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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
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1334 RAOC RS04870 WP 004918236.1
NTDB id 1389 A4U84 RS07560 WP 021112712.1
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NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
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Sequence	Score
DEKIGGGA ¹ E ² KA ³ KN ⁴ YL ⁵ KE ⁶ HQ ⁷ DV ⁸ FD ⁹ EID ¹⁰ HK ¹¹ VRAAH ¹² GL ¹³ LD ¹⁴ SEVAETEEETTA...SKTKAKAKKEEKAVETEEIELELED.	387
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQD ¹² TENKK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQD ¹² TENKK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PEIF ⁶ DEID ⁷ KQ ⁸ VR ⁹ SKF ¹⁰ GL ¹¹ IDGEEVSEQD ¹² TENKK...DE...PKKEEA...VNEEVPLDLGDE	381
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEVFA ⁶ EID ⁷ HQ ⁸ VR ⁹ VQF ¹⁰ GL ¹¹ IDGEEAAE...SKK...DE...VAQVDS...VNEEVTLDLGDE	377
DEKIGGGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PEIF ⁶ DEID ⁷ HQ ⁸ VR ⁹ VQF ¹⁰ GL ¹¹ IDGEEIAE...SKK...DE...AAQVDS...VNEEVTLDLGDE	377
GEKIGGGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ RK ⁹ VR ¹⁰ VKF ¹¹ GL ¹² LEESEESAMAVASE...E...TDDLALDLNG	373
GEKIGGGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PEIF ⁶ DD ⁷ ID ⁸ HK ⁹ VR ¹⁰ VQY ¹¹ GL ¹² IEEDNTEEKQSSKEK...ETDEK...ADKNLVLELDDT	378
EE ¹ RL ² GG ³ RENA ⁴ KQ ⁵ FL ⁶ KN ⁷ KD ⁸ IM ⁹ LI ¹⁰ QE ¹¹ Q ¹² IREHY ¹³ GL ¹⁴ DNNGVVQQAEETQE...EL ¹⁵ .EFE.E...E...	348
SERIGGG ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ VR ⁷ LK ⁸ VRAAY ⁹ GIS ¹⁰ DVPEEDLPTTEDE...QI.NILPDDST...EE...	355
DERIGGG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ EME ⁷ QE ⁸ IRDRV ⁹ MAA ¹⁰ IRAGNAGEAPALAPAPAAPEAA ¹¹ EA...	363
DKKLGGG ¹ RENSKA ² FL ³ KN ⁴ PEIA ⁵ DEIT ⁶ KA ⁷ IQNSM ⁸ G ⁹ IEGMI...SGSEDD...EGEE...	343
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEI...MPLPDE...PLEEME...	347
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ LK ⁷ IKESIG ⁸ SNEEI...MPLPDE...PLEEME...	347
DTKLGGGR ¹ DTV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LEAK ⁸ IREKLQAK...	343
GTKIGGG ¹ KNN ² AVK ³ WL ⁴ KN ⁵ PEIA ⁶ DK ⁷ LE ⁸ QEI ⁹ RNTLA ¹⁰ SNPNS...VLKATASDSN ¹¹ DES ¹² DVEEFS...EEEL...	372
GAKIGGG ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ G ¹⁰ VMHI...TEGTQDET ¹¹ D...GERP...EE...	348
GAKIGGG ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ G ¹⁰ VMHI...TEGTQDET ¹¹ D...GERP...EE...	348
GAKIGGG ¹ KDN ² VR ³ VL ⁴ KN ⁵ PEIS ⁶ DEID ⁷ AK ⁸ IRALN ⁹ G ¹⁰ VMHI...TEGTQDET ¹¹ D...GERP...EE...	348
GERIGGG ¹ RD ² NC ³ REFL ⁴ RENA ⁵ EL ⁶ LA ⁷ REI ⁸ ENK ⁹ VREHL ¹⁰ GVTPMG...AVTL.AEEVE ¹¹ ED...	352
GEKIGGG ¹ KANAT ² NWL ³ KN ⁴ PEI ⁵ ATA ⁶ IE ⁷ KKL ⁸ RELLLNQDS...TPDFSVDSDG ⁹ EDV...KETN...EDF...	354
GDKIGGG ¹ KANACKY ² L ³ KN ⁴ PEIA ⁵ AKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENM...QLIAETSSAAD ¹⁰ VEFGAVP...EEF...	354
GDKIGGG ¹ KANACKY ² L ³ KN ⁴ PEIA ⁵ AKT ⁶ L ⁷ DKKL ⁸ REMLLN ⁹ PENM...QLIAETSSAAD ¹⁰ VEFGAVP...EEF...	354
GSKIGGG ¹ KANA ² AKY ³ LEEN ⁴ PEIG ⁵ Q ⁶ EIE ⁷ QQ ⁸ IRAKLL ⁹ V ¹⁰ TSAN...TKATPVAEDLADADI...	347
GNKIGGG ¹ KNN ² VIRY ³ LEEN ⁴ PQ ⁵ ISTE ⁶ IE ⁷ EAV ⁸ IREQLLT ⁹ KASD...QTA ¹⁰ .HDETE ¹¹ EE ¹² PDLLES...	349
GNKIGGG ¹ KNN ² VIRY ³ FENN ⁴ QIA ⁵ EIE ⁶ ERN ⁷ IREQLLT ⁸ TGTN...GAVQ.I.EDEE ⁹ EE ¹⁰ PDLLES...	349

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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved