div#header', 'body > *:nth-child(1)'])
});</script>
<link rel="stylesheet" type="text/css" href="css/header.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/google-fonts.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/footer.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/main.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/blastRes.css" media="screen" />
<!--[if IE]>
<link rel="stylesheet" type="text/css" href="css/descriptionsIE.css" media="screen" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/print.css" media="print" />
<!--[if lte IE 6]>
<link rel="stylesheet" type="text/css" href="css/ie6_or_less.css" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/blastReq.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/results.css" media="screen" />


</head>

<body id="type-a" class="noToggleCheck " >
<div id="wrap">

<header id="page_header" role="banner">
<ul class="skip_nav">
<li><a accesskey="1" title="NCBI Homepage" href="https://www.ncbi.nlm.nih.gov/">NCBI Home</a><
<li><a accesskey="2" title="MyNCBI" href="https://www.ncbi.nlm.nih.gov/myncbi">Sign in to NCBI<
<li><a accesskey="3" title="Skip to main content" href="#content">Skip to Main Content</a></li
<li><a accesskey="4" title="Skip to navigation" href="#navcontent">Skip to Navigation</a></li>
<li><a accesskey="0" title="About NCBI Accesskeys" href="https://www.ncbi.nlm.nih.gov/guide/br
</ul>
<nav class="blue_nav_bar">
<div class="nih">
<a id="page_header_6" href="https://www.nih.gov/" class="left norm_height">
<img src="images/nih_logo.svg" alt="NIH logo" class="left"/></a>
<a id="page_header_7" href="https://www.nlm.nih.gov/" class="left header_link">U.S. National L
</div>

<div class="left">
<img src="images/arrow.svg" class="left norm_height" alt=""/>
</div>
```

BLAST INFORMATION

```
<div class="ncbi">
<a id="page_header_8" href="https://www.ncbi.nlm.nih.gov/" class="header_link">
<span class="ncbi_name">NCBI</span>
<span class="med_hidden">National Center for Biotechnology Information</span></a>

<div class="right sign-in">
<ul class="myncbi2">
<li id="myncbiusername">
<span id="mnu">
<a id="mnu_0" href="https://www.ncbi.nlm.nih.gov/account/settings/" title="Edit account setting
</span>
</li>
<li id="myncbi"><a id="myncbi_0"  href="https://www.ncbi.nlm.nih.gov/myncbi/">My NCBI</a></li>
<li id="myncbi_sign_in"><a id="myncbi_sign_in_0" href="https://www.ncbi.nlm.nih.gov/account/?ba
<li id="myncbi_register"><a id="myncbi_register_0" href="https://www.ncbi.nlm.nih.gov/account/
<li id="myncbi_sign_out"><a id="myncbi_sign_out_0" href="https://www.ncbi.nlm.nih.gov/account/
</ul>
</div>
</div>
</nav>

<div class="bg-gray header-div">
<nav class="top-nav" id="navcontent" role="navigation">
<a class="lf" href="Blast.cgi">BLAST <sup>&reg;</sup></a> <span id="brc"><span class="brcrmbsig
<span class="rf">
<ul id="blnav">
<li  class="first "><a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastHome" title="BLAST Home">Home
<li  class="recent "><a href="Blast.cgi?CMD=GetSaved&amp;RECENT_RESULTS=on" title="Unexpired Bl
<li  class="saved "><a href="Blast.cgi?CMD=GetSaved" title="Saved sets of BLAST search paramete
<li  class= "last documentation "> <a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs" title="
</ul>
</span>
</nav>
</div>
</header>

<div id="content-wrap">

<div class="pageTitle">
BLAST Results
</div>
<div class="inlineDiv resHeader resPage">

</div>
<ul class="print-log-res"><li></li></ul>

<!-- CDD info for old design -->
```

BLAST INFORMATION

```html
<div id="content">

<!--<ul id="msg" class="msg"><li class=""><p class=""></p><p class=""></p><p class=""></p></li
<ul id="msg" class="msg"><li class=""></li></ul>
<a  href="#" class="resLink resPage" id="searchOptions" submitForm="setSavedOptions">Edit and
<a  href="#" class="resLink resPage hidden" id="saveSearchOptions" submitForm="saveOptions">Sav
<span class="reslink  resPage" >[Sign in above to save your search strategy]</span>
<a  id="showFormat" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggler
<span class="ui-ncbitoggler-master-text">Formatting options </span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<a  id="showDownload" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggle
<span class="ui-ncbitoggler-master-text">Download</span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<span id="hnr">
<a id="ytb" class="ytb " title="External link to YouTube" href="https://www.youtube.com/playli
<a id="brFtp" class="" title="Blast report description" href="ftp://ftp.ncbi.nlm.nih.gov/pub/fa
</span>
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST" id="results

<input name="QUERY_INDEX" type="hidden" value="0">
<input name="_PGR" type="hidden" value="" >
<input id="seqViewUrl" type="hidden" value="https://www.ncbi.nlm.nih.gov" >
<input id="userAgent" type="hidden" value="">
<input name="CMD" type="hidden" value="Get">
</form>
<!-- Reformat and downlaod for new design -->
<div class="ui-helper-reset" aria-live="assertive" >
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="Format
<table class="options blastn ">
<tr>
<td class="frh" colspan=2>
<div class="fi">
<div class="tb">Formatting options</div>
<input type="image"  border="0" id="onPageReformat" src="css/images/reformat.jpg" class="blast
</div>
</tr>
<tr class="paramSet xgl">
```

BLAST INFORMATION

```
<td class="hd"><label for="FORMAT_OBJECT">Show</label></td>
<td>
<div class="fi">
<input type="hidden" id="FORMAT_OBJECT" value="Alignment" name="FORMAT_OBJECT" />
<label for="FORMAT_TYPE" id="nft">Alignment as</label>
<select name="FORMAT_TYPE" id="FORMAT_TYPE" class="reset" defVal="HTML">
<option value="HTML"  >HTML</option>
<option value="Text"  >Plain text</option>

</select>

<span id="advView" class="">
<span class=""><input name="OLD_VIEW" id="OLD_VIEW" type="checkbox" class="cb reset" defVal="u
<label for="OLD_VIEW">Old View</label></span>
</span>
<a class="resetAll" id="resetAll" >Reset form to defaults</a>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments object formatting
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp1">
These options control formatting of alignments in results pages. The
default is HTML, but other formats (including plain text) are available.
PSSM and PssmWithParameters are representations of Position Specific Scoring Matrices and are
The Advanced view option allows the database descriptions to be sorted by various indices in a
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="odd paramSet">
<td class="hd"><label for="ALIGNMENT_VIEW">Alignment View</label></td>
<td>
<div class="fi">
<select name="ALIGNMENT_VIEW" id="ALIGNMENT_VIEW" defVal="Pairwise" class="reset">
<option value="Pairwise" selected="selected" >Pairwise</option>
<option value="PairwiseWithIdentities"  >Pairwise with dots for identities</option>
<option value="QueryAnchored"  >Query-anchored with dots for identities</option>
<option value="QueryAnchoredNoIdentities"  >Query-anchored with letters for identities</option
<option value="FlatQueryAnchored"  >Flat query-anchored with dots for identities</option>
<option value="FlatQueryAnchoredNoIdentities"  >Flat query-anchored with letters for identitie

</select>


<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments view options help
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
```

BLAST INFORMATION

```
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp2">
Choose how to view alignments.
The default "pairwise" view shows how each subject sequence aligns
individually to the query sequence. The "query-anchored" view shows how
all subject sequences align to the query sequence. For each view type,
you can choose to show "identities" (matching residues) as letters or
dots.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#alignment_view" targe
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet">
<td class="hd"><label>Display</label></td>
<td class="cb">
<div class="fi">
<input name="SHOW_OVERVIEW" id="SHOW_OVERVIEW" type="checkbox" class="cb reset" defVal="checke
<label class="rb" for="SHOW_OVERVIEW">Graphical Overview</label>

<span id="shl" >
<input name="SHOW_LINKOUT" id="SHOW_LINKOUT" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="SHOW_LINKOUT">Linkout</label>
</span>
<span id="gts" >
<input name="GET_SEQUENCE" id="GET_SEQUENCE" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="GET_SEQUENCE">Sequence Retrieval</label>
</span>

<input name="NCBI_GI" id="NCBI_GI" type="checkbox" class="cb reset" defVal="unchecked" false /
<label class="rb" for="NCBI_GI">NCBI-gi</label>
<span id="scf" >
<input name="SHOW_CDS_FEATURE" id="SHOW_CDS_FEATURE" type="checkbox" class="cb reset blastn" d
<label for="SHOW_CDS_FEATURE" class="blastn">CDS feature</label>
</span>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments display options h
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp3">
<li>Graphical Overview: Graphical Overview: Show graph of similar sequence regions aligned to
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_overview" target
</li>
<li>NCBI-gi: Show NCBI gi identifiers.
</li>
<li>CDS feature: Show annotated coding region and translation.
```

BLAST INFORMATION

```
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_cds_feature" ti
</li></ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"><label>Masking</label></td>
<td>
<div class="fi">
<label for="MASK_CHAR"> Character: </label>
<select name="MASK_CHAR" id="MASK_CHAR"  class="reset" defVal="2">
<option value="0"  >X for protein, n for nucleotide</option>
<option value="2" selected="selected" >Lower Case</option>
</select>
<label for="MASK_COLOR"> Color:</label>
<select name="MASK_COLOR" id="MASK_COLOR" class="reset" defVal="1">
<option value="0"  >Black
</option>

