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NTDB id 625 LCA RS02525 WP 011374196.1	IVEIYGPESGKTTVALHVAEVAQKQGTTAAAYIDAENAMDPKYATALGVNIDDLLSQPDTGEQGLEIADALVSSGAVDI	140
NTDB id 410273 D5E69 RS10500 WP 048003984.1	IEEYGPESGKTTVALHVAEVAQKQGQAFAFIDAEHALDPVYAQKLGVNIIDELLSPQDTGEQALEIAEALVRSGAVDA	138
NTDB id 115 BSU 16940 NP 389576.2	IEEYGPESGKTTVALHVAEVAQKQGQAFAFIDAEHALDPVYAQKLGVNIIDELLSPQDTGEQALEIAEALVRSGAVDI	138
NTDB id 600 KW2 RS01765 WP 011675413.1	IVEIYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPEYAKALGVNIDELLSPQDYGEQGLQIAEKLITSGAVDL	154
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 228 SPD RS09265 WP 001085462.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 194 SPR RS08825 WP 001085462.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 159 SP RS09750 WP 001085462.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 453 Spy49 1753c ACI62003.1	IEEYGPESGKTTVALHVAEVAQKQEGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 408 SMU RS09530 WP 002262392.1	IVEIYGPESGKTTVALHVAEVAQKQDGGIAAFIDAEHALDPAYAAAALGVNIDELLSPQDSGEQGLEIAGKLIDSGAVDL	153
NTDB id 1313 DR RS12030 WP 010888966.1	ITEIYGPESGKTTVALHVAEVAQKQAGGTCFAFIDAEHALDPVYARALGVNTDELLVSPQDNGEQALEIIMELLVRSGATDV	152
NTDB id 1245 Cj1673c YP 002345041.1	IEEYGPESGKTTTLHLIAEACQKAGGVCFAFIDAEHALDVKYAKNLGVNTDLYVSPQDFGEQALEIIVETIARSGAVDL	139
NTDB id 1211 C694 RS00795 WP 000963128.1	IEEYGPESGKTTLSLHIAEACQKNGGVCFAFIDAEHALDVHYAKRLGVDTENLLVSPQDTGEQALEILETITRSGGIDL	141
NTDB id 1214 NCTC11637 00359 SQJ03206.1	IEEYGPESGKTTLSLHIAEACQKNGGVCFAFIDAEHALDVHYAKRLGVDTENLLVSPQDTGEQALEILETITRSGGIDL	141
NTDB id 1334 RAOC RS04870 WP 004918236.1	IVEIYGPESGKTTTLHLIAEAAQKVGTTAAFAFIDAEHAFDMHYAEKLGINLEELIVSQPDNGEQALEIADSLTRSGGVDI	148
NTDB id 1389 A4U84 RS07560 WP 021112712.1	IVEIYGPESGKTTTLSLIAQAQKGNKTCFAFIDAEHALDPVYARNLGVNTDELLSPQDNGEQALEICDALVRSGAVDV	156
NTDB id 1130 NGFG RS03960 WP 003688695.1	IVEIFGPESGKTTLCLEAVAQCQKNGGVCFAFVDAEHAFDPVYARKLGVKVEELYLSQPDTEQALEICDTLVRSGGIDM	140
NTDB id 1124 NGFG RS03960 WP 003688695.1	IVEIFGPESGKTTLCLEAVAQCQKNGGVCFAFVDAEHAFDPVYARKLGVKVEELYLSQPDTEQALEICDTLVRSGGIDM	140
NTDB id 1123 OK783 RS03845 WP 003688695.1	IVEIFGPESGKTTLCLEAVAQCQKNGGVCFAFVDAEHAFDPVYARKLGVKVEELYLSQPDTEQALEICDTLVRSGGIDM	140
NTDB id 1427 RS RS02760 WP 011000510.1	VVEIYGPESGKTTTLQVVAEMQKLGTCFAFIDAEHALDVTYADKLGVKVPDLLISQPDTEQALEIADALVRSGSVDL	148
NTDB id 1165 A1552VC RS01565 WP 000344154.1	IVEIFGPESGKTTTLELIAAAQREGKTCFAFIDAEHALDPVYAKKLGVNIIDELLVSPQDTGEQALEICDALARSGAVDV	139
NTDB id 1142 GTF74 RS11550 WP 000344154.1	IVEIFGPESGKTTTLELIAAAQREGKTCFAFIDAEHALDPVYAKKLGVNIIDELLVSPQDTGEQALEICDALARSGAVDV	139
NTDB id 1205 PSJM300 05545 AFN77183.1	IVEIYGPESGKTTTLQVVAEMQKLGTCFAFVDAEHAFDPYAGKLGVNVDLLVSPQDTGEQALEITDMLVRSNAVDV	139
NTDB id 1022 ACIAD RS06390 WP 004925639.1	IVEIYGPESGKTTMTLQAIQAQCQKAGGTCFAFIDAEHALDPQYARKLGVDIDNLLVSPQDPHGEQALEIADMLVRSGATDL	139
NTDB id 1074 ABD1 RS10195 WP 000344167.1	IEEYGPESGKTTMTLQAIQAQCQKSGGTCFAFIDAEHALDPQYARKLGVDIDNLLVSPQDNGEQALEIADMLVRSGATDL	139
consensus	**!***!!!!*!!!!* ! **! !* ** !***!!!!*!* !! !!***!!***!!!!*!!!!*!*! * ***!***!*	

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NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRRAETIKNGT....DMIGNRARIKVVKNKVAPPFKVAEVDIMYGGQGISRTGELVDMAVEKDIINKSGSWYSYG	294
NTDB id 410273 D5E69 RS10500 WP 048003984.1	SVRLEVRRRAETLKQGN....EMVGNKTKIKVVKNKVAPPFRVAEVDIMYGGEGISKEGETVDLGSLEDIILKSGAWYSYN	292
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRRAEQLKQGN....DVMGNKTKIKVVKNKVAPPFRVAEVDIMYGGEGISKEGETIDLGTLEDIVQKSGSWYSYE	292
NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQIGKITIKVVKNKVAPPFKVALVDIMFGEGISSTGELLNIAVEEGIINKSGAWFAYN	312
NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNVGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNVGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNVGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNVGKETKIKVVKNKVAPPFKAEVVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTNVGKETKIKVVKNKVAPPFKAEAFVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTNVGKETKIKVVKNKVAPPFKAEAFVEIMYGGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSSIGKETKIKVVKNKVAPPFKVAEVEIMYGGEGISRTGELVKIASDLDIQKAGAWFSYN	311
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSNIGKETKIKVVKNKVAPPFKAEAFVEIYYGGEGISRTGELVKIASDLGIQKAGAWFSYN	311
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGNDAVANTVKTITVKNKVAAPFKVEVELALVYGGKGFQDLSDLVGLAADMDIINKAGSFYSYG	307
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKIVAT....L.KQNEEPIGNRVKVVKNKVAPPFRQAEFDMVFGGELSREGELIDYGVKLDIVDKSGAWFSYK	294
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS....L.KQNEQHIGNRAKAKVVKNKVAPPFRQAEFDIMFGEGISKEGETIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA....L.KQNEQHIGNRAKAKVVKNKVAPPFRQAEFDIMFGEGISKEGETIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEVIGNRTKVVKNKVAPPFKSAEFDIMYGGEGVSKVGEILDVATDLDIQKSGSWFSYQ	307
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KGDDEIIGSETKVVKNKVAPPFRVQFQDIMYGGEGISRMNELLILAEANGFIKKSGAWFSYD	310
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEVVLGNETRKKVKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEVVLGNETRKKVKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS....I.KKGEVVLGNETRKKVKNKVAPPFRQAEFDILYGGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS....I.KKGEDEVGNETKVVKNKVAPPFRQAEIFDILYGGAGVSREGEIIDLGVKAKVVEKSGAWYSYN	302
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA....I.KEGEEVVGNETRIKVVKNKIAAPFKAEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEEVVGNETRIKVVKNKIAAPFKAEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEVVGSETRKKVVKNKVAPPFRQAEFQILYGGKGIYRNGETIDLGVQQGLVEKSGAWYAYK	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEIIGSETKVVKNKMAPPFREAIQILYGGKGVNQLGELVDLAVQQNIVQKAGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEIIGSETKVVKNKMAPPFREAIQILYGGKGTNQLGELVDLAVQQDIVQKAGAWYSYQ	293
consensus	*!!**!* * ** *****!!*!!*!!*!!* * *****!!*** ** ** ** **	

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NTDB id 625 LCA RS02525 WP 011374196.1
 NTDB id 410273 D5E69 RS10500 WP 048003984.1
 NTDB id 115 BSU 16940 NP 389576.2
 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 1313 DR RS12030 WP 010888966.1
 NTDB id 1245 Cj1673c YP 002345041.1
 NTDB id 1211 C694 RS00795 WP 000963128.1
 NTDB id 1214 NCTC11637 00359 SQJ03206.1
 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 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



