

CLUSTAL W (1.83) multiple sequence alignment

Geobacillus MPINIPKDLPAKEILEQENIFVMDEERAYSQDIRPLNIIILNLMPEK--EKAETQLLRLL 58
Clostridium MPIKIPDSLPAKEVLTNENIFVMDEHRALHQDVRPLRIAILNLMPTK--ITTETQLLRLLI 58
Thermotoga MPINVPSGLPAVKVLAKEGIFVMTEKRAIHQDIRPLEILILNLMMPDK--IKTEIQLLRLL 58
Streptococcus MPIKLDNKLPAALDVLRSSENVFIMDENRASSQDIRPMEVLILNLMPTK--EVTETQLLRLL 58
Escherichia MPIRVDELPAVNFVLRSENVFVMTTSRASGQEI RPLKVLILNLMPPK--IETENQFLRLL 58
Methylococcus MPLVAHTDLPTFQRLREEGQDVLSVERAARQDIREMHIGLLNMPDAALEATERQFFRLV 60
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Geobacillus G--NSPLQVNVTFRLRPATHEPKTTSKHHLEQFYTIFPHIRHRKFDGMIITGAPVEQMPFE 116
Clostridium G--NTPIQVEI ELLHPKTHVSKNTP EEHLTKFYKTFDEVKDEKFDGLIITGAPVEQMEFE 116
Thermotoga G--NTPLQVNVTLTYTETHKPKHTPIEHILKFYTTFSAVKDRKFDGFIITGAPVELLPFE 116
Streptococcus A--NTPLQINVEFLYMASHKSKNTHAEHMETFYKTFDEIKDKYDGLIVTGAPVEQMPFE 116
Escherichia S--NSPLQVDIQLLRIDSRESRNTPAEHLN NFYCNFEDIQQDNFDGLIVTGAPLGLVEFN 116
Methylococcus GGANPIVQFHMHPFTIEGLPRGDQAAEHIARYYESFDRIREEGLDGLIVSGANVTQPHLQ 120
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Geobacillus EVNYWGE L TEIM EWTKTNVTSTLHCWGAQAGLYYHYGIPKYELPEKCFGVFNHTVEVKN 176
Clostridium EVNYWEE L KKIMDWSVHNVYSTFHICWGAQAALYHHYGIKKYELPEKCFGVFNHTVEVKN 176
Thermotoga EVDYWEE L TEIM EWSRHNVYSTMFICWAAQAGLYYFYGIPKYELPQKLSGVYKHRVAK-D 175
Streptococcus EVDYWQE L TRVFDWSKKHVYSTLHLCWGAQAGLYYKHGVDKFFLSEKLSGIYKQTVDMPE 176
Escherichia DVAYWPQ L KQVLEWSKDHTVSTL FVCWAVQAALNILYGI PKQTRTEKLSGVYEHHLHPH 176
Methylococcus QEAFWQ L TEVFDWARSNVT SILCSCLATHALFQYSYGVERTHLGFKRWGVYSHRVVEPL 180
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Geobacillus VKLLRGFD DVFRMPSRHTDVKREDIEKVPDLTILSMSDKAGVCLVASNDG-RRIFLTGH 235
Clostridium TMLLRGFDDCFYAPHSRHT EVRREDIEKVG EIDILSDSEEAGVYIMKTRGG-RQVFVTGH 235
Thermotoga SVLFRGHDDFFWAPHSRYTEVKKEIDDKVPELEILAESDEAGVYVANKSE-RQIFVTGH 234
Streptococcus NFLMNGFDDSFVSPHSRYTEVTLEDIKNKTDLDVVASGQEVGLSILASKDL-REVYSFGH 235
Escherichia ALLTRGFDDSF LAPHSRYADFPALIRDYTDLEILAETEEDAYLFASKDK-RIAFVTGH 235
Methylococcus HPLVADINTRFDVPHSRYNEIFREDME AAG-LRVLVESEEAGVHLAVSPDLFRVIYFQAH 239
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Geobacillus PEYDATT LKEEYERDLAKGLP-----IHIPESYF----- 264
Clostridium SEYDQFT LKEEYERDLAKGLK-----IKMPKNYF----- 264
Thermotoga PEYDRYTLRDEYRDIGRNLK-----VPI PANYF----- 263
Streptococcus FEYDRDTLAREYRRDLEVGIN-----PDVPANYF----- 264
Escherichia PEYDAQTLAQEFFRDVEAGLD-----PDVPYNYF----- 264
Methylococcus PEYDTVSL LKEYKREILRYFSGEREDYPPFPEHYFSLEVGAA LNDYGQALRSARRAGRAP 299
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Geobacillus ---PNDDPSQPPLNTWRSHANLLFVNWLNYYVYQETPYEWE----- 302
Clostridium ---PDDDPTKPPVNWNRGHANLLFSNWLNYVYQETPFDLNELK----- 305
Thermotoga ---PNDDPTKTPILTWSHAHLFFSNWLN YCIYQKTPYRLEDIH----- 304
Streptococcus ---PGDDPSQEPKLRWNLAASTFFSNW INYAVYQETPYRLEELEDDFSFYGYL--- 314
Escherichia ---PHNDPQNTPRASWRSHGNLLFTNWLNYVYQITPYDLRHMNPTLD----- 309
Methylococcus PPFPEEFVLRHLDNTWRDTAKAVFNWNLGKIYQITDQDRRKPFMAHIDPDNPLGLA 355
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Figure S1.