

CLUSTAL 2.1 multiple sequence alignment

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VPCI_470/P/14      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_672/P/12      -----TTTAACTAACCCAACGTTAAGTTCAACT 29
VPCI_673/P/12      -----CTAACCCAACGTTAAGTTCAACT 23
VPCI_676/P/12      -----TAACCCAACGTTAAGTTCAACT 22
VPCI_107/P/14      -----CTAACCCAACGTTAAGTTCAACT 23
VPCI_711/P/12      -----CTAACCCAACGTTAAGTTCAACT 23
VPCI_709/P/12      -----CTAACCCAACGTTAAGTTCAACT 23
VPCI_671/P/12      -----AACTAACCCAACGTTAAGTTCAACT 26
VPCI_677/P/12      -----TTAAACTAACCCAACGTTAAGTTCAACT 29
6684              TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_692/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_105/P/14      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_106/P/14      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_717/P/14      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_683/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_1130/P/13     TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_670/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_708/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_669/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60
VPCI_712/P/12      TTGATATTTTGCATACACACTGATTGGATTTTAACTAACCCAACGTTAAGTTCAACT 60

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VPCI_470/P/14      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_672/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 88
VPCI_673/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 82
VPCI_676/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 81
VPCI_107/P/14      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGCTATCGATGAAGAAC 83
VPCI_711/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 82
VPCI_709/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 82
VPCI_671/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 85
VPCI_677/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 88
6684              AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_692/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_105/P/14      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_106/P/14      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_717/P/14      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_683/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_1130/P/13     AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_670/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_708/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_669/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119
VPCI_712/P/12      AAAACAAAACATAAACTTTCAACAACGGATCTCTGGTTCTCGC-ATCGATGAAGAAC 119

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VPCI_470/P/14      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_672/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 148
VPCI_673/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 142
VPCI_676/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 141
VPCI_107/P/14      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 143
VPCI_711/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 142
VPCI_709/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 142
VPCI_671/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 145
VPCI_677/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 148
6684              GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_692/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_105/P/14      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_106/P/14      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_717/P/14      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_683/P/12      GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179
VPCI_1130/P/13     GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA 179

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VPCI_670/P/12	GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA	179
VPCI_708/P/12	GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA	179
VPCI_669/P/12	GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA	179
VPCI_712/P/12	GCAGCGAAATGCGATACGTAGTATGACTTGCAGACGTGAATCATCGAATCTTTGAACGCA	179

VPCI_470/P/14	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_672/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	207
VPCI_673/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	201
VPCI_676/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	200
VPCI_107/P/14	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	202
VPCI_711/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	201
VPCI_709/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	201
VPCI_671/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	204
VPCI_677/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	207
6684	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_692/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_105/P/14	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_106/P/14	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_717/P/14	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_683/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_1130/P/13	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_670/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_708/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	239
VPCI_669/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238
VPCI_712/P/12	CATTGCGCCTTGGGGTATTCCCCAAGGCATGCCTGTTTGAGC-GTGATGTCTTCTCACCA	238

VPCI_470/P/14	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_672/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	267
VPCI_673/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	261
VPCI_676/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	260
VPCI_107/P/14	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	262
VPCI_711/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	261
VPCI_709/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	261
VPCI_671/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	264
VPCI_677/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	267
6684	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_692/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_105/P/14	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_106/P/14	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_717/P/14	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_683/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_1130/P/13	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_670/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	295
VPCI_708/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	298
VPCI_669/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	295
VPCI_712/P/12	ATCTTCGCGGTGGCGTTGCATTACAAAAATTACAGCTTGCACGAAAAAAATCTACGCTTT	297

VPCI_470/P/14	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	351
VPCI_672/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	320
VPCI_673/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	314
VPCI_676/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	313
VPCI_107/P/14	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	315
VPCI_711/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	314
VPCI_709/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	314
VPCI_671/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	317
VPCI_677/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	320
6684	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	351
VPCI_692/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	352
VPCI_105/P/14	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	351
VPCI_106/P/14	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACCTAA	351

VPCI_717/P/14	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACTTAA	351
VPCI_683/P/12	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACTTAA	351
VPCI_1130/P/13	TTTTTTCGTTTTGTTGTCGCC-TCAAATCAGGTAGGACTACCCGCTGAACTTAA	351
VPCI_670/P/12	-----	
VPCI_708/P/12	-----	
VPCI_669/P/12	-----	
VPCI_712/P/12	-----	