

logo

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 499 SM12261 RS08315 WP 078228268.1
NTDB id 527 SMSK321 RS11065 WP 001085454.1
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
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 221476 BS653 RS11740 WP 000963143.1
NTDB id 1165 A1552VC RS01565 WP 000344154.1
NTDB id 1142 GTF74 RS11550 WP 000344154.1
NTDB id 1205 PSJM300 05545 AFN77183.1
NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQIGKITKIKVVKNKVAPPFKVALVDIMFGEGISSTGELINIAVEEGI	I	IKKSGAWFAYN	312			
NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKEAFVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKEAFVEIMYEGEGISKTGELLKIASDL	D	IIKKAGAWYSYK	311		
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSN	IGKETKIKVVKNKVAPPFKVAEVEIMYEGEGISRTGELVKIASDL	D	IIQKAGAWFSYN	311		
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKEAFVEIIMYEGEGISRTGELVKIASDL	G	IIQKAGAWYSYN	311		
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DVMGNKTKIKVVKNKVAPPFRTA	EVDIMYEGEGISKEGEIIDLGTEL	D	IVQKSGSWYSYE	292		
NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT.....DMIGNRARIKVVKNKVAPPFKVAEVD	IMYGGISRTGELVDMAVEK	DI	INKSGSWYSYG	294		
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ.....PTKVGND	AVANTVKIKTVKNKVAAPFKEVELALVYGKGF	QDLS	DLVGLAADMD	IIKKAGSFYSYG	307	
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKVAT.....L.KQNEEP	IGNRVKVVKNKVAPPFRQAEFDVMFGEGLS	REGELIDYGV	KLDIVDKSGAWFSYK	294		
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRDIRRIAA.....L.KQNEQH	IGNRAKAKVVKNKVAPPFR	EA	EFDIMFGEGISKEGEIIDYGV	KLDIVDKSGAWLSYQ	296	
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRDIRRIAS.....L.KQNEQH	IGNRAKAKVVKNKVAPPFR	EA	EFDIMFGEGISKEGEIIDYGV	KLDIVDKSGAWLSYQ	296	
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRDIRRSLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPFKSA	AEFDIMYEGGVSKVGEILD	VATDLDIIQKSGSWFSYQ	307		
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV.....V.KDGDEI	IGSETKVVKNKVAPPFR	EVQFDIMYEGEGISRMNELL	ILAEANGFI	IKKSGAWFSYD	310	
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS.....I.KKGE	EEVLGNETRVKVIKNKVAPPFRQAEFD	DILYEGEGISWEGELID	IGVKNDIINKSGAWYSYN	294		
NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS.....I.KKGE	EEVLGNETRVKVIKNKVAPPFRQAEFD	DILYEGEGISWEGELID	IGVKNDIINKSGAWYSYN	294		
NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS.....I.KKGE	EEVLGNETRVKVIKNKVAPPFRQAEFD	DILYEGEGISWEGELID	IGVKNDIINKSGAWYSYN	294		
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS.....I.KKGE	DEVGNETKVVKNKVAPPFR	EA	IFDILYAGVSR	REGELIDLGVEAKVVEKSGAWYSYN	302	
NTDB id 221476 BS653 RS11740 WP 000963143.1	SVRLDIRRIGA.....V.KEGENV	VGS	ETRVKVVKNKIAAPFKQAEFQ	ILYGE	GINFYGELVDLGVKEKLLIEKAGAWYSYK	295	
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA.....I.KEG	EEVLGNETRIKVVKNKIAAPFKEANTQIMYGG	GFNR	REGELIDLGVKHKMVEKSGAWYSYN	293		
NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA.....I.KEG	EEVLGNETRIKVVKNKIAAPFKEANTQIMYGG	GFNR	REGELIDLGVKHKMVEKSGAWYSYN	293		
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA.....V.KEG	DEVVGS	ETRVKVVKNKVAPPFRQAEFQ	ILYGKGIYRNGE	IDLG	VQQGLVEKSGAWYAYK	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ.....V.KEG	DEIIGSETKVVKNKMAPPFR	EA	IFQILYGKGVNQLGELVDLAVQQ	NIVQKAGAWYSYK	293	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ.....V.KEG	DEIIGSETKVVKNKMAPPFK	EA	IFQILYGKGTNQLGELVDLAVQQ	NIVQKAGAWYSYQ	293	
consensus	*!!**!* *	*	**	*****!*****!*****!*	*	*****!*!***** ***** *	*** ! !*****!

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NTDB id 1022 ACIAD RS06390 WP 004925639.1
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Sequence	Score
DEKIGGGAEKAKNYLKEHQDVFEIDHKVRAAHGLDDSEVAETEEETTASKTAKAKKKEKAVETEEIELELED....	387
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSENAKKYLAHNPEIFDEIDHQRVVFGLIDGEEIAES...KKDE...AAQVDS..VNEEVTLDLGDELEIE	381
DEKIGQGSENAKKYLAHNPEVFAEIDHQRVVFGLIDGEEAAES...KKDE...VAQVDS..VNEEVTLDLGDELEIE	381
GEKIGQGSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGQGRENAKQFLKENKDIMLMIQEQUIREHYGLDNGGVVQQAEETQEEL.EFE.E.....	348
SERIGQGRENAKNYLADHEDVEDEVRLKVRAAAYGISDVPEEDLPTTEDE.QI.NILPDDST....EE.....	355
DERIGQGEKTIATYIAERPMEQEIRDRVMMAAIRAGNAGEAPALAPAPAAPEAA...EA.....	363
DKKLGQGRNSKAFLENPEIADEITKATINSMGTIEGM.....ISGSEDDEG.....EE.....	343
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DKKLGQGRENAKALLKEDKALADEITLKIKESIGSNEE....IMPLPDEPL.....EEME.....	347
DTKLGQGRDTPVKELIKDNPELAELEAKIREKLQAK.....	343
GTKIGQGKNNAVKWLKENPEIADKLEQIRNTLASNPN....SVLKATASDSN...DES.DVEEFSEEL	372
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMH....ITEG.....T...QDETGDGERPEE	348
GERIGQGRDNCREFLRENAELAREIENKVRHGLVTPM.....GAVTLAEE.VE...ED.....	352
GEKIGQGANATAWLKDNPETAKIEKKVRELLNSNP....STPDFSV..D..DSEGVATNEDF	353
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA..DDVEFGAVPEEF	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPN....MQLIAETSSAA..DDVEFGAVPEEF	354
GSKIGGQKANAAKYLEENPEIGQIEEQIRAKLLVTSA....NTKATPVAEDL..ADADI.....	347
GNKIGGQKNNVIRYLEENPQISTEIEAVIREQLLTKAS....DQTAA.HDETE...EEDPLLLES	349
GNKIGGQKNNVIRIFYENNQIAEIERNIEREQLLTGT....NGAVQ.I.EDE...EEDPLLLES	349

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NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384
NTDB id 453 Spy49 1753c ACI62003.1	D..	378
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383
NTDB id 115 BSU 16940 NP 389576.2	...	348
NTDB id 625 LCA RS02525 WP 011374196.1	...	355
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consensus

 non conserved
 similar
 ≥ 50% conserved