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NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
NTDB id 159 SP RS09750 WP 001085462.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
NTDB id 499 SM12261 RS08315 WP 078228268.1
NTDB id 453 Spy49 1753c ACI62003.1
NTDB id 408 SMU RS09530 WP 002262392.1
NTDB id 115 BSU 16940 NP 389576.2
NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1313 DR RS12030 WP 010888966.1
NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
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NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
NTDB id 1130 NGFG RS03960 WP 003688695.1
NTDB id 1124 NGFG RS03960 WP 003688695.1
NTDB id 1123 OK783 RS03845 WP 003688695.1
NTDB id 1427 RS RS02760 WP 011000510.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 224816 B7L46 RS19920 WP 000344169.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1205 PSJM300 05545 AFN77183.1
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Sequence	Score
DEKIGGGA ⁺ E ⁺ KA ⁺ KNYLKEHQ ⁺ DV ⁺ FEID ⁺ HKVRAAHG ⁺ LDDSEVAETEEEE.TTAS ⁺ KTK..AKAKKEEKAVETEEIELELED..	387
DEKIGQGSEN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ EHPEIF ⁺ DEID ⁺ KQVRSKFG ⁺ LIDGEEVSEQDTE.NKKD ⁺ E.....PKKEEA..VNEEVPLDLGDEL	382
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ ADNP ⁺ EVFAEID ⁺ HQVRVQFGLIDGEEAAE.....SKKD ⁺ E.....VAQVDS..VNEEVTLDLGDEL	378
DEKIGQGS ⁺ EN ⁺ AKKYLA ⁺ ADNP ⁺ EVFAEID ⁺ HQVRVQFGLIDGEEAAE.....SKKD ⁺ E.....AAQVDS..VNEEVTLDLGDEL	378
GEKIGQGS ⁺ EN ⁺ AKRYLADHP ⁺ QLFDEID ⁺ DKVRVKFGLLEESEEESAMAV.ASE.....E.....TDDLALDLNGI	374
GEKIGQGS ⁺ EN ⁺ AKKFLADNP ⁺ EIFDD ⁺ IDHKVRVQYGLIEEDNTEEKQSS.KEK.....ETDEK..ADKNLVLELDDTI	379
EERLGGGREN ⁺ AKQFLKEN ⁺ KDIMLMIQEQIREHYGLDNGGVVQQAAEE.TQEEL.E..FE.E.....	348
SERIGGGREN ⁺ AKNYLADHED ⁺ VEDEVRLK ⁺ VRAAYGISDVPEEDLP ⁺ TTE.DE.QI.N..ILPDDST.....EE	355
DERIGGGKEKT ⁺ IAYIA ⁺ ERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA..	363
DKKLGGGREN ⁺ SKAFLKEN ⁺ PEIADEIT ⁺ KATQNSMGIEGMISGS..EDDEGE..E.....	343
DKKLGGGREN ⁺ AKALLKED ⁺ KALADEIT ⁺ LKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DKKLGGGREN ⁺ AKALLKED ⁺ KALADEIT ⁺ LKIKESIGSNEEIMPL..PDEPLE..EME.....	347
DTKLGGGRD ⁺ TVKELIK ⁺ DNPELAE ⁺ ELEAKIREKLQAK.....	343
GTKIGQGKNN ⁺ AVKWLKEN ⁺ PEIAD ⁺ KLQEIRNTLASNPNSVLK..ATASDSND ⁺ ESDVEEFSE.....EEL	372
GAKIGGQKDN ⁺ VRVWLKEN ⁺ PEISDEID ⁺ AKIRALNGVEMHITEG..TQDET.....GERPE..E.....	348
GAKIGGQKDN ⁺ VRVWLKEN ⁺ PEISDEID ⁺ AKIRALNGVEMHITEG..TQDET.....GERPE..E.....	348
GAKIGGQKDN ⁺ VRVWLKEN ⁺ PEISDEID ⁺ AKIRALNGVEMHITEG..TQDET.....GERPE..E.....	348
GERIGGGRDN ⁺ CREFLRENA ⁺ ELAREIENK ⁺ VREHLGVTPMGAV..TLAEEVEED ⁺	352
GDKIGGQKAN ⁺ ACKYLKEN ⁺ PEIAKTLDKKLREMLLNPNMQLI..AETSSAAD ⁺ VEFGAVPE.....EF	354
GDKIGGQKAN ⁺ ACKYLKEN ⁺ PEIAKTLDKKLREMLLNPNMQLI..AETSSAAD ⁺ VEFGAVPE.....EF	354
GNKIGGQKNN ⁺ VIRYFEENT ⁺ QIAE ⁺ EIERNIREQLLTTGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQKNN ⁺ VIRYFEENN ⁺ QIAE ⁺ EIERNIREQLLTTGTNGAV..Q.I.EDEE ⁺ EPD..LLE.....S.....	349
GNKIGGQKNN ⁺ VIRYLEEN ⁺ PQISTE ⁺ IEAVIREQLLTKASDQTA..A.HDETEE ⁺ EPD..LLES.....	349
GSKIGGQKANA ⁺ KYLEEN ⁺ PEIQ ⁺ EIEQVIRAKLLVTSANTKA..TPVAEDLAD ⁺ AD..I.....	347

logo

		EIEIEE	
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved