

CLUSTAL 2.1 multiple sequence alignment

KC470224.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470223.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470225.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470214.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470215.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470216.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470217.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470218.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470219.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470220.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470221.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470222.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470228.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470227.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470226.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470230.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470229.1	ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KX514433.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KU298886.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
KC470213.1	ATGCATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCC
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KC470224.1	TCAAAATGAAATTCCGGTTGACCTTTTATGTCACGAGCAATTAAGCGACT
KC470223.1	TCAAAATGAAATTCCGGTTGACCTTTTATGTCACGAGCAATTAAGCGACT
KC470225.1	TCAAAATGACATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470214.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470215.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470216.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470217.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470218.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470219.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470220.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470221.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470222.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470228.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470227.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470226.1	TCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470230.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470229.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KX514433.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KU298886.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT
KC470213.1	CCAAAATGAAATTCCGGTTGACCTTCTATGTCACGAGCAATTAAGCGACT

KC470224.1	CAGAGGAAGAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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CLUSTAL 2.1 multiple sequence alignment

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KC470223.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470225.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470214.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470215.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470216.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470217.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470218.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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KC470220.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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KC470222.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470228.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470227.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470226.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470230.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470229.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KX514433.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KU298886.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
KC470213.1      CAGAGGAAGAAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCA
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KC470224.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
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KC470225.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470214.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470215.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470216.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470217.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470218.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470219.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470220.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470221.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470222.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470228.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470227.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470226.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470230.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470229.1      GCCCGACGAGCCGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KX514433.1      GCCCGACGAGCTGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KU298886.1      GCCCGACGAGCTGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
KC470213.1      GCCCGACGAGCTGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAA
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KC470224.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470223.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470225.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
KC470214.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAGACGACCTTC
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CLUSTAL 2.1 multiple sequence alignment

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KC470215.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
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KC470218.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470219.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470220.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470221.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470222.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470228.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470227.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470226.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470230.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470229.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KX514433.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KU298886.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
KC470213.1      GTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAAGCTCAGCAGACGACCTTC
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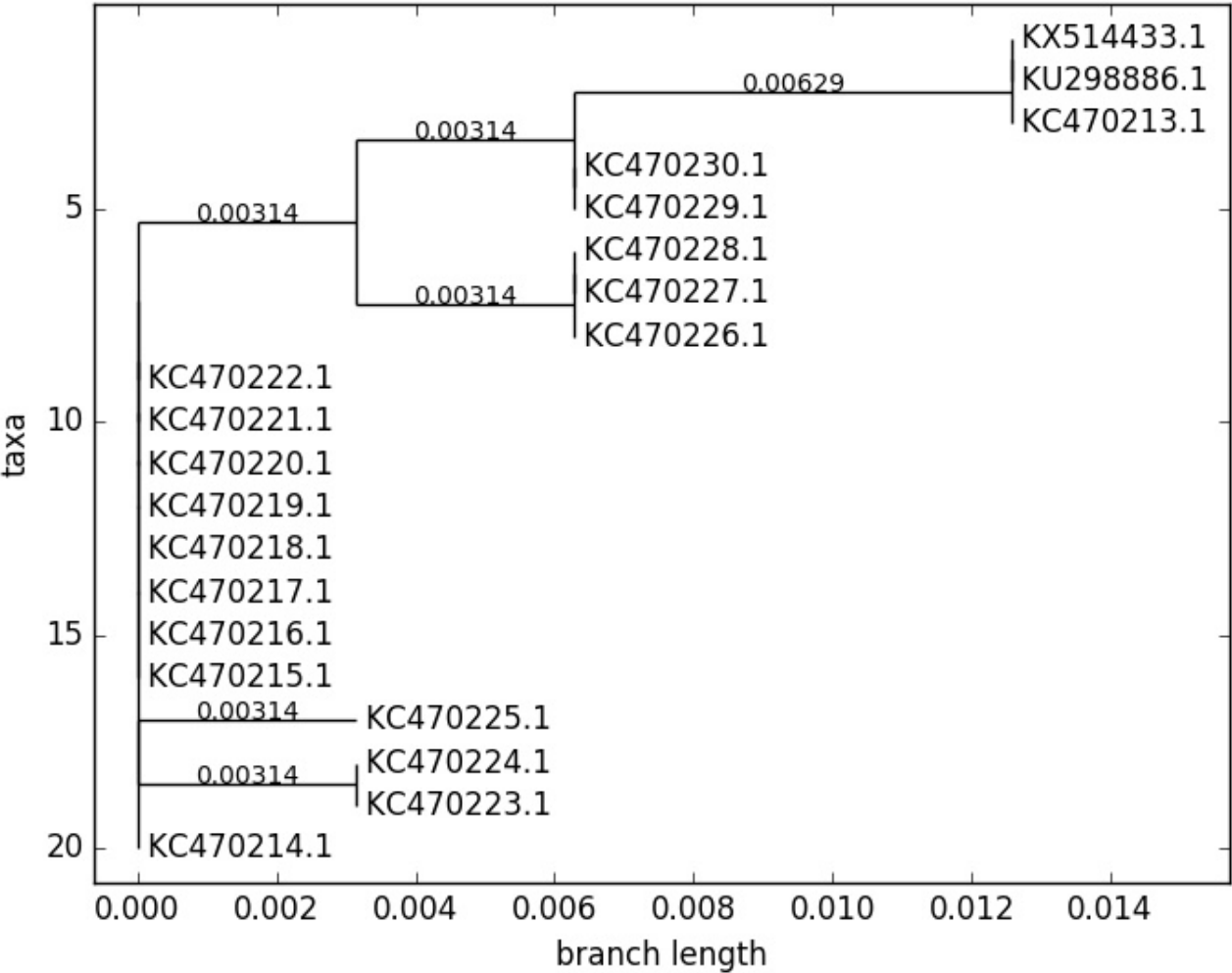
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KC470224.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
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KC470225.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470214.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470215.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470216.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470217.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470218.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470219.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470220.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470221.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470222.1      GAGCATTCCAGCAGCTGTTTCTGAGCACCTGTCCTTTGTGTGTCCGTGG
KC470228.1      GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470227.1      GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470226.1      GAGCATTCCAGCAGCTGTTTCTGAAAACCCTGTCCTTTGTGTGTCCGTGG
KC470230.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KC470229.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KX514433.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KU298886.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
KC470213.1      GAGCATTCCAGCAGCTGTTTCTGAACACCCTGTCCTTTGTGTGTCCGTGG
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KC470224.1      TGTGCATCCCAGCAGTAA
KC470223.1      TGTGCATCCCAGCAGTAA
KC470225.1      TGTGCATCCCAGCAGTAA
KC470214.1      TGTGCATCCCAGCAGTAA
KC470215.1      TGTGCATCCCAGCAGTAA
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KC470217.1      TGTGCATCCCAGCAGTAA
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CLUSTAL 2.1 multiple sequence alignment

KC470218.1	TGTGCATCCCAGCAGTAA
KC470219.1	TGTGCATCCCAGCAGTAA
KC470220.1	TGTGCATCCCAGCAGTAA
KC470221.1	TGTGCATCCCAGCAGTAA
KC470222.1	TGTGCATCCCAGCAGTAA
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KC470230.1	TGTGCATCCCAGCAGTAA
KC470229.1	TGTGCATCCCAGCAGTAA
KX514433.1	TGTGCATCCCAGCAGTAA
KU298886.1	TGTGCATCCCAGCAGTAA
KC470213.1	TGTGCATCCCAGCAGTAA

Multiple Sequence Alignment tree



Consensus sequence

ATGTATGGACCTAAGGCAACATTGCAAGACATTGTATTGCATTTAGAGCCTCAAAATGAAATTCCGGTTGACCTTCTATGT
CACGAGCAATTAAGCGACTCAGAGGAAGAAAACGATGAAATAGATGGAGTTAATCATCAACATTTACCAGCCCGACGAGC
CGAACCACAACGTCACACAATGTTGTGTATGTGTTGTAAGTGTGAAGCCAGAATTGAGCTAGTAGTAGAAAGCTCAGCAG

Primers data

ACCEPTABLE LEFT PRIMERS

#	sequence	0-based		#	GC%	Tm	self		self hair-	qual-
		start	ln				any_th	end_th		
0	TGTATGGACCTAAGGCAACATTG	1	23	0	43.48	58.731	0.00	0.00	41.41	4.269
1	TGTATGGACCTAAGGCAACATT	1	22	0	40.91	57.415	0.00	0.00	41.41	4.585
2	ATGTATGGACCTAAGGCAACAT	0	22	0	40.91	57.204	0.00	0.00	41.41	4.796
3	ATGTATGGACCTAAGGCAACATTG	0	24	0	41.67	59.111	0.00	0.00	41.41	4.889
4	GTATGGACCTAAGGCAACATTG	2	22	0	45.45	57.099	0.00	0.00	41.41	4.901
5	ATGTATGGACCTAAGGCAACATT	0	23	0	39.13	57.871	0.00	0.00	41.41	5.129

ACCEPTABLE RIGHT PRIMERS

#	sequence	0-based		#	GC%	Tm	self		self hair-	qual-
		start	ln				any_th	end_th		
0	GAAGGTCGTCTGCTGAGCTT	249	20	0	55.00	60.038	7.47	7.47	38.04	0.038
1	AGGTCGTCTGCTGAGCTTTC	247	20	0	55.00	60.038	0.00	0.00	0.00	0.038
2	GGTCGTCTGCTGAGCTTTCT	246	20	0	55.00	60.038	0.00	0.00	0.00	0.038
3	CTCGTCGGGCTGGTAAATGT	159	20	0	55.00	60.108	0.00	0.00	0.00	0.108
4	GGACAGGGTGCTCAGAAACA	284	20	0	55.00	59.891	0.00	0.00	0.00	0.109
5	CTGGAATGCTCGAAGGTCGT	260	20	0	55.00	60.109	0.00	0.00	43.45	0.109
6	TGGAATGCTCGAAGGTCGTC	259	20	0	55.00	60.109	0.00	0.00	43.45	0.109
7	ACAAAGGACAGGGTGCTCAG	289	20	0	55.00	59.891	0.00	0.00	31.83	0.109
8	GGAATGCTCGAAGGTCGTCT	258	20	0	55.00	59.826	0.00	0.00	43.45	0.174
9	ACACAAAGGACAGGGTGCTC	291	20	0	55.00	60.179	0.00	0.00	31.83	0.179
10	CACAAAGGACAGGGTGCTCA	290	20	0	55.00	60.179	0.00	0.00	31.83	0.179
11	ACGGACACACAAAGGACAGG	297	20	0	55.00	60.179	0.00	0.00	0.00	0.179
12	CTCGAAGGTCGTCTGCTGAG	252	20	0	60.00	60.179	0.00	0.00	43.45	0.179
13	GGACACACAAAGGACAGGGT	295	20	0	55.00	59.817	0.00	0.00	0.00	0.183
14	GTGCTCAGAAACAGCTGCTG	277	20	0	55.00	59.762	27.02	27.02	37.79	0.238
15	CAGGGTGCTCAGAAACAGCT	281	20	0	55.00	60.251	3.10	0.00	37.79	0.251
16	AGGGTGCTCAGAAACAGCTG	280	20	0	55.00	60.251	13.48	13.48	37.79	0.251
17	TCGTCGGGCTGGTAAATGTT	158	20	0	50.00	59.678	0.00	0.00	0.00	0.322
18	TTACTGCTGGGATGCACACC	317	20	0	55.00	60.322	0.00	0.00	38.12	0.322
19	CACACCACGGACACACAAAG	303	20	0	55.00	59.623	0.00	0.00	0.00	0.377
20	TGCTGGAATGCTCGAAGGTC	262	20	0	55.00	60.392	0.00	0.00	0.00	0.392
21	CTGCTGGAATGCTCGAAGGT	263	20	0	55.00	60.392	0.00	0.00	0.00	0.392
22	AAGGTCGTCTGCTGAGCTTT	248	20	0	50.00	59.605	4.25	0.00	34.76	0.395
23	CAAAGGACAGGGTGCTCAGA	288	20	0	55.00	59.602	0.00	0.00	31.83	0.398
24	AGGACAGGGTGCTCAGAAAC	285	20	0	55.00	59.602	0.00	0.00	24.24	0.398
25	CGTCGGGCTGGTAAATGTTG	157	20	0	55.00	59.554	0.00	0.00	0.00	0.446
26	CACCACGGACACACAAAGGA	301	20	0	55.00	60.463	0.00	0.00	0.00	0.463
27	CCACGGACACACAAAGGACA	299	20	0	55.00	60.463	0.00	0.00	0.00	0.463
28	ACCACGGACACACAAAGGAC	300	20	0	55.00	60.463	0.00	0.00	0.00	0.463
29	CACACAAAGGACAGGGTGCT	292	20	0	55.00	60.466	0.00	0.00	35.27	0.466
30	ACAGGGTGCTCAGAAACAGC	282	20	0	55.00	60.536	0.00	0.00	37.40	0.536
31	GCTCAGAAACAGCTGCTGGA	275	20	0	55.00	60.605	31.00	17.77	35.51	0.605
32	TTGTGTGACGTTGTGGTTCG	180	20	0	50.00	59.278	0.00	0.00	0.00	0.722

Primers data

33	AATGCTCGAAGGTCGTCTGC	256	20	0	55.00	60.738	6.26	6.26	43.45	0.738
34	AGCTGCTGGAATGCTCGAAG	265	20	0	55.00	60.744	0.00	0.00	30.41	0.744
35	ACACCACGGACACACAAAGG	302	20	0	55.00	60.747	0.00	0.00	0.00	0.747
36	ACACACAAAGGACAGGGTGC	293	20	0	55.00	60.752	0.00	0.00	34.69	0.752
37	CGGACACACAAAGGACAGGG	296	20	0	60.00	60.885	0.00	0.00	0.00	0.885
38	AGAAACAGCTGCTGGAATGC	271	20	0	50.00	59.113	11.85	0.18	35.51	0.887
39	GAAACAGCTGCTGGAATGCT	270	20	0	50.00	59.113	12.08	0.00	35.51	0.887
40	AAACAGCTGCTGGAATGCTC	269	20	0	50.00	59.113	31.00	0.00	35.51	0.887
41	TGCTCAGAAACAGCTGCTGG	276	20	0	55.00	60.888	31.00	14.58	37.79	0.888
42	GGTGCTCAGAAACAGCTGCT	278	20	0	55.00	60.888	1.22	0.00	37.79	0.888
43	CACGGACACACAAAGGACAG	298	20	0	55.00	59.063	0.00	0.00	0.00	0.937
44	CAGCTGCTGGAATGCTCGAA	266	20	0	55.00	61.023	21.71	0.00	34.51	1.023
45	TGTGTGACGTTGTGGTTTCGG	179	20	0	55.00	61.085	0.00	0.00	0.00	1.085
46	GAAACAGCTGCTGGAATGCTC	270	21	0	52.38	60.135	12.08	0.00	35.51	1.135
47	AAAGGACAGGGTGCTCAGAA	287	20	0	50.00	58.860	0.00	0.00	31.83	1.140
48	AAGGACAGGGTGCTCAGAAA	286	20	0	50.00	58.860	0.00	0.00	31.83	1.140
49	GCTCGTCGGGCTGGTAAAT	160	19	0	57.89	60.153	10.59	0.00	0.00	1.153
50	ATGCTCGAAGGTCGTCTGC	255	19	0	57.89	60.154	6.26	6.26	43.45	1.154
51	GGTCGTCTGCTGAGCTTTCTA	246	21	0	52.38	59.797	0.00	0.00	0.00	1.203
52	CAAAGGACAGGGTGCTCAGAA	288	21	0	52.38	60.203	0.00	0.00	31.83	1.203
53	AAGGACAGGGTGCTCAGAAAC	286	21	0	52.38	60.203	0.00	0.00	31.83	1.203
54	GAATGCTCGAAGGTCGTCTG	257	20	0	55.00	58.727	0.00	0.00	43.45	1.273
55	AGCTGCTGGAATGCTCGAA	265	19	0	52.63	59.702	0.00	0.00	30.41	1.298
56	TACTGCTGGGATGCACACC	316	19	0	57.89	59.700	0.00	0.00	38.12	1.300
57	AACAGCTGCTGGAATGCTCG	268	20	0	55.00	61.304	31.00	5.48	35.51	1.304
58	GACACACAAAGGACAGGGTG	294	20	0	55.00	58.691	0.00	0.00	37.29	1.309
59	ATTGTGTGACGTTGTGGTTTCG	181	21	0	47.62	59.671	0.00	0.00	0.00	1.329
60	CAGAAACAGCTGCTGGAATGC	272	21	0	52.38	60.402	12.65	0.18	35.51	1.402
61	GCTGGAATGCTCGAAGGTCG	261	20	0	60.00	61.424	0.00	0.00	44.56	1.424
62	GCTCGTCGGGCTGGTAAATG	160	20	0	60.00	61.429	10.59	0.00	0.00	1.429
63	CAGCTGCTGGAATGCTCGA	266	19	0	57.89	60.449	21.71	0.00	34.51	1.449
64	TACTGCTGGGATGCACACCA	316	20	0	55.00	61.488	6.10	4.92	38.12	1.488
65	AAAGGACAGGGTGCTCAGAAA	287	21	0	47.62	59.505	0.00	0.00	31.83	1.495
66	GACAGGGTGCTCAGAAACAG	283	20	0	55.00	58.483	0.00	0.00	0.00	1.517
67	AGAAACAGCTGCTGGAATGCT	271	21	0	47.62	60.547	14.60	5.01	35.51	1.547
68	GGTGCTCAGAAACAGCTGC	278	19	0	57.89	59.422	15.27	0.00	37.79	1.578
69	GAAGGTCGTCTGCTGAGCT	249	19	0	57.89	59.411	5.83	0.00	0.00	1.589
70	TGACGTTGTGGTTTCGGCTC	175	19	0	57.89	60.593	0.00	0.00	35.95	1.593
71	GATGCACACCACGGACACA	307	19	0	57.89	60.597	0.00	0.00	0.00	1.597
72	ATGCTCGAAGGTCGTCTGCT	255	20	0	55.00	61.600	11.58	0.55	43.45	1.600
73	GAAGGTCGTCTGCTGAGCTTT	249	21	0	52.38	60.607	8.40	2.28	36.71	1.607
74	AAGGTCGTCTGCTGAGCTTTC	248	21	0	52.38	60.607	4.25	0.00	34.76	1.607
75	GTGTGACGTTGTGGTTTCGG	178	19	0	57.89	59.360	0.00	0.00	0.00	1.640
76	GCACACCACGGACACACAAA	304	20	0	55.00	61.649	0.00	0.00	0.00	1.649
77	CTCGTCGGGCTGGTAAATGTT	159	21	0	52.38	60.675	0.00	0.00	0.00	1.675
78	TGCTGGAATGCTCGAAGGT	262	19	0	52.63	59.321	0.00	0.00	0.00	1.679
79	GCTGCTGGAATGCTCGAAGG	264	20	0	60.00	61.713	0.00	0.00	0.00	1.713

Primers data

80	GCTGCTGGAATGCTCGAAG	264	19	0	57.89	59.280	0.00	0.00	0.00	1.720
81	CGTTTTCTTCCTCTGAGTCGC	114	21	0	52.38	59.278	0.00	0.00	0.00	1.722
82	ACAGCTGCTGGAATGCTCG	267	19	0	57.89	60.744	31.00	5.48	35.51	1.744
83	ACATTGTGTGACGTTGTGGT	183	20	0	45.00	58.255	0.00	0.00	0.00	1.745
84	GCTCGAAGGTCGTCTGCTG	253	19	0	63.16	60.804	6.06	0.00	43.45	1.804
85	CGAAGGTCGTCTGCTGAGC	250	19	0	63.16	60.804	0.00	0.00	37.02	1.804
86	GTCGGGCTGGTAAATGTTGA	156	20	0	50.00	58.184	0.00	0.00	0.00	1.816
87	GTGACGTTGTGGTTCGGCTC	176	20	0	60.00	61.828	0.00	0.00	35.95	1.828
88	GATGCACACCACGGACACAC	307	20	0	60.00	61.842	0.00	0.00	0.00	1.842
89	GGGTGCTCAGAAACAGCTGC	279	20	0	60.00	61.860	15.27	0.00	37.79	1.860
90	GCTCAGAAACAGCTGCTGG	275	19	0	57.89	59.125	31.00	14.58	35.51	1.875
91	CTCGAAGGTCGTCTGCTGA	252	19	0	57.89	59.123	0.00	0.00	43.45	1.877
92	TCGAAGGTCGTCTGCTGAG	251	19	0	57.89	59.123	0.00	0.00	43.45	1.877
93	GGACAGGGTGCTCAGAAACAG	284	21	0	57.14	60.880	0.00	0.00	0.00	1.880
94	GTGACGTTGTGGTTCGGCT	176	19	0	57.89	60.886	0.00	0.00	35.95	1.886
95	CTCAGAAACAGCTGCTGGAA	274	20	0	50.00	58.112	31.00	10.35	35.51	1.888
96	ATGCACACCACGGACACAC	306	19	0	57.89	60.892	0.00	0.00	0.00	1.892
97	ACCACGGACACACAAAGGA	300	19	0	52.63	59.091	0.00	0.00	0.00	1.909
98	ACACAAAGGACAGGGTGCT	291	19	0	52.63	59.077	0.00	0.00	35.27	1.923
99	TCGTCGGGCTGGTAAATGTTG	158	21	0	52.38	60.942	0.00	0.00	0.00	1.942
100	CGTCGGGCTGGTAAATGTTGA	157	21	0	52.38	60.942	0.00	0.00	0.00	1.942
101	TGGAATGCTCGAAGGTCGT	259	19	0	52.63	59.028	0.00	0.00	43.45	1.972
102	TCGTCGGGCTGGTAAATGT	158	19	0	52.63	59.023	0.00	0.00	0.00	1.977
103	TGAGTCGCTTAATTGCTCGTG	101	21	0	47.62	59.007	0.00	0.00	0.00	1.993
104	AGTCGCTTAATTGCTCGTGAC	99	21	0	47.62	59.007	4.62	4.62	0.00	1.993
105	CACCACGGACACACAAAGG	301	19	0	57.89	58.978	0.00	0.00	0.00	2.022
106	TCGGGCTGGTAAATGTTGATGA	155	22	0	45.45	60.027	0.00	0.00	0.00	2.027
107	GAGTCGCTTAATTGCTCGTGAC	100	22	0	50.00	59.972	4.62	4.62	0.00	2.028
108	CTGAGTCGCTTAATTGCTCGTG	102	22	0	50.00	59.971	0.00	0.00	0.00	2.029
109	GGATGCACACCACGGACA	308	18	0	61.11	59.968	6.86	0.00	0.00	2.032
110	CACACAAAGGACAGGGTGC	292	19	0	57.89	58.967	0.00	0.00	34.69	2.033
111	CTGCTGGGATGCACACCA	314	18	0	61.11	59.965	6.10	4.92	38.12	2.035
112	ACTGCTGGGATGCACACC	315	18	0	61.11	59.965	0.00	0.00	38.12	2.035
113	AAGGTCGTCTGCTGAGCTT	248	19	0	52.63	58.946	5.83	4.25	34.13	2.054
114	AGGTCGTCTGCTGAGCTTT	247	19	0	52.63	58.946	5.83	0.00	0.00	2.054
115	CTGGAATGCTCGAAGGTCGTC	260	21	0	57.14	61.064	0.00	0.00	43.45	2.064
116	GGAATGCTCGAAGGTCGTCTG	258	21	0	57.14	61.064	0.00	0.00	43.45	2.064
117	GGACACACAAAGGACAGGGTG	295	21	0	57.14	61.085	0.00	0.00	37.29	2.085
118	AACATTGTGTGACGTTGTGGT	184	21	0	42.86	58.912	0.00	0.00	0.00	2.088
119	ACATTGTGTGACGTTGTGGTT	183	21	0	42.86	58.912	0.00	0.00	0.00	2.088
120	TCTGAGTCGCTTAATTGCTCGT	103	22	0	45.45	60.095	0.00	0.00	0.00	2.095
121	GTCGTCTGCTGAGCTTTCTACT	245	22	0	50.00	60.095	0.00	0.00	0.00	2.095
122	ACATTGTGTGACGTTGTGGTTC	183	22	0	45.45	59.903	0.00	0.00	0.00	2.097
123	GTCGGGCTGGTAAATGTTGATG	156	22	0	50.00	59.903	0.00	0.00	0.00	2.097
124	GCACACCACGGACACACAA	304	19	0	57.89	61.110	0.00	0.00	0.00	2.110
125	AGGGTGCTCAGAAACAGCT	280	19	0	52.63	58.850	3.10	0.00	37.79	2.150
126	CACAAAGGACAGGGTGCTCAG	290	21	0	57.14	61.150	0.00	0.00	31.83	2.150

Primers data

127	GCTCAGAAACAGCTGCTGGAA	275	21	0	52.38	61.150	31.00	10.35	35.51	2.150
128	TCAGAAACAGCTGCTGGAATG	273	21	0	47.62	58.843	22.36	15.68	35.51	2.157
129	AGCTCAATTCTGGCTTCACAC	220	21	0	47.62	58.842	0.00	0.00	0.00	2.158
130	GCTCAATTCTGGCTTCACACT	219	21	0	47.62	58.842	0.00	0.00	0.00	2.158
131	ACAACATTGTGTGACGTTGTGG	186	22	0	45.45	60.159	5.36	0.00	41.89	2.159
132	CAACATTGTGTGACGTTGTGGT	185	22	0	45.45	60.159	0.00	0.00	0.00	2.159
133	CTCAGAAACAGCTGCTGGAATG	274	22	0	50.00	59.838	22.36	15.68	35.51	2.162
134	TCGTCTGCTGAGCTTTCTACT	244	21	0	47.62	58.836	0.18	0.00	0.00	2.164
135	TGTGACGTTGTGGTTTCGGC	177	19	0	57.89	61.175	0.00	0.00	35.47	2.175
136	ACAGCTGCTGGAATGCTCGA	267	20	0	55.00	62.176	31.00	0.00	35.51	2.176
137	GCTCGAAGGTCGTCTGCTGA	253	20	0	60.00	62.201	6.06	0.00	43.45	2.201
138	TCGAAGGTCGTCTGCTGAGC	251	20	0	60.00	62.201	0.00	0.00	43.45	2.201
139	CGAAGGTCGTCTGCTGAGCT	250	20	0	60.00	62.207	5.83	0.00	37.02	2.207
140	AGCTCAATTCTGGCTTCACACT	220	22	0	45.45	60.225	0.00	0.00	0.00	2.225
141	ACAAAGGACAGGGTGCTCA	289	19	0	52.63	58.769	0.00	0.00	31.83	2.231
142	CAGGGTGCTCAGAAACAGC	281	19	0	57.89	58.748	0.00	0.00	37.40	2.252
143	GGGTGCTCAGAAACAGCTG	279	19	0	57.89	58.748	13.48	13.48	37.79	2.252
144	GTCGTCTGCTGAGCTTTCTAC	245	21	0	52.38	58.745	0.00	0.00	0.00	2.255
145	TGCTCGAAGGTCGTCTGC	254	18	0	61.11	59.741	6.26	6.26	43.45	2.259
146	GAGTCGCTTAATTGCTCGTGA	100	21	0	47.62	58.740	0.00	0.00	0.00	2.260
147	CTGAGTCGCTTAATTGCTCGT	102	21	0	47.62	58.737	0.00	0.00	0.00	2.263
148	GCTCGTCGGGCTGGTAAA	160	18	0	61.11	59.736	10.59	0.00	0.00	2.264
149	TGCTCGAAGGTCGTCTGCT	254	19	0	57.89	61.269	11.58	0.00	43.45	2.269
150	TGCTGGGATGCACACCAC	313	18	0	61.11	60.282	3.46	0.78	38.12	2.282
151	CCACGGACACACAAAGGAC	299	19	0	57.89	58.683	0.00	0.00	0.00	2.317
152	ACAAAGGACAGGGTGCTCAGA	289	21	0	52.38	61.318	0.00	0.00	31.83	2.318
153	AGGACAGGGTGCTCAGAAACA	285	21	0	52.38	61.318	0.00	0.00	24.24	2.318
154	GGATGCACACCACGGACAC	308	19	0	63.16	61.325	6.86	0.00	0.00	2.325
155	CTGCTGGAATGCTCGAAGGTC	263	21	0	57.14	61.338	0.00	0.00	0.00	2.338
156	CTGCTGGGATGCACACCAC	314	19	0	63.16	61.338	3.46	0.78	38.12	2.338
157	TGAGTCGCTTAATTGCTCGTGA	101	22	0	45.45	60.352	0.00	0.00	0.00	2.352
158	TTGTGGTTTCGGCTCGTCG	170	18	0	61.11	60.355	0.00	0.00	0.00	2.355
159	TGAGTCGCTTAATTGCTCGT	101	20	0	45.00	57.636	0.00	0.00	0.00	2.364
160	AGTCGCTTAATTGCTCGTGA	99	20	0	45.00	57.636	0.00	0.00	0.00	2.364
161	TCGGGCTGGTAAATGTTGATG	155	21	0	47.62	58.635	0.00	0.00	0.00	2.365
162	CGGGCTGGTAAATGTTGATGA	154	21	0	47.62	58.635	0.00	0.00	0.00	2.365
163	GTCGGGCTGGTAAATGTTGAT	156	21	0	47.62	58.634	0.00	0.00	0.00	2.366
164	GTGTGACGTTGTGGTTTCGGC	178	20	0	60.00	62.369	0.00	0.00	35.47	2.369
165	TGTGTGACGTTGTGGTTTCG	179	19	0	52.63	58.625	0.00	0.00	0.00	2.375
166	GCTGGAATGCTCGAAGGTC	261	19	0	57.89	58.612	0.00	0.00	0.00	2.388
167	CTGCTGGAATGCTCGAAGG	263	19	0	57.89	58.609	0.00	0.00	0.00	2.391
168	CCACGGACACACAAAGGACAG	299	21	0	57.14	61.406	0.00	0.00	0.00	2.406
169	CACGGACACACAAAGGACAGG	298	21	0	57.14	61.406	0.00	0.00	0.00	2.406
170	CACACAAAGGACAGGGTGCTC	292	21	0	57.14	61.417	0.00	0.00	31.83	2.417
171	CTCAGAAACAGCTGCTGGAAT	274	21	0	47.62	58.566	31.00	17.58	35.51	2.434
172	AGGTCGTCTGCTGAGCTTTCT	247	21	0	52.38	61.436	0.00	0.00	0.00	2.436
173	CAACATTGTGTGACGTTGTGG	185	21	0	47.62	58.551	0.00	0.00	0.00	2.449

Primers data

174	GGTCGTCTGCTGAGCTTTTC	246	19	0	57.89	58.549	0.00	0.00	0.00	2.451
175	CACACCACGGACACACAAA	303	19	0	52.63	58.528	0.00	0.00	0.00	2.472
176	GACAGGGTGCTCAGAAACAGC	283	21	0	57.14	61.478	0.00	0.00	37.40	2.478
177	TGCTCGAAGGTCGTCTGCTG	254	20	0	60.00	62.478	11.58	0.00	43.45	2.478
178	CAGGGTGCTCAGAAACAGCTG	281	21	0	57.14	61.480	13.48	13.48	37.79	2.480
179	AACATTGTGTGACGTTGTGGTT	184	22	0	40.91	59.510	0.00	0.00	0.00	2.490
180	TCCTCTGAGTCGCTTAATTGCT	106	22	0	45.45	59.502	3.66	0.00	0.00	2.498
181	TGGAATGCTCGAAGGTCGTCT	259	21	0	52.38	61.498	0.00	0.00	43.45	2.498
182	TGACGTTGTGGTTCGGCT	175	18	0	55.56	59.498	0.00	0.00	35.95	2.502
183	ATGCACACCACGGACACA	306	18	0	55.56	59.492	0.00	0.00	0.00	2.508
184	TGCACACCACGGACACAC	305	18	0	61.11	60.513	0.00	0.00	0.00	2.513
185	GCACACCACGGACACACA	304	18	0	61.11	60.513	0.00	0.00	0.00	2.513
186	TCTGAGTCGCTTAATTGCTCG	103	21	0	47.62	58.470	0.00	0.00	0.00	2.530
187	CTCTGAGTCGCTTAATTGCTCG	104	22	0	50.00	59.466	0.00	0.00	0.00	2.534
188	GCTCAATTCTGGCTTCACACTT	219	22	0	45.45	59.444	0.00	0.00	0.00	2.556
189	AACAGCTGCTGGAATGCTC	268	19	0	52.63	58.436	31.00	0.00	35.51	2.564
190	GCTCGAAGGTCGTCTGCT	253	18	0	61.11	59.431	6.06	0.00	43.45	2.569
191	TCAGAAACAGCTGCTGGAAT	273	20	0	45.00	57.426	31.00	17.58	35.51	2.574
192	AGCTCAATTCTGGCTTCACA	220	20	0	45.00	57.426	0.00	0.00	0.00	2.574
193	TGTGACGTTGTGGTTCGGCT	177	20	0	55.00	62.581	0.00	0.00	35.95	2.581
194	GGCTCGTCGGGCTGGTAAAT	161	20	0	60.00	62.589	8.47	0.00	0.00	2.589
195	TTGTGTGACGTTGTGGTTCGG	180	21	0	52.38	61.599	0.00	0.00	0.00	2.599
196	ATGCACACCACGGACACACA	306	20	0	55.00	62.601	0.00	0.00	0.00	2.601
197	TCGTTTTCTTCCTCTGAGTCGC	115	22	0	50.00	60.607	0.00	0.00	0.00	2.607
198	CGTTTTCTTCCTCTGAGTCGCT	114	22	0	50.00	60.608	0.00	0.00	0.00	2.608
199	AGTCGCTTAATTGCTCGTGACA	99	22	0	45.45	60.609	11.57	0.00	0.00	2.609
200	CGGACACACAAAGGACAGG	296	19	0	57.89	58.383	0.00	0.00	0.00	2.617
201	TGCTCAGAAACAGCTGCTG	276	19	0	52.63	58.375	27.02	27.02	37.79	2.625
202	GCTCAATTCTGGCTTCACAC	219	20	0	50.00	57.374	0.00	0.00	0.00	2.626
203	GTGCTCAGAAACAGCTGCT	277	19	0	52.63	58.373	1.22	0.00	37.79	2.627
204	GTGACGTTGTGGTTCGGC	176	18	0	61.11	59.370	0.00	0.00	35.47	2.630
205	CAGAAACAGCTGCTGGAATG	272	20	0	50.00	57.369	19.76	10.50	35.51	2.631
206	CACAAAGGACAGGGTGCTC	290	19	0	57.89	58.366	0.00	0.00	31.83	2.634
207	GTCGTCTGCTGAGCTTTCTA	245	20	0	50.00	57.361	0.00	0.00	0.00	2.639
208	TCGTCTGCTGAGCTTTCTAC	244	20	0	50.00	57.361	0.00	0.00	0.00	2.639
209	CGTCTGCTGAGCTTTCTACT	243	20	0	50.00	57.354	0.18	0.00	0.00	2.646
210	GAATGCTCGAAGGTCGTCTGC	257	21	0	57.14	61.648	6.26	6.26	43.45	2.648
211	GACGTTGTGGTTCGGCTCG	174	19	0	63.16	61.655	0.00	0.00	31.86	2.655
212	CGTTGTGGTTCGGCTCGTC	172	19	0	63.16	61.655	0.00	0.00	0.00	2.655
213	GTTGTGGTTCGGCTCGTCG	171	19	0	63.16	61.655	0.00	0.00	0.00	2.655
214	ACGTTGTGGTTCGGCTCG	173	18	0	61.11	60.661	0.00	0.00	0.00	2.661
215	CGTTGTGGTTCGGCTCGT	172	18	0	61.11	60.661	0.00	0.00	0.00	2.661
216	GGAATGCTCGAAGGTCGTC	258	19	0	57.89	58.333	0.00	0.00	43.45	2.667
217	CACCACGGACACACAAAGGAC	301	21	0	57.14	61.670	0.00	0.00	0.00	2.670
218	CTGGAATGCTCGAAGGTCG	260	19	0	57.89	58.329	0.00	0.00	44.56	2.671
219	CTCGTCGGGCTGGTAAATG	159	19	0	57.89	58.322	0.00	0.00	0.00	2.678
220	GACACACAAAGGACAGGGTGC	294	21	0	57.14	61.682	0.00	0.00	34.69	2.682

Primers data

221	GAGTCGCTTAATTGCTCGTG	100	20	0	50.00	57.297	0.00	0.00	0.00	2.703
222	CATTGTGTGACGTTGTGGTTC	182	21	0	47.62	58.285	0.00	0.00	0.00	2.715
223	GGGATGCACACCACGGAC	309	18	0	66.67	60.746	12.79	0.00	0.00	2.746
224	CTGGGATGCACACCACGG	311	18	0	66.67	60.747	2.08	0.00	0.00	2.747
225	CAAAGGACAGGGTGCTCAGAAA	288	22	0	50.00	60.749	0.00	0.00	31.83	2.749
226	AAAGGACAGGGTGCTCAGAAAC	287	22	0	50.00	60.750	0.00	0.00	31.83	2.750
227	ACACCACGGACACACAAAG	302	19	0	52.63	58.225	0.00	0.00	0.00	2.775
228	TCGGGCTGGTAAATGTTGAT	155	20	0	45.00	57.201	0.00	0.00	0.00	2.799
229	TGCACACCACGGACACACAA	305	20	0	55.00	62.805	0.00	0.00	0.00	2.805
230	AAACAGCTGCTGGAATGCTCG	269	21	0	52.38	61.812	31.00	5.48	35.51	2.812
231	ACTGCTGGGATGCACACCA	315	19	0	57.89	61.833	6.10	4.92	38.12	2.833
232	AACATTGTGTGACGTTGTGG	184	20	0	45.00	57.158	0.00	0.00	0.00	2.842
233	CATTGTGTGACGTTGTGGTT	182	20	0	45.00	57.158	0.00	0.00	0.00	2.842
234	CGTCGGGCTGGTAAATGTT	157	19	0	52.63	58.151	0.00	0.00	0.00	2.849
235	CATTGTGTGACGTTGTGGTTTCG	182	22	0	50.00	60.849	0.00	0.00	0.00	2.849
236	CGGGCTGGTAAATGTTGATG	154	20	0	50.00	57.150	0.00	0.00	0.00	2.850
237	AAAGGACAGGGTGCTCAGA	287	19	0	52.63	58.146	0.00	0.00	31.83	2.854
238	AAGGACAGGGTGCTCAGAA	286	19	0	52.63	58.146	0.00	0.00	31.83	2.854
239	AGGACAGGGTGCTCAGAAA	285	19	0	52.63	58.146	0.00	0.00	24.24	2.854
240	CCTCTGAGTCGCTTAATTGCTC	105	22	0	50.00	59.137	3.66	0.00	0.00	2.863
241	ACACAAAGGACAGGGTGCTCA	291	21	0	52.38	61.869	0.00	0.00	31.83	2.869
242	TCCTCTGAGTCGCTTAATTGC	106	21	0	47.62	58.106	3.66	0.00	0.00	2.894
243	CCTCTGAGTCGCTTAATTGCT	105	21	0	47.62	58.101	3.66	0.00	0.00	2.899
244	CAGCTGCTGGAATGCTCGAAG	266	21	0	57.14	61.927	21.71	0.00	34.51	2.927
245	ACAGGGTGCTCAGAAACAGCT	282	21	0	52.38	61.933	3.10	0.00	37.79	2.933
246	GGACAGGGTGCTCAGAAAC	284	19	0	57.89	58.066	0.00	0.00	0.00	2.934
247	CACACCACGGACACACAAAGG	303	21	0	57.14	61.935	0.00	0.00	0.00	2.935
248	CAAAGGACAGGGTGCTCAG	288	19	0	57.89	58.062	0.00	0.00	31.83	2.938
249	CTGGCTTCACACTTACAACACA	211	22	0	45.45	59.058	0.00	0.00	0.00	2.942
250	CGGGCTGGTAAATGTTGATGAT	154	22	0	45.45	59.048	0.00	0.00	0.00	2.952
251	AGCTGCTGGAATGCTCGA	265	18	0	55.56	59.015	0.00	0.00	30.41	2.985
252	CTGAGTCGCTTAATTGCTCG	102	20	0	50.00	57.013	0.00	0.00	0.00	2.987
253	GGTCGTCTGCTGAGCTTTCTAC	246	22	0	54.55	60.987	0.00	0.00	0.00	2.987
254	TGGCTTCACACTTACAACACA	210	21	0	42.86	58.007	0.00	0.00	0.00	2.993
255	TTACTGCTGGGATGCACACCA	317	21	0	52.38	62.004	6.10	4.92	38.12	3.004
256	ACTAGCTCAATTCTGGCTTCACA	223	23	0	43.48	59.992	2.49	0.00	33.07	3.008
257	TAGCTCAATTCTGGCTTCACACT	221	23	0	43.48	59.992	2.49	0.00	33.07	3.008
258	GGACACACAAAGGACAGGG	295	19	0	57.89	57.979	0.00	0.00	0.00	3.021
259	GTTTTCTTCCTCTGAGTCGCT	113	21	0	47.62	57.967	0.00	0.00	0.00	3.033
260	AAACAGCTGCTGGAATGCT	269	19	0	47.37	57.953	31.00	8.45	35.51	3.047
261	TTCCTCTGAGTCGCTTAATTGCT	107	23	0	43.48	60.056	0.00	0.00	0.00	3.056
262	GGTGCTCAGAAACAGCTGCTG	278	21	0	57.14	62.068	27.02	27.02	37.79	3.068
263	GTGCTCAGAAACAGCTGCTGG	277	21	0	57.14	62.068	31.00	14.58	37.79	3.068
264	CACGGACACACAAAGGACA	298	19	0	52.63	57.927	0.00	0.00	0.00	3.073
265	AATGCTCGAAGGTCGTCTGCT	256	21	0	52.38	62.099	11.58	0.55	43.45	3.099
266	CAGCTGCTGGAATGCTCG	266	18	0	61.11	58.901	21.71	0.00	34.51	3.099
267	ACACCACGGACACACAAAGGA	302	21	0	52.38	62.124	0.00	0.00	0.00	3.124

Primers data

268	ACCACGGACACACAAAGGACA	300	21	0	52.38	62.124	0.00	0.00	0.00	3.124
269	GTCGTCTGCTGAGCTTTCTACTA	245	23	0	47.83	59.873	0.00	0.00	0.00	3.127
270	TCGTCTGCTGAGCTTTCTACTAC	244	23	0	47.83	59.873	0.18	0.00	0.00	3.127
271	CGTCTGCTGAGCTTTCTACTACT	243	23	0	47.83	59.872	0.18	0.00	0.00	3.128
272	ACAACATTGTGTGACGTTGTG	186	21	0	42.86	57.870	5.36	0.00	41.89	3.130
273	AGGTCGTCTGCTGAGCTTTCTA	247	22	0	50.00	61.142	0.00	0.00	0.00	3.142
274	ACACACAAAGGACAGGGTGCT	293	21	0	52.38	62.146	0.00	0.00	35.27	3.146
275	TCTGGCTTCACACTTACAACAC	212	22	0	45.45	58.797	0.00	0.00	0.00	3.203
276	GACGTTGTGGTTTCGGCTC	174	18	0	61.11	58.759	0.00	0.00	31.86	3.241
277	GTTGTGGTTTCGGCTCGTC	171	18	0	61.11	58.759	0.00	0.00	0.00	3.241
278	TGGGATGCACACCACGGA	310	18	0	61.11	61.245	6.10	0.00	0.00	3.245
279	TTACTGCTGGGATGCACAC	317	19	0	52.63	57.752	0.00	0.00	38.12	3.248
280	CTGGGATGCACACCACGGA	311	19	0	63.16	62.253	2.08	0.00	0.00	3.253
281	GATGCACACCACGGACAC	307	18	0	61.11	58.746	0.00	0.00	0.00	3.254
282	CGTCGGGCTGGTAAATGTTGAT	157	22	0	50.00	61.256	0.00	0.00	0.00	3.256
283	TGCTCAGAAACAGCTGCTGGA	276	21	0	52.38	62.259	31.00	17.77	37.79	3.259
284	TTCTCTGAGTCGCTTAATTGC	107	22	0	45.45	58.738	0.00	0.00	0.00	3.262
285	TCGTTTTCTTCCTCTGAGTCG	115	21	0	47.62	57.716	0.00	0.00	0.00	3.284
286	GGCTCGTCGGGCTGGTAAA	161	19	0	63.16	62.305	8.47	0.00	0.00	3.305
287	CTTCCTCTGAGTCGCTTAATTGC	108	23	0	47.83	59.692	0.00	0.00	0.00	3.308
288	TGCACACCACGGACACACA	305	19	0	57.89	62.317	0.00	0.00	0.00	3.317
289	TAGCTCAATTCTGGCTTCACAC	221	22	0	45.45	58.662	2.49	0.00	33.07	3.338
290	TCGTCTGCTGAGCTTTCTACTA	244	22	0	45.45	58.655	0.18	0.00	0.00	3.345
291	TCTGGCTTCACACTTACAACACA	212	23	0	43.48	60.370	0.00	0.00	0.00	3.370
292	TCGGGCTGGTAAATGTTGATGAT	155	23	0	43.48	60.371	0.00	0.00	0.00	3.371
293	CTAGCTCAATTCTGGCTTCACAC	222	23	0	47.83	59.627	2.49	0.00	33.07	3.373
294	ACGGACACACAAAGGACAG	297	19	0	52.63	57.620	0.00	0.00	0.00	3.380
295	CGGGCTGGTAAATGTTGATGATT	154	23	0	43.48	59.619	0.00	0.00	0.00	3.381
296	GTTTTCTTCCTCTGAGTCGCTT	113	22	0	45.45	58.605	0.00	0.00	0.00	3.395
297	GAAACAGCTGCTGGAATGC	270	19	0	52.63	57.586	9.13	0.00	35.51	3.414
298	AATGCTCGAAGGTCGTCTG	256	19	0	52.63	57.574	0.00	0.00	43.45	3.426
299	AACATTGTGTGACGTTGTGGTTC	184	23	0	43.48	60.427	0.00	0.00	0.00	3.427
300	TCCTCTGAGTCGCTTAATTGCTC	106	23	0	47.83	60.430	3.66	0.00	0.00	3.430
301	CGTCTGCTGAGCTTTCTACTAC	243	22	0	50.00	58.569	0.18	0.00	0.00	3.431
302	GCTGGGATGCACACCACG	312	18	0	66.67	61.434	3.27	0.42	0.00	3.434
303	ACGTTGTGGTTTCGGCTCGT	173	19	0	57.89	62.435	0.00	0.00	0.00	3.435
304	GCTCAGAAACAGCTGCTGGAAT	275	22	0	50.00	61.457	31.00	17.58	35.51	3.457
305	AGAAACAGCTGCTGGAATGCTC	271	22	0	50.00	61.457	14.60	5.05	35.51	3.457
306	GAAGGTCGTCTGCTGAGCTTTC	249	22	0	54.55	61.494	3.04	0.30	36.71	3.494
307	ACACACAAAGGACAGGGTG	293	19	0	52.63	57.505	0.00	0.00	37.29	3.495
308	GTCGTCTGCTGAGCTTTCT	245	19	0	52.63	57.494	0.00	0.00	0.00	3.506
309	GCACACCACGGACACACAAAG	304	21	0	57.14	62.514	0.00	0.00	0.00	3.514
310	ACGGACACACAAAGGACAGGG	297	21	0	57.14	62.522	0.00	0.00	0.00	3.522
311	CGGACACACAAAGGACAGGGT	296	21	0	57.14	62.522	0.00	0.00	0.00	3.522
312	TGGGATGCACACCACGGAC	310	19	0	63.16	62.545	6.10	0.00	0.00	3.545
313	GGGATGCACACCACGGACA	309	19	0	63.16	62.545	12.79	0.00	0.00	3.545
314	TGGCTTCACACTTACAACACAT	210	22	0	40.91	58.449	0.00	0.00	0.00	3.551

