

CLUSTAL O(1.2.4) multiple sequence alignment

MchSLE1 KX018543.1	tgtaacatgtatagatgtcagtactttgataatgcacgtgtaataactcatgcgactg -----	60 0
MchSLE1 KX018543.1	gcacttccaccaactgtgttacacatgttattcttgtaacaatgtagactaacatgc -----	120 0
MchSLE1 KX018543.1	tgatatattaacgtagttcactataacttggttctctcttaatggtatactatgggatat -----	180 0
MchSLE1 KX018543.1	aaacatgggtgtcagatgttaaaacccgatgtcagacaacgaggaaaaacgaaaacataaat -----	240 0
MchSLE1 KX018543.1	gagccggaagaagatcatccagaggaacaagcgatagaaccacaagcagaactagcg -----	300 0
MchSLE1 KX018543.1	attgaaatggcagccgtcccaccattgtttaacattccattcccgggaaactggacttg -----	360 0
MchSLE1 KX018543.1	gatggaaatataatcaacaaaactggaaaaattcaagcggacatgggacaattatgaaatc -----	420 0
MchSLE1 KX018543.1	gcatcaggtttatctacaaaagatacaaaaactacgtactgcaacattgcttacttgatt -----	480 0
MchSLE1 KX018543.1	ggcccagaagcaatggatatttttgatggactagctttcgaaaatgaagaagacaagaag -----	540 0
MchSLE1 KX018543.1	gacatagcaaaaagtgatcgaaaagtttgaagcgttttgatataggcaaaacaaacgaaaca -----	600 0
MchSLE1 KX018543.1	tttgaaagatacactttcaacatatgtaatcaaagcgaagccgaaaacatcgacacttac -----	660 0
MchSLE1 KX018543.1	gtctcaaagctaagaaaacttgcaaaaacatgcaactaccaggatttaataagaaagcctc -----	720 0
MchSLE1 KX018543.1	atccgtgatagaattgtctgtggaatacgggacaacacggcaagaaaagacttttgcaa -----	780 0
MchSLE1 KX018543.1	gaagacaaattgactttgaataagtgcatagatatttgccgtgctttagaatctacttca -----	840 0
MchSLE1 KX018543.1	gcaaaaatgaaaaccatgacagggatcctaacaacttggataaaggagaagacattaag -----	900 0
MchSLE1 KX018543.1	gcggtagaagtaaatcatcttttaacaagcataaaaacatttacacaaaagcaaagcaaa -----	960 0
MchSLE1 KX018543.1	agaaactgttctactgtggaaaacaatgcactaaaggaaaatgtcctgcatatggaaaa -----	1020 0

MchSLE1 KX018543.1	aagtgcgacagttgctgcaaaactaaatcatttcgcttcccaatgcagacaaaaatgaaa -----	1080 0
MchSLE1 KX018543.1	cctagaggtaaagatcagatgtaaggcaatttaacacattatcaacagacgagagcgat -----	1140 0
MchSLE1 KX018543.1	agcgaatatgaaataatggctgtagaacagacgatgtaaacgtaaacatgatacagaat -----	1200 0
MchSLE1 KX018543.1	aagatatttgcaaggatgctattaatagatgagaacaagagggttaagtttcaattagat -----	1260 0
MchSLE1 KX018543.1	agcgggtgcgactgctaacctaattccgagatcttatctcattcattcaciaattgagagt -----	1320 0
MchSLE1 KX018543.1	ggaaatgacaagttaacgatgtataatcagctactatgaaatcgatggcacatgcatg -----	1380 0
MchSLE1 KX018543.1	ctgcgtgtaaagaatccaaaaacacacaaacggttacaagggtcaagtttattgttggat -----	1440 0
MchSLE1 KX018543.1	gataaatacacacctctactagaggcaaaaggccattcaagctatgaaatctaattaagata -----	1500 0
MchSLE1 KX018543.1	caatttcaaacattatggatgcgataaccagaatgcaacaggcattgctctatggaa -----	1560 0
MchSLE1 KX018543.1	agcattatttctgaatactctgacgtatttgaggagaaggaaacatttaaggggagcctta -----	1620 0
MchSLE1 KX018543.1	aaattagaaattgatgagtcacatacctcctgttaagtctccgttaagacgcatacctatt -----	1680 0
MchSLE1 KX018543.1	gcacttaagccgaagttaaagacagaacttcaagactggaaaaactaggagttattaaa -----	1740 0
MchSLE1 KX018543.1	ccagttgatacaccaacagattgggtatccagccttgaattgtcaagaaacctagtggg -----	1800 0
MchSLE1 KX018543.1	aaaaaagactatgcattgacccaaagccattaaataaagcattaaagcgggtgtcattat -----	1860 0
MchSLE1 KX018543.1	ccgttgccaattatcgaagatttacttccagaattaagcaaagctaaagtataattccaag -----	1920 0
MchSLE1 KX018543.1	tgtgatgttaaaaatggattttggcatgtaaacctagcagacgagtcaagctttttaact -----	1980 0
MchSLE1 KX018543.1	acttttgaaacaccggttcggaagataccggttgacaaagatgccatttggatttcgcct -----	2040 0
MchSLE1 KX018543.1	gccccgaatatttccaacaatttttgaaaagagaaattgaaaatctaccgggagtccga -----	2100 0


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                **   **   *   *   *   *   *   *   *   *   *   *   *   *   *   *
MchSLE1      aacggcattatattcaaaaggtgatcgatgtataatacctaaatgcaatgagaaacg---aa   3231
KX018543.1   GATGGACTACTTTACAAAAGCCAACGTATATTCATACCTAAATCACTTCAACGAGAGATG   455
                *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
MchSLE1      atactgagccagattcactactcatattggcattgaaggatgtttaaaacgtgcacgagaa   3291
KX018543.1   TTAGTGAATTTGCACGAAGCACAATCTTGGCATTTGTTAAGACAAAACAGCGTGCCCGTGAA   515
                *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
MchSLE1      tgcgtatactggcctagaatgaattcagaattgagagactacatcagtaaatgcatgtg   3351
KX018543.1   ATACTATCTGGCGTAATATGAACAGTGATATTGAAAACCTCATTAAAAACTGTAGCATA   575
                *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
MchSLE1      tgccagtcacttgctatgaaacaaccgaaagaactttaagtcacacgacgtgccatcg   3411
KX018543.1   TGTAACAAGTTTAGAAAGGCAAACTGTAGAGAACCGCTCAATCTCATGATATTCGCTCG   635
                *   *   *   *   *   *   *   *   *   *   *   *   *   *   *
MchSLE1      agaccgtgggctaagataggaaccgatttattcacactatcgggaaatgactatattgatt   3471
KX018543.1   CGTCCGTGGGCCAAAGTCGGAA-----
                *   *   *   *   *   *   *   *   *
MchSLE1      actgtagattattacagcagttttttcggagtgatagactttatgatacttcgtcaaag   3531
KX018543.1   -----
MchSLE1      acagtaatcaataaaacttaacaacatttcgctagatggggaatccctgaaacagttatc   3591
KX018543.1   -----
MchSLE1      tcagacaatggaccgcaatatttcgctccgaacaatttaaacagttcagcaagcaatgggat   3651
KX018543.1   -----
MchSLE1      tttcaacataaaaacatctagtcgggacatgcacaatctaattgggaaagtcgaaaacgca   3711
KX018543.1   -----
MchSLE1      gtgaaaacagcaaaacgcctaattgcaaaaagcgaaaaaatcaaacagtgaccggtacatt   3771
KX018543.1   -----
MchSLE1      gcgttactgaattttagaaatacaccacaacaagtgacaaaatacagtcgggtacaacaa   3831
KX018543.1   -----
MchSLE1      atgatcaacagaaggacacgaacattgctaccaatgaaatcagcattatgtgaatcgaaa   3891
KX018543.1   -----
MchSLE1      attccagaaaatgtacgaagcaacatcatggataataaaaaacgtcaagaaaaatattac   3951
KX018543.1   -----
MchSLE1      aatagatccgcaagagacttaaacgaacttaacaagggtgaaattgtcagattaacacca   4011
KX018543.1   -----
MchSLE1      caagatcgacaaaaagaatgggaaaaaggagtgatcaagaataaaaaatccgagagatcg   4071
KX018543.1   -----
MchSLE1      tatgaagtcgaaaaggaaaatggacgtaccgtaagacgtaacagaaaatatttgcgtaga   4131
KX018543.1   -----
MchSLE1      actaatgaacaattcaatccgaaatgtcaaacggaagaaattaacattgatccgaatgaa   4191
KX018543.1   -----
MchSLE1      caagagatatctcatgatgaaaacaaaaacaatagttcggaccctaaacattcagtcgtg   4251

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KX018543.1 ----- 657

MchSLE1      cccgatgttgaagagaaatctcaaccgtgtagccgttatggaagaccaattcagaaacca 4311
KX018543.1 ----- 657

MchSLE1      agctggatgaaagattacgatttaaagtgacttttaacggttgaacattgtaaatattag 4371
KX018543.1 ----- 657

MchSLE1      ttagagactagaagttaggtttagttaatttagtatttgaactttaaatgacagtgcctt 4431
KX018543.1 ----- 657

MchSLE1      agaaaattcatttagattctagaacatatacatggacagttaaatatagcagttaaagaa 4491
KX018543.1 ----- 657

MchSLE1      ttttataatgttgcagtaattatgtttagattttctgataatgtgatataagc 4551
KX018543.1 ----- 657

MchSLE1      ttcaagttgaaaaaagaaggatgtaacatgtatagtagtcagtactttgataatgcac 4611
KX018543.1 ----- 657

MchSLE1      gtgtaataactcatgcgcactggcacttccgccaactgtgttacacatgttattcttgt 4671
KX018543.1 ----- 657

MchSLE1      aaacaatgtagactaaccatgctgtatattaacgtagttcactataacttggttctcac 4731
KX018543.1 ----- 657

MchSLE1      ttaatggtatactatgggatataaaca 4758
KX018543.1 ----- 657

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# Percent Identity Matrix - created by Clustal2.1
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1: MchSLE1      100.00  52.16
2: KX018543.1  52.16  100.00

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CLUSTAL O(1.2.4) multiple sequence alignment

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MchSLE2      GCACATATATGCATCTATGAAAATAATAGGCAGAATGAGAAAAGCAACTTAACAAGATTT 60
KX018543.1 ----- 0

MchSLE2      CAATTAGACAGTGGAGCAACATGCAATATAATCACTGCAAGAACATTGAAAGAGCTTGAT 120
KX018543.1 -----TTGAAAGCG----- 9
                      ***** *

MchSLE2      ATTAACCAATTACAGAAAACAAGTCAAATACTGACAATGTACAACAATACCACAATAAAA 180
KX018543.1 ----ACCA----C-----AAACCGTTAGTTGCAATCTACGACAAACCGC----- 45
                      **** * * * * * * * * * *

MchSLE2      CCGATAGGAACATGCATTCTAAAAATTGGTGAATCCAAAGAACAATAAAGTTCAAGGCA 240
KX018543.1 -----TTTATCGAGCTA----- 57
                      * * * * *

MchSLE2      GAATTTGTAGTAGTAAAAGATGGCACTTTGACTCCGTTGTTAGGTAGCAAAGCAGTGCAA 300
KX018543.1 ----- 57

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