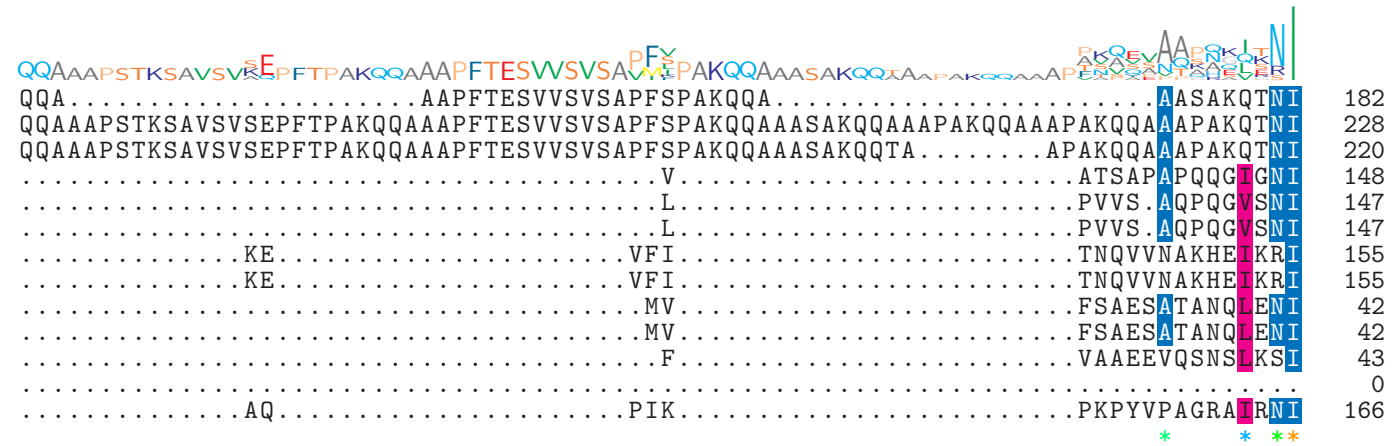


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NTDB id 1100 NMB RS09455 WP 002225652.1
NTDB id 1092 CAD91899.1 1..2286( )
NTDB id 1009 ACIAD RS15175 WP 004923730.1
NTDB id 1052 ABD1 RS15850 WP 001017033.1
NTDB id 1039 HON27 RS01460 WP 031993779.1
NTDB id 1284 ACE17W RS12370 WP 010946666.1
NTDB id 1257 GC085 RS04855 WP 163621000.1
NTDB id 1186 GTF74 RS01320 WP 000788426.1
NTDB id 1175 A1552VC RS12105 WP 000788426.1
NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 357191 E5221 RS26365 WP 082044629.1
NTDB id 1193 PAKAF RS26665 WP 003161249.1
consensus

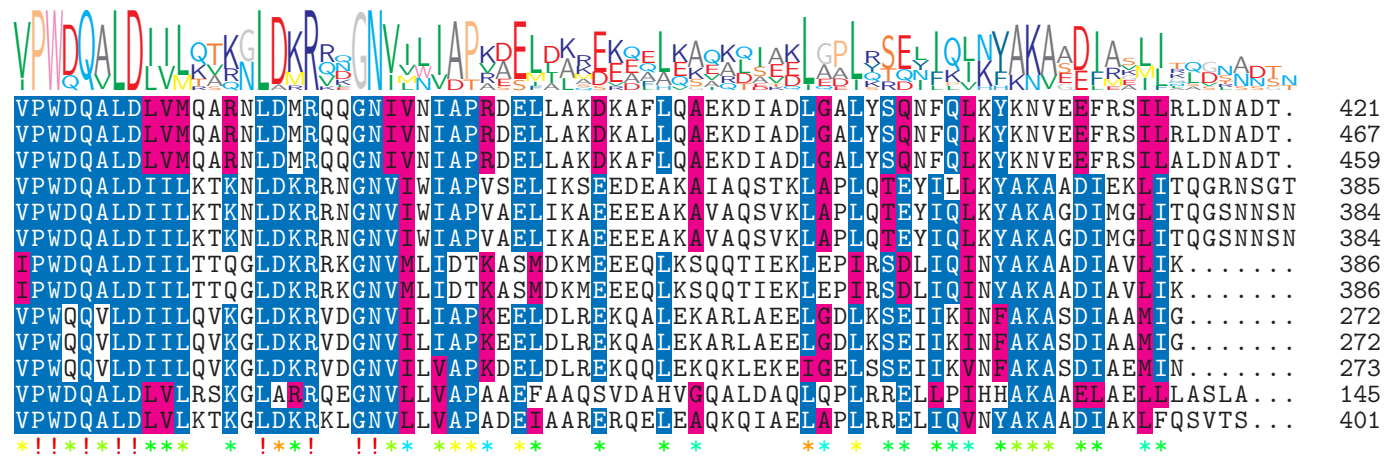
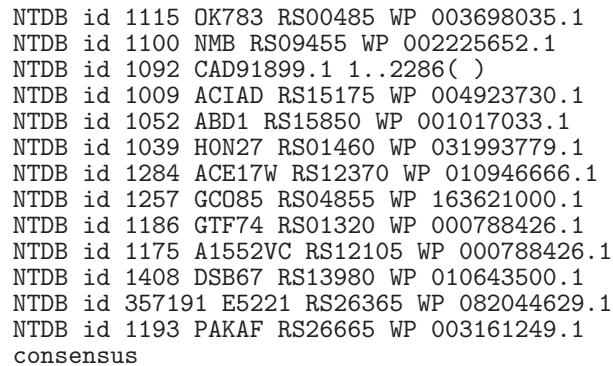
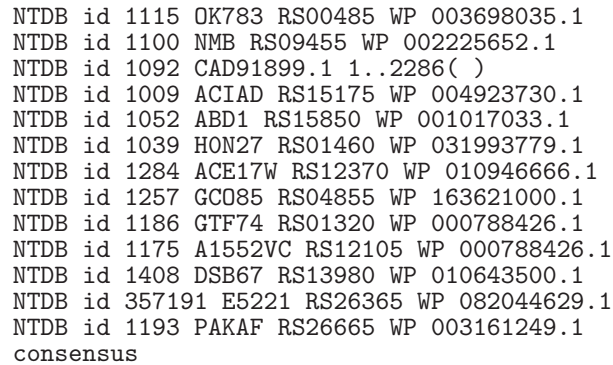
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NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 357191 E5221 RS26365 WP 082044629.1
NTDB id 1193 PAKAF RS26665 WP 003161249.1
consensus

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NTDB id	1115	OK783	RS00485	WP	003698035.1		TGNRNTLVSGRGSVLIDPATNTLIIVTDTRSVIEKFRKLIDEVDVPAQVMIEARIVE	478
NTDB id	1100	NMB	RS09455	WP	002225652.1		TGNRNTLISGRGSVLIDPATNTLIIVTDTRSVIEKFRKLIDEVDVPAQVMIEARIVE	524
NTDB id	1092	CAD91899.1	1..2286()				TGNRNTLVSGRGSVLIDPATNTLIIVTDTRSVIEKFRKLIDEVDVPAQVMIEARIVE	516
NTDB id	1009	ACIAD	RS15175	WP	004923730.1	SNSN.....TNGSATVEPLGDSVGTLSPRGITSