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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 499 SM12261 RS08315 WP 078228268.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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Sequence	Score
DEKIGQGA 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 DDSEVAETEEETTAS ¹⁵ KT ¹⁶ KAKAK ¹⁷ KE ¹⁸ KA ¹⁹ VETEEIELE ²⁰ ED... 387	387
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GL ¹³ ID ¹⁴ GEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE... PK ¹⁸ KEEA... V ¹⁹ NEEVPLDLG ²⁰ DELEIE 385	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GL ¹³ ID ¹⁴ GEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE... PK ¹⁸ KEEA... V ¹⁹ NEEVPLDLG ²⁰ DELEIE 385	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ EH ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ KQ ¹⁰ VR ¹¹ SKF ¹² GL ¹³ ID ¹⁴ GEEVSEQD ¹⁵ TEN ¹⁶ KK ¹⁷ DE... PK ¹⁸ KEEA... V ¹⁹ NEEVPLDLG ²⁰ DELEIE 385	385
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQF ¹² GL ¹³ ID ¹⁴ GEEIAES... KK ¹⁵ DE... AA ¹⁶ QV ¹⁷ DS... V ¹⁸ NEEVTLDLG ¹⁹ DELEIE 381	381
DEKIGQGS ¹ EN ² AK ³ KYLA ⁴ DN ⁵ PE ⁶ IF ⁷ DE ⁸ ID ⁹ HQ ¹⁰ VR ¹¹ VQF ¹² GL ¹³ ID ¹⁴ GEEAAES... KK ¹⁵ DE... VA ¹⁶ QV ¹⁷ DS... V ¹⁸ NEEVTLDLG ¹⁹ DELEIE 381	381
GEKIGQGS ¹ EN ² AK ³ RYLA ⁴ DHP ⁵ QL ⁶ FD ⁷ EID ⁸ DK ⁹ VR ¹⁰ VKF ¹¹ GL ¹² LEESEESAMAVASE... E... TDD ¹³ LALDL ¹⁴ NG ¹⁵ IEIE 377	377
GEKIGQGS ¹ EN ² AK ³ KFLA ⁴ DN ⁵ PE ⁶ IF ⁷ DD ⁸ ID ⁹ HK ¹⁰ VR ¹¹ VQY ¹² GL ¹³ IEEDNTEEKQSSKEK... ET ¹⁴ DEK... AD ¹⁵ KNLVLEL ¹⁶ DD ¹⁷ TIELE 382	382
EE ¹ RL ² GG ³ RENA ⁴ KQ ⁵ FL ⁶ KN ⁷ KD ⁸ IM ⁹ LM ¹⁰ IQEQ ¹¹ IREHY ¹² GL ¹³ DNNGVVQQAEETQEEL ¹⁴ .EFE.E... 348	348
SERIGQGS ¹ RENA ² KNYLA ³ DH ⁴ ED ⁵ VE ⁶ DEV ⁷ RL ⁸ KV ⁹ RAAY ¹⁰ GIS ¹¹ SDVPEEDLPTTEDE.QI.NILPDDST... EE... 355	355
DERIGQG ¹ KE ² KTI ³ AY ⁴ IA ⁵ ERP ⁶ EME ⁷ QE ⁸ IRDR ⁹ VMAA ¹⁰ IRAGNAGEAPALAPAPAAPEAA... EA... 363	363
DKKLGGG ¹ RENS ² KA ³ FL ⁴ IKEN ⁵ PEIA ⁶ DEIT ⁷ KA ⁸ IQNSM ⁹ GI ¹⁰ EGM... ISGSEDDEG... EF... 343	343
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ TL ⁷ KIKES ⁸ IG ⁹ SNEE... IMPLPDEPL... EEME... 347	347
DKKLGGG ¹ RENA ² KALL ³ KED ⁴ KALA ⁵ DEIT ⁶ TL ⁷ KIKES ⁸ IG ⁹ SNEE... IMPLPDEPL... EEME... 347	347
DTKLGGGR ¹ DTV ² KEL ³ IK ⁴ DN ⁵ PELA ⁶ E ⁷ LEAK ⁸ IREKLQAK... 343	343
GTKIGQG ¹ KNN ² AVK ³ WL ⁴ KEN ⁵ PEIA ⁶ DK ⁷ LEQEI ⁸ RNTLA ⁹ SNPN... SVLKATASDSN... DES ¹⁰ DVEEFSEEL... 372	372
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH... ITEG... T... QDET ⁹ DGERPEE... 348	348
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH... ITEG... T... QDET ⁹ DGERPEE... 348	348
GAKIGQG ¹ KDN ² VR ³ VL ⁴ KEN ⁵ PEIS ⁶ DEIDAK ⁷ IRALNG ⁸ VMH... ITEG... T... QDET ⁹ DGERPEE... 348	348
GERIGQGR ¹ DN ² CRE ³ FL ⁴ RENA ⁵ E ⁶ LARE ⁷ IE ⁸ KN ⁹ KV ¹⁰ REHL ¹¹ GV ¹² TPM... GAVTLAEE.VE... ED... 352	352
GEKIGQGG ¹ KANATA ² WL ³ KN ⁴ PETAK ⁵ EIEKK ⁶ VRELLSNPN... STPDFSV... D... DSEGVAETNEDF... 353	353
GDKIGQG ¹ KANACKY ² LKEN ³ PEIA ⁴ KT ⁵ LDKKL ⁶ REMLLN ⁷ PNEN... MQLIAETSSAA... DDVEFGAVPEEF... 354	354
GDKIGQG ¹ KANACKY ² LKEN ³ PEIA ⁴ KT ⁵ LDKKL ⁶ REMLLN ⁷ PNEN... MQLIAETSSAA... DDVEFGAVPEEF... 354	354
GSKIGQG ¹ KANA ² AKY ³ LEEN ⁴ PEIG ⁵ QIE ⁶ EQQ ⁷ IRAKLL ⁸ VTSA... NTKATPVAEDL... ADADI... 347	347
GNKIGQG ¹ KNN ² VIRY ³ LEEN ⁴ PQISTE ⁵ IE ⁶ EAV ⁷ IREQLLTKAS... DQ ⁸ TAA.HDETE... EEP ⁹ DLLES... 349	349
GNKIGQG ¹ KNN ² VIRY ³ FEENN ⁴ QIAE ⁵ IE ⁶ ERN ⁷ IREQLLTGT... NGA ⁸ VQ.I.EDE... EEP ⁹ DLLES... 349	349

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		IEE	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
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consensus			

-  non conserved
-  similar
-  ≥ 50% conserved