<option value="1" selected="selected" >Grey
</option>

<option value="2"  >Red
</option>

</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments masking help" id=
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp4">
<li>Masking Character: Display masked (filtered) sequence regions as lower-case or as specific
</li>
<li>Masking Color: Display masked sequence regions in the given color.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr id="lr" class="paramSet xgl">
<td class="hd"><label>Limit results</label></td>
<td>
<div class="fi">
```

BLAST INFORMATION

```html
<label for="FRM_DESCRIPTIONS">Descriptions:</label>
<select name="DESCRIPTIONS" id="FRM_DESCRIPTIONS" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"    >1000</option>
<option value="5000"    >5000</option>
<option value="10000"   >10000</option>
<option value="20000"   >20000</option>
</select>

<label for="FRM_NUM_OVERVIEW">Graphical overview:</label>
<select name="NUM_OVERVIEW" id="FRM_NUM_OVERVIEW" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"   >500</option>
<option value="1000"    >1000</option>
</select>
<span id="frmAln">
<label for="FRM_ALIGNMENTS">Alignments:</label>
<select name="ALIGNMENTS" id="FRM_ALIGNMENTS" class="reset" defVal="100">
<option value="0"       >0</option>
<option value="10"      >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"     >100</option>
<option value="250"     >250</option>
<option value="500"     >500</option>
<option value="1000"    >1000</option>
<option value="5000"    >5000</option>
<option value="10000"   >10000</option>
<option value="20000"   >20000</option>
</select>
</span>
<label for="FRM_LINE_LENGTH">Line length:</label>
<select name="LINE_LENGTH" id="FRM_LINE_LENGTH" class="reset" defVal="60">
<option value="60"    selected="selected" >60</option>
<option value="90"       >90</option>
<option value="120"       >120</option>
<option value="150"       >150</option>
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit number of descriptions
```

BLAST INFORMATION

```html
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp5">
<li>Descriptions: Show short descriptions for up to the given number of  sequences.</li>
<li>Alignments:  Show alignments for up to the given number of sequences, in order of statistic
<li>Line lenghth:  Number of letters to show on one line in an alignment.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl ">
<td class="hd"></td>
<td>
<div class="">
<label for="qorganism">Organism</label>
<span class="instr">Type common name, binomial, taxid, or group name. Only 20 top taxa will be
<input name="FORMAT_ORGANISM" size="55"  type="text" id="qorganism" value="" data-jigconfig="d
<input type="checkbox" name="FORMAT_ORG_EXCLUDE"  class="oExclR cb" id="orgExcl"/>
<input type="hidden" value = "1" name="FORMAT_NUM_ORG" id="numOrg" />
<label for="orgExcl" class="right">Exclude</label>
<a href="#" title="Add organism" id="addOrg"><img border="0" src="css/images/addOrg.jpg" id="a
<div id="orgs">

</div>
<div class="fi">
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by organism he
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp6">
Show only sequences from the given organism.
</p>
</div><!-- ARIA -->
</div>
</div>
</td>
</tr>

<tr class="paramSet xgl ">
<td class="hd"></td>
<td>
<div class="fi">
<label for="FORMAT_EQ_TEXT">Entrez query:</label>
<input name="FORMAT_EQ_TEXT" id="FORMAT_EQ_TEXT" size="60" type="text" value="" class="reset" 
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by Entrez query
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
```

BLAST INFORMATION

```
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp7">
Show only those sequences that match the given Entrez query.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#limit_result" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="EXPECT_LOW">Expect Min:</label> <input name="EXPECT_LOW" id="EXPECT_LOW" size="10"
<label for="EXPECT_HIGH">Expect Max:</label> <input name="EXPECT_HIGH" id="EXPECT_HIGH" size="
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by expect valu
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp8">
Show only sequences with expect values in the given range.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#expect_range" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="paramSet xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="PERC_IDENT_LOW">Percent Identity Min:</label> <input name="PERC_IDENT_LOW" id="PERC
<label for="PERC_IDENT_HIGH">Percent Identity Max:</label> <input name="PERC_IDENT_HIGH" id="P
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by percent iden
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp10">
Show only sequences with percent identity values in the given range.
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="psiBlast odd paramSet xgl">
<td class="hd"><label>Format for</label></td>
<td>
```

BLAST INFORMATION

```html
<div class="fi">
<input name="RUN_PSIBLAST_FORM" id="RUN_PSIBLAST" type="checkbox" class="cb psiBlast"  />
<label class="rb psiBlast" for="RUN_PSIBLAST">PSI-BLAST</label>
<label for="I_THRESH">with inclusion threshold:</label>
<input name="I_THRESH" id="I_THRESH" size="10" type="text" value="" defVal="0.005" />
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="PSI BLAST formatting help" i
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp9">
<li>Format for PSI-BLAST: The Position-Specific Iterated BLAST (PSI-BLAST) program performs ite
in which sequences found in one round of search are used to build a custom score model for the
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#psiblast" target="he
</li>
<li>Inclusion Threshold: This sets the statistical significance threshold for including a seque
by PSI-BLAST to create the PSSM on the next iteration.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>
</table>


<input name="ViewReport" value="ViewReport" type="hidden" />
<input name="REFORMAT_REPORT" value="shown" type="hidden" />
<input name="RID" value="P7XAXRST014" type="hidden" />
<input name="CDD_RID" value="" type="hidden" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />

<input name="STEP_NUMBER" value="" id="stepNumber" type="hidden" />
<input name="CMD" value="Get" type="hidden" />
<input name="FORMAT_EQ_OP" value="AND" type="hidden" />
<input name="RESULTS_PAGE_TARGET" type="hidden" id="resPageTarget" value="" />
<!-- <input name="QUERY_INFO" type="hidden" value="" /> -->
<!-- <input name="ENTREZ_QUERY" type="hidden" value="" /> -->
<input name="QUERY_INDEX" type="hidden" value="0"/>
<input name="NUM_QUERIES" type="hidden" value="1"/>

<!-- Those params are set in the template (blastn.dat, blastp.dat etc. -->
<input name="BLAST_PROGRAMS" type="hidden" value="blastn"/>
<input name="PAGE" type="hidden" value="Nucleotides"/>
<input name="PROGRAM" type="hidden" value="blastn"/>
<input name="MEGABLAST" type="hidden" value="" />
<input name="RUN_PSIBLAST" type="hidden" value="" />
<input name="BLAST_SPEC" id="blastSpec" type="hidden" value=""/>
```

BLAST INFORMATION

```
<input name="QUERY" type="hidden" value="GCTTTGAGGATCCAACACGG"/>
<input name="JOB_TITLE" type="hidden" value="Nucleotide Sequence (20 letters)"/>
<input name="QUERY_TO" type="hidden" value=""/>
<input name="QUERY_FROM" type="hidden" value=""/>
<input name="SUBJECTS_FROM" type="hidden" value=""/>
<input name="SUBJECTS_TO" type="hidden" value=""/>
<input name="EQ_TEXT" type="hidden" value=""/>
<input name="ORGN" type="hidden" value=""/>
<input name="EQ_MENU" type="hidden" value=""/>
<input name="ORG_EXCLUDE" type="hidden" value=""/>
<input name="PHI_PATTERN" type="hidden" value=""/>
<input name="EXPECT" type="hidden" value="10"/>
<input name="DATABASE" type="hidden" value="nt"/>
<input name="DB_GROUP" type="hidden" value=""/>
<input name="SUBGROUP_NAME" type="hidden" value=""/>

<input name="GENETIC_CODE" type="hidden" value=""/>
<input name="WORD_SIZE" type="hidden" value="11"/>
<input name="MATCH_SCORES" type="hidden" value="2,-3"/>
<input name="MATRIX_NAME" type="hidden" value=""/>
<input name="GAPCOSTS" type="hidden" value="5 2"/>
<input name="MAX_NUM_SEQ" id="maxNumSeq" type="hidden" value="50"/>
<input name="COMPOSITION_BASED_STATISTICS" type="hidden" value=""/>
<input name="NEWWIN" type="hidden" value=""/>
<input name="SHORT_QUERY_ADJUST" type="hidden" value=""/>
<input name="FILTER" type="hidden" value="L;m;"/>
<input name="REPEATS" type="hidden" value=""/>
<input name="ID_FOR_PSSM" type="hidden" value=""/>
<input name="EXCLUDE_MODELS" type="hidden" value=""/>
<input name="EXCLUDE_SEQ_UNCULT" type="hidden" value=""/>
<input name="WP_PROTEINS" type="hidden" value=""/>
<input name="SEQ_FROM_TYPE" type="hidden" value=""/>
<input name="ENTREZ_QUERY" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET_EXCL" type="hidden" value=""/>
<input name="NUM_ORG" type="hidden" value = "1" />

<!-- PSSM -->
<input name="LCASE_MASK" type="hidden" value=""/>
<input name="TEMPLATE_TYPE" type="hidden" value=""/>
<input name="TEMPLATE_LENGTH" type="hidden" value=""/>
<input name="I_THRESH" type="hidden" value=""/>
<input name="PSI_PSEUDOCOUNT" type="hidden" value=""/>
<input name="DI_THRESH" type="hidden" id="diThresh" value=""/>
<input name="HSP_RANGE_MAX" type="hidden" value="0"/>
```

BLAST INFORMATION

```
<input name="ADJUSTED_FOR_SHORT_QUERY" type="hidden" value=""/>
<input name="MIXED_QUERIES" type="hidden" value=""/>
<input name="MIXED_DATABASE" id="mixedDb" type="hidden" value=""/>
<input name="BUILD_NAME"  type="hidden" value=""/>
<input name="ORG_DBS"  type="hidden" value=""/>
<input name="WWW_BLAST_TYPE" type="hidden" value="newblast"/>


</form>
</div> <!-- aria -->
<div class="ui-helper-reset" aria-live="assertive" >
<form  name="FormatDownload" id="FormatDownload" class="resbox ui-ncbitoggler-slave">
<table class="options dwnl blastn ">
<tr><td class="frh" colspan=6><div class="tb">Download</div></td></tr>
<tr>
<td id="tdal">
<div class="dnHeader">Alignment</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=Text&FORMAT_OBJECT=Alignment&D
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=XML&FORMAT_OBJECT=2
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=Alignment&C
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=JSONSA&FORMAT_OBJECT=Alignment&
<a  id="hitText" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=Text&FORMAT_OBJECT
<a  id="hitCvs" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=CSV&FORMAT_OBJECT=2
<a  class="xgl" href="Blast.cgi?RID=P7XAXRST014&FORMAT_TYPE=XML2&FORMAT_OBJECT=Alignment&CMD=Ge
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=XML2_S&FORMAT_OBJEC
<a  class="xgl" href="Blast.cgi?RID=P7XAXRST014&FORMAT_TYPE=JSON2&FORMAT_OBJECT=Alignment&CMD=C
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=JSON2_S&FORMAT_OBJ
<a  class="xgl blastn" href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=SAM_SQ&FORM
</div>
</td>
<td class="dnl xgl">
<div class="dnHeader">Search Strategies</div>
<div class="dnLinks">
<a  href="Blast.cgi?CMD=GetSaved&RECENT_RESULTS=on&RID=P7XAXRST014&DOWNLOAD_OPTIONS=true">ASN.
</div>
</td>
<td class="dnl" id="dnPSSMPar">
<div class="dnHeader">PSSM to restart search</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XAXRST014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=PSSM_Score
</div>
</td>
<td>
<a class="helplink ui-ncbitoggler" data-jig="ncbitoggler" title="Download help" data-ncbitoggle
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
</td>
```

BLAST INFORMATION
```
</tr>
</table>
<div class="ui-helper-reset" aria-live="assertive" >
<div class="helpbox ui-ncbitoggler-slave" id="hlp11">
The Download link provides BLAST output that may be used as input to another program.
This includes parseable formats such as the tabular report or XML as well as the Search Strateg
More details on the parseable (XML, tabular, and ASN.1) reports can be found at
<a href="https://www.ncbi.nlm.nih.gov/books/NBK153387/" target="helpWin" >https://www.ncbi.nlm
<br/>
<p>
The following formats are offered under the Alignment section:<br/>
1). "Text". Non-HTML standard BLAST report.<br/>
2). "XML". XML report based upon the DTD at <a href="https://www.ncbi.nlm.nih.gov/data_specs/d
3). "ASN.1". Alignment written out in Abstract Syntax Notation 1.<br/>
4). "JSON Seq-align". Alignment written out in JSON.<br/>
4). "Hit Table(text)". The tabular report as text.<br/>
5). "Hit Table(csv)". The tabular report ready for import into spread-sheet programs like Excel
6). "XML2". New XML format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NEW
7). "JSON". New JSON format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NE
8). "SAM". Sequence Alignment Map format.<br/>
</p>
<p>
XML2 and JSON can be downloaded either as one file per query (multiple-file) or one file for al
</p>
<p>
The following report is offered under the Search Strategy section:<br/>
1). "ASN.1" Search Strategy. A record of the parameters, query, and database used in the search
<a href="https://www.ncbi.nlm.nih.gov/books/NBK1763/#CmdLineAppsManual.I455_BLAST_search_stra"
</p>
</div>
</div><!-- ARIA -->
</form>
</div> <!-- aria -->
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST"  name="over

<input name="CMD" type="hidden" value="">
<p><!--
QBlastInfoBegin
Status=READY
QBlastInfoEnd
--><p>
<PRE>
BLASTN 2.6.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
```

RID: P7XAXRST014

Database: Nucleotide collection (nt)
43,324,577 sequences; 150,093,331,920 total letters
Query=
Length=20


```
                                                             Score    E
Sequences producing significant alignments:                 (Bits)  Value

KY457840.1  Human papillomavirus type 18 strain 18CNTZ36 E6 (E...  37.4   2.6
KY457839.1  Human papillomavirus type 18 strain 18CNTZ35 E6 (E...  37.4   2.6
KY457838.1  Human papillomavirus type 18 strain 18CNTZ34 E6 (E...  37.4   2.6
KY457837.1  Human papillomavirus type 18 strain 18CNTZ33 E6 (E...  37.4   2.6
KY457836.1  Human papillomavirus type 18 strain 18CNTZ32 E6 (E...  37.4   2.6
KY457835.1  Human papillomavirus type 18 strain 18CNTZ31 E6 (E...  37.4   2.6
KY457834.1  Human papillomavirus type 18 strain 18CNTZ30 E6 (E...  37.4   2.6
KY457833.1  Human papillomavirus type 18 strain 18CNTZ29 E6 (E...  37.4   2.6
KY457832.1  Human papillomavirus type 18 strain 18CNTZ28 E6 (E...  37.4   2.6
KY457831.1  Human papillomavirus type 18 strain 18CNTZ27 E6 (E...  37.4   2.6
KY457830.1  Human papillomavirus type 18 strain 18CNTZ26 E6 (E...  37.4   2.6
KY457829.1  Human papillomavirus type 18 strain 18CNTZ25 E6 (E...  37.4   2.6
KY457828.1  Human papillomavirus type 18 strain 18CNTZ24 E6 (E...  37.4   2.6
KY457827.1  Human papillomavirus type 18 strain 18CNTZ23 E6 (E...  37.4   2.6
KY457826.1  Human papillomavirus type 18 strain 18CNTZ22 E6 (E...  37.4   2.6
KY457825.1  Human papillomavirus type 18 strain 18CNTZ21 E6 (E...  37.4   2.6
KY457824.1  Human papillomavirus type 18 strain 18CNTZ20 E6 (E...  37.4   2.6
KY457823.1  Human papillomavirus type 18 strain 18CNTZ19 E6 (E...  37.4   2.6
KY457822.1  Human papillomavirus type 18 strain 18CNTZ18 E6 (E...  37.4   2.6
KY457821.1  Human papillomavirus type 18 strain 18CNTZ17 E6 (E...  37.4   2.6
KY457820.1  Human papillomavirus type 18 strain 18CNTZ16 E6 (E...  37.4   2.6
KY457819.1  Human papillomavirus type 18 strain 18CNTZ15 E6 (E...  37.4   2.6
KY457818.1  Human papillomavirus type 18 strain 18CNTZ14 E6 (E...  37.4   2.6
KY457817.1  Human papillomavirus type 18 strain 18CNTZ13 E6 (E...  37.4   2.6
KY457816.1  Human papillomavirus type 18 strain 18CNTZ12 E6 (E...  37.4   2.6
KY457815.1  Human papillomavirus type 18 strain 18CNTZ11 E6 (E...  37.4   2.6
KY457814.1  Human papillomavirus type 18 strain 18CNTZ10 E6 (E...  37.4   2.6
KY457813.1  Human papillomavirus type 18 strain 18CNTZ09 E6 (E...  37.4   2.6
KY457812.1  Human papillomavirus type 18 strain 18CNTZ08 E6 (E...  37.4   2.6
KY457811.1  Human papillomavirus type 18 strain 18CNTZ07 E6 (E...  37.4   2.6
KY457810.1  Human papillomavirus type 18 strain 18CNTZ06 E6 (E...  37.4   2.6
KY457809.1  Human papillomavirus type 18 strain 18CNTZ05 E6 (E...  37.4   2.6
```

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

```
||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG  20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG  20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG  20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457828.1 Human papillomavirus type 18 strain 18CNTZ24 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||
Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457827.1 Human papillomavirus type 18 strain 18CNTZ23 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
            ||||||||||||||||||||
Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457826.1 Human papillomavirus type 18 strain 18CNTZ22 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
            ||||||||||||||||||||
Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457825.1 Human papillomavirus type 18 strain 18CNTZ21 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
            ||||||||||||||||||||
Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457824.1 Human papillomavirus type 18 strain 18CNTZ20 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457823.1 Human papillomavirus type 18 strain 18CNTZ19 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457822.1 Human papillomavirus type 18 strain 18CNTZ18 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
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>KY457821.1 Human papillomavirus type 18 strain 18CNTZ17 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
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>KY457820.1 Human papillomavirus type 18 strain 18CNTZ16 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds

BLAST INFORMATION

Length=2502

Score = 37.4 bits (40), Expect = 2.6
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Query 1   GCTTTGAGGATCCAACACGG   20
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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457819.1 Human papillomavirus type 18 strain 18CNTZ15 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||
Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457818.1 Human papillomavirus type 18 strain 18CNTZ14 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20
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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457817.1 Human papillomavirus type 18 strain 18CNTZ13 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20
            ||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457816.1 Human papillomavirus type 18 strain 18CNTZ12 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
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Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457815.1 Human papillomavirus type 18 strain 18CNTZ11 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
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Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457814.1 Human papillomavirus type 18 strain 18CNTZ10 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG 20
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Sbjct 8   GCTTTGAGGATCCAACACGG 27

>KY457813.1 Human papillomavirus type 18 strain 18CNTZ09 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6

BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457812.1 Human papillomavirus type 18 strain 18CNTZ08 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457811.1 Human papillomavirus type 18 strain 18CNTZ07 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY457810.1 Human papillomavirus type 18 strain 18CNTZ06 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

BLAST INFORMATION

>KY457809.1 Human papillomavirus type 18 strain 18CNTZ05 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG  20
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Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457808.1 Human papillomavirus type 18 strain 18CNTZ04 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG  20
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Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457807.1 Human papillomavirus type 18 strain 18CNTZ03 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG  20
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Sbjct  8    GCTTTGAGGATCCAACACGG  27
```

>KY457806.1 Human papillomavirus type 18 strain 18CNTZ02 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY457805.1 Human papillomavirus type 18 strain 18CNTZ01 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KX514433.1 Human papillomavirus type 18 isolate pam9, complete genome
Length=7857

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Strand=Plus/Plus

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>KY502096.1 Human papillomavirus isolate HPV18 P2-50 transforming protein
E6 (E6) gene, partial cds
Length=474

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```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY502095.1 Human papillomavirus isolate HPV18 P2-40 transforming protein
E6 (E6) gene, partial cds
Length=474

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCTTTGAGGATCCAACACGG  20
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Sbjct  8   GCTTTGAGGATCCAACACGG  27
```

>KY502094.1 Human papillomavirus isolate HPV18 P2-30 transforming protein
E6 (E6) gene, partial cds
Length=474

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCTTTGAGGATCCAACACGG  20
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Sbjct  8   GCTTTGAGGATCCAACACGG  27
```

>KY502093.1 Human papillomavirus isolate HPV18 P2-20 transforming protein
E6 (E6) gene, partial cds
Length=474

```
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Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCTTTGAGGATCCAACACGG  20
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Sbjct  8   GCTTTGAGGATCCAACACGG  27
```

>KY502092.1 Human papillomavirus isolate HPV18 P2-10 transforming protein
E6 (E6) gene, partial cds
Length=474

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   GCTTTGAGGATCCAACACGG  20
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Sbjct  8   GCTTTGAGGATCCAACACGG  27
```

>KY502091.1 Human papillomavirus isolate HPV18 P2 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20
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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY502090.1 Human papillomavirus isolate HPV18 P1-50 transforming protein
E6 (E6) gene, partial cds
Length=474

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Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY502089.1 Human papillomavirus isolate HPV18 P1-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20
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Sbjct 8   GCTTTGAGGATCCAACACGG   27

>KY502088.1 Human papillomavirus isolate HPV18 P1-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY502086.1 Human papillomavirus isolate HPV18 P1-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KY502085.1 Human papillomavirus isolate HPV18 P1 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KX545359.1 Human papillomavirus type 18 isolate NGSk274-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=516

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    GCTTTGAGGATCCAACACGG   20
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Sbjct  8    GCTTTGAGGATCCAACACGG   27
```

>KX545354.1 Human papillomavirus type 18 isolate NGSk256-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds

BLAST INFORMATION

Length=579

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   GCTTTGAGGATCCAACACGG   20

||||||||||||||||||||

Sbjct 8   GCTTTGAGGATCCAACACGG   27

Database: Nucleotide collection (nt)

Posted date: Jul 8, 2017 5:09 AM

Number of letters in database: 150,093,331,920

Number of sequences in database: 43,324,577

Lambda   K   H

0.634   0.408   0.912

Gapped

Lambda   K   H

0.625   0.410   0.780

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 43324577

Number of Hits to DB: 799697

Number of extensions: 249

Number of successful extensions: 249

Number of sequences better than 10: 17

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 249

Number of HSP's successfully gapped: 17

Length of query: 20

Length of database: 150093331920

Length adjustment: 17

Effective length of query: 3

Effective length of database: 149356814111

Effective search space: 448070442333

Effective search space used: 448070442333

A: 0

X1: 22 (20.1 bits)

X2: 33 (29.8 bits)

X3: 110 (99.2 bits)

S1: 28 (26.5 bits)

S2: 38 (35.6 bits)

BLAST INFORMATION

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<!-- TO DO: test all of those changes -->
<!-- Psi blast params  PSI_BLAST_PARAMS - commented- using forms[0] from fromatter> -->
<!-- Current Formatting options FORMATTING_OPTIONS- commented- using forms[0] from fromatter> 
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</div><!-- /#content-wrap -->

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<div class="left col two_col">
BLAST is a registered trademark of the National Library of Medicine
</div>
<div class="right">
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Ncbi_App=blast&amp;Page=oldblastresults&Time=2017-07-10T17:45:28&amp;Host=blast339&amp;ncbi_ph
</a>
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=MailList">Mailing list</a>
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BLAST INFORMATION

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<!-- bottom section of footer -->
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BLAST INFORMATION

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<span class="p-postal-code">20894</span>
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<meta name="referrer" content="origin-when-cross-origin" />
<meta name="ncbi_app" content="blast" />
```

BLAST INFORMATION

```html
<meta name="ncbi_pdid" content="oldblastresults" />

<meta name="ncbi_db" content="nt" />
<meta name="ncbi_program" content="blastn" />
<meta name="ncbi_algorithm" content="blastn" />

<meta name="ncbi_stat" content="false" />
<meta name="ncbi_sessionid" content="5AABF963963F5951_0000SID" />
<meta name="ncbi_phid" content="5AABF963963F59510000000000000001" />
<script type="text/javascript"> var ncbi_startTime = new Date(); </script>
<title>NCBI Blast:Nucleotide Sequence (20 letters)</title>
<script type="text/javascript" src="/core/jig/1.14.8/js/jig.min.js          "></script>
<script type="text/javascript">    jQuery.getScript("/core/alerts/alerts.js", function() {
                                galert(['div#header', 'body > *:nth-child(1)'])
});</script>
<link rel="stylesheet" type="text/css" href="css/header.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/google-fonts.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/footer.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/main.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/blastRes.css" media="screen" />
<!--[if IE]>
<link rel="stylesheet" type="text/css" href="css/descriptionsIE.css" media="screen" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/print.css" media="print" />
<!--[if lte IE 6]>
<link rel="stylesheet" type="text/css" href="css/ie6_or_less.css" />
<![endif]-->
<link rel="stylesheet" type="text/css" href="css/blastReq.css" media="screen" />
<link rel="stylesheet" type="text/css" href="css/results.css" media="screen" />


</head>

<body id="type-a" class="noToggleCheck " >
<div id="wrap">

<header id="page_header" role="banner">
<ul class="skip_nav">
<li><a accesskey="1" title="NCBI Homepage" href="https://www.ncbi.nlm.nih.gov/">NCBI Home</a><
<li><a accesskey="2" title="MyNCBI" href="https://www.ncbi.nlm.nih.gov/myncbi">Sign in to NCBI
<li><a accesskey="3" title="Skip to main content" href="#content">Skip to Main Content</a></li
<li><a accesskey="4" title="Skip to navigation" href="#navcontent">Skip to Navigation</a></li>
<li><a accesskey="0" title="About NCBI Accesskeys" href="https://www.ncbi.nlm.nih.gov/guide/bro
</ul>
<nav class="blue_nav_bar">
<div class="nih">
<a id="page_header_6" href="https://www.nih.gov/" class="left norm_height">
```

```html
<img src="images/nih_logo.svg" alt="NIH logo" class="left"/></a>
<a id="page_header_7" href="https://www.nlm.nih.gov/" class="left header_link">U.S. National L
</div>


<div class="left">
<img src="images/arrow.svg" class="left norm_height" alt=""/>
</div>



<div class="ncbi">
<a id="page_header_8" href="https://www.ncbi.nlm.nih.gov/" class="header_link">
<span class="ncbi_name">NCBI</span>
<span class="med_hidden">National Center for Biotechnology Information</span></a>

<div class="right sign-in">
<ul class="myncbi2">
<li id="myncbiusername">
<span id="mnu">
<a id="mnu_0" href="https://www.ncbi.nlm.nih.gov/account/settings/" title="Edit account setting
</span>
</li>
<li id="myncbi"><a id="myncbi_0"  href="https://www.ncbi.nlm.nih.gov/myncbi/">My NCBI</a></li>
<li id="myncbi_sign_in"><a id="myncbi_sign_in_0" href="https://www.ncbi.nlm.nih.gov/account/?ba
<li id="myncbi_register"><a id="myncbi_register_0" href="https://www.ncbi.nlm.nih.gov/account/r
<li id="myncbi_sign_out"><a id="myncbi_sign_out_0" href="https://www.ncbi.nlm.nih.gov/account/s
</ul>
</div>
</div>
</nav>

<div class="bg-gray header-div">
<nav class="top-nav" id="navcontent" role="navigation">
<a class="lf" href="Blast.cgi">BLAST <sup>&reg;</sup></a> <span id="brc"><span class="brcrmbsig
<span class="rf">
<ul id="blnav">
<li  class="first "><a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastHome" title="BLAST Home">Home
<li  class="recent "><a href="Blast.cgi?CMD=GetSaved&amp;RECENT_RESULTS=on" title="Unexpired Bl
<li  class="saved "><a href="Blast.cgi?CMD=GetSaved" title="Saved sets of BLAST search paramete
<li  class= "last documentation "> <a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs" title="
</ul>
</span>
</nav>
</div>
</header>

<div id="content-wrap">
```

