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Multalin version 5.4.1

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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: 275 Check: 0 ..

Name: China1_YP_0097 Len: 275 Check: 2511 Weight: 1.00

Name: India_QIA98584 Len: 275 Check: 2511 Weight: 1.00

Name: USA1_QH060595. Len: 275 Check: 2511 Weight: 1.00

Name: Nepal_QIB84674 Len: 275 Check: 2511 Weight: 1.00

Name: Italy_QIA98555 Len: 275 Check: 2856 Weight: 1.00

Name: Consensus Len: 275 Check: 2511 Weight: 0.00

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1
China1_YP_ MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS 180
India_QIA9 MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS
USA1_QH060 MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS
Nepal_QIB8 MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS
Italy_QIA9 MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS
Consensus MDLFMRIFTI GTVTLKQGEI KDATPSDFVR ATATIPIQAS LPFGWLIVGV ALLAVFQSAS KIITLKKRWQ LALSKGVHVF CNLLLLFVTV YSHLLLVAAG LEAPFLYLYA LVYFLQSFN VRIIMRLWLC WKCRSKNPLL YDANYFLCWH TNCYDYCIPY NSVTSSIVIT SGDGTSPIS

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181
China1_YP_ EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID GSSGVVNPVM EPIYDEPTTT TSVPL 275
India_QIA9 EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID GSSGVVNPVM EPIYDEPTTT TSVPL
USA1_QH060 EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID GSSGVVNPVM EPIYDEPTTT TSVPL
Nepal_QIB8 EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID GSSGVVNPVM EPIYDEPTTT TSVPL
Italy_QIA9 EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID VSSGVVNPVM EPIYDEPTTT TSVPL
Consensus EHDYQIGGYT EKWESGVKDC VVLHSYFTSD YYQLYSTQLS TDTGVEHVTF FIYNKIVDEP EEHVQIHTID gSSGVVNPVM EPIYDEPTTT TSVPL

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