Go directly to Alignment

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Published research using this software should cite
Multiple sequence alignment with hierarchical clustering
F. CORPET, 1988, Nucl. Acids Res., 16 (22), 10881-10890
Symbol comparison table: blosum62
Gap weight: 12
Gap length weight: 2
Consensus levels: high=90% low=50%
Consensus symbols:
 ! is anyone of IV
 $ is anyone of LM
 % is anyone of FY
 # is anyone of NDQEBZ

 MSF:   1140    Check:   0          ..
 Name: gi|3241889|dbj Len:  1140  Check: 4993  Weight:  0.66
 Name: gi|3241883|dbj Len:  1140  Check: 5503  Weight:  0.66
 Name: gi|3241885|dbj Len:  1140  Check: 4360  Weight:  0.91
 Name: gi|3241877|dbj Len:  1140  Check: 5292  Weight:  1.39
 Name: gi|3241897|dbj Len:  1140  Check: 5774  Weight:  1.39
 Name: Consensus      Len:  1140  Check: 6399  Weight:  0.00

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            1                                                                                                                              120
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gi|3241883  ATGACCAACA TCCGAAAATC ACACCCACTA ATAAAAATTA TCAACAACGC ATTCATTGAC CTCCCAGCCC CCTCAAACAT CTCATCATGA TGAAACTTCG GTTCCCTCTT AGGCATCTGC
gi|3241885  ATGACCAACA TCCGAAAATC ACACCCACTA ATAAAAATTA TCAACAACGC ATTCATTGAC CTCCCAGCCC CCTCAAACAT CTCATCATGA TGAAACTTCG GTTCCCTCTT AGGCATCTGC
gi|3241877  ATGACCAACA TCCGAAAATC ACACCCACTA ATAAAAATTA TCAACAACGC ATTCATTGAC CTCCCAGCCC CCTCAAACAT CTCATCATGA TGAAACTTCG GTTCCCTCTT AGGCATCTGC
gi|3241897  ATGATCAACA TCCGAAAATC ACACCCACTA ATAAAAATTA TCAACAACGC ATTCATTGAC CTCCCAGCCC CCTCAAACAT CCCATCATGA TGAAACTTCG GTTCCCTCTT AGGCATCTGC
 Consensus  ATGAcCAACA TCCGAAAATC ACACCCACTA ATAAAAATTA TCAACAACGC ATTCATTGAC CTCCCAGCCC CCTCAAACAT CtCATCATGA TGAAACTTCG GTTCCCTCTT AGGCATCTGC

            121                                                                                                                            240
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gi|3241885  CTAATCTTGC AAATCCTAAC AGGCCTGTTC TTAGCAATAC ATTACACATC AGACACAACA ACAGCTTTCT CATCAGTTAC ACACATCTGT CGAGACGTAA ATTACGGATG AGTTATTCGC
gi|3241877  CTAATCTTGC AAATCCTAAC AGGCCTGTTC TTAGCAATAC ATTACACATC AGACACAACA ACAGCTTTCT CATCAGTTAC ACACATCTGT CGAGACGTAA ATTACGGATG AGTTATTCGC
gi|3241897  CTAATCTTGC AAATCCTAAC AGGCCTATTC TTAGCAATAC ATTACACATC AGACACAACA ACAGCTTTCT CATCAGTTAC ACACATCTGT CGAGACGTAA ATTACGGATG AGTTATTCGC
 Consensus  CTAATCTTGC AAATCCTAAC AGGCCTgTTC TTAGCAATAC ATTACACATC AGACACAACA ACAGCTTTCT CATCAGTTAC ACACATCTGT CGAGAcGTAA ATTACGGATG AGTTATTCGC

            241                                                                                                                            360
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gi|3241885  TACCTACATG CAAACGGAGC ATCCATGTTC TTTATTTGCC TATTCATCCA CGTAGGCCGA GGCCTATACT ACGGATCCTA TATATTCCTA GAAACATGAA ACATTGGAGT AGTCCTACTA
gi|3241877  TACCTACATG CAAACGGAGC ATCCATATTC TTTATTTGCC TATTCATCCA CGTAGGCCGA GGTCTATACT ACGGATCCTA TATATTCCTA GAAACATGAA ACATTGGAGT AGTCCTACTA
gi|3241897  TACCTACATG CAAACGGAGC ATCCATATTC TTTATTTGCC TATTCATCCA CGTAGGCCGA GGTCTATACT ACGGATCCTA TATATTCCTA GAAACATGAA ACATTGGAGT AGTCCTACTA
 Consensus  TACCTACATG CAAACGGAGC ATCCATaTTC TTTATTTGCC TATTCATCCA CGTAGGCCGA GGtCTATACT ACGGATCCTA TATATTCCTA GAAACATGAA ACATTGGAGT AGTCCTACTA

            361                                                                                                                            480
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gi|3241883  TTTACCGTTA TAGCAACAGC CTTCATAGGC TACGTCCTGC CCTGAGGACA AATATCATTC TGAGGAGCTA CAGTCATCAC AAATCTACTA TCAGCTATCC CTTATATCGG AACAGACCTC
gi|3241885  TTTACCGTTA TAGCAACAGC CTTCATAGGC TACGTCCTGC CCTGAGGACA AATATCATTC TGAGGAGCTA CGGTCATCAC AAATCTACTA TCAGCTATCC CTTATATCGG AACAGACCTC
gi|3241877  TTTACCGTTA TAGCAACAGC CTTCATAGGC TACGTCCTGC CCTGAGGACA AATATCATTC TGAGGAGCTA CGGTCATCAC AAATCTACTA TCAGCTATCC CTTATATCGG AACAGACCTC
gi|3241897  TTTACCGTTA TAGCAACAGC CTTCATAGGC TACGTCCTGC CCTGAGGACA AATATCATTC TGAGGAGCTA CGGTCATCAC AAATCTACTA TCAGCTATCC CTTATATCGG AACAGACCTC
 Consensus  TTTACCGTTA TAGCAACAGC CTTCATAGGC TACGTCCTGC CCTGAGGACA AATATCATTC TGAGGAGCTA CgGTCATCAC AAATCTACTA TCAGCTATCC CTTATATCGG AACAGACCTC

            481                                                                                                                            600
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gi|3241883  GTAGAATGAA TCTGAGGGGG CTTTTCCGTC GACAAAGCAA CCCTCACACG ATTCTTCGCC TTTCACTTTA TCCTGCCATT CATCATTACC GCCCTCGCAG CCGTACATCT CCTATTCCTG
gi|3241885  GTAGAATGAA TCTGAGGGGG CTTTTCCGTC GACAAAGCAA CCCTCACACG ATTCTTCGCC TTTCACTTTA TCCTGCCATT CATCATTACC GCCCTCGCAG CCGTACATCT CCTATTCCTG
gi|3241877  GTAGAATGAA TCTGAGGGGG CTTTTCCGTC GACAAAGCAA CCCTCACACG ATTCTTCGCC TTTCACTTTA TCCTGCCATT CATCATTACC GCCCTCGCAG CCGTACATCT CCTATTCCTG
gi|3241897  GTAGAATGAA TCTGAGGGGG CTTTTCCGTC GACAAAGCAA CCCTCACACG ATTCTTCGCC TTTCACTTTA TCCTGCCATT CATCATTACC GCCCTCGCAG CCGTACATCT CCTATTCCTG
 Consensus  GTAGAATGAA TCTGAGGGGG CTTTTCCGTC GACAAAGCAA CCCTCACACG ATTCTTCGCC TTtCACTTTA TCCTGCCATT CATCATTACC GCCCTCGCAG CCGTACATCT CCTATTCCTG

            601                                                                                                                            720
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gi|3241883  CACGAAACCG GATCCAACAA CCCTACCGGA ATCTCATCAG ACATAGACAA AATTCCATTT CACCCATACT ACACTATTAA AGACATTCTA GGGGCCTTAT TTATAATACT AATCCTACTA
gi|3241885  CACGAAACCG GATCCAACAA CCCTACCGGA ATCTCATCAG ACATAGACAA AATTCCATTT CACCCATACT ACACTATTAA AGACATTCTA GGGGCCTTAT TTATAATACT AATCCTACTA
gi|3241877  CACGAAACCG GATCCAATAA CCCTACCGGA ATCTCATCAG ACATAGACAA AATTCCATTT CACCCATACT ACACTATTAA AGACATTCTA GGAGCCTTAT TTATAATACT AATCCTACTA
gi|3241897  CACGAAACCG GATCCAATAA CCCTACCGGA ATCTCATCAG ACATAGACAA AATTCCATTT CACCCATACT ACACTATTAA AGACATTCTA GGAGCCTTAT TTATAATACT AATCCTACTA
 Consensus  CACGAAACCG GATCCAAtAA CCCTACCGGA ATCTCATCAG ACATAGACAA AATTCCATTT CACCCATACT ACACTATTAA AGACATTCTA GGaGCCTTAT TTATAATACT AATCCTACTA

            721                                                                                                                            840
gi|3241889  ATCCTTGTAC TATTCTCACC AGACCTACTA GGAGACCCAG ACAACTACAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATC
gi|3241883  ATCCTTGTAC TATTCTCACC AGACCTACTA GGAGACCCAG ACAACTACAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATC
gi|3241885  ATCCTTGTAC TATTCTCACC AGACCTACTA GGAGACCCAG ACAACTACAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATC
gi|3241877  ATCCTCGTAC TATTCTCACC AGACCTACTA GGAGACCCAG ACAACTACAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATT
gi|3241897  ATCCTTGTAC TATTCTCACC AGACCTACTA GGGGACCCAG ACAACTATAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATT
 Consensus  ATCCTtGTAC TATTCTCACC AGACCTACTA GGaGACCCAG ACAACTAcAC CCCAGCAAAC CCACTAAACA CCCCACCCCA TATTAAACCA GAATGATATT TCTTATTCGC CTACGCTATt

            841                                                                                                                            960
gi|3241889  CTACGTTCAA TTCCTAATAA ACTAGGTGGA GTGCTAGCTC TAGTAGCCTC CATCCTAATC CTAATTTTAA TGCCCATACT ACACACATCC AAACAACGAA GCATAATATT TCGACCACTA
gi|3241883  CTACGTTCAA TTCCTAATAA ACTAGGTGGA GTGCTAGCTC TAGTAGCCTC CATCCTAATC CTAATTTTAA TGCCCATACT ACACACATCC AAACAACGAA GCATAATATT TCGACCACTA
gi|3241885  CTACGTTCAA TTCCTAATAA ACTAGGTGGA GTGCTAGCTC TAATAGCCTC CATCCTAATC CTAATTTTAA TGCCCATACT ACACACATCC AAACAACGAA GCATAATATT TCGACCACTA
gi|3241877  CTACGTTCAA TTCCTAACAA ACTAGGTGGA GTGTTAGCTC TAGTAGCCTC CATCCTAATC CTAATTTTAA TACCCATACT ACACACATCC AAACAACGAA GCATAATATT TCGACCACTA
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 Consensus  CTACGTTCAA TTCCTAAtAA ACTAGGTGGA GTGtTaGCTC TAgTAGCCTC CATCCTAATC CTAATTTTAA TgCCCATACT ACACACATCC AAACAACGAA GCATAATATT TCGACCACTA

            961                                                                                                                           1080
gi|3241889  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCATT CATCATCATT GGCCAACTAG CCTCCATCTT ATATTTCCTA
gi|3241883  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCATT CATCATCATT GGCCAACTAG CCTCCATCTT ATATTTCCTA
gi|3241885  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCATT CATCATCATC GGCCAACTAG CCTCCATCTT ATATTTCCTA
gi|3241877  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCATT CATCATCATC GGCCAACTAG CCTCCATCTT ATATTTCCTA
gi|3241897  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCGTT CATCATCATC GGCCAACTAG CCTCCATCTT ATACTTCCTA
 Consensus  AGTCAATGCC TATTCTGAAT ACTAGTAGCA GACCTCATTA CACTAACATG AATTGGAGGA CAACCCGTAG AACACCCaTT CATCATCATc GGCCAACTAG CCTCCATCTT ATAtTTCCTA

            1081                                                         1140
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gi|3241883  ATCATTCTAG TATTGATACC AATCACTAGC ATCATCGAAA ACAACCTATT AAAGTGAAGA
gi|3241885  ATCATTCTAG TATTGATACC AATCACTAGC ATCATCGAAA ACAACCTATT AAAGTGAAGA
gi|3241877  ATCATTCTAG TATTGATACC AATCACTAGC ATCATCGAAA ACAACCTATT AAAGTGAAGA
gi|3241897  ATCATTCTAG TATTGATACC AATCACTAGC ATCATCGAAA ACAACCTATT AAAGTGAAGA
 Consensus  ATCATTCTAG TATTGATACC AATCACTAGC ATCATCGAAA ACAACCTATT AAAGTGAAGA
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