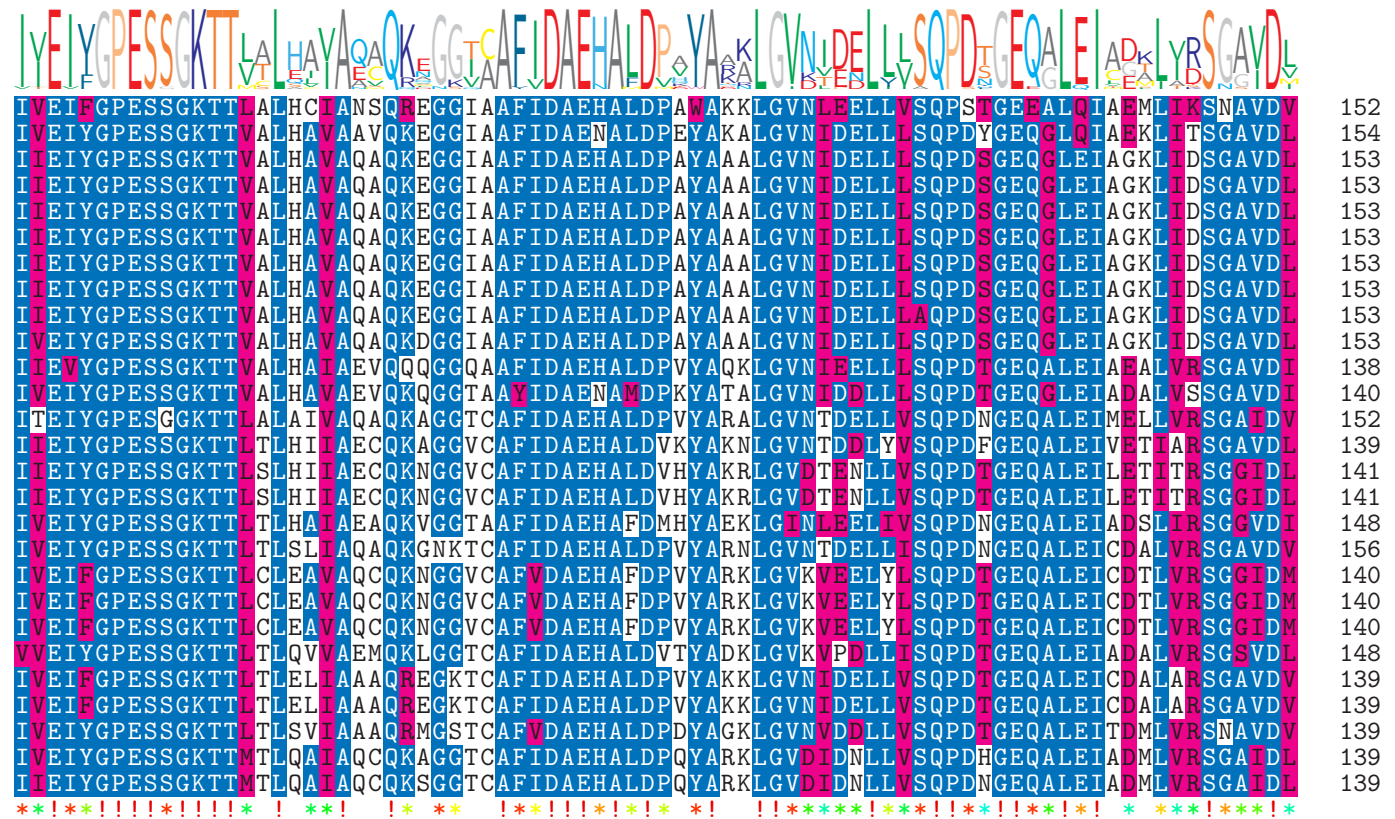


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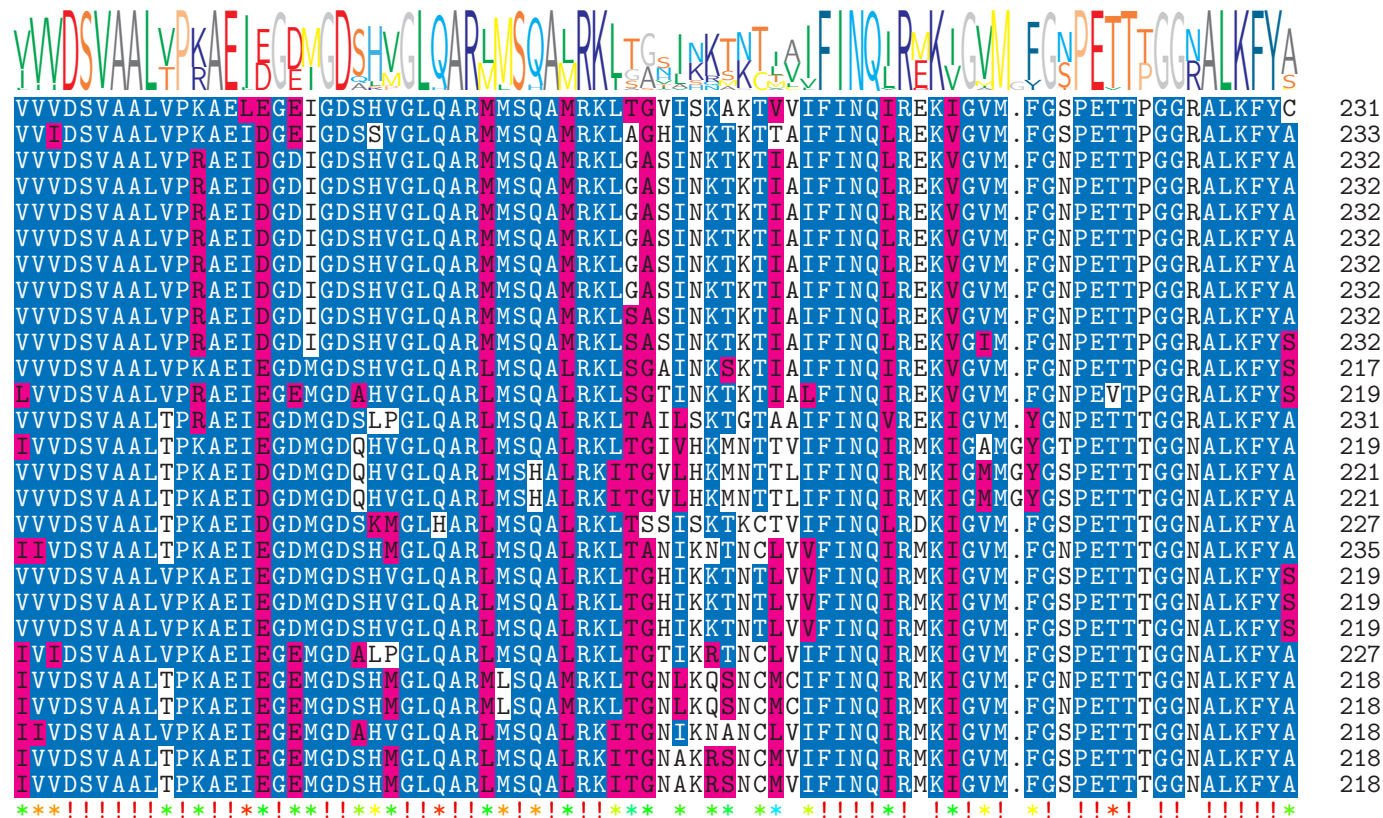
NTDB id 347927 Spb1 RS15650 WP 145302180.1
NTDB id 600 KW2 RS01765 WP 011675413.1
NTDB id 269 KZH43 RS08665 WP 001085462.1
NTDB id 228 SPD RS09265 WP 001085462.1
NTDB id 194 SPR RS08825 WP 001085462.1
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NTDB id 527 SMSK321 RS11065 WP 001085454.1
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NTDB id 1245 Cj1673c YP 002345041.1
NTDB id 1211 C694 RS00795 WP 000963128.1
NTDB id 1214 NCTC11637 00359 SQJ03206.1
NTDB id 1334 RA0C RS04870 WP 004918236.1
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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
consensus

Sequence	Score
. MSPK AKPDKKSAAEVER EHV KL L DN T LG Q IEKAFGRGSIMKLTDA . GMDV D GTGS G ALSLDLALGGKGFPRGR	72
MATKK KTNFDDITKKYGA ERD KALADALALIEKD F GKGSIMRLGEA . ANQKVSV V SSGSLALDIALGAGGYPKGR	74
. MAKK PKKLEEISKKFGA ERE KALNDALKLIEKD F GKGSIMRLGER . AEQKVQVMSSGSLALDIALGSGGYPKGR	73
. MAKK PKKLEEISKKFGA ERE KALNDALKLIEKD F GKGSIMRLGER . AEQKVQVMSSGSLALDIALGSGGYPKGR	73
. MAKK PKKLEEISKKFGA ERE KALNDALKLIEKD F GKGSIMRLGER . AEQKVQVMSSGSLALDIALGSGGYPKGR	73
. MAKK PKKLEEISKKFGA ERE KALNDALKLIEKD F GKGSIMRLGER . AEQKVQVMSSGSLALDIALGSGGYPKGR	73
. MAKK PKKLEEISKKFGA ERE KALNDALKLIEKD F GKGSIMRLGER . AEQKVQVMSSGSLALDIALGSGGYPKGR	73
. MAKK LKKNEEITKKFGD ERR KALDDALK N IEKD F GKGAVMRLGER . AEQKVQVMSSGSLALDIALGAGGYPKGR	73
. MAKR IKKTEEITKKFGD ERR KALDDALK N IEKD F GKGAVMRLGER . AEQKVQVMSSGSLALDIALGAGGYPKGR	73
. MS DR QAALDMALK Q IEK F GKGSIMK L CEK . TDTR I STVPSSGSLALDTALGIGGYPGR	58
. MAKD ER QAALDAALK I EKN F GKGSIMR M CEK . VDTQVSTVSSGSLALDEALGVGGYPGR	60
. MSKDATKEISAPTD AK ERS KATETAM S QIEKAFGKGSIMKLGAE . SKLDVQV V STGSLSLDLALGVGGIPGR	72
. MDDN KR KS L DAALKS L DKT F GKGTILRLCDK . EVEQ I DS I GTGSVGLDLALGIGGVPKGR	59
. MAID DK QK A ISLA I KQIDKV F GKGALVRLCDK . QVEK I DS I STGSLGLDLALGIGGVPKGR	61
. MAID DK QK A ISLA I KQIDKV F GKGALVRLCDK . QVEK I DA I STGSLGLDLALGIGGVPKGR	61
. MAKT ETTSPND KK KALAAVLEK L DKTY G KGTVMK L CDGTVDNH I EV I PSGSLGLDLALGVGGYPKGR	68
. MAENKKSSKNNTV VKQVEPEQK K QALEAALAQIEK F GKGSIMK L QQT . EQLD I ESV I STGSLGLDLALGIGGLPMGR	76
. MSD DK SKALAAALAQIEK S FGKGAIMKMDGSQQUEEN L EV I STGSLGLDLALGVGGLPRGR	60
. MSD DK SKALAAALAQIEK S FGKGAIMKMDGSQQUEEN L EV I STGSLGLDLALGVGGLPRGR	60
. MSD DK SKALAAALAQIEK S FGKGAIMKMDGSQQUEEN L EV I STGSLGLDLALGVGGLPRGR	60
. MEDG K KAASMSA E KQKALAAALAQIEK F GKGSIMK N GD . EVEPVQV V STGSLGLDLALGVGGLPRGR	68
. MDEN K QKALAAALGQIEK F GKGSIMRLCDN . RAMDVET I STGSLSLDIALGAGGLPMGR	59
. MDEN K QKALAAALGQIEK F GKGSIMRLCDN . RAMDVET I STGSLSLDIALGAGGLPMGR	59
. MDEN K KRALAAALGQIEK F GKGAVMR M CDH . DRQA I PS I STGSLGLDIALGIGGLPKGR	59
. MDDN K SKALQAAL S QIEK F GKNTVMRLCDN . TVQAV E AV I STGSLTLDIALGIGGLPKGR	59
. MDEN K SKALQAAL S QIEK F GKNTVMRLCDN . TVQAV E AV I STGSLTLDIALGIGGLPKGR	59