BLAST INFORMATION

```
<div class="pageTitle">
BLAST Results
</div>
<div class="inlineDiv resHeader resPage">

</div>
<ul class="print-log-res"><li></li></ul>


<!-- CDD info for old design -->
```

```
<div id="content">

<!--<ul id="msg" class="msg"><li class=""><p class=""></p><p class=""></p><p class=""></p></li
<ul id="msg" class="msg"><li class=""></li></ul>
<a  href="#" class="resLink resPage" id="searchOptions" submitForm="setSavedOptions">Edit and 
<a  href="#" class="resLink resPage hidden" id="saveSearchOptions" submitForm="saveOptions">Sav
<span class="reslink  resPage" >[Sign in above to save your search strategy]</span>
<a  id="showFormat" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggler"
<span class="ui-ncbitoggler-master-text">Formatting options </span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<a  id="showDownload" class="resLink resPage resArrowLinkB ui-ncbitoggler" data-jig="ncbitoggle
<span class="ui-ncbitoggler-master-text">Download</span>
<span class="ui-icon ui-icon-triangle-1-e"></span>
</a>
<span id="hnr">
<a id="ytb" class="ytb " title="External link to YouTube" href="https://www.youtube.com/playli
<a id="brFtp" class="" title="Blast report description" href="ftp://ftp.ncbi.nlm.nih.gov/pub/fa
</span>
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="POST" id="results 

<input name="QUERY_INDEX" type="hidden" value="0">
<input name="_PGR" type="hidden" value="" >
<input id="seqViewUrl" type="hidden" value="https://www.ncbi.nlm.nih.gov" >
<input id="userAgent" type="hidden" value="">
<input name="CMD" type="hidden" value="Get">
</form>
<!-- Reformat and downlaod for new design -->
<div class="ui-helper-reset" aria-live="assertive" >
<form action="Blast.cgi" enctype="application/x-www-form-urlencoded" method="post" name="Format
```

BLAST INFORMATION

```
<table class="options blastn ">
<tr>
<td class="frh" colspan=2>
<div class="fi">
<div class="tb">Formatting options</div>
<input type="image"  border="0" id="onPageReformat" src="css/images/reformat.jpg" class="blast
</div>
</tr>
<tr class="paramSet xgl">
<td class="hd"><label for="FORMAT_OBJECT">Show</label></td>
<td>
<div class="fi">
<input type="hidden" id="FORMAT_OBJECT" value="Alignment" name="FORMAT_OBJECT" />
<label for="FORMAT_TYPE" id="nft">Alignment as</label>
<select name="FORMAT_TYPE" id="FORMAT_TYPE" class="reset" defVal="HTML">
<option value="HTML"  >HTML</option>
<option value="Text"  >Plain text</option>

</select>

<span id="advView" class="">
<span class=""><input name="OLD_VIEW" id="OLD_VIEW" type="checkbox" class="cb reset" defVal="un
<label for="OLD_VIEW">Old View</label></span>
</span>
<a class="resetAll" id="resetAll" >Reset form to defaults</a>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments object formatting
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp1">
These options control formatting of alignments in results pages. The
default is HTML, but other formats (including plain text) are available.
PSSM and PssmWithParameters are representations of Position Specific Scoring Matrices and are
The Advanced view option allows the database descriptions to be sorted by various indices in a
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="odd paramSet">
<td class="hd"><label for="ALIGNMENT_VIEW">Alignment View</label></td>
<td>
<div class="fi">
<select name="ALIGNMENT_VIEW" id="ALIGNMENT_VIEW" defVal="Pairwise" class="reset">
<option value="Pairwise" selected="selected" >Pairwise</option>
<option value="PairwiseWithIdentities"  >Pairwise with dots for identities</option>
<option value="QueryAnchored"  >Query-anchored with dots for identities</option>
```

```
<option value="QueryAnchoredNoIdentities"  >Query-anchored with letters for identities</option
<option value="FlatQueryAnchored"  >Flat query-anchored with dots for identities</option>
<option value="FlatQueryAnchoredNoIdentities"  >Flat query-anchored with letters for identitie

</select>


<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments view options help
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp2">
Choose how to view alignments.
The default "pairwise" view shows how each subject sequence aligns
individually to the query sequence. The "query-anchored" view shows how
all subject sequences align to the query sequence. For each view type,
you can choose to show "identities" (matching residues) as letters or
dots.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#alignment_view" targe
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet">
<td class="hd"><label>Display</label></td>
<td class="cb">
<div class="fi">
<input name="SHOW_OVERVIEW" id="SHOW_OVERVIEW" type="checkbox" class="cb reset" defVal="checke
<label class="rb" for="SHOW_OVERVIEW">Graphical Overview</label>

<span id="shl" >
<input name="SHOW_LINKOUT" id="SHOW_LINKOUT" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="SHOW_LINKOUT">Linkout</label>
</span>
<span id="gts" >
<input name="GET_SEQUENCE" id="GET_SEQUENCE" type="checkbox" class="cb reset" defVal="checked"
<label class="rb" for="GET_SEQUENCE">Sequence Retrieval</label>
</span>


<input name="NCBI_GI" id="NCBI_GI" type="checkbox" class="cb reset" defVal="unchecked" false /
<label class="rb" for="NCBI_GI">NCBI-gi</label>
<span id="scf" >
<input name="SHOW_CDS_FEATURE" id="SHOW_CDS_FEATURE" type="checkbox" class="cb reset blastn" d
<label for="SHOW_CDS_FEATURE" class="blastn">CDS feature</label>
</span>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments display options h
```

BLAST INFORMATION

```
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp3">
<li>Graphical Overview: Graphical Overview: Show graph of similar sequence regions aligned to
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_overview" targe
</li>
<li>NCBI-gi: Show NCBI gi identifiers.
</li>
<li>CDS feature: Show annotated coding region and translation.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#show_cds_feature" ti
</li></ul>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"><label>Masking</label></td>
<td>
<div class="fi">
<label for="MASK_CHAR"> Character: </label>
<select name="MASK_CHAR" id="MASK_CHAR"  class="reset" defVal="2">
<option value="0"  >X for protein, n for nucleotide</option>
<option value="2" selected="selected" >Lower Case</option>
</select>
<label for="MASK_COLOR"> Color:</label>
<select name="MASK_COLOR" id="MASK_COLOR" class="reset" defVal="1">
<option value="0"  >Black
</option>

<option value="1" selected="selected" >Grey
</option>

<option value="2"  >Red
</option>

</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Alignments masking help" id=
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp4">
<li>Masking Character: Display masked (filtered) sequence regions as lower-case or as specific
</li>
<li>Masking Color: Display masked sequence regions in the given color.</li>
</ul>
</div><!-- ARIA -->
```

BLAST INFORMATION
```
</div>
</td>
</tr>


<tr id="lr" class="paramSet xgl">
<td class="hd"><label>Limit results</label></td>
<td>
<div class="fi">
<label for="FRM_DESCRIPTIONS">Descriptions:</label>
<select name="DESCRIPTIONS" id="FRM_DESCRIPTIONS" class="reset" defVal="100">
<option value="0"        >0</option>
<option value="10"       >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"      >100</option>
<option value="250"      >250</option>
<option value="500"      >500</option>
<option value="1000"     >1000</option>
<option value="5000"     >5000</option>
<option value="10000"   >10000</option>
<option value="20000"   >20000</option>
</select>

<label for="FRM_NUM_OVERVIEW">Graphical overview:</label>
<select name="NUM_OVERVIEW" id="FRM_NUM_OVERVIEW" class="reset" defVal="100">
<option value="0"        >0</option>
<option value="10"       >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"      >100</option>
<option value="250"      >250</option>
<option value="500"   >500</option>
<option value="1000"   >1000</option>
</select>
<span id="frmAln">
<label for="FRM_ALIGNMENTS">Alignments:</label>
<select name="ALIGNMENTS" id="FRM_ALIGNMENTS" class="reset" defVal="100">
<option value="0"        >0</option>
<option value="10"       >10</option>
<option value="50"    selected="selected" >50</option>
<option value="100"      >100</option>
<option value="250"      >250</option>
<option value="500"      >500</option>
<option value="1000"    >1000</option>
<option value="5000"     >5000</option>
<option value="10000"   >10000</option>
<option value="20000"   >20000</option>
</select>
```

BLAST INFORMATION

```
</span>
<label for="FRM_LINE_LENGTH">Line length:</label>
<select name="LINE_LENGTH" id="FRM_LINE_LENGTH" class="reset" defVal="60">
<option value="60"    selected="selected" >60</option>
<option value="90"      >90</option>
<option value="120"      >120</option>
<option value="150"      >150</option>
</select>
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit number of descriptions
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp5">
<li>Descriptions: Show short descriptions for up to the given number of  sequences.</li>
<li>Alignments:  Show alignments for up to the given number of sequences, in order of statisti
<li>Line lenghth:  Number of letters to show on one line in an alignment.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>

<tr class="paramSet odd xgl ">
<td class="hd"></td>
<td>
<div class="">
<label for="qorganism">Organism</label>
<span class="instr">Type common name, binomial, taxid, or group name. Only 20 top taxa will be
<input name="FORMAT_ORGANISM" size="55"  type="text" id="qorganism" value="" data-jigconfig="d:
<input type="checkbox" name="FORMAT_ORG_EXCLUDE"  class="oExclR cb" id="orgExcl"/>
<input type="hidden" value = "1" name="FORMAT_NUM_ORG" id="numOrg" />
<label for="orgExcl" class="right">Exclude</label>
<a href="#" title="Add organism" id="addOrg"><img border="0" src="css/images/addOrg.jpg" id="ac
<div id="orgs">

</div>
<div class="fi">
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by organism hel
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp6">
Show only sequences from the given organism.
</p>
</div><!-- ARIA -->
</div>
</div>
</td>
</tr>
```

BLAST INFORMATION

```
<tr class="paramSet xgl ">
<td class="hd"></td>
<td>
<div class="fi">
<label for="FORMAT_EQ_TEXT">Entrez query:</label>
<input name="FORMAT_EQ_TEXT" id="FORMAT_EQ_TEXT" size="60" type="text" value="" class="reset"
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by Entrez query
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp7">
Show only those sequences that match the given Entrez query.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#limit_result" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>


<tr class="paramSet odd xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="EXPECT_LOW">Expect Min:</label> <input name="EXPECT_LOW" id="EXPECT_LOW" size="10"
<label for="EXPECT_HIGH">Expect Max:</label> <input name="EXPECT_HIGH" id="EXPECT_HIGH" size="1
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by expect value
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp8">
Show only sequences with expect values in the given range.
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#expect_range" target=
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="paramSet xgl">
<td class="hd"></td>
<td>
<div class="fi">
<label for="PERC_IDENT_LOW">Percent Identity Min:</label> <input name="PERC_IDENT_LOW" id="PERC
<label for="PERC_IDENT_HIGH">Percent Identity Max:</label> <input name="PERC_IDENT_HIGH" id="PI
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="Limit results by percent iden
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<p class="helpbox ui-ncbitoggler-slave" id="hlp10">
```

BLAST INFORMATION

Show only sequences with percent identity values in the given range.
```
</p>
</div><!-- ARIA -->
</div>
</td>
</tr>
<tr class="psiBlast odd paramSet xgl">
<td class="hd"><label>Format for</label></td>
<td>
<div class="fi">
<input name="RUN_PSIBLAST_FORM" id="RUN_PSIBLAST" type="checkbox" class="cb psiBlast"  />
<label class="rb psiBlast" for="RUN_PSIBLAST">PSI-BLAST</label>
<label for="I_THRESH">with inclusion threshold:</label>
<input name="I_THRESH" id="I_THRESH" size="10" type="text" value="" defVal="0.005" />
<a class="helplink  ui-ncbitoggler" data-jig="ncbitoggler" title="PSI BLAST formatting help" i
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
<div class="ui-helper-reset" aria-live="assertive" >
<ul class="helpbox ui-ncbitoggler-slave" id="hlp9">
<li>Format for PSI-BLAST: The Position-Specific Iterated BLAST (PSI-BLAST) program performs ite
in which sequences found in one round of search are used to build a custom score model for the
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=BlastHelp#psiblast" target="hel
</li>
<li>Inclusion Threshold: This sets the statistical significance threshold for including a seque
by PSI-BLAST to create the PSSM on the next iteration.</li>
</ul>
</div><!-- ARIA -->
</div>
</td>
</tr>
</table>


<input name="ViewReport" value="ViewReport" type="hidden" />
<input name="REFORMAT_REPORT" value="shown" type="hidden" />
<input name="RID" value="P7XBUUX2014" type="hidden" />
<input name="CDD_RID" value="" type="hidden" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />

<input name="STEP_NUMBER" value="" id="stepNumber" type="hidden" />
<input name="CMD" value="Get" type="hidden" />
<input name="FORMAT_EQ_OP" value="AND" type="hidden" />
<input name="RESULTS_PAGE_TARGET" type="hidden" id="resPageTarget" value="" />
<!-- <input name="QUERY_INFO" type="hidden" value="" /> -->
<!-- <input name="ENTREZ_QUERY" type="hidden" value="" /> -->
<input name="QUERY_INDEX" type="hidden" value="0"/>
<input name="NUM_QUERIES" type="hidden" value="1"/>
```

BLAST INFORMATION

```
<!-- Those params are set in the template (blastn.dat, blastp.dat etc. -->
<input name="BLAST_PROGRAMS" type="hidden" value="blastn"/>
<input name="PAGE" type="hidden" value="Nucleotides"/>
<input name="PROGRAM" type="hidden" value="blastn"/>
<input name="MEGABLAST" type="hidden" value="" />
<input name="RUN_PSIBLAST" type="hidden" value="" />
<input name="BLAST_SPEC" id="blastSpec" type="hidden" value=""/>


<input name="QUERY" type="hidden" value="TTTGAGGATCCAACACGGCG"/>
<input name="JOB_TITLE" type="hidden" value="Nucleotide Sequence (20 letters)"/>
<input name="QUERY_TO" type="hidden" value=""/>
<input name="QUERY_FROM" type="hidden" value=""/>
<input name="SUBJECTS_FROM" type="hidden" value=""/>
<input name="SUBJECTS_TO" type="hidden" value=""/>
<input name="EQ_TEXT" type="hidden" value=""/>
<input name="ORGN" type="hidden" value=""/>
<input name="EQ_MENU" type="hidden" value=""/>
<input name="ORG_EXCLUDE" type="hidden" value=""/>
<input name="PHI_PATTERN" type="hidden" value=""/>
<input name="EXPECT" type="hidden" value="10"/>
<input name="DATABASE" type="hidden" value="nt"/>
<input name="DB_GROUP" type="hidden" value=""/>
<input name="SUBGROUP_NAME" type="hidden" value=""/>


<input name="GENETIC_CODE" type="hidden" value=""/>
<input name="WORD_SIZE" type="hidden" value="11"/>
<input name="MATCH_SCORES" type="hidden" value="2,-3"/>
<input name="MATRIX_NAME" type="hidden" value=""/>
<input name="GAPCOSTS" type="hidden" value="5 2"/>
<input name="MAX_NUM_SEQ" id="maxNumSeq" type="hidden" value="50"/>
<input name="COMPOSITION_BASED_STATISTICS" type="hidden" value=""/>
<input name="NEWWIN" type="hidden" value=""/>
<input name="SHORT_QUERY_ADJUST" type="hidden" value=""/>
<input name="FILTER" type="hidden" value="L;m;"/>
<input name="REPEATS" type="hidden" value=""/>
<input name="ID_FOR_PSSM" type="hidden" value=""/>
<input name="EXCLUDE_MODELS" type="hidden" value=""/>
<input name="EXCLUDE_SEQ_UNCULT" type="hidden" value=""/>
<input name="WP_PROTEINS" type="hidden" value=""/>
<input name="SEQ_FROM_TYPE" type="hidden" value=""/>
<input name="ENTREZ_QUERY" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET" type="hidden" value=""/>
<input name="ENTREZ_QUERY_PRESET_EXCL" type="hidden" value=""/>
<input name="NUM_ORG" type="hidden" value = "1" />

<!-- PSSM -->
```

BLAST INFORMATION

```
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</form>
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<tr><td class="frh" colspan=6><div class="tb">Download</div></td></tr>
<tr>
<td id="tdal">
<div class="dnHeader">Alignment</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=Text&FORMAT_OBJECT=Alignment&DI
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=XML&FORMAT_OBJECT=A
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=Alignment&C
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=JSONSA&FORMAT_OBJECT=Alignment&
<a  id="hitText" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=Text&FORMAT_OBJEC
<a  id="hitCvs" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=CSV&FORMAT_OBJECT=A
<a  class="xgl" href="Blast.cgi?RID=P7XBUUX2014&FORMAT_TYPE=XML2&FORMAT_OBJECT=Alignment&CMD=Ge
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=XML2_S&FORMAT_OBJEC
<a  class="xgl" href="Blast.cgi?RID=P7XBUUX2014&FORMAT_TYPE=JSON2&FORMAT_OBJECT=Alignment&CMD=G
<a  class="xgl" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=JSON2_S&FORMAT_OBJE
<a  class="xgl blastn" href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=SAM_SQ&FORMA
</div>
</td>
<td class="dnl xgl">
<div class="dnHeader">Search Strategies</div>
<div class="dnLinks">
<a  href="Blast.cgi?CMD=GetSaved&RECENT_RESULTS=on&RID=P7XBUUX2014&DOWNLOAD_OPTIONS=true">ASN.
</div>
</td>
<td class="dnl" id="dnPSSMPar">
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BLAST INFORMATION

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<div class="dnHeader">PSSM to restart search</div>
<div class="dnLinks">
<a  href="Blast.cgi?RESULTS_FILE=on&RID=P7XBUUX2014&FORMAT_TYPE=ASN.1&FORMAT_OBJECT=PSSM_Scorer
</div>
</td>
<td>
<a class="helplink ui-ncbitoggler" data-jig="ncbitoggler" title="Download help" data-ncbitoggle
<span class="ui-icon ui-icon-triangle-1-e"></span></a>
</td>
</tr>
</table>
<div class="ui-helper-reset" aria-live="assertive" >
<div class="helpbox ui-ncbitoggler-slave" id="hlp11">
The Download link provides BLAST output that may be used as input to another program.
This includes parseable formats such as the tabular report or XML as well as the Search Strateg
More details on the parseable (XML, tabular, and ASN.1) reports can be found at
<a href="https://www.ncbi.nlm.nih.gov/books/NBK153387/" target="helpWin" >https://www.ncbi.nlm
<br/>
<p>
The following formats are offered under the Alignment section:<br/>
1). "Text". Non-HTML standard BLAST report.<br/>
2). "XML". XML report based upon the DTD at <a href="https://www.ncbi.nlm.nih.gov/data_specs/d
3). "ASN.1". Alignment written out in Abstract Syntax Notation 1.<br/>
4). "JSON Seq-align". Alignment written out in JSON.<br/>
4). "Hit Table(text)". The tabular report as text.<br/>
5). "Hit Table(csv)". The tabular report ready for import into spread-sheet programs like Exce
6). "XML2". New XML format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/NE
7). "JSON". New JSON format described at <a href="ftp://ftp.ncbi.nlm.nih.gov/blast/documents/N
8). "SAM". Sequence Alignment Map format.<br/>
</p>
<p>
XML2 and JSON can be downloaded either as one file per query (multiple-file) or one file for a
</p>
<p>
The following report is offered under the Search Strategy section:<br/>
1). "ASN.1" Search Strategy. A record of the parameters, query, and database used in the searc
<a href="https://www.ncbi.nlm.nih.gov/books/NBK1763/#CmdLineAppsManual.I455_BLAST_search_stra"
</p>
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</form>
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BLAST INFORMATION
Status=READY
QBlastInfoEnd
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<PRE>
BLASTN 2.6.1+
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro
A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and
David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new
generation of protein database search programs", Nucleic
Acids Res. 25:3389-3402.

RID: P7XBUUX2014

Database: Nucleotide collection (nt)
43,324,577 sequences; 150,093,331,920 total letters
Query=
Length=20


```
                                                                    Score     E
Sequences producing significant alignments:                        (Bits)  Value

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KY457839.1  Human papillomavirus type 18 strain 18CNTZ35 E6 (E...   37.4    2.6
KY457838.1  Human papillomavirus type 18 strain 18CNTZ34 E6 (E...   37.4    2.6
KY457837.1  Human papillomavirus type 18 strain 18CNTZ33 E6 (E...   37.4    2.6
KY457836.1  Human papillomavirus type 18 strain 18CNTZ32 E6 (E...   37.4    2.6
KY457835.1  Human papillomavirus type 18 strain 18CNTZ31 E6 (E...   37.4    2.6
KY457834.1  Human papillomavirus type 18 strain 18CNTZ30 E6 (E...   37.4    2.6
KY457833.1  Human papillomavirus type 18 strain 18CNTZ29 E6 (E...   37.4    2.6
KY457832.1  Human papillomavirus type 18 strain 18CNTZ28 E6 (E...   37.4    2.6
KY457831.1  Human papillomavirus type 18 strain 18CNTZ27 E6 (E...   37.4    2.6
KY457830.1  Human papillomavirus type 18 strain 18CNTZ26 E6 (E...   37.4    2.6
KY457829.1  Human papillomavirus type 18 strain 18CNTZ25 E6 (E...   37.4    2.6
KY457828.1  Human papillomavirus type 18 strain 18CNTZ24 E6 (E...   37.4    2.6
KY457827.1  Human papillomavirus type 18 strain 18CNTZ23 E6 (E...   37.4    2.6
KY457826.1  Human papillomavirus type 18 strain 18CNTZ22 E6 (E...   37.4    2.6
KY457825.1  Human papillomavirus type 18 strain 18CNTZ21 E6 (E...   37.4    2.6
KY457824.1  Human papillomavirus type 18 strain 18CNTZ20 E6 (E...   37.4    2.6
KY457823.1  Human papillomavirus type 18 strain 18CNTZ19 E6 (E...   37.4    2.6
KY457822.1  Human papillomavirus type 18 strain 18CNTZ18 E6 (E...   37.4    2.6
KY457821.1  Human papillomavirus type 18 strain 18CNTZ17 E6 (E...   37.4    2.6
KY457820.1  Human papillomavirus type 18 strain 18CNTZ16 E6 (E...   37.4    2.6
KY457819.1  Human papillomavirus type 18 strain 18CNTZ15 E6 (E...   37.4    2.6
KY457818.1  Human papillomavirus type 18 strain 18CNTZ14 E6 (E...   37.4    2.6
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KY457817.1  Human papillomavirus type 18 strain 18CNTZ13 E6 (E...    37.4    2.6
KY457816.1  Human papillomavirus type 18 strain 18CNTZ12 E6 (E...    37.4    2.6
KY457815.1  Human papillomavirus type 18 strain 18CNTZ11 E6 (E...    37.4    2.6
KY457814.1  Human papillomavirus type 18 strain 18CNTZ10 E6 (E...    37.4    2.6
KY457813.1  Human papillomavirus type 18 strain 18CNTZ09 E6 (E...    37.4    2.6
KY457812.1  Human papillomavirus type 18 strain 18CNTZ08 E6 (E...    37.4    2.6
KY457811.1  Human papillomavirus type 18 strain 18CNTZ07 E6 (E...    37.4    2.6
KY457810.1  Human papillomavirus type 18 strain 18CNTZ06 E6 (E...    37.4    2.6
KY457809.1  Human papillomavirus type 18 strain 18CNTZ05 E6 (E...    37.4    2.6
KY457808.1  Human papillomavirus type 18 strain 18CNTZ04 E6 (E...    37.4    2.6
KY457807.1  Human papillomavirus type 18 strain 18CNTZ03 E6 (E...    37.4    2.6
KY457806.1  Human papillomavirus type 18 strain 18CNTZ02 E6 (E...    37.4    2.6
KY457805.1  Human papillomavirus type 18 strain 18CNTZ01 E6 (E...    37.4    2.6
KX514433.1  Human papillomavirus type 18 isolate pam9, complet...    37.4    2.6
KY502096.1  Human papillomavirus isolate HPV18 P2-50 transform...    37.4    2.6
KY502095.1  Human papillomavirus isolate HPV18 P2-40 transform...    37.4    2.6
KY502094.1  Human papillomavirus isolate HPV18 P2-30 transform...    37.4    2.6
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KY502092.1  Human papillomavirus isolate HPV18 P2-10 transform...    37.4    2.6
KY502091.1  Human papillomavirus isolate HPV18 P2 transforming...    37.4    2.6
KY502090.1  Human papillomavirus isolate HPV18 P1-50 transform...    37.4    2.6
KY502089.1  Human papillomavirus isolate HPV18 P1-40 transform...    37.4    2.6
KY502088.1  Human papillomavirus isolate HPV18 P1-30 transform...    37.4    2.6
KY502086.1  Human papillomavirus isolate HPV18 P1-10 transform...    37.4    2.6
KY502085.1  Human papillomavirus isolate HPV18 P1 transforming...    37.4    2.6
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KX545354.1  Human papillomavirus type 18 isolate NGSk256-18 E6...    37.4    2.6


ALIGNMENTS
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and L1 (L1) genes, complete cds
Length=2502


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Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


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Sbjct  10  TTTGAGGATCCAACACGGCG  29



>KY457839.1 Human papillomavirus type 18 strain 18CNTZ35 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502


Score = 37.4 bits (40),  Expect = 2.6
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BLAST INFORMATION

Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457838.1 Human papillomavirus type 18 strain 18CNTZ34 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457837.1 Human papillomavirus type 18 strain 18CNTZ33 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457836.1 Human papillomavirus type 18 strain 18CNTZ32 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
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Sbjct 10   TTTGAGGATCCAACACGGCG   29

BLAST INFORMATION

>KY457835.1 Human papillomavirus type 18 strain 18CNTZ31 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457834.1 Human papillomavirus type 18 strain 18CNTZ30 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

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Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457833.1 Human papillomavirus type 18 strain 18CNTZ29 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457832.1 Human papillomavirus type 18 strain 18CNTZ28 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

BLAST INFORMATION

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Query  1    TTTGAGGATCCAACACGGCG   20
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Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY457831.1 Human papillomavirus type 18 strain 18CNTZ27 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

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Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    TTTGAGGATCCAACACGGCG   20
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Sbjct  10   TTTGAGGATCCAACACGGCG   29
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>KY457830.1 Human papillomavirus type 18 strain 18CNTZ26 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

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Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    TTTGAGGATCCAACACGGCG   20
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Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY457829.1 Human papillomavirus type 18 strain 18CNTZ25 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1    TTTGAGGATCCAACACGGCG   20
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Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY457828.1 Human papillomavirus type 18 strain 18CNTZ24 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457827.1 Human papillomavirus type 18 strain 18CNTZ23 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457826.1 Human papillomavirus type 18 strain 18CNTZ22 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457825.1 Human papillomavirus type 18 strain 18CNTZ21 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

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Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457824.1 Human papillomavirus type 18 strain 18CNTZ20 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457823.1 Human papillomavirus type 18 strain 18CNTZ19 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   TTTGAGGATCCAACACGGCG  20
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Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457822.1 Human papillomavirus type 18 strain 18CNTZ18 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457821.1 Human papillomavirus type 18 strain 18CNTZ17 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)