Primers data

315	TCTGGCTTCACACTTACAACA	212	21	0	42.86	57.448	0.00	0.00	0.00	3.552
316	CTGGCTTCACACTTACAACACAT	211	23	0	43.48	59.435	0.00	0.00	0.00	3.565
317	CTAGCTCAATTCTGGCTTCACA	222	22	0	45.45	58.396	2.49	0.00	33.07	3.604
318	ACTAGCTCAATTCTGGCTTCAC	223	22	0	45.45	58.395	2.49	0.00	33.07	3.605
319	CTGGCTTCACACTTACAACAC	211	21	0	47.62	57.391	0.00	0.00	0.00	3.609
320	CATCGTTTTCTTCCTCTGAGTCG	117	23	0	47.83	59.390	0.00	0.00	0.00	3.610
321	CTCAGAAACAGCTGCTGGA	274	19	0	52.63	57.380	31.00	17.77	35.51	3.620
322	TTCTGGCTTCACACTTACAACAC	213	23	0	43.48	59.374	0.00	0.00	0.00	3.626
323	AACAGCTGCTGGAATGCTCGA	268	21	0	52.38	62.651	31.00	0.00	35.51	3.651
324	ACAGCTGCTGGAATGCTCGAA	267	21	0	52.38	62.651	31.00	0.00	35.51	3.651
325	TACTGCTGGGATGCACACCAC	316	21	0	57.14	62.660	3.46	0.78	38.12	3.660
326	CGAAGGTCGTCTGCTGAGCTT	250	21	0	57.14	62.671	7.47	7.47	38.04	3.671
327	CAACATTGTGTGACGTTGTGGTT	185	23	0	43.48	60.672	0.00	0.00	0.00	3.672
328	TAGCTCAATTCTGGCTTCACA	221	21	0	42.86	57.299	2.49	0.00	33.07	3.701
329	GACAGGGTGCTCAGAAACA	283	19	0	52.63	57.294	0.00	0.00	0.00	3.706
330	TCAGAAACAGCTGCTGGAATGC	273	22	0	50.00	61.711	22.78	10.47	35.51	3.711
331	ACAGGGTGCTCAGAAACAG	282	19	0	52.63	57.286	0.00	0.00	0.00	3.714
332	CAGAAACAGCTGCTGGAATGCT	272	22	0	50.00	61.715	14.60	5.01	35.51	3.715
333	GAATGCTCGAAGGTCGTCT	257	19	0	52.63	57.276	0.00	0.00	43.45	3.724
334	ATGCTCGAAGGTCGTCTGCTG	255	21	0	57.14	62.738	11.58	0.00	43.45	3.738
335	AGCTCAATTCTGGCTTCACACTT	220	23	0	43.48	60.750	0.00	0.00	0.00	3.750
336	GCTCAATTCTGGCTTCACACTTA	219	23	0	43.48	59.247	0.00	0.00	0.00	3.753
337	TTTTCTTCCTCTGAGTCGCTT	112	21	0	42.86	57.247	0.00	0.00	0.00	3.753
338	CGTCTGCTGAGCTTTCTACTA	243	21	0	47.62	57.233	0.18	0.00	0.00	3.767
339	GGCTCGTCGGGCTGGTAA	161	18	0	66.67	61.767	8.47	0.00	0.00	3.767
340	AAGGTCGTCTGCTGAGCT	248	18	0	55.56	58.215	5.83	0.00	0.00	3.785
341	AGGTCGTCTGCTGAGCTT	247	18	0	55.56	58.215	5.83	0.00	0.00	3.785
342	GACACACAAAGGACAGGGT	294	19	0	52.63	57.199	0.00	0.00	0.00	3.801
343	CTCGTCGGGCTGGTAAATGTTG	159	22	0	54.55	61.813	0.00	0.00	0.00	3.813
344	ACAAAGGACAGGGTGCTCAGAA	289	22	0	50.00	61.821	0.00	0.00	31.83	3.821
345	AAGGACAGGGTGCTCAGAAACA	286	22	0	50.00	61.821	0.00	0.00	31.83	3.821
346	ATCGTTTTCTTCCTCTGAGTCG	116	22	0	45.45	58.161	0.00	0.00	0.00	3.839
347	TTGTGGTTTCGGCTCGTCGG	170	19	0	63.16	62.852	0.00	0.00	0.00	3.852
348	TTCTGGCTTCACACTTACAACA	213	22	0	40.91	58.120	0.00	0.00	0.00	3.880
349	ATTGTGTGACGTTGTGGTTCGG	181	22	0	50.00	61.883	0.00	0.00	0.00	3.883
350	GCTGCTGGAATGCTCGAA	264	18	0	55.56	58.105	0.00	0.00	0.00	3.895
351	ATCGTTTTCTTCCTCTGAGTCGC	116	23	0	47.83	60.919	0.00	0.00	0.00	3.919
352	AGTCGCTTAATTGCTCGTGACAT	99	23	0	43.48	60.923	11.57	0.17	0.00	3.923
353	AAGGTCGTCTGCTGAGCTTTCT	248	22	0	50.00	61.926	4.25	0.00	34.76	3.926
354	CTCTGAGTCGCTTAATTGCTCGT	104	23	0	47.83	60.977	0.00	0.00	0.00	3.977
355	ACTAGCTCAATTCTGGCTTCA	223	21	0	42.86	57.011	0.00	0.00	33.07	3.989
356	TCGAAGGTCGTCTGCTGA	251	18	0	55.56	57.925	0.00	0.00	43.45	4.075
357	CGTTTTCTTCCTCTGAGTCGCTT	114	23	0	47.83	61.103	0.00	0.00	0.00	4.103
358	TGTGACGTTGTGGTTCGG	177	18	0	55.56	57.888	0.00	0.00	0.00	4.112
359	GAAGGTCGTCTGCTGAGC	249	18	0	61.11	57.823	0.00	0.00	0.00	4.177
360	GTCGGGCTGGTAAATGTTGATGA	156	23	0	47.83	61.178	0.00	0.00	0.00	4.178
361	AGGACAGGGTGCTCAGAAACAG	285	22	0	54.55	62.197	0.00	0.00	24.24	4.197

Primers data

362	CACACCACGGACACACAA	303	18	0	55.56	57.790	0.00	0.00	0.00	4.210
363	TCTGAGTCGCTTAATTGCTCGTG	103	23	0	47.83	61.218	0.00	0.00	0.00	4.218
364	CTGAGTCGCTTAATTGCTCGTGA	102	23	0	47.83	61.218	0.00	0.00	0.00	4.218
365	TACTAGCTCAATTCTGGCTTCACA	224	24	0	41.67	59.777	0.00	0.00	33.07	4.223
366	TCGTCGGGCTGGTAAATGTTGA	158	22	0	50.00	62.244	0.00	0.00	0.00	4.244
367	TGCTGAGCTTTCTACTACTAGCT	239	23	0	43.48	58.726	5.83	0.00	0.00	4.274
368	ATTCTGGCTTCACACTTACAACAC	214	24	0	41.67	59.724	0.00	0.00	0.00	4.276
369	ACAGCTGCTGGAATGCTC	267	18	0	55.56	57.684	31.00	0.00	35.51	4.316
370	CGTCTGCTGAGCTTTCTACTACTA	243	24	0	45.83	59.667	0.18	0.00	0.00	4.333
371	TCTGCTGAGCTTTCTACTACTAGC	241	24	0	45.83	59.663	5.83	0.00	0.00	4.337
372	TGCTGAGCTTTCTACTACTAGCTC	239	24	0	45.83	59.663	14.27	14.27	40.31	4.337
373	GCTGAGCTTTCTACTACTAGCTCA	238	24	0	45.83	59.663	20.97	20.97	44.16	4.337
374	CTGCTGAGCTTTCTACTACTAGCT	240	24	0	45.83	59.662	5.83	0.00	0.00	4.338
375	CTGGAATGCTCGAAGGTCGTCT	260	22	0	54.55	62.350	0.00	0.00	43.45	4.350
376	TGTGGTTCGGCTCGTCTGG	169	18	0	66.67	62.352	0.00	0.00	0.00	4.352
377	GCTCAATTCTGGCTTCACACTTAC	219	24	0	45.83	60.379	0.00	0.00	0.00	4.379
378	CACAAAGGACAGGGTGCTCAGA	290	22	0	54.55	62.453	0.00	0.00	31.83	4.453
379	TGAGTCGCTTAATTGCTCGTGAC	101	23	0	47.83	61.459	4.62	4.62	0.00	4.459
380	GAGTCGCTTAATTGCTCGTGACA	100	23	0	47.83	61.459	11.57	0.00	0.00	4.459
381	ATTCTGGCTTCACACTTACAACA	214	23	0	39.13	58.540	0.00	0.00	0.00	4.460
382	CTCGAAGGTCGTCTGCTG	252	18	0	61.11	57.533	0.00	0.00	43.45	4.467
383	CGAAGGTCGTCTGCTGAG	250	18	0	61.11	57.533	0.00	0.00	37.02	4.467
384	ACTACTAGCTCAATTCTGGCTTCA	226	24	0	41.67	59.532	0.00	0.00	33.07	4.468
385	TAGCTCAATTCTGGCTTCACACTT	221	24	0	41.67	60.506	2.49	0.00	33.07	4.506
386	AGCTCAATTCTGGCTTCACACTTA	220	24	0	41.67	60.506	0.00	0.00	0.00	4.506
387	TGGCTTCACACTTACAACACATAC	210	24	0	41.67	59.486	0.00	0.00	0.00	4.514
388	GGCTTCACACTTACAACACATACA	209	24	0	41.67	59.486	0.00	0.00	0.00	4.514
389	ACCACGGACACACAAAGG	300	18	0	55.56	57.448	0.00	0.00	0.00	4.552
390	GTTTTCTTCTCTGAGTCGCTTA	113	23	0	43.48	58.443	0.00	0.00	0.00	4.557
391	CCTCTGAGTCGCTTAATTGCTCG	105	23	0	52.17	61.577	3.66	0.00	0.00	4.577
392	CGGGCTGGTAAATGTTGATGATTA	154	24	0	41.67	59.421	0.00	0.00	0.00	4.579
393	ACACAAAGGACAGGGTGC	291	18	0	55.56	57.421	0.00	0.00	34.69	4.579
394	TGGAATGCTCGAAGGTCGTCTG	259	22	0	54.55	62.599	0.00	0.00	43.45	4.599
395	CTGCTGAGCTTTCTACTACTAGC	240	23	0	47.83	58.393	5.83	0.00	0.00	4.607
396	CGTCGGGCTGGTAAATGT	157	18	0	55.56	57.390	0.00	0.00	0.00	4.610
397	TCATCGTTTTCTTCTCTGAGTCG	118	24	0	45.83	60.616	0.00	0.00	0.00	4.616
398	TGCTGGAATGCTCGAAGG	262	18	0	55.56	57.376	0.00	0.00	0.00	4.624
399	AAGGTCGTCTGCTGAGCTTTCTA	248	23	0	47.83	61.624	4.25	0.00	34.76	4.624
400	GCTGGAATGCTCGAAGGT	261	18	0	55.56	57.374	0.00	0.00	0.00	4.626
401	GAAACAGCTGCTGGAATGCTCG	270	22	0	54.55	62.627	12.08	0.00	35.51	4.627
402	TGCTGAGCTTTCTACTACTAGC	239	22	0	45.45	57.359	5.83	0.00	0.00	4.641
403	AAGGACAGGGTGCTCAGA	286	18	0	55.56	57.352	0.00	0.00	31.83	4.648
404	AGGACAGGGTGCTCAGAA	285	18	0	55.56	57.352	0.00	0.00	24.24	4.648
405	ACAACATTGTGTGACGTTGTGGT	186	23	0	43.48	61.671	5.36	0.00	41.89	4.671
406	AGTCGCTTAATTGCTCGTGACATA	99	24	0	41.67	60.677	11.57	0.00	0.00	4.677
407	GGTCGTCTGCTGAGCTTT	246	18	0	55.56	57.317	5.83	0.00	0.00	4.683
408	TCTGGCTTCACACTTACAACACAT	212	24	0	41.67	60.686	0.00	0.00	0.00	4.686

Primers data

409	TGGCTTCACACTTACAACACATA	210	23	0	39.13	58.291	0.00	0.00	0.00	4.709
410	GTCTGCTGAGCTTTTCTACTACT	242	22	0	45.45	57.288	0.00	0.00	0.00	4.712
411	TGCTCAGAAACAGCTGCTGGAA	276	22	0	50.00	62.712	31.00	10.35	37.79	4.712
412	TCAATTCTGGCTTCACACTTACA	217	23	0	39.13	58.286	0.00	0.00	0.00	4.714
413	ACACAAAGGACAGGGTGCTCAG	291	22	0	54.55	62.714	0.00	0.00	31.83	4.714
414	TCTTCCTCTGAGTCGCTTAATTG	109	23	0	43.48	58.251	0.00	0.00	0.00	4.749
415	CTGGCTTCACACTTACAACACATA	211	24	0	41.67	59.245	0.00	0.00	0.00	4.755
416	CTCAATTCTGGCTTCACACTTACA	218	24	0	41.67	59.243	0.00	0.00	0.00	4.757
417	TACTAGCTCAATTCTGGCTTCAC	224	23	0	43.48	58.240	0.00	0.00	33.07	4.760
418	GACAGGGTGCTCAGAAACAGCT	283	22	0	54.55	62.766	3.10	0.00	37.79	4.766
419	CTACTAGCTCAATTCTGGCTTCAC	225	24	0	45.83	59.192	2.49	0.00	33.07	4.808
420	AGGGTGCTCAGAAACAGC	280	18	0	55.56	57.191	0.00	0.00	37.40	4.809
421	GGGTGCTCAGAAACAGCT	279	18	0	55.56	57.191	3.10	0.00	37.79	4.809
422	TCATCGTTTTTCTTCCTCTGAGTC	118	23	0	43.48	58.189	0.00	0.00	0.00	4.811
423	AACAGCTGCTGGAATGCT	268	18	0	50.00	57.163	31.00	8.45	35.51	4.837
424	CGTTTTTCTTCCTCTGAGTCGCTTA	114	24	0	45.83	60.851	0.00	0.00	0.00	4.851
425	CAAAGGACAGGGTGCTCAGAAAC	288	23	0	52.17	61.855	0.00	0.00	31.83	4.855
426	GCTGAGCTTTTCTACTACTAGCTC	238	23	0	47.83	58.144	14.27	14.27	40.31	4.856
427	TCGTTTTCTTCCTCTGAGTCGCT	115	23	0	47.83	61.861	0.00	0.00	0.00	4.861
428	CTAGCTCAATTCTGGCTTCACACT	222	24	0	45.83	60.862	2.49	0.00	33.07	4.862
429	TTCTGGCTTCACACTTACAACACA	213	24	0	41.67	60.865	0.00	0.00	0.00	4.865
430	TTTTCTTCCTCTGAGTCGCTTA	112	22	0	40.91	57.133	0.00	0.00	0.00	4.867
431	TTTCTTCCTCTGAGTCGCTTAA	111	22	0	40.91	57.133	0.00	0.00	0.00	4.867
432	CCACGGACACACAAAGGA	299	18	0	55.56	57.132	0.00	0.00	0.00	4.868
433	TCGGGCTGGTAAATGTTGATGATT	155	24	0	41.67	60.870	0.00	0.00	0.00	4.870
434	TCATCGTTTTTCTTCCTCTGAGT	118	22	0	40.91	57.126	3.66	0.00	0.00	4.874
435	AATTCTGGCTTCACACTTACAACA	215	24	0	37.50	59.113	0.00	0.00	0.00	4.887
436	GAATGCTCGAAGGTCGTCTGCT	257	22	0	54.55	62.906	11.58	0.55	43.45	4.906
437	CACAAAGGACAGGGTGCT	290	18	0	55.56	57.093	0.00	0.00	35.27	4.907
438	TGGAATGCTCGAAGGTCG	259	18	0	55.56	57.089	0.00	0.00	44.56	4.911
439	GCTGAGCTTTTCTACTACTAGCT	238	22	0	45.45	57.088	0.00	0.00	0.00	4.912
440	GGAATGCTCGAAGGTCGT	258	18	0	55.56	57.087	0.00	0.00	43.45	4.913
441	TCTTCCTCTGAGTCGCTTAATTGC	109	24	0	45.83	60.916	0.00	0.00	0.00	4.916
442	TTCTCTGAGTCGCTTAATTGCTC	107	24	0	45.83	60.916	0.00	0.00	0.00	4.916
443	CTTCCTCTGAGTCGCTTAATTGCT	108	24	0	45.83	60.917	0.00	0.00	0.00	4.917
444	TCGTCGGGCTGGTAAATG	158	18	0	55.56	57.076	0.00	0.00	0.00	4.924
445	ACCACGGACACACAAAGGACAG	300	22	0	54.55	62.945	0.00	0.00	0.00	4.945
446	GTCGTCTGCTGAGCTTTTCTACTAC	245	24	0	50.00	60.962	0.00	0.00	0.00	4.962
447	CACACAAAGGACAGGGTGCTCA	292	22	0	54.55	62.966	0.00	0.00	31.83	4.966
448	GACACACAAAGGACAGGGTGCT	294	22	0	54.55	62.968	0.00	0.00	35.27	4.968
449	ACACACAAAGGACAGGGTGCTC	293	22	0	54.55	62.968	0.00	0.00	31.83	4.968
450	GTTTTCTTCCTCTGAGTCGCTTAA	113	24	0	41.67	59.011	0.00	0.00	0.00	4.989
451	GCTTCACACTTACAACACATACACA	208	25	0	40.00	59.993	0.00	0.00	0.00	5.007
452	TCAATTCTGGCTTCACACTTACAAC	217	25	0	40.00	59.991	0.00	0.00	0.00	5.009
453	CTACTAGCTCAATTCTGGCTTCA	225	23	0	43.48	57.984	0.00	0.00	33.07	5.016
454	ACTACTAGCTCAATTCTGGCTTC	226	23	0	43.48	57.983	2.49	0.00	33.07	5.017
455	GGCTTCACACTTACAACACATAC	209	23	0	43.48	57.969	0.00	0.00	0.00	5.031

Primers data

456	CGGGCTGGTAAATGTTGATGATTAA	154	25	0	40.00	59.933	0.00	0.00	0.00	5.067
457	ACTAGCTCAATTCTGGCTTCACAC	223	24	0	45.83	61.100	2.49	0.00	33.07	5.100
458	TCGTCTGCTGAGCTTTCTACTACT	244	24	0	45.83	61.104	0.18	0.00	0.00	5.104
459	TCAATTCTGGCTTCACACTTACAA	217	24	0	37.50	58.870	0.00	0.00	0.00	5.130
460	GCTGAGCTTTCTACTACTAGCTCAA	238	25	0	44.00	60.164	21.58	9.71	44.95	5.164
461	TTCTTCCTCTGAGTCGCTTAATTG	110	24	0	41.67	58.829	0.00	0.00	0.00	5.171
462	TTTTCTTCCTCTGAGTCGCTTAA	112	23	0	39.13	57.790	0.00	0.00	0.00	5.210
463	CAATTCTGGCTTCACACTTACAAC	216	24	0	41.67	58.785	0.00	0.00	0.00	5.215
464	TTCATCGTTTTCTTCCTCTGAGT	119	23	0	39.13	57.785	3.66	0.00	0.00	5.215
465	CAATTCTGGCTTCACACTTACAACA	216	25	0	40.00	60.221	0.00	0.00	0.00	5.221
466	AATTCTGGCTTCACACTTACAACAC	215	25	0	40.00	60.221	0.00	0.00	0.00	5.221
467	AGGTCGTCTGCTGAGCTTTCTAC	247	23	0	52.17	62.224	0.00	0.00	0.00	5.224
468	GGTCGTCTGCTGAGCTTTCTACT	246	23	0	52.17	62.224	2.49	0.00	0.00	5.224
469	TTCATCGTTTTCTTCCTCTGAGTC	119	24	0	41.67	58.769	0.00	0.00	0.00	5.231
470	CTCAATTCTGGCTTCACACTTACAA	218	25	0	40.00	59.761	0.00	0.00	0.00	5.239
471	TAGCTCAATTCTGGCTTCACACTTA	221	25	0	40.00	60.280	2.49	0.00	33.07	5.280
472	ACAAAGGACAGGGTGCTCAGAAA	289	23	0	47.83	62.280	0.00	0.00	31.83	5.280
473	AAAGGACAGGGTGCTCAGAAACA	287	23	0	47.83	62.280	0.00	0.00	31.83	5.280
474	CTCAATTCTGGCTTCACACTTAC	218	23	0	43.48	57.711	0.00	0.00	0.00	5.289
475	ACATTGTGTGACGTTGTGGTTCG	183	23	0	47.83	62.310	0.00	0.00	0.00	5.310
476	CGTCGGGCTGGTAAATGTTGATG	157	23	0	52.17	62.314	0.00	0.00	0.00	5.314
477	CTGGCTTCACACTTACAACACATAC	211	25	0	44.00	60.334	0.00	0.00	0.00	5.334
478	TTTCTTCCTCTGAGTCGCTTAAT	111	23	0	39.13	57.593	0.00	0.00	0.00	5.407
479	TTCTTCCTCTGAGTCGCTTAATT	110	23	0	39.13	57.593	0.00	0.00	0.00	5.407
480	CAATTCTGGCTTCACACTTACAA	216	23	0	39.13	57.563	0.00	0.00	0.00	5.437
481	AATTCTGGCTTCACACTTACAAC	215	23	0	39.13	57.561	0.00	0.00	0.00	5.439
482	GCTTCACACTTACAACACATACAC	208	24	0	41.67	58.559	0.00	0.00	0.00	5.441
483	TCTACTACTAGCTCAATTCTGGCT	229	24	0	41.67	58.550	2.60	2.60	34.62	5.450
484	TCTGGCTTCACACTTACAACACATA	212	25	0	40.00	60.454	0.00	0.00	0.00	5.454
485	GTCGGGCTGGTAAATGTTGATGAT	156	24	0	45.83	61.461	0.00	0.00	0.00	5.461
486	CAACATTGTGTGACGTTGTGGTTC	185	24	0	45.83	61.480	0.00	0.00	0.00	5.480
487	TCGTCTGGGCTGGTAAATGTTGAT	158	23	0	47.83	62.497	0.00	0.00	0.00	5.497
488	CGTCTGCTGAGCTTTCTACTACTAG	243	25	0	48.00	60.503	0.18	0.00	0.00	5.503
489	CTGCTGAGCTTTCTACTACTAGCTC	240	25	0	48.00	60.506	14.27	14.27	40.31	5.506
490	GCTCAGAAACAGCTGCTGGAATG	275	23	0	52.17	62.510	22.36	15.68	35.51	5.510
491	CTCAGAAACAGCTGCTGGAATGC	274	23	0	52.17	62.510	22.78	10.47	35.51	5.510
492	CAGAAACAGCTGCTGGAATGCTC	272	23	0	52.17	62.510	14.60	5.05	35.51	5.510
493	GGCTTCACACTTACAACACATACAC	209	25	0	44.00	60.560	0.00	0.00	0.00	5.560
494	TTTCATCGTTTTCTTCCTCTGAGT	120	24	0	37.50	58.389	3.66	0.00	0.00	5.611
495	CTACTAGCTCAATTCTGGCTTCACA	225	25	0	44.00	60.625	0.00	0.00	33.07	5.625
496	ACTACTAGCTCAATTCTGGCTTCAC	226	25	0	44.00	60.626	2.49	0.00	33.07	5.626
497	TCGGGCTGGTAAATGTTGATGATTA	155	25	0	40.00	60.630	0.00	0.00	0.00	5.630
498	AAGGACAGGGTGCTCAGAAACAG	286	23	0	52.17	62.635	0.00	0.00	31.83	5.635
499	TTTCTTCCTCTGAGTCGCTTAATTG	111	25	0	40.00	59.360	0.00	0.00	0.00	5.640
500	GTTTTCTTCCTCTGAGTCGCTTAAT	113	25	0	40.00	59.360	0.00	0.00	0.00	5.640
501	TACTACTAGCTCAATTCTGGCTTCA	227	25	0	40.00	59.343	0.00	0.00	33.07	5.657
502	GCTTCACACTTACAACACATACA	208	23	0	39.13	57.333	0.00	0.00	0.00	5.667

Primers data

503	TTTCATCGTTTTCTTCCTCTGAGTC	120	25	0	40.00	59.303	0.00	0.00	0.00	5.697
504	GAAGGTCGTCTGCTGAGCTTTTCT	249	23	0	52.17	62.716	5.55	0.00	36.71	5.716
505	GAGTCGCTTAATTGCTCGTGACAT	100	24	0	45.83	61.724	11.57	1.91	0.00	5.724
506	GTCTGCTGAGCTTTTCTACTACTAGC	242	25	0	48.00	60.732	0.00	0.00	0.00	5.732
507	TCTACTACTAGCTCAATTCTGGC	229	23	0	43.48	57.224	0.00	0.00	0.00	5.776
508	CTACTACTAGCTCAATTCTGGCT	228	23	0	43.48	57.217	2.60	2.60	34.62	5.783
509	TTTTCTTCCTCTGAGTCGCTTAAT	112	24	0	37.50	58.205	0.00	0.00	0.00	5.795
510	TTTCTTCCTCTGAGTCGCTTAATT	111	24	0	37.50	58.205	0.00	0.00	0.00	5.795
511	GTCTGCTGAGCTTTTCTACTACTAG	242	24	0	45.83	58.183	0.00	0.00	0.00	5.817
512	GTCTGCTGAGCTTTTCTACTACTA	242	23	0	43.48	57.178	0.00	0.00	0.00	5.822
513	TACTAGCTCAATTCTGGCTTCACAC	224	25	0	44.00	60.855	0.00	0.00	33.07	5.855
514	TCGTCTGCTGAGCTTTTCTACTACTA	244	25	0	44.00	60.857	0.18	0.00	0.00	5.857
515	TCTGCTGAGCTTTTCTACTACTAGCT	241	25	0	44.00	60.864	5.83	0.00	0.00	5.864
516	TCACACTTACAACACATACACAACA	205	25	0	36.00	59.125	0.00	0.00	0.00	5.875
517	CACAAAGGACAGGGTGCTCAGAA	290	23	0	52.17	62.878	0.00	0.00	31.83	5.878
518	TTCTACTACTAGCTCAATTCTGGCT	230	25	0	40.00	59.106	2.60	2.60	34.62	5.894
519	TCTACTACTAGCTCAATTCTGGCTT	229	25	0	40.00	59.106	2.49	0.00	33.07	5.894
520	CATTGTGTGACGTTGTGGTTTCGG	182	23	0	52.17	62.896	0.00	0.00	0.00	5.896
521	TGGCTTCACACTTACAACACATACA	210	25	0	40.00	60.917	0.00	0.00	0.00	5.917
522	GGTCGTCTGCTGAGCTTTTCTACTA	246	24	0	50.00	61.927	2.49	0.00	0.00	5.927
523	TGCTCAGAAACAGCTGCTGGAAT	276	23	0	47.83	62.948	31.00	17.58	37.79	5.948
524	TCAGAAACAGCTGCTGGAATGCT	273	23	0	47.83	62.948	22.78	12.14	35.51	5.948
525	CATCGTTTTCTTCCTCTGAGTCGC	117	24	0	50.00	61.949	0.00	0.00	0.00	5.949
526	CTCTGAGTCGCTTAATTGCTCGTG	104	24	0	50.00	61.998	0.00	0.00	0.00	5.998
527	TCTACTACTAGCTCAATTCTGGCTTC	229	26	0	42.31	59.960	2.49	0.00	33.07	6.040
528	TTCATCGTTTTCTTCCTCTGAGTCG	119	25	0	44.00	61.074	0.00	0.00	0.00	6.074
529	TGCTGAGCTTTTCTACTACTAGCTCA	239	25	0	44.00	61.094	20.97	20.97	44.16	6.094
530	GGGCTGGTAAATGTTGATGATTAAC	153	26	0	38.46	59.903	1.77	0.00	0.00	6.097
531	ACAACATTGTGTGACGTTGTGGTT	186	24	0	41.67	62.107	5.36	0.00	41.89	6.107
532	CACACTTACAACACATACACAACA	204	24	0	37.50	57.887	0.00	0.00	0.00	6.113
533	ATCGTTTTCTTCCTCTGAGTCGCT	116	24	0	45.83	62.118	0.00	0.00	0.00	6.118
534	TTTTCTTCCTCTGAGTCGCTTAATTG	112	26	0	38.46	59.852	0.00	0.00	0.00	6.148
535	GTTTTCTTCCTCTGAGTCGCTTAATT	113	26	0	38.46	59.852	0.00	0.00	0.00	6.148
536	ATTCTGGCTTCACACTTACAACACA	214	25	0	40.00	61.150	0.00	0.00	0.00	6.150
537	TTCTGGCTTCACACTTACAACACAT	213	25	0	40.00	61.150	0.00	0.00	0.00	6.150
538	TTCTACTACTAGCTCAATTCTGGC	230	24	0	41.67	57.850	0.00	0.00	0.00	6.150
539	TACTACTAGCTCAATTCTGGCTTC	227	24	0	41.67	57.850	2.49	0.00	33.07	6.150
540	CTACTACTAGCTCAATTCTGGCTT	228	24	0	41.67	57.845	2.49	0.00	33.07	6.155
541	CTACTACTAGCTCAATTCTGGCTTCA	228	26	0	42.31	60.183	0.00	0.00	33.07	6.183
542	CTACTACTAGCTCAATTCTGGCTTC	228	25	0	44.00	58.787	2.49	0.00	33.07	6.213
543	CTGAGTCGCTTAATTGCTCGTGAC	102	24	0	50.00	62.225	4.62	4.62	0.00	6.225
544	TTTTCTTCCTCTGAGTCGCTTAATT	112	25	0	36.00	58.769	0.00	0.00	0.00	6.231
545	ATTTTCATCGTTTTCTTCCTCTGAGT	121	25	0	36.00	58.766	3.66	0.00	0.00	6.234
546	GGGCTGGTAAATGTTGATGATTAAC	153	25	0	40.00	58.727	0.00	0.00	0.00	6.273
547	TCGTTTTCTTCCTCTGAGTCGCTT	115	24	0	45.83	62.290	0.00	0.00	0.00	6.290
548	CGTTTTCTTCCTCTGAGTCGCTTAA	114	25	0	44.00	61.299	0.00	0.00	0.00	6.299
549	CTAGCTCAATTCTGGCTTCACACTT	222	25	0	44.00	61.316	2.49	0.00	33.07	6.316

Primers data

550	TCACACTTACAACACATACACAAC	205	24	0	37.50	57.647	0.00	0.00	0.00	6.353
551	TTCTTCCTCTGAGTCGCTTAATTGC	110	25	0	44.00	61.364	0.00	0.00	0.00	6.364
552	ATTTTCATCGTTTTCTTCCTCTGAGTC	121	26	0	38.46	59.630	0.00	0.00	0.00	6.370
553	TTCACACTTACAACACATACACAACA	206	26	0	34.62	59.628	0.00	0.00	0.00	6.372
554	TTTCTACTACTAGCTCAATTCTGGCT	231	26	0	38.46	59.619	2.60	2.60	34.62	6.381
555	TTCTACTACTAGCTCAATTCTGGCTT	230	26	0	38.46	59.619	2.49	0.00	33.07	6.381
556	TCTGAGTCGCTTAATTGCTCGTGA	103	24	0	45.83	62.394	0.00	0.00	0.00	6.394
557	GAAGGTCGTCGCTGAGCTTTCTA	249	24	0	50.00	62.400	5.55	0.00	36.71	6.400
558	TACTACTAGCTCAATTCTGGCTTCAC	227	26	0	42.31	60.406	0.00	0.00	33.07	6.406
559	CTGAGCTTTCTACTACTAGCTCAA	237	24	0	41.67	57.556	21.58	9.71	44.95	6.444
560	GCTTCACACTTACAACACATACACAA	208	26	0	38.46	60.458	0.00	0.00	0.00	6.458
561	GAGTCGCTTAATTGCTCGTGACATA	100	25	0	44.00	61.461	11.57	0.00	0.00	6.461
562	GCTGAGCTTTCTACTACTAGCTCAAT	238	26	0	42.31	60.461	21.58	0.00	44.95	6.461
563	AGTCGCTTAATTGCTCGTGACATAG	99	25	0	44.00	61.464	11.57	0.00	0.00	6.464
564	GGGCTGGTAAATGTTGATGATTAA	153	24	0	37.50	57.536	0.00	0.00	0.00	6.464
565	TCACACTTACAACACATACACAACAT	205	26	0	34.62	59.459	0.00	0.00	0.00	6.541
566	AGCTCAATTCTGGCTTCACACTTAC	220	25	0	44.00	61.544	0.00	0.00	0.00	6.544
567	TTTCTACTACTAGCTCAATTCTGGC	231	25	0	40.00	58.426	0.00	0.00	0.00	6.574
568	CTTCACACTTACAACACATACACA	207	24	0	37.50	57.403	0.00	0.00	0.00	6.597
569	AAGGTCGTCGCTGAGCTTTCTAC	248	24	0	50.00	62.636	4.25	0.00	34.76	6.636
570	CTTCCTCTGAGTCGCTTAATTGCTC	108	25	0	48.00	61.692	0.00	0.00	0.00	6.692
571	GCTTTCTACTACTAGCTCAATTCTGG	233	26	0	42.31	59.300	0.00	0.00	0.00	6.700
572	CTTTCTACTACTAGCTCAATTCTGGC	232	26	0	42.31	59.300	0.00	0.00	0.00	6.700
573	AACATTGTGTGACGTTGTGGTTTCG	184	24	0	45.83	62.712	0.00	0.00	0.00	6.712
574	CACACTTACAACACATACACAACAT	204	25	0	36.00	58.276	0.00	0.00	0.00	6.724
575	ATTTTCATCGTTTTCTTCCTCTGAG	121	24	0	37.50	57.266	0.00	0.00	0.00	6.734
576	TCCTCTGAGTCGCTTAATTGCTCG	106	24	0	50.00	62.737	3.66	0.00	0.00	6.737
577	GCTCAATTCTGGCTTCACACTTACA	219	25	0	44.00	61.769	0.00	0.00	0.00	6.769
578	TTCACACTTACAACACATACACAAC	206	25	0	36.00	58.223	0.00	0.00	0.00	6.777
579	CTCAATTCTGGCTTCACACTTACAAC	218	26	0	42.31	60.785	0.00	0.00	0.00	6.785
580	TGAGTCGCTTAATTGCTCGTGACA	101	24	0	45.83	62.859	11.57	2.96	0.00	6.859
581	GTCGGGCTGGTAAATGTTGATGATT	156	25	0	44.00	61.891	0.00	0.00	0.00	6.891
582	CTTCACACTTACAACACATACACAAC	207	26	0	38.46	59.095	0.00	0.00	0.00	6.905
583	TTCTGGCTTCACACTTACAACACATA	213	26	0	38.46	60.910	0.00	0.00	0.00	6.910
584	ACACTTACAACACATACACAACAT	203	24	0	33.33	57.064	0.00	0.00	0.00	6.936
585	CGGGCTGGTAAATGTTGATGATTAA	154	26	0	42.31	60.951	0.00	0.00	0.00	6.951
586	CCTCTGAGTCGCTTAATTGCTCGT	105	24	0	50.00	62.972	3.66	0.00	0.00	6.972
587	TTCACACTTACAACACATACACAA	206	24	0	33.33	57.013	0.00	0.00	0.00	6.987
588	TCGTTTTCTTCCTCTGAGTCGCTTA	115	25	0	44.00	62.001	0.00	0.00	0.00	7.001
589	CTTCACACTTACAACACATACACAA	207	25	0	36.00	57.989	0.00	0.00	0.00	7.011
590	CTGAGCTTTCTACTACTAGCTCAAT	237	25	0	40.00	57.962	21.58	0.00	44.95	7.038
591	TTCACACTTACAACACATACACAACAT	206	27	0	33.33	59.934	0.00	0.00	0.00	7.066
592	TCACACTTACAACACATACACAACATT	205	27	0	33.33	59.934	0.00	0.00	0.00	7.066
593	CTAGCTCAATTCTGGCTTCACACTTA	222	26	0	42.31	61.072	2.49	0.00	33.07	7.072
594	TCTTCCTCTGAGTCGCTTAATTGCT	109	25	0	44.00	62.076	0.00	0.00	0.00	7.076
595	TCGGGCTGGTAAATGTTGATGATTAA	155	26	0	38.46	61.081	0.00	0.00	0.00	7.081
596	TTTCTACTACTAGCTCAATTCTGGCTT	231	27	0	37.04	60.093	2.49	0.00	33.07	7.093

Primers data

597	GGCTGGTAAATGTTGATGATTA	152	25	0	36.00	57.900	1.77	0.00	0.00	7.100
598	GTCGTCTGCTGAGCTTTCTACT	245	25	0	48.00	62.102	0.14	0.00	0.00	7.102
599	GCTGGTAAATGTTGATGATTA	151	27	0	37.04	60.148	3.92	3.92	0.00	7.148
600	ACACTTACAACACATACACA	203	27	0	33.33	60.148	0.00	0.00	44.94	7.148
601	CACACTTACAACACATACACA	204	27	0	37.04	59.834	0.00	0.00	0.00	7.166
602	CACACTTACAACACATACACA	204	26	0	34.62	58.807	0.00	0.00	0.00	7.193
603	ACACTTACAACACATACACA	203	26	0	34.62	58.807	0.00	0.00	0.00	7.193
604	CACTTACAACACATACACA	202	26	0	34.62	58.807	0.00	0.00	44.94	7.193
605	GGCTGGTAAATGTTGATGAT	152	26	0	38.46	58.804	0.00	0.00	0.00	7.196
606	GCTGGTAAATGTTGATGAT	151	26	0	38.46	58.804	0.00	0.00	0.00	7.196
607	CAATTCTGGCTTCACACTT	216	26	0	42.31	61.220	0.00	0.00	0.00	7.220
608	ACTAGCTCAATTCTGGCTTC	223	25	0	44.00	62.263	2.49	0.00	33.07	7.263
609	ACTCCATCTATTTTCATCGT	130	27	0	37.04	59.719	0.00	0.00	0.00	7.281
610	TAGCTCAATTCTGGCTTCAC	221	26	0	42.31	61.292	2.49	0.00	33.07	7.292
611	ACACTTACAACACATACACA	203	25	0	32.00	57.672	0.00	0.00	0.00	7.328
612	ACTTACAACACATACACA	201	25	0	32.00	57.672	0.00	0.00	44.94	7.328
613	TCCATCTATTTTCATCGT	128	26	0	34.62	58.661	0.00	0.00	0.00	7.339
614	TGAGCTTTCTACTACTAGCT	236	27	0	37.04	59.659	20.65	0.00	43.75	7.341
615	TCAATTCTGGCTTCACACTT	217	26	0	38.46	61.356	0.00	0.00	0.00	7.356
616	TATTTTCATCGTTTTTCTTC	122	26	0	34.62	58.613	3.66	0.00	0.00	7.387
617	TGAGCTTTCTACTACTAGCT	236	25	0	36.00	57.589	20.65	0.00	43.75	7.411
618	CTTCACACTTACAACACAT	207	27	0	37.04	60.414	0.00	0.00	0.00	7.414
619	ATTCTGGCTTCACACTTACA	214	26	0	38.46	61.415	0.00	0.00	0.00	7.415
620	TTCTACTACTAGCTCAATT	230	27	0	40.74	60.417	2.49	0.00	33.07	7.417
621	AGCTTTCTACTACTAGCTCA	234	27	0	40.74	60.417	0.00	0.00	0.00	7.417
622	CTTTCTACTACTAGCTCAAT	232	27	0	40.74	60.417	2.60	2.60	34.62	7.417
623	TCTGGCTTCACACTTACAAC	212	26	0	42.31	61.454	0.00	0.00	0.00	7.454
624	TGAGCTTTCTACTACTAGCT	236	26	0	38.46	58.515	20.65	0.82	43.75	7.485
625	CTGAGCTTTCTACTACTAG	237	26	0	38.46	58.512	21.58	0.00	44.95	7.488
626	AGCTTTCTACTACTAGCTCA	234	26	0	38.46	58.512	0.00	0.00	0.00	7.488
627	TCCATCTATTTTCATCGT	128	27	0	37.04	59.504	0.00	0.00	0.00	7.496
628	TTTCATCGTTTTTCTTCCT	120	26	0	42.31	61.497	0.00	0.00	0.00	7.497
629	CTCCATCTATTTTCATCGT	129	27	0	37.04	59.503	0.00	0.00	0.00	7.497
630	CCATCTATTTTCATCGT	127	27	0	37.04	59.503	0.00	0.00	0.00	7.497
631	ATCGTTTTTCTTCCTCTGA	116	25	0	44.00	62.521	0.00	0.00	0.00	7.521
632	TGCTGAGCTTTCTACTACT	239	26	0	42.31	61.526	21.58	9.36	44.95	7.526
633	TATTTTCATCGTTTTTCTTC	122	27	0	37.04	59.454	0.00	0.00	0.00	7.546
634	CTATTTTCATCGTTTTTCTTC	123	27	0	37.04	59.453	3.66	0.00	0.00	7.547
635	CGTTTTTCTTCCTCTGAGT	114	26	0	42.31	61.553	0.00	0.00	0.00	7.553
636	TCCATCTATTTTCATCGT	128	25	0	36.00	57.446	0.00	0.00	0.00	7.554
637	CCATCTATTTTCATCGT	127	25	0	36.00	57.440	0.00	0.00	0.00	7.560
638	AATTCTGGCTTCACACTTACA	215	26	0	38.46	61.579	0.00	0.00	0.00	7.579
639	CACTTACAACACATACACA	202	25	0	36.00	57.392	0.00	0.00	0.00	7.608
640	CTACTAGCTCAATTCTGGCT	225	26	0	46.15	61.610	2.49	0.00	33.07	7.610
641	TCTATTTTCATCGTTTTTCTTC	124	26	0	34.62	58.388	0.00	0.00	0.00	7.612
642	TCGTCTGCTGAGCTTTCTACT	244	26	0	46.15	61.615	0.18	0.00	0.00	7.615
643	TCTGCTGAGCTTTCTACTACT	241	26	0	46.15	61.625	14.27	14.27	40.31	7.625

Primers data

644	GTCGGGCTGGTAAATGTTGATGATTA	156	26	0	42.31	61.625	0.00	0.00	0.00	7.625
645	CTCCATCTATTTTCATCGTTTTCTTCC	129	26	0	38.46	58.365	0.00	0.00	0.00	7.635
646	CCATCTATTTTCATCGTTTTCTTCCTC	127	26	0	38.46	58.365	0.00	0.00	0.00	7.635
647	CTGAGCTTTCTACTACTAGCTCAATTC	237	27	0	40.74	59.352	21.58	0.92	44.95	7.648
648	GAGCTTTCTACTACTAGCTCAATTCTG	235	27	0	40.74	59.352	15.79	0.00	39.93	7.648
649	AGCTTTCTACTACTAGCTCAATTCT	234	25	0	36.00	57.346	0.00	0.00	0.00	7.654
650	CTGGCTTCACACTTACAACACATACA	211	26	0	42.31	61.674	0.00	0.00	0.00	7.674
651	GGGCTGGTAAATGTTGATGATTAAGTC	153	27	0	40.74	60.682	0.00	0.00	0.00	7.682
652	GGCTGGTAAATGTTGATGATTAAGTCC	152	27	0	40.74	60.682	0.00	0.00	0.00	7.682
653	GCTTTCTACTACTAGCTCAATTCTG	233	25	0	40.00	57.307	0.00	0.00	0.00	7.693
654	GAGCTTTCTACTACTAGCTCAATTCT	235	26	0	38.46	58.287	15.79	0.00	39.93	7.713
655	TCTATTTTCATCGTTTTCTTCCTCTGAG	124	27	0	37.04	59.238	0.00	0.00	0.00	7.762
656	TTTCTTCCTCTGAGTCGCTTAATTGC	111	26	0	42.31	61.778	0.00	0.00	0.00	7.778
657	ACAACATTGTGTGACGTTGTGGTTC	186	25	0	44.00	62.821	5.36	0.00	41.89	7.821
658	GTCGTCTGCTGAGCTTTCTACTACTA	245	26	0	46.15	61.832	0.14	0.00	0.00	7.832
659	GTTTTCTTCCTCTGAGTCGCTTAATTG	113	27	0	40.74	60.832	0.00	0.00	0.00	7.832
660	TCTATTTTCATCGTTTTCTTCCTCTG	124	25	0	36.00	57.166	0.00	0.00	0.00	7.834
661	CTATTTTCATCGTTTTCTTCCTCTGA	123	25	0	36.00	57.166	0.00	0.00	0.00	7.834
662	TATTTTCATCGTTTTCTTCCTCTGAG	122	25	0	36.00	57.166	0.00	0.00	0.00	7.834
663	CTGCTGAGCTTTCTACTACTAGCTCA	240	26	0	46.15	61.846	20.97	20.97	44.16	7.846
664	GTCTGCTGAGCTTTCTACTACTAGCT	242	26	0	46.15	61.847	0.00	0.00	0.00	7.847
665	GGTCGTCTGCTGAGCTTTCTACTAC	246	25	0	52.00	62.874	2.49	0.00	0.00	7.874
666	TGGCTTCACACTTACAACACATACAC	210	26	0	42.31	61.891	0.00	0.00	0.00	7.891
667	GGCTTCACACTTACAACACATACACA	209	26	0	42.31	61.891	0.00	0.00	0.00	7.891
668	GCTGAGCTTTCTACTACTAGCTCAATT	238	27	0	40.74	60.897	21.58	0.00	44.95	7.897
669	CTATTTTCATCGTTTTCTTCCTCTGAG	123	26	0	38.46	58.096	0.00	0.00	0.00	7.904
670	GAGCTTTCTACTACTAGCTCAATTC	235	25	0	40.00	57.076	15.79	0.00	39.93	7.924
671	ACTACTAGCTCAATTCTGGCTTCACA	226	26	0	42.31	61.981	0.00	0.00	33.07	7.981
672	TACTAGCTCAATTCTGGCTTCACACT	224	26	0	42.31	61.981	0.00	0.00	33.07	7.981
673	CTACTACTAGCTCAATTCTGGCTTCAC	228	27	0	44.44	61.158	2.49	0.00	33.07	8.158
674	GCTCAATTCTGGCTTCACACTTACAA	219	26	0	42.31	62.169	0.00	0.00	0.00	8.169
675	GAGTCGCTTAATTGCTCGTGACATAG	100	26	0	46.15	62.174	11.57	0.00	0.00	8.174
676	ATTCTGGCTTCACACTTACAACACATA	214	27	0	37.04	61.174	0.00	0.00	0.00	8.174
677	ACTCCATCTATTTTCATCGTTTTCTTC	130	26	0	34.62	57.797	0.00	0.00	0.00	8.203
678	ATCGTTTTCTTCCTCTGAGTCGCTTA	116	26	0	42.31	62.233	0.00	0.00	0.00	8.233
679	ATCTATTTTCATCGTTTTCTTCCTCTGA	125	27	0	33.33	58.739	0.00	0.00	0.00	8.261
680	CTGGTAAATGTTGATGATTAAGTCCA	150	26	0	34.62	57.720	3.92	3.92	0.00	8.280
681	TCTACTACTAGCTCAATTCTGGCTTCA	229	27	0	40.74	61.289	0.00	0.00	33.07	8.289
682	CATCTATTTTCATCGTTTTCTTCCTCTG	126	27	0	37.04	58.666	0.00	0.00	0.00	8.334
683	TCGTTTTCTTCCTCTGAGTCGCTTAA	115	26	0	42.31	62.393	0.00	0.00	0.00	8.393
684	GCTTCACACTTACAACACATACACAAC	208	27	0	40.74	61.404	0.00	0.00	0.00	8.404
685	CATCTATTTTCATCGTTTTCTTCCTCT	126	26	0	34.62	57.569	0.00	0.00	0.00	8.431
686	ATCTATTTTCATCGTTTTCTTCCTCTG	125	26	0	34.62	57.569	0.00	0.00	0.00	8.431
687	TTCTTCCTCTGAGTCGCTTAATTGCT	110	26	0	42.31	62.469	0.00	0.00	0.00	8.469
688	AGTCGCTTAATTGCTCGTGACATAGA	99	26	0	42.31	62.549	11.57	0.00	0.00	8.549
689	AACTCCATCTATTTTCATCGTTTTCTT	131	26	0	30.77	57.433	0.00	0.00	0.00	8.567
690	GCTTTCTACTACTAGCTCAATTCTGGC	233	27	0	44.44	61.632	0.00	0.00	0.00	8.632

