

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 625 LCA RS02525 WP 011374196.1
NTDB id 241897 CGP85 RS06195 WP 000368166.1
NTDB id 115 BSU 16940 NP 389576.2
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 1022 ACIAD RS06390 WP 004925639.1
NTDB id 1074 ABD1 RS10195 WP 000344167.1
NTDB id 1205 PSJM300 05545 AFN77183.1
consensus



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NTDB id 600 KW2 RS01765 WP 011675413.1	SVRLDVRGSTKIEEGS.GDNKTQIGKITKIKVVKNKVAPPFKEAVALVDIMFGEGISSTGELINIAVEEGITIKKSGAWFAYN	312
NTDB id 269 KZH43 RS08665 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNKGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
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NTDB id 194 SPR RS08825 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNKGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 159 SP RS09750 WP 001085462.1	SVRLDVRGNTQIKGTG.DQKETNKGKETKIKVVKNKVAPPFKEAVVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 499 SM12261 RS08315 WP 078228268.1	SVRLDVRGSTQIKGTG.DQKDTNKGKETKIKVVKNKVAPPFKEAFVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 527 SMSK321 RS11065 WP 001085454.1	SVRLDVRGSTQIKGTG.DQKDTNKGKETKIKVVKNKVAPPFKEAFVEIMYEGEGISKTGELLKIASDLDIKKAGAWYSYK	311
NTDB id 453 Spy49 1753c ACI62003.1	SVRLDVRGTTQIKGTG.DQKDSIGKETKIKVVKNKVAPPFKEAEVEIMYEGEGISRTGELVKIASDLDIQKAGAWFSYN	311
NTDB id 408 SMU RS09530 WP 002262392.1	SVRLDVRGNTQIKGTG.EQKDSNIGKETKIKVVKNKVAPPFKEAFVEIIMYEGEGISRTGELVKIASDLGIQKAGAWYSYN	311
NTDB id 625 LCA RS02525 WP 011374196.1	TVRLEVRRRAETIKNGT.....DMIGNRARIKVVKNKVAPPFKEAEVDIMYGGGISRTGELVDMAVEKDIINKSGSWYSYG	294
NTDB id 241897 CGP85 RS06195 WP 000368166.1	SVRLEVRRAEQLKQGQ.....EIVGNRTKIKVVKNKVAPPFRVAEVDIMYGGGISKEGELIDLGVENDIVDKSGAWYSYN	293
NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DVMGNKTKIKVVKNKVAPPFRTAEVDIMYEGEGISKEGETIIDLGTELIDIVQKSGSWYSYE	292
NTDB id 1313 DR RS12030 WP 010888966.1	SVRLDVRKIGQ....PTKVGNDAAVANTVKIKTVKNKVAAPFKEVELALVYGKGFQDQLSDLVGLAADMDIINKAGSFYSYG	307
NTDB id 1245 Cj1673c YP 002345041.1	SVRLDVRKVAT....L.KQNEEPIGNRVKVVKNKVAPPFRQAEFDVMFGEGLSREGELIDYGVKLDIVDKSGAWFSYK	294
NTDB id 1211 C694 RS00795 WP 000963128.1	SVRIDIRRIAS....L.KQNEQHIGNRAKAKVVKNKVAPPFREAEFDIMFGEGISKEGETIIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1214 NCTC11637 00359 SQJ03206.1	SVRIDIRRIAA....L.KQNEQHIGNRAKAKVVKNKVAPPFREAEFDIMFGEGISKEGETIIDYGVKLDIVDKSGAWLSYQ	296
NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEVIGNRTKVVVVKNKVAPPFKSAEFDIMYEGEGVSKVGEILDVATDLDIQKSGSWFSYQ	307
NTDB id 1389 A4U84 RS07560 WP 021112712.1	SVRLDIRRCGV....V.KDGDEIIGSETKVVVVKNKVAPPFREVEQFDIMYEGEGISRMNELLILAEANGFIKKSGAWFSYD	310
NTDB id 1130 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEVVLGNETRKKVKNKVAPPFRQAEFDILYEGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
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NTDB id 1123 OK783 RS03845 WP 003688695.1	SVRLDIRRTGS....I.KKGEVVLGNETRKKVKNKVAPPFRQAEFDILYEGEGISWEGELIDIGVKNDIINKSGAWYSYN	294
NTDB id 1427 RS RS02760 WP 011000510.1	SVRLDIRRIGS....I.KKGEDEVGNETKVVVVKNKVAPPFREAIFFDILYGAGVSREGEIIDLGVEAKVVEKSGAWYSYN	302
NTDB id 1165 A1552VC RS01565 WP 000344154.1	SVRLDIRRTGA....I.KEGEEVVGNETRIKVVKNKIAAPFKEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1142 GTF74 RS11550 WP 000344154.1	SVRLDIRRTGA....I.KEGEEVVGNETRIKVVKNKIAAPFKEANTQIMYGGGFNREGELIDLGVKHKMVEKSGAWYSYN	293
NTDB id 1022 ACIAD RS06390 WP 004925639.1	SVRLDIRRIGQ....V.KEGDEIIGSETKVVVVKNKMAPPFREAIFFQILYGKGYNQLGELVDLAVQQNIVQKAGAWYSYQ	293
NTDB id 1074 ABD1 RS10195 WP 000344167.1	SVRLDIRRIGQ....V.KEGDEIIGSETKVVVVKNKMAPPFREAIFFQILYGKGYNQLGELVDLAVQQNIVQKAGAWYSYQ	293
NTDB id 1205 PSJM300 05545 AFN77183.1	SVRLDIRRTGA....V.KEGDEVVGSETRVVVVKNKVAPPFRQAEFFQILYGKGIIYRNGEIIDLGVQQGLVEKSGAWAYK	293
consensus	*!!**!* * ** *****!*****!!*!!*!!* * *****!*!*** ***** ** ***** ! !*****!	

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DEKIGQGS	ENAKKYLA	AH	PEIF	FEID	KQV	RSK	FG	LIDGE	EV	SEQD	TENK	KDE	...	PKKEEA	..	VNEEV	PLDL	GD	DELEIE	385																			
DEKIGQGS	ENAKKYLA	AH	PEIF	FEID	KQV	RSK	FG	LIDGE	EV	SEQD	TENK	KDE	...	PKKEEA	..	VNEEV	PLDL	GD	DELEIE	385																			
DEKIGQGS	ENAKKYLA	AH	PEIF	FEID	KQV	RSK	FG	LIDGE	EV	SEQD	TENK	KDE	...	PKKEEA	..	VNEEV	PLDL	GD	DELEIE	385																			
DEKIGQGS	ENAKKYLA	AH	PEIF	FEID	KQV	RSK	FG	LIDGE	EV	SEQD	TENK	KDE	...	PKKEEA	..	VNEEV	PLDL	GD	DELEIE	385																			
DEKIGQGS	ENAKKYLA	AD	NPEIF	FEID	HQV	RV	QF	LIDGE	EE	IAES	...	KKDE	...	AAQVDS	..	VNEEV	TLDL	GD	DELEIE	381																			
DEKIGQGS	ENAKKYLA	AD	NPEV	FA	IED	HQV	RV	QF	LIDGE	EE	AAES	...	KKDE	...	VAQVDS	..	VNEEV	TLDL	GD	DELEIE	381																		
GEKIGQGS	ENAKRYL	AD	HP	Q	FEID	RK	VR	VK	FG	LEE	SEES	AM	AVASE		E		TDDL	AL	DL	NGIEIE	377																		
GEKIGQGS	ENAKKFL	AD	NPEIF	DD	ID	HK	VR	VQ	GL	IED	NTE	EK	QSSKEK		ETDEK	..	ADKN	LV	LE	DDTIELE	382																		
SERIGQGR	ENAKNYL	AD	HED	VE	VR	LK	VRA	AY	G	ISD	V	PEED	LP	TT	DE	QIN	IL	P	DD	STEE		355																	
GERMGQGS	KEN	V	KMYL	KEN	P	Q	I	KEE	I	DR	K	RE	KL	G	ISD	G	V	E	E	T	E	DA	..	PKSL	F	DEE		347											
EERLGG	REN	AK	QFL	KEN	D	IM	L	IQE	Q	I	RE	HY	G	L	DN	NG	V	V	Q	Q	A	E	E	T	E	E	E		348										
DERIGQG	KEK	TI	AY	IA	ER	PE	ME	Q	E	I	R	D	R	V	MAA	A	I	R	A	G	N	A	G	E	A	P	A	P	A		363								
DKKLGG	RENSK	AF	L	KEN	PEI	AD	EIT	K	A	I	Q	N	S	M	G	I	E	G	M	I		SG	SEDD	..	E	G	E		343										
DKKLGG	REN	AK	L	KED	K	AL	AD	EIT	L	K	I	K	E	S	I	G	S	N	E	E	I		MPL	P	D	E	..	P	L	E	E	M	E		347				
DKKLGG	REN	AK	L	KED	K	AL	AD	EIT	L	K	I	K	E	S	I	G	S	N	E	E	I		MPL	P	D	E	..	P	L	E	E	M	E		347				
DTKLGG	R	D	T	V	KEL	I	K	D	N	P	E	L	A	E	E	L	E	A	K	I	R	E	K	L	Q	A	K		343										
GKIGQG	KNN	AV	K	L	KEN	PEI	AD	K	L	E	Q	E	I	R	N	T	L	A	S	N	P	N	S		V	L	K	A	T	A	S	D	S	N	D	E	S		372
GAKIGQG	KDN	VR	V	L	KEN	PEI	S	DEI	D	A	K	I	R	A	L	N	G	V	E	M	H	I		T	E	G	T	Q	D	E	T	D	G	E	R		348		
GAKIGQG	KDN	VR	V	L	KEN	PEI	S	DEI	D	A	K	I	R	A	L	N	G	V	E	M	H	I		T	E	G	T	Q	D	E	T	D	G	E	R		348		
GAKIGQG	KDN	VR	V	L	KEN	PEI	S	DEI	D	A	K	I	R	A	L	N	G	V	E	M	H	I		T	E	G	T	Q	D	E	T	D	G	E	R		348		
GERIGQ	R	D	N	C	R	E	F	L	R	E	N	A	E	L	A	R	E	I	E	N	K	V	R	E	H	L	G	V	T	P	M	G		352					
GDKIGQG	KAN	ACK	YL	KEN	PEI	AKT	L	D	K	K	R	E	M	L	L	N	P	E	N	M		Q	L	I	A	E	T	S	S	A	A	D	D	V	E				

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consensus			

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