SERIGQGRENAKNYLADHEDVEDEVRLKVR AAYGTS DVP EEDLPT...TED.EQINIL.....PDD 351
 EERLGQGRENAKVFLKENPDIRNEIMLKI RDHYGLDTGRAETEDM...EEM...SLL.....DD. 345
 DEKIGQGRENAKQFLKENKDIMLMIQE QIREHYGLDNNGVVQQA...EETQELEFE.....E.. 348
 DEKIGQGAEKAKNYLKEHQDV FDEIDHKVRAAHGLLDDSEVAETE...EETTAS KTKAKAKKEEKAVETEEIELELED 387
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD...TENKKDE...PKKEEA..VNEEVPLDLGD 380
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD...TENKKDE...PKKEEA..VNEEVPLDLGD 380
 DEKIGQGS ENAKKYLA EHPEIFDEIDKQVRSKFG LIDGEEVSEQD...TENKKDE...PKKEEA..VNEEVPLDLGD 380
 DEKIGQGS ENAKKYLA DNPEIFDEIDHQV RVVQFGLIDGEEIAES.....KKDE...AAQVDS..VNEEVTLDLGD 376
 DEKIGQGS ENAKKYLA DNPEVFAEIDHQV RVVQFGLIDGEEAAES.....KKDE...VAQVDS..VNEEVTLDLGD 376
 GEKIGQGS ENAKRYLADHPQLFDEIDRKV RVVKFGLLEESEEEESAM...AVASE.....E.....TDDLALDLDN 372
 GEKIGQGS ENAKKFLADNPEIFDDIDHKV RVVQYGLIEEDNTEEKQ...SSKEK.....ETDEK..ADKNLVLELDD 377
 DERIGQGKEKTIAYIAERP EMEQEIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA..... 363
 DKKLGQGRENSKAF LKENPEIAD EITKAIQNSMG IEGMI...SGSEDDE..GEE..... 343
 DKKLGQGRENAKALLKEDKALADEITLKI KESIGSNEEI...MPLPDEP..LEEME..... 347
 DKKLGQGRENAKALLKEDKALADEITLKI KESIGSNEEI...MPLPDEP..LEEME..... 347
 DTKLGQGRD TVKELTKDNPELA EEL EAKIREKLQAK..... 343
 GTKIGQGNNAVKWLKENPEIADKLEQEIRNTLASNPN S...VLKATASDSNDES DVEEFS.....EEEL..... 372
 GAKIGQKDNV RVVWLKENPEISDEIDAKIRALNGVEMHI...TEGT...QDET DGERP.....EE..... 348
 GAKIGQKDNV RVVWLKENPEISDEIDAKIRALNGVEMHI...TEGT...QDET DGERP.....EE..... 348
 GAKIGQKDNV RVVWLKENPEISDEIDAKIRALNGVEMHI...TEGT...QDET DGERP.....EE..... 348
 GERIGQGRDNCREFLRENAELAREIENKVREHLG VTPMG...AV.TLAE EVEED..... 352
 GDKIGQK KANACKY LKENPEIAKTL DKKLREMLLN PENM...QLIAETSSAADDVEFGAVP.....EEF..... 354
 GDKIGQK KANACKY LKENPEIAKTL DKKLREMLLN PENM...QLIAETSSAADDVEFGAVP.....EEF..... 354
 GSKIGQK KANA AKYLEENPEIGQEIEQQIRAKLLVTSAN...TKATPVAEDLADADI..... 347
 GNKIGQKKNNVIRYLEENPQISTEIEAVIREQLLTKASD...QTAA.HDETEE EPDLL..E.....S..... 349
 GNKIGQKKNNVIRYFEENNQIAE EIERNIREQLLTTGTN...GAVQ.I.EDEE EPDLL..L.....ES..... 349

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NTDB id	Accession	Sequence	Score
625	LCA RS02525 WP 011374196.1	STEE....	355
410273	D5E69 RS10500 WP 048003984.1	345
115	BSU 16940 NP 389576.2	348
600	KW2 RS01765 WP 011675413.1	387
269	KZH43 RS08665 WP 001085462.1	ELEIEIEE	388
228	SPD RS09265 WP 001085462.1	ELEIEIEE	388
194	SPR RS08825 WP 001085462.1	ELEIEIEE	388
159	SP RS09750 WP 001085462.1	ELEIEIEE	388
499	SM12261 RS08315 WP 078228268.1	ELEIEIEE	384
527	SMSK321 RS11065 WP 001085454.1	ELEIEIEE	384
453	Spy49 1753c ACI62003.1	GIEIED..	378
408	SMU RS09530 WP 002262392.1	TIELED..	383
1313	DR RS12030 WP 010888966.1	363
1245	Cj1673c YP 002345041.1	343
1211	C694 RS00795 WP 000963128.1	347
1214	NCTC11637 00359 SQJ03206.1	347
1334	RAOC RS04870 WP 004918236.1	343
1389	A4U84 RS07560 WP 021112712.1	372
1130	NGFG RS03960 WP 003688695.1	348
1124	NGFG RS03960 WP 003688695.1	348
1123	OK783 RS03845 WP 003688695.1	348
1427	RS RS02760 WP 011000510.1	352
1165	A1552VC RS01565 WP 000344154.1	354
1142	GTF74 RS11550 WP 000344154.1	354
1205	PSJM300 05545 AFN77183.1	347
1022	ACIAD RS06390 WP 004925639.1	349
1074	ABD1 RS10195 WP 000344167.1	349

consensus

- X non conserved
- X similar
- X ≥ 50% conserved