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NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus



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NTDB id 347927 Spb1 RS15650 WP 145302180.1	SVRADVRRLATL....KEG	DVTTGMRMKVKIVKNKVAPPF	RVAEF	DMLSSQG	ISFSGD	LLIDLGVAAR	LID	RS	GS	WFTY	G	306	
NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQ	IGKITKIKVVKNKVAPPF	KVALVDIM	F	GEGISST	GELINIAVEEG	I	IKK	SG	AWFAY	N	312	
NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPF	KEAVVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 228 SPD RS09265 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPF	KEAVVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPF	KEAVVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETN	VGKETKIKVVKNKVAPPF	KEAVVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPF	KEAFVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTN	VGKETKIKVVKNKVAPPF	KEAFVEIMY	GEGISKT	GELLKIASDL	DI	IKK	A	G	AWYSYK		311	
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSN	IGKETKIKVVKNKVAPPF	KVAEVEIMY	GEGISRT	GELVKIASDL	DI	IKK	A	G	AWFSYN		311	
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSN	IGKETKIKVVKNKVAPPF	KEAFVEI	IY	GEGISRT	GELVKIASDL	GI	IKK	A	AWFSYN		311	
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DV	MGNKTKIKVVKNKVAPPF	RTAEVDIMY	GEGISKEGE	IIDL	GT	ELDI	VQK	SG	SWYSYE		292	
NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRAETIKNGT.....DM	IGNRARIKVVKNKVAPPF	KVAEVDIMY	G	QGISRT	GELVDM	AVEKDI	INK	SG	SWYSYG		294	
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGND	AVANTV	KIKTVKNKVAAPF	KEVELALVY	GKGF	DLSDLVGL	A	ADM	DI	IKK	AGS	FYSYG	307
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKVAT....L.KQNEEP	IGNRVKVVKNKVAPPF	RQAEFDV	M	F	GEGLS	REGELIDY	GVKLDI	V	DK	SG	AWFSYK	294
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS....L.KQNEQH	IGNRAKAKVVKNKVAPPF	REAEFDIM	F	GEGISKEGE	I	IDY	GVKLDI	V	DK	SG	AWLSYQ	296
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA....L.KQNEQH	IGNRAKAKVVKNKVAPPF	REAEFDIM	F	GEGISKEGE	I	IDY	GVKLDI	V	DK	SG	AWLSYQ	296
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPF	KSAEFDIMY	GEGVSKVGE	ILDVATDL	DI	I	QK	SG	SW	FSYQ		307
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEI	IGSETKVVKNKVAPPF	REVQFDIMY	GEGISRMNELL	ILAEANG	F	I	KK	SG	AW	FSYD		310
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPF	RQAEFDILY	GEGISWEGEL	IDIGVKN	DI	I	NK	SG	AW	SYN		294
NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPF	RQAEFDILY	GEGISWEGEL	IDIGVKN	DI	I	NK	SG	AW	SYN		294
NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPF	RQAEFDILY	GEGISWEGEL	IDIGVKN	DI	I	NK	SG	AW	SYN		294
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS....I.KKGEV	VGNETKVVKNKVAPPF	REAI	F	DILY	GAGVS	REGE	IIDL	LGVEAK	VVEK	SGAWSYN		302
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPF	KEANTQIMY	G	GFN	REGELID	LG	VKHKM	V	E	K	SGAWSYN	293
NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEEV	VGNETRIKVVKNKIAAPF	KEANTQIMY	G	GFN	REGELID	LG	VKHKM	V	E	K	SGAWSYN	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEV	VGSETRVKNKVAPPF	RQAEFQILY	GKGIY	R	N	GE	IIDL	LG	VQ	GLVEK	SGAWYAYK	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEI	IGSETKVVKNKMAPPF	REAI	FQILY	GKGVN	QLGELVD	LAV	QQN	I	V	QK	AGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEI	VGSETKVVKNKMAPPF	KEAI	FQILY	GKGTN	QLGELVD	LAV	QQD	I	V	QK	AGAWYSYQ	293
consensus	*!!**!* *	*	**	*****!*****!*	*	*****!*****	*****	*****	*****	*****	*****	*****!	

