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NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT....DM	IGNRARIKVVKNKVAPPFKVAEVDIMYGGGISRTGELVDMAVEKDIINKSGSWYSYG	294
NTDB id 119587 A418 RS07660 WP 003725961.1	TVRLEVRRAEQLKQGT....DV	MGNKTKIKVVKNKVAPPFRFAEVDIMYGGEGISREGELVDMAAEVDVINKSGSWYSYK	292
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN....DV	MGNKTKIKVVKNKVAPPFRFAEVDIMYGGEGISKEGEIDLGTELDIVQKSGSWYSYE	292
NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQ	IGKITIKVVKNKVAPPFKVALVDIMFGEGISSTGELLNIAVEEGIINKSGAWFAYN	312
NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKAEAFVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPFKAEAFVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDS	IGKETKIKVVKNKVAPPFKVAEVEIMYGGEGISRTGELVKIASDLDIQKAGAWFSYN	311
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPFKAEAFVEIYGGEGISRTGELVKIASDLGIQKAGAWYSYN	311
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTVKIKTVKNKVAAPFKLEVELALVYGGKGFQDLSDLVGLAADMDIINKAGSFYSYG	307
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKIVAT....L.KQNEEP	IGNRVKVVKNKVAPPFRQAEFDMVFGGELSREGELIDYGVKLDIVDKSGAWFSYK	294
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS....L.KQNEQH	IGNRAKAKVVKNKVAPPFRFAEAFDIMFGEGISKEGETIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA....L.KQNEQH	IGNRAKAKVVKNKVAPPFRFAEAFDIMFGEGISKEGETIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPFKSAEAFDIMYGGEGVSKVGEILDVATDLDIQKSGSWFSYQ	307
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPFRFVQFDIMYGGEGISRMNELLILAEANGFIKKSGAWFSYD	310
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS....I.KKGEV	VGNETKVVKNKVAPPFRFAEAFDILYGGAGVSREGEIDLGVKAEKVVVEKSGAWYSYN	302
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPFKAEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPFKAEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	VGSETKVVKNKMAPPFKAEAFQILYGGKGTNQLGELVDLAVQQDIVQKAGAWYSYQ	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVKNKMAPPFRFAEAFQILYGGKGVNQLGELVDLAVQQNIVQKAGAWYSYQ	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKNKVAPPFRQAEFQILYGGKIYRNGEIDLGVQQGLVEKSGAWAYK	293
consensus	*!!**!* * ** *****!!*!!*!!*!!* * *****!*!*** **	*** ! !*****!	

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 NTDB id 408 SMU RS09530 WP 002262392.1
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 NTDB id 1165 A1552VC RS01565 WP 000344154.1
 NTDB id 1142 GTF74 RS11550 WP 000344154.1
 NTDB id 1074 ABD1 RS10195 WP 000344167.1
 NTDB id 1022 ACIAD RS06390 WP 004925639.1
 NTDB id 1205 PSJM300 05545 AFN77183.1

consensus



SERIGQGRENAKNYLADHEDVEDEVRLKVRRAAYGTSVPEEDLPTTEDEQINILPDDSTEE..... 355
 EERIGQGRENAKQYLKEHTDIRDEISKRVREEYEIDGSNKEPLD..EGEETLSLLDDE..... 348
 EERLGQGRENAKQFLKENKDIMLMIQEQIREHYGLDNNGVVQQAEETQEELEFEE..... 348
 DEKIGQGAEKAKNYLKEHQDVFEIDHKVRAAHGLLDDSEVAETEETTASKTKAKAKKEEKAVETEEIELELED..... 387
 DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE....PKKEEA..VNEEVPLDLGDELEIE 385
 DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE....PKKEEA..VNEEVPLDLGDELEIE 385
 DEKIGQGSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQD TENKKDE....PKKEEA..VNEEVPLDLGDELEIE 385
 DEKIGQGSENAKKYLADNPEIFDEIDHQVVRVQFGLIDGEEIAES....KKDE....AAQVDS..VNEEVTLDLGDELEIE 381
 DEKIGQGSENAKKYLADNPEVFAEIDHQVVRVQFGLIDGEEAAES....KKDE....VAQVDS..VNEEVTLDLGDELEIE 381
 GEKIGQGSENAKRYLADHPQLFDEIDRKVVRVKFGLLEESEEEESAMAVASE.....E.....TDDLALDLNGIEIE 377
 GEKIGQGSENAKKFLADNPEIFDDIDHKVVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE 382
 DERIGQGKEKTIAYIAERPMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA..... 363
 DKKLGQGRENSKAFLENPEIAD EITKAIQNSMGT EGM I....SGSEDDE..GEE..... 343
 DKKLGQGRENAKALLKEDKALADEITLTKESIGSNEEI....MPLPDEP..LEEME..... 347
 DKKLGQGRENAKALLKEDKALADEITLTKESIGSNEEI....MPLPDEP..LEEME..... 347
 DTKLGQGRD TVKELTKDNPELAELEAKIREKLQAK..... 343
 GTKIGQGNNAVKWLKENPEIADKLEQEIRNTLASNPNS....VLKATASDSNDES DVEE..FSEEEL..... 372
 GAKIGQKDNVVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDETD.....GE..RPEE..... 348
 GAKIGQKDNVVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDETD.....GE..RPEE..... 348
 GAKIGQKDNVVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDETD.....GE..RPEE..... 348
 GERIGQGRDNCREFLRENAELAREIENKVRHLGVTPMG....AV.TLAEVEED..... 352
 GDKIGQGANACKY LKENPEIAKTLDKKLREMLLN PENM....QLIAETSSAADDVEFGA..VPEEF..... 354
 GDKIGQGANACKY LKENPEIAKTLDKKLREMLLN PENM....QLIAETSSAADDVEFGA..VPEEF..... 354
 GNKIGQGNNVIRYFEENNQIAEEIERNIREQLLTTGTN....GAVQ.I.EDEE EPD..L..LLES..... 349
 GNKIGQGNNVIRYLEENPQISTEIEAVIREQLLTKASD....QTAA.HDETEE EPD..L..LLES..... 349
 GSKIGQGANAAKYLEENPEIGQEIEQQIRAKLLVTSAN....TKATPVAEDLADAD..I..... 347

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NTDB id 453 Spy49 1753c ACI62003.1	D..	378
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consensus

 non conserved
 similar
 ≥ 50% conserved