Primers data

691	ACTAGCTCAATTCTGGCTTCACACTT	223	26	0	42.31	62.651	2.49	0.00	33.07	8.651
692	AACTCCATCTATTTTCATCGTTTTCTTC	131	27	0	33.33	58.331	0.00	0.00	0.00	8.669
693	TACTACTAGCTCAATTCTGGCTTCACA	227	27	0	40.74	61.718	0.00	0.00	33.07	8.718
694	ATTTTCATCGTTTTCTTCCTCTGAGTCG	121	27	0	40.74	61.736	0.00	0.00	0.00	8.736
695	TGAGTCGCTTAATTGCTCGTGACATA	101	26	0	42.31	62.762	11.57	2.02	0.00	8.762
696	TGCTGAGCTTTCTACTACTAGCTCAAT	239	27	0	40.74	61.769	21.58	0.00	44.95	8.769
697	TCTTCCTCTGAGTCGCTTAATTGCTC	109	26	0	46.15	62.773	0.00	0.00	0.00	8.773
698	AATTCTGGCTTCACACTTACAACACAT	215	27	0	37.04	61.819	0.00	0.00	0.00	8.819
699	TGGTAAATGTTGATGATTAAGTCCAT	149	26	0	30.77	57.178	4.34	0.00	0.00	8.822
700	CGTCTGCTGAGCTTTCTACTACTAGC	243	26	0	50.00	62.842	0.18	0.00	0.00	8.842
701	TTCTGGCTTCACACTTACAACACATAC	213	27	0	40.74	61.852	0.00	0.00	0.00	8.852
702	AGCTCAATTCTGGCTTCACACTTACA	220	26	0	42.31	62.867	0.00	0.00	0.00	8.867
703	TGGTAAATGTTGATGATTAAGTCCATC	149	27	0	33.33	58.097	7.15	7.15	0.00	8.903
704	CTGGTAAATGTTGATGATTAAGTCCAT	150	27	0	33.33	58.093	4.98	0.00	0.00	8.907
705	CGTTTTCTTCCTCTGAGTCGCTTAATT	114	27	0	40.74	61.943	0.00	0.00	0.00	8.943
706	CTAGCTCAATTCTGGCTTCACACTTAC	222	27	0	44.44	62.000	2.49	0.00	33.07	9.000
707	GTCGGGCTGGTAAATGTTGATGATTAA	156	27	0	40.74	62.018	0.00	0.00	0.00	9.018
708	TCGGGCTGGTAAATGTTGATGATTAAAC	155	27	0	40.74	62.018	0.00	0.00	0.00	9.018
709	CGGGCTGGTAAATGTTGATGATTAACT	154	27	0	40.74	62.022	1.77	0.00	0.00	9.022
710	CTCAATTCTGGCTTCACACTTACAACA	218	27	0	40.74	62.067	0.00	0.00	0.00	9.067
711	GGTAAATGTTGATGATTAAGTCCATCT	148	27	0	33.33	57.875	12.60	0.00	0.00	9.125
712	TTTTCTTCCTCTGAGTCGCTTAATTGC	112	27	0	40.74	62.162	0.00	0.00	0.00	9.162
713	CTGCTGAGCTTTCTACTACTAGCTCAA	240	27	0	44.44	62.230	21.58	10.71	44.95	9.230
714	GGCTTCACACTTACAACACATACACAA	209	27	0	40.74	62.271	0.00	0.00	0.00	9.271
715	TCAATTCTGGCTTCACACTTACAACAC	217	27	0	40.74	62.275	0.00	0.00	0.00	9.275
716	TACTAGCTCAATTCTGGCTTCACACTT	224	27	0	40.74	62.365	0.00	0.00	33.07	9.365
717	ACTAGCTCAATTCTGGCTTCACACTTA	223	27	0	40.74	62.365	2.49	0.00	33.07	9.365
718	TGATGATTAACTCCATCTATTTTCATCG	139	27	0	33.33	57.572	12.60	0.00	0.00	9.428
719	GATGATTAACTCCATCTATTTTCATCGT	138	27	0	33.33	57.571	6.94	0.00	0.00	9.429
720	CAATTCTGGCTTCACACTTACAACACA	216	27	0	40.74	62.486	0.00	0.00	0.00	9.486
721	GTCGTCTGCTGAGCTTTCTACTACTAG	245	27	0	48.15	62.510	0.14	0.00	0.00	9.510
722	GTCTGCTGAGCTTTCTACTACTAGCTC	242	27	0	48.15	62.526	14.27	14.27	40.31	9.526
723	CTGGCTTCACACTTACAACACATACAC	211	27	0	44.44	62.568	0.00	0.00	0.00	9.568
724	TAGCTCAATTCTGGCTTCACACTTACA	221	27	0	40.74	62.575	2.49	0.00	33.07	9.575
725	ATCGTTTTCTTCCTCTGAGTCGCTTAA	116	27	0	40.74	62.603	0.00	0.00	0.00	9.603
726	TCGTTTTCTTCCTCTGAGTCGCTTAAT	115	27	0	40.74	62.603	0.00	0.00	0.00	9.603
727	TGATTAACTCCATCTATTTTCATCGTTT	136	27	0	29.63	57.387	0.00	0.00	0.00	9.613
728	CTACTAGCTCAATTCTGGCTTCACACT	225	27	0	44.44	62.667	0.00	0.00	33.07	9.667
729	TTAACTCCATCTATTTTCATCGTTTTCT	133	27	0	29.63	57.333	0.00	0.00	0.00	9.667
730	TAACTCCATCTATTTTCATCGTTTTCTT	132	27	0	29.63	57.333	0.00	0.00	0.00	9.667
731	TCTGGCTTCACACTTACAACACATACA	212	27	0	40.74	62.729	0.00	0.00	0.00	9.729
732	ATGATTAACTCCATCTATTTTCATCGTT	137	27	0	29.63	57.215	0.00	0.00	0.00	9.785
733	TTTCTTCCTCTGAGTCGCTTAATTGCT	111	27	0	40.74	62.833	0.00	0.00	0.00	9.833
734	ACTACTAGCTCAATTCTGGCTTCACAC	226	27	0	44.44	62.875	2.49	0.00	33.07	9.875
735	TCTGCTGAGCTTTCTACTACTAGCTCA	241	27	0	44.44	62.901	20.97	20.97	44.16	9.901
736	TGTTGATGATTAACTCCATCTATTTCA	142	27	0	29.63	57.096	4.15	0.00	0.00	9.904
737	AGTCGCTTAATTGCTCGTGACATAGAA	99	27	0	40.74	62.905	11.57	0.00	0.00	9.905

Primers data

BLAST INFORMATION

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: PD7PEV0E014

Database: Nucleotide collection (nt)

43,336,626 sequences; 150,108,365,041 total letters

Query=

Length=23

Score E

Sequences producing significant alignments: (Bits) Value

KX545354.1	Human papillomavirus type 18 isolate NGSk256-18 E6...	42.8	0.060
KC470230.1	Human papillomavirus type 18 isolate BF226, comple...	42.8	0.060
KC470229.1	Human papillomavirus type 18 isolate Qv39775, comp...	42.8	0.060
KC470228.1	Human papillomavirus type 18 isolate BF380, comple...	42.8	0.060
KC470227.1	Human papillomavirus type 18 isolate Qv12693, comp...	42.8	0.060
KC470226.1	Human papillomavirus type 18 isolate Z125, complet...	42.8	0.060
KC470225.1	Human papillomavirus type 18 isolate BF172, comple...	42.8	0.060
KC470224.1	Human papillomavirus type 18 isolate BF288, comple...	42.8	0.060
KC470223.1	Human papillomavirus type 18 isolate BF309, comple...	42.8	0.060
KC470222.1	Human papillomavirus type 18 isolate Z100, complet...	42.8	0.060
KC470221.1	Human papillomavirus type 18 isolate Qv28775, comp...	42.8	0.060
KC470219.1	Human papillomavirus type 18 isolate Rw57, complet...	42.8	0.060
KC470218.1	Human papillomavirus type 18 isolate Rw687, comple...	42.8	0.060
KC470217.1	Human papillomavirus type 18 isolate Rw750, comple...	42.8	0.060
KC470216.1	Human papillomavirus type 18 isolate Z53, complete...	42.8	0.060
KC470215.1	Human papillomavirus type 18 isolate Z63, complete...	42.8	0.060
KC470214.1	Human papillomavirus type 18 isolate Z52, complete...	42.8	0.060
KC662605.1	Human papillomavirus type 18 isolate B8890 E7 (E7)...	42.8	0.060
JN416175.1	Human papillomavirus isolate LSCG E7 (E7) gene, co...	42.8	0.060
JN416174.1	Human papillomavirus isolate LSCE E7 (E7) gene, co...	42.8	0.060
JN416165.1	Human papillomavirus isolate LSM4 E7 (E7) gene, co...	42.8	0.060
JN416163.1	Human papillomavirus isolate LSM2 E7 (E7) gene, co...	42.8	0.060
EF422144.1	Human papillomavirus type 18 strain P629 E7 protei...	42.8	0.060
EF202155.1	Human papillomavirus type 18 isolate Qv04924, comp...	42.8	0.060
EF202154.1	Human papillomavirus type 18 isolate Qv03814, comp...	42.8	0.060
EF202153.1	Human papillomavirus type 18 isolate Qv21444, comp...	42.8	0.060
EF202152.1	Human papillomavirus type 18 isolate Qv17199, comp...	42.8	0.060

BLAST INFORMATION

AF339137.1	Homo sapiens clone CC-2 sequence flanking Human pa...	42.8	0.060
KY457840.1	Human papillomavirus type 18 strain 18CNTZ36 E6 (E...	37.4	2.5
KY457839.1	Human papillomavirus type 18 strain 18CNTZ35 E6 (E...	37.4	2.5
KY457838.1	Human papillomavirus type 18 strain 18CNTZ34 E6 (E...	37.4	2.5
KY457837.1	Human papillomavirus type 18 strain 18CNTZ33 E6 (E...	37.4	2.5
KY457836.1	Human papillomavirus type 18 strain 18CNTZ32 E6 (E...	37.4	2.5
KY457835.1	Human papillomavirus type 18 strain 18CNTZ31 E6 (E...	37.4	2.5
KY457834.1	Human papillomavirus type 18 strain 18CNTZ30 E6 (E...	37.4	2.5
KY457833.1	Human papillomavirus type 18 strain 18CNTZ29 E6 (E...	37.4	2.5
KY457832.1	Human papillomavirus type 18 strain 18CNTZ28 E6 (E...	37.4	2.5
KY457831.1	Human papillomavirus type 18 strain 18CNTZ27 E6 (E...	37.4	2.5
KY457830.1	Human papillomavirus type 18 strain 18CNTZ26 E6 (E...	37.4	2.5
KY457829.1	Human papillomavirus type 18 strain 18CNTZ25 E6 (E...	37.4	2.5
KY457828.1	Human papillomavirus type 18 strain 18CNTZ24 E6 (E...	37.4	2.5
KY457827.1	Human papillomavirus type 18 strain 18CNTZ23 E6 (E...	37.4	2.5
KY457826.1	Human papillomavirus type 18 strain 18CNTZ22 E6 (E...	37.4	2.5
KY457825.1	Human papillomavirus type 18 strain 18CNTZ21 E6 (E...	37.4	2.5
KY457824.1	Human papillomavirus type 18 strain 18CNTZ20 E6 (E...	37.4	2.5
KY457823.1	Human papillomavirus type 18 strain 18CNTZ19 E6 (E...	37.4	2.5
KY457822.1	Human papillomavirus type 18 strain 18CNTZ18 E6 (E...	37.4	2.5
KY457821.1	Human papillomavirus type 18 strain 18CNTZ17 E6 (E...	37.4	2.5
KY457820.1	Human papillomavirus type 18 strain 18CNTZ16 E6 (E...	37.4	2.5
KY457819.1	Human papillomavirus type 18 strain 18CNTZ15 E6 (E...	37.4	2.5

ALIGNMENTS

>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 = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG  23
             |||
Sbjct 487    TGTATGGACCTAAGGCAACATTG  509
```

>KC470230.1 Human papillomavirus type 18 isolate BF226, complete genome
Length=7837

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG  23
             |||
```

BLAST INFORMATION

Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470229.1 Human papillomavirus type 18 isolate Qv39775, complete genome
Length=7837

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470228.1 Human papillomavirus type 18 isolate BF380, complete genome
Length=7844

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470227.1 Human papillomavirus type 18 isolate Qv12693, complete genome
Length=7844

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470226.1 Human papillomavirus type 18 isolate Z125, complete genome
Length=7844

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
```

BLAST INFORMATION

|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470225.1 Human papillomavirus type 18 isolate BF172, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470224.1 Human papillomavirus type 18 isolate BF288, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470223.1 Human papillomavirus type 18 isolate BF309, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470222.1 Human papillomavirus type 18 isolate Z100, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

BLAST INFORMATION

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470221.1 Human papillomavirus type 18 isolate Qv28775, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470219.1 Human papillomavirus type 18 isolate Rw57, complete genome
KC470220.1 Human papillomavirus type 18 isolate Rw830, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470218.1 Human papillomavirus type 18 isolate Rw687, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>KC470217.1 Human papillomavirus type 18 isolate Rw750, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)

BLAST INFORMATION

Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470216.1 Human papillomavirus type 18 isolate Z53, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470215.1 Human papillomavirus type 18 isolate Z63, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC470214.1 Human papillomavirus type 18 isolate Z52, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>KC662605.1 Human papillomavirus type 18 isolate B8890 E7 (E7) gene, complete
cds
Length=422

BLAST INFORMATION

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1  TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 2  TGTATGGACCTAAGGCAACATTG 24
```

>JN416175.1 Human papillomavirus isolate LSCG E7 (E7) gene, complete cds
Length=318

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1  TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 2  TGTATGGACCTAAGGCAACATTG 24
```

>JN416174.1 Human papillomavirus isolate LSCE E7 (E7) gene, complete cds
Length=318

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1  TGTATGGACCTAAGGCAACATTG 23
          |||||||||||||||||||||
Sbjct 2  TGTATGGACCTAAGGCAACATTG 24
```