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NTDB id 600 KW2 RS01765 WP 011675413.1
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NTDB id 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
consensus

Sequence	Score
EVKLGQGRDKARIYLEEHPPELMAETIKAKVLELHAAGQHISSSKGE.....	352
DEKIGQGGAEKAKNYLKEHQDVDFEIDHKVRAAHGLDDSEVAETEETETASKTKAKAKKEEKAVETEEIELELED....	387
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGLIDGEEVSEQDTENKKDE...PKKEEA..VNEEVPLDLGDELEIE	385
DEKIGQGSSENAKKYLAADNPEVFAEIDHQVRVQFGLIDGEEAAE...SKKDE...VAQVDS..VNEEVTLDLGDLEIE	381
DEKIGQGSSENAKKYLAADNPEIFDEIDHQVRVQFGLIDGEEIAE...AAQVDS..VNEEVTLDLGDLEIE	381
GEKIGQGSSENAKRYLADHPQLFDEIDRKVRVKFGLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGSSENAKKFLADNPEIFDDIDHKVRVQYGLIEEDNTEEKQSSKEK.....ETDEK..ADKNLVLELDDTIELE	382
EERLGGGRENAAKFLKENKDIMLMIQEIGIREHYGLDNGGVVQQAAETQEEL.EFE.E.....	348
SERIGQGRENAAKLYLADHEDVEIVRLKVRVQYGLSDVPEEDLPTTEDE.QI.NILPDST.....EE.....	355
DERIGQGEKTIAYIAIERPEMEQEIIRDRVMAAIRAGNAGEAPALAPAPAAPEAAE..A.....	363
DKKLGQGRNSKAFLEKNEPEIADAITKAIQNSMGIEGMI....SGSEDDE..GE..E.....	343
DKKLGQGRNSKAFLEKNEPEIADAITKAIQNSMGIEGMI....MPLPDEP..LE..EME.....	347
DKKLGQGRNSKAFLEKNEPEIADAITKAIQNSMGIEGMI....MPLPDEP..LE..EME.....	347
DTKLGGGRDTPVKELIKDNPPELAELEAKIREKLQAK.....	343
GTKIGQGGKNNAVKWLKENPEIADKLEQEIIRNTLASNPNS....VLKATASDSND..ESDVVEEFSEEEEL..	372
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
GAKIGQGGKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGT.....Q..DETDERPEE.....	348
GERIGQGRDNCREFLNARNAELARIEIENKVRHLGVTPMG....AV.TLAEVEEVE..D.....	352
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GDKIGQGGKANACKYLKENPEIAKTLDDKKLREMLLNPNEM....QLIAETSSAAD..DVEFGAVPEEF.....	354
GSKIGQGGKANAAKYLEENPEIGQIEEQIRAKLLVTSAN....TKATPVAEDLA..DADI.....	347
GNIKIGQGGKNNVIRYLEENPEIISTEIEAVIREQLLTKASD....QTA..HDETEE..EPDLL..ES.....	349
GNKIGQGGKNNVIRYLEENPEIISTEIEAVIREQLLTKASD....QTA..HDETEE..EPDLL..LES.....	349

logo

		IEE	
NTDB id 347927 Spb1 RS15650 WP 145302180.1	...	352	
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NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388	
NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384	
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384	
NTDB id 453 Spy49 1753c ACI62003.1	D..	378	
NTDB id 408 SMU RS09530 WP 002262392.1	D..	383	
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NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
consensus			

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