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NTDB id 625 LCA RS02525 WP 011374196.1
NTDB id 1165355 ACE4RD RS11635 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
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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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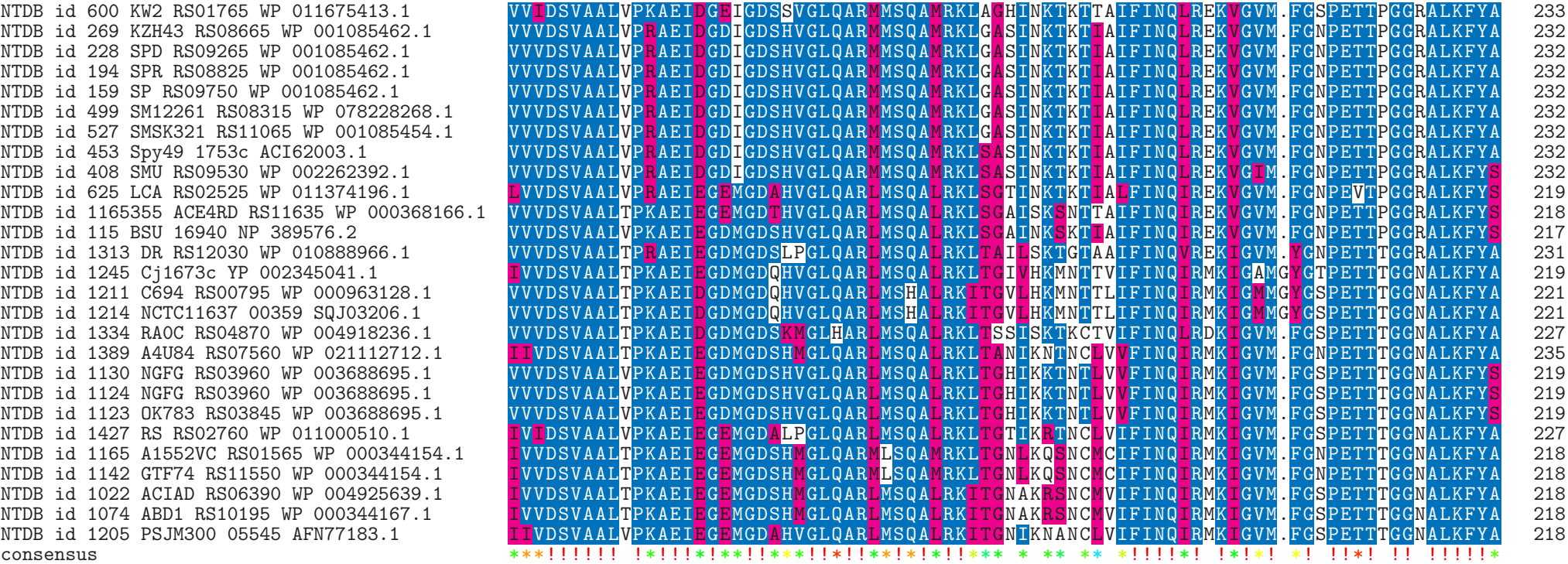
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IY	EI	YG	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	A	V	Q	K	E	G	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	K	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	Y	G	E	Q	G	L	I	A	E	K	L	I	T	S	G	A	V	D	L	
I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	K	E	G	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L
I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	K	E	G	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L
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I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	K	E	G	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L
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I	E	I	Y	G	P	E	S	S	G	K	T	T	V	A	L	H	A	V	A	Q	K	E	G	G	I	A	F	D	A	E	H	A	L	D	P	Y	A	A	A	L	G	V	N	I	D	E	L	L	S	Q	P	D	S	G	E	Q	G	L	E	I	A	G	K	L	I	D	S	G	A	V	D	L
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logo



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Sequence	Score
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DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAEHPEIF DEID KQVRSKF LIDGEEVSEQDTEN KKDE ...PKKEEA...VNEEVPLDLGDELEIE	385
DEKIGQGS ENAKKYLAADNPEIF FEID HQVRVQF LIDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDLEIE	381
DEKIGQGS ENAKKYLAADNPEIF FEID HQVRVQF LIDGEEIAES...KKDE...AAQVDS...VNEEVTLDLGDLEIE	381
GEKIGQGS ENAKRYLADHPQLF FEID RKVRVKF GLLEESEESAMAVASE.....E.....TDDLALDLNGIEIE	377
GEKIGQGS ENAKKFLADNPEIF DDID HQVRVQY GLIEEDNTEEKQSSKEK.....ETDEK...ADKNLVLELDDTIELE	382
SERIGQGR ENAKNYLADHEDVE DEV RLKVR AAYGISDVPEEDLPTTEDEQINILPDDSTEE.....	355
GERMGQG KENVKMYLKENPQIKEE ID RKLREKL GISDGDVEETEDA...PKSLFDEE.....	347
EERLGG RENAKQFLKENK IMLM IQEQIREHY GLDNNGVVQQAAETQEELEFEE.....	348
DERIGQG EKTIAYIAERPEMEQ EIRDRVMAAIRAGNAGEAPALAPAPAAPEAAEA.....	363
DKKLGG RENSKAF LKENPEIAD EITKAIQNSM GIEGMI....SGSEDD..EGEE.....	343
DKKLGG RENAKALLKEDKAL AD EITLKIKESIG SNEEI....MPLPDE..PLEEME.....	347
DKKLGG RENAKALLKEDKAL AD EITLKIKESIG SNEEI....MPLPDE..PLEEME.....	347
DTKLGG RD TVKELIK DNPELA ELEAKIREKLQAK.....	343
GKIGQG KNN AVKWLKENPEIAD KLEQEI RNTLASNPNS....VLKATASDSNDESD..VEEFSEEEL.....	372
GAKIGQG KDNVRVWLKENPEIS DEIDAKIRALN GVEMHITEGTQDET DGERPEE.....	348
GAKIGQG KDNVRVWLKENPEIS DEIDAKIRALN GVEMHITEGTQDET DGERPEE.....	348
GAKIGQG KDNVRVWLKENPEIS DEIDAKIRALN GVEMHITEGTQDET DGERPEE.....	348
GERIGQ RD NCREFL RNAELAR EIENK VREHL GVTPMG....AVTLA.EEEVE.....	352
GDKIGQG KANACKYLKENPEIAKT LDKKLREMLLN PNEMQLIAETSSAADDVE..FGAVPEEF.....	354
GDKIGQG KANACKYLKENPEIAKT LDKKLREMLLN PNEMQLIAETSSAADDVE..FGAVPEEF.....	354
GNKIGQG KNN VIRYLEENPQISTEIEAVIREQLLT TKASDQTAA.HDETEEEP D ..LL..ES.....	349
GNKIGQG KNN VIRYFEENNQIAEIEIERNIREQLLT TGTNGAVQ.I.EDEEEP D ..LL..LES.....	349
GSKIGQ KANA AKY LE NPQIEEQIRAKLL VT SAN....TKATPVAEDLADAD..I.....	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1	... 387
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
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	... 349
NTDB id 1205 PSJM300 05545 AFN77183.1	... 347
consensus	

-  non conserved
-  similar
-  ≥ 50% conserved