>JN416165.1 Human papillomavirus isolate LSM4 E7 (E7) gene, complete cds
JN416169.1 Human papillomavirus isolate LSC9 E7 (E7) gene, complete cds
JN416172.1 Human papillomavirus isolate LSCC E7 (E7) gene, complete cds
JN416177.1 Human papillomavirus isolate LSCI E7 (E7) gene, complete cds
JN416189.1 Human papillomavirus isolate LSCY E7 (E7) gene, complete cds
JN416201.1 Human papillomavirus isolate LSML1 E7 (E7) gene, complete cds
KC456641.1 Human papillomavirus type 18 strain 18-558 E7 protein (E7) gene,
complete cds
Length=318

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

BLAST INFORMATION

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 2 TGTATGGACCTAAGGCAACATTG 24

>JN416163.1 Human papillomavirus isolate LSM2 E7 (E7) gene, complete cds
Length=318

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 2 TGTATGGACCTAAGGCAACATTG 24

>EF422144.1 Human papillomavirus type 18 strain P629 E7 protein (E7) gene,
complete cds

JN416164.1 Human papillomavirus isolate LSM3 E7 (E7) gene, complete cds
JN416199.1 Human papillomavirus isolate LSCJ1 E7 (E7) gene, complete cds
JN416210.1 Human papillomavirus isolate LSCU1 E7 (E7) gene, complete cds
Length=318

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 2 TGTATGGACCTAAGGCAACATTG 24

>EF202155.1 Human papillomavirus type 18 isolate Qv04924, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATTG 613

>EF202154.1 Human papillomavirus type 18 isolate Qv03814, complete genome
Length=7824

BLAST INFORMATION

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>EF202153.1 Human papillomavirus type 18 isolate Qv21444, complete genome
Length=7824

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>EF202152.1 Human papillomavirus type 18 isolate Qv17199, complete genome
Length=7844

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATTG 613
```

>AF339137.1 Homo sapiens clone CC-2 sequence flanking Human papillomavirus
type 18 E6 protein (E6) gene, partial cds; and E7 protein
(E7) gene, complete cds
Length=1288

Score = 42.8 bits (46), Expect = 0.060
Identities = 23/23 (100%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           |||||||||||||||||||||
Sbjct 165    TGTATGGACCTAAGGCAACATTG 187
```


BLAST INFORMATION

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||||||||||||||||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||||||||||||||||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||||||||||||||||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||||||||||||||||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

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

BLAST INFORMATION

Length=2502

Score = 37.4 bits (40), Expect = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
```

BLAST INFORMATION

Sbjct 479 TGCATGGACCTAAGGCAACATTG 501

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|| |||||
Sbjct 479 TGCATGGACCTAAGGCAACATTG 501

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|| |||||
Sbjct 479 TGCATGGACCTAAGGCAACATTG 501

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATTG 23
|| |||||
Sbjct 479 TGCATGGACCTAAGGCAACATTG 501

>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 = 2.5

BLAST INFORMATION

Identities = 22/23 (96%), Gaps = 0/23 (0%)

Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATTG 23
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATTG 501
```

>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 = 2.5
Identities = 22/23 (96%), Gaps = 0/23 (0%)
Strand=Plus/Plus

BLAST INFORMATION

Query 1 TGTATGGACCTAAGGCAACATTG 23
|| |||||
Sbjct 479 TGCATGGACCTAAGGCAACATTG 501

Database: Nucleotide collection (nt)
Posted date: Jul 10, 2017 6:27 PM
Number of letters in database: 150,108,365,041
Number of sequences in database: 43,336,626

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: 43336626
Number of Hits to DB: 691816
Number of extensions: 224
Number of successful extensions: 224
Number of sequences better than 10: 1
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 224
Number of HSP's successfully gapped: 1
Length of query: 23
Length of database: 150108365041
Length adjustment: 20
Effective length of query: 3
Effective length of database: 149241632521
Effective search space: 447724897563
Effective search space used: 447724897563
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)

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

BLAST INFORMATION

Acids Res. 25:3389-3402.

RID: PD7S1B7E015

Database: Nucleotide collection (nt)

43,336,626 sequences; 150,108,365,041 total letters

Query=

Length=22

Score E

Sequences producing significant alignments: (Bits) Value

KX545354.1	Human papillomavirus type 18 isolate	NGSk256-18 E6...	41.0	0.21
KC470230.1	Human papillomavirus type 18 isolate	BF226, comple...	41.0	0.21
KC470229.1	Human papillomavirus type 18 isolate	Qv39775, comp...	41.0	0.21
KC470228.1	Human papillomavirus type 18 isolate	BF380, comple...	41.0	0.21
KC470227.1	Human papillomavirus type 18 isolate	Qv12693, comp...	41.0	0.21
KC470226.1	Human papillomavirus type 18 isolate	Z125, complet...	41.0	0.21
KC470225.1	Human papillomavirus type 18 isolate	BF172, comple...	41.0	0.21
KC470224.1	Human papillomavirus type 18 isolate	BF288, comple...	41.0	0.21
KC470223.1	Human papillomavirus type 18 isolate	BF309, comple...	41.0	0.21
KC470222.1	Human papillomavirus type 18 isolate	Z100, complet...	41.0	0.21
KC470221.1	Human papillomavirus type 18 isolate	Qv28775, comp...	41.0	0.21
KC470219.1	Human papillomavirus type 18 isolate	Rw57, complet...	41.0	0.21
KC470218.1	Human papillomavirus type 18 isolate	Rw687, comple...	41.0	0.21
KC470217.1	Human papillomavirus type 18 isolate	Rw750, comple...	41.0	0.21
KC470216.1	Human papillomavirus type 18 isolate	Z53, complete...	41.0	0.21
KC470215.1	Human papillomavirus type 18 isolate	Z63, complete...	41.0	0.21
KC470214.1	Human papillomavirus type 18 isolate	Z52, complete...	41.0	0.21
KC662605.1	Human papillomavirus type 18 isolate	B8890 E7 (E7)...	41.0	0.21
JN416175.1	Human papillomavirus isolate	LSCG E7 (E7) gene, co...	41.0	0.21
JN416174.1	Human papillomavirus isolate	LSCE E7 (E7) gene, co...	41.0	0.21
JN416165.1	Human papillomavirus isolate	LSM4 E7 (E7) gene, co...	41.0	0.21
JN416163.1	Human papillomavirus isolate	LSM2 E7 (E7) gene, co...	41.0	0.21
EF422144.1	Human papillomavirus type 18 strain	P629 E7 protei...	41.0	0.21
EF202155.1	Human papillomavirus type 18 isolate	Qv04924, comp...	41.0	0.21
EF202154.1	Human papillomavirus type 18 isolate	Qv03814, comp...	41.0	0.21
EF202153.1	Human papillomavirus type 18 isolate	Qv21444, comp...	41.0	0.21
EF202152.1	Human papillomavirus type 18 isolate	Qv17199, comp...	41.0	0.21
AF339137.1	Homo sapiens clone CC-2 sequence	flanking Human pa...	41.0	0.21
KY457840.1	Human papillomavirus type 18 strain	18CNTZ36 E6 (E...	35.6	8.9
KY457839.1	Human papillomavirus type 18 strain	18CNTZ35 E6 (E...	35.6	8.9
KY457838.1	Human papillomavirus type 18 strain	18CNTZ34 E6 (E...	35.6	8.9
KY457837.1	Human papillomavirus type 18 strain	18CNTZ33 E6 (E...	35.6	8.9

BLAST INFORMATION

KY457836.1	Human papillomavirus type 18 strain 18CNTZ32	E6 (E...	35.6	8.9
KY457835.1	Human papillomavirus type 18 strain 18CNTZ31	E6 (E...	35.6	8.9
KY457834.1	Human papillomavirus type 18 strain 18CNTZ30	E6 (E...	35.6	8.9
KY457833.1	Human papillomavirus type 18 strain 18CNTZ29	E6 (E...	35.6	8.9
KY457832.1	Human papillomavirus type 18 strain 18CNTZ28	E6 (E...	35.6	8.9
KY457831.1	Human papillomavirus type 18 strain 18CNTZ27	E6 (E...	35.6	8.9
KY457830.1	Human papillomavirus type 18 strain 18CNTZ26	E6 (E...	35.6	8.9
KY457829.1	Human papillomavirus type 18 strain 18CNTZ25	E6 (E...	35.6	8.9
KY457828.1	Human papillomavirus type 18 strain 18CNTZ24	E6 (E...	35.6	8.9
KY457827.1	Human papillomavirus type 18 strain 18CNTZ23	E6 (E...	35.6	8.9
KY457826.1	Human papillomavirus type 18 strain 18CNTZ22	E6 (E...	35.6	8.9
KY457825.1	Human papillomavirus type 18 strain 18CNTZ21	E6 (E...	35.6	8.9
KY457824.1	Human papillomavirus type 18 strain 18CNTZ20	E6 (E...	35.6	8.9
KY457823.1	Human papillomavirus type 18 strain 18CNTZ19	E6 (E...	35.6	8.9
KY457822.1	Human papillomavirus type 18 strain 18CNTZ18	E6 (E...	35.6	8.9
KY457821.1	Human papillomavirus type 18 strain 18CNTZ17	E6 (E...	35.6	8.9
KY457820.1	Human papillomavirus type 18 strain 18CNTZ16	E6 (E...	35.6	8.9
KY457819.1	Human papillomavirus type 18 strain 18CNTZ15	E6 (E...	35.6	8.9

ALIGNMENTS

>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 = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query	1	TGTATGGACCTAAGGCAACATT	22
Sbjct	487	TGTATGGACCTAAGGCAACATT	508

>KC470230.1 Human papillomavirus type 18 isolate BF226, complete genome
Length=7837

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query	1	TGTATGGACCTAAGGCAACATT	22
Sbjct	591	TGTATGGACCTAAGGCAACATT	612

>KC470229.1 Human papillomavirus type 18 isolate Qv39775, complete genome
Length=7837

BLAST INFORMATION

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470228.1 Human papillomavirus type 18 isolate BF380, complete genome
Length=7844

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470227.1 Human papillomavirus type 18 isolate Qv12693, complete genome
Length=7844

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470226.1 Human papillomavirus type 18 isolate Z125, complete genome
Length=7844

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470225.1 Human papillomavirus type 18 isolate BF172, complete genome

BLAST INFORMATION

Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470224.1 Human papillomavirus type 18 isolate BF288, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470223.1 Human papillomavirus type 18 isolate BF309, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470222.1 Human papillomavirus type 18 isolate Z100, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

BLAST INFORMATION

>KC470221.1 Human papillomavirus type 18 isolate Qv28775, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470219.1 Human papillomavirus type 18 isolate Rw57, complete genome
KC470220.1 Human papillomavirus type 18 isolate Rw830, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470218.1 Human papillomavirus type 18 isolate Rw687, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470217.1 Human papillomavirus type 18 isolate Rw750, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

BLAST INFORMATION

>KC470216.1 Human papillomavirus type 18 isolate Z53, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470215.1 Human papillomavirus type 18 isolate Z63, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC470214.1 Human papillomavirus type 18 isolate Z52, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          |||||||||||||||||||||
Sbjct 591    TGTATGGACCTAAGGCAACATT  612
```

>KC662605.1 Human papillomavirus type 18 isolate B8890 E7 (E7) gene, complete
cds
Length=422

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
```

BLAST INFORMATION

```
|||||
Sbjct  2   TGTATGGACCTAAGGCAACATT   23
```

>JN416175.1 Human papillomavirus isolate LSCG E7 (E7) gene, complete cds
Length=318

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query  1   TGTATGGACCTAAGGCAACATT   22
|||||
Sbjct  2   TGTATGGACCTAAGGCAACATT   23
```

>JN416174.1 Human papillomavirus isolate LSCE E7 (E7) gene, complete cds
Length=318

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query  1   TGTATGGACCTAAGGCAACATT   22
|||||
Sbjct  2   TGTATGGACCTAAGGCAACATT   23
```

>JN416165.1 Human papillomavirus isolate LSM4 E7 (E7) gene, complete cds
JN416169.1 Human papillomavirus isolate LSC9 E7 (E7) gene, complete cds
JN416172.1 Human papillomavirus isolate LSCC E7 (E7) gene, complete cds
JN416177.1 Human papillomavirus isolate LSCI E7 (E7) gene, complete cds
JN416189.1 Human papillomavirus isolate LSCY E7 (E7) gene, complete cds
JN416201.1 Human papillomavirus isolate LSML1 E7 (E7) gene, complete cds
KC456641.1 Human papillomavirus type 18 strain 18-558 E7 protein (E7) gene,
complete cds
Length=318

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query  1   TGTATGGACCTAAGGCAACATT   22
|||||
Sbjct  2   TGTATGGACCTAAGGCAACATT   23
```

BLAST INFORMATION

>JN416163.1 Human papillomavirus isolate LSM2 E7 (E7) gene, complete cds
Length=318

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1 TGTATGGACCTAAGGCAACATT 22
      |||||||||||||||||||||
Sbjct 2 TGTATGGACCTAAGGCAACATT 23
```

>EF422144.1 Human papillomavirus type 18 strain P629 E7 protein (E7) gene, complete cds
JN416164.1 Human papillomavirus isolate LSM3 E7 (E7) gene, complete cds
JN416199.1 Human papillomavirus isolate LSCJ1 E7 (E7) gene, complete cds
JN416210.1 Human papillomavirus isolate LSCU1 E7 (E7) gene, complete cds
Length=318

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1 TGTATGGACCTAAGGCAACATT 22
      |||||||||||||||||||||
Sbjct 2 TGTATGGACCTAAGGCAACATT 23
```

>EF202155.1 Human papillomavirus type 18 isolate Qv04924, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1 TGTATGGACCTAAGGCAACATT 22
      |||||||||||||||||||||
Sbjct 591 TGTATGGACCTAAGGCAACATT 612
```

>EF202154.1 Human papillomavirus type 18 isolate Qv03814, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

BLAST INFORMATION

Query 1 TGTATGGACCTAAGGCAACATT 22
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATT 612

>EF202153.1 Human papillomavirus type 18 isolate Qv21444, complete genome
Length=7824

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATT 22
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATT 612

>EF202152.1 Human papillomavirus type 18 isolate Qv17199, complete genome
Length=7844

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATT 22
|||||
Sbjct 591 TGTATGGACCTAAGGCAACATT 612

>AF339137.1 Homo sapiens clone CC-2 sequence flanking Human papillomavirus
type 18 E6 protein (E6) gene, partial cds; and E7 protein
(E7) gene, complete cds
Length=1288

Score = 41.0 bits (44), Expect = 0.21
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Plus

Query 1 TGTATGGACCTAAGGCAACATT 22
|||||
Sbjct 165 TGTATGGACCTAAGGCAACATT 186

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

BLAST INFORMATION

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT 500
```

BLAST INFORMATION

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
           || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

BLAST INFORMATION

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

BLAST INFORMATION

Length=2502

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
```

BLAST INFORMATION

Sbjct 479 TGCATGGACCTAAGGCAACATT 500

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479 TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479 TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT 22
           || |||||
Sbjct 479 TGCATGGACCTAAGGCAACATT 500
```

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

Score = 35.6 bits (38), Expect = 8.9

BLAST INFORMATION

Identities = 21/22 (95%), Gaps = 0/22 (0%)

Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

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

Score = 35.6 bits (38), Expect = 8.9
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Plus

```
Query 1      TGTATGGACCTAAGGCAACATT  22
          || |||||
Sbjct 479    TGCATGGACCTAAGGCAACATT  500
```

BLAST INFORMATION

Database: Nucleotide collection (nt)

Posted date: Jul 10, 2017 6:27 PM

Number of letters in database: 150,108,365,041

Number of sequences in database: 43,336,626

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: 43336626

Number of Hits to DB: 562980

Number of extensions: 142

Number of successful extensions: 142

Number of sequences better than 10: 24

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

Number of HSP's gapped: 142

Number of HSP's successfully gapped: 24

Length of query: 22

Length of database: 150108365041

Length adjustment: 19

Effective length of query: 3

Effective length of database: 149284969147

Effective search space: 447854907441

Effective search space used: 447854907441

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)