BLAST INFORMATION

Strand=Plus/Plus

```
Query   1    TTTGAGGATCCAACACGGCG   20
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Sbjct   10   TTTGAGGATCCAACACGGCG   29
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>KY457820.1 Human papillomavirus type 18 strain 18CNTZ16 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

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Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query   1    TTTGAGGATCCAACACGGCG   20
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Sbjct   10   TTTGAGGATCCAACACGGCG   29
```

>KY457819.1 Human papillomavirus type 18 strain 18CNTZ15 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query   1    TTTGAGGATCCAACACGGCG   20
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Sbjct   10   TTTGAGGATCCAACACGGCG   29
```

>KY457818.1 Human papillomavirus type 18 strain 18CNTZ14 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query   1    TTTGAGGATCCAACACGGCG   20
             ||||||||||||||||||||
Sbjct   10   TTTGAGGATCCAACACGGCG   29
```

>KY457817.1 Human papillomavirus type 18 strain 18CNTZ13 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20

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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457816.1 Human papillomavirus type 18 strain 18CNTZ12 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20

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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457815.1 Human papillomavirus type 18 strain 18CNTZ11 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20

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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457814.1 Human papillomavirus type 18 strain 18CNTZ10 E6 (E6), E7 (E7),

and L1 (L1) genes, complete cds

Length=2502

Score = 37.4 bits (40), Expect = 2.6

Identities = 20/20 (100%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20

||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457813.1 Human papillomavirus type 18 strain 18CNTZ09 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
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Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457812.1 Human papillomavirus type 18 strain 18CNTZ08 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457811.1 Human papillomavirus type 18 strain 18CNTZ07 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
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Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
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Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY457810.1 Human papillomavirus type 18 strain 18CNTZ06 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

BLAST INFORMATION

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457809.1 Human papillomavirus type 18 strain 18CNTZ05 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457808.1 Human papillomavirus type 18 strain 18CNTZ04 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457807.1 Human papillomavirus type 18 strain 18CNTZ03 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

```
Score = 37.4 bits (40),  Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus


Query  1   TTTGAGGATCCAACACGGCG  20
           ||||||||||||||||||||
Sbjct  10  TTTGAGGATCCAACACGGCG  29
```

>KY457806.1 Human papillomavirus type 18 strain 18CNTZ02 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY457805.1 Human papillomavirus type 18 strain 18CNTZ01 E6 (E6), E7 (E7),
and L1 (L1) genes, complete cds
Length=2502

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KX514433.1 Human papillomavirus type 18 isolate pam9, complete genome
Length=7857

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
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Sbjct  114  TTTGAGGATCCAACACGGCG   133
```

>KY502096.1 Human papillomavirus isolate HPV18 P2-50 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY502095.1 Human papillomavirus isolate HPV18 P2-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY502094.1 Human papillomavirus isolate HPV18 P2-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY502093.1 Human papillomavirus isolate HPV18 P2-20 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

```
Query  1    TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct  10   TTTGAGGATCCAACACGGCG   29
```

>KY502092.1 Human papillomavirus isolate HPV18 P2-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY502091.1 Human papillomavirus isolate HPV18 P2 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY502090.1 Human papillomavirus isolate HPV18 P1-50 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY502089.1 Human papillomavirus isolate HPV18 P1-40 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KY502088.1 Human papillomavirus isolate HPV18 P1-30 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG 20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG 29

>KY502086.1 Human papillomavirus isolate HPV18 P1-10 transforming protein
E6 (E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG 20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG 29

>KY502085.1 Human papillomavirus isolate HPV18 P1 transforming protein E6
(E6) gene, partial cds
Length=474

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG 20
            ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG 29

>KX545359.1 Human papillomavirus type 18 isolate NGSk274-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=516

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)

BLAST INFORMATION

Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
           ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

>KX545354.1 Human papillomavirus type 18 isolate NGSk256-18 E6 protein (E6)
gene, complete cds; and E7 protein (E7) gene, partial cds
Length=579

Score = 37.4 bits (40), Expect = 2.6
Identities = 20/20 (100%), Gaps = 0/20 (0%)
Strand=Plus/Plus

Query 1   TTTGAGGATCCAACACGGCG   20
           ||||||||||||||||||||
Sbjct 10   TTTGAGGATCCAACACGGCG   29

Database: Nucleotide collection (nt)
Posted date: Jul 8, 2017 5:09 AM
Number of letters in database: 150,093,331,920
Number of sequences in database: 43,324,577

Lambda   K   H
0.634   0.408   0.912
Gapped
Lambda   K   H
0.625   0.410   0.780
Matrix: blastn matrix:2 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 43324577
Number of Hits to DB: 697064
Number of extensions: 225
Number of successful extensions: 225
Number of sequences better than 10: 54
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 225
Number of HSP's successfully gapped: 54
Length of query: 20
Length of database: 150093331920
Length adjustment: 17
Effective length of query: 3
Effective length of database: 149356814111
Effective search space: 448070442333
Effective search space used: 448070442333

BLAST INFORMATION

```
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 28 (26.5 bits)
S2: 38 (35.6 bits)




</form>
</div><!-- /#content -->
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<input name="QUERY_INFO" type="hidden" value="" />
<input name="ENTREZ_QUERY" type="hidden" value="" />
<input name="CDD_RID" type="hidden" value="" />
<input name="CDD_SEARCH_STATE" type="hidden" value="" />
<input name="RID" type="hidden" value="P7XBUUX2014" />
<input name="STEP_NUMBER" type="hidden" value="" />
<input name="CMD" type="hidden" value="Web"/>
<input NAME="PAGE_TYPE" type="hidden"  value="BlastFormatting"/>

<!-- TO DO: test all of those changes -->
<!-- Psi blast params  PSI_BLAST_PARAMS - commented- using forms[0] from fromatter> -->
<!-- Current Formatting options FORMATTING_OPTIONS- commented- using forms[0] from fromatter>
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="setSa
<input name="PAGE_TYPE" type="hidden" value="BlastSearch" />
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<input name="CMD" type="hidden" value="Web" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from fromatter> -->
</form>

<form action="Blast.cgi" enctype="application/x-www-form-urlencoded"  method="post" name="save
<input name="SAVE" type="hidden" value="true"/>
<input name="CMD" type="hidden" value="GetSaved" />
<!-- Current Search options CURR_SAVED_OPTIONS - commented- using forms[0] from formatter> -->
</form>
</div><!-- /#content-wrap -->

<footer id="page_footer">
<div class="foot_wrap">
<div class="left col two_col">
BLAST is a registered trademark of the National Library of Medicine
</div>
<div class="right">
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BLAST INFORMATION

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<a class="help_desk jig-ncbihelpwindow" target="_blank" href="https://support.ncbi.nlm.nih.gov
Ncbi_App=blast&amp;Page=oldblastresults&Time=2017-07-10T17:45:57&amp;Host=blast359&amp;ncbi_ph
</a>
<a href="Blast.cgi?CMD=Web&amp;PAGE_TYPE=BlastDocs&amp;DOC_TYPE=MailList">Mailing list</a>
<a href="https://www.youtube.com/ncbinlm" target="_blank" id="page_footer_54">
<img class="icon-medium gray-medium" src="images/youtube.svg" alt="">
<span class="icon-fallback-text">YouTube</span>
</a>
</div>

</div>


<!-- bottom section of footer -->
<div class="col" id="contentinfo">
<ul class="right inline_list logos">
<li>
<a href="https://www.nlm.nih.gov" id="page_footer_60">
<img class="gray-medium" src="images/nlm-logo.svg" alt="">
<span class="icon-fallback-text">National Library Of Medicine</span>
</a>
</li>
<li>
<a href="https://www.nih.gov" id="page_footer_61">
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<span class="icon-fallback-text">National Institutes Of Health</span>
</a>
</li>
<li>
<a href="https://www.hhs.gov" id="page_footer_62">
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<span class="icon-fallback-text">U.S. Department of Health &amp; Human Services</span>
</a>
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<img class="icon-large-wide gray-medium" src="images/usagov-logo.svg" alt="">
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</ul>

<div class="footer_padding">

<div class="footer_border h-card">

<a href="https://www.ncbi.nlm.nih.gov/" class="u-url" id="page_footer_64">
<h3 role="heading" aria-level="3" class="ncbi_blue p-org">NCBI</h3>
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BLAST INFORMATION

```html
</a>

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<a href="https://www.ncbi.nlm.nih.gov/" class="u-url p-org" id="page_footer_65">National Center
<a href="https://www.nlm.nih.gov/" id="page_footer_66"> U.S. National Library of Medicine</a>

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<span class="p-street-address">8600 Rockville Pike</span>,
<span class="p-locality">Bethesda</span>
<span class="p-region"> MD</span>,
<span class="p-postal-code">20894</span>
<span class="p-country-name">USA</span>
</span>

</address>

</div>
<div class="inline_list about_list">
<a href="https://www.ncbi.nlm.nih.gov/home/about/policies.shtml" id="page_footer_67">Policies
|
<a href="https://www.ncbi.nlm.nih.gov/home/about/contact.shtml" id="page_footer_68">Contact</a
</div>
</div>
</div>
</footer>
<script type="text/javascript" src="js/header.js"> </script>
</div><!--/#wrap-->

<script type="text/javascript" src="js/utils.js"></script>
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<script type="text/javascript" src="/portal/portal3rc.fcgi/rlib/js/InstrumentOmnitureBaseJS/In
<!--
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<script type="text/javascript">$("#browsers_ajax").browserCheck();</script>
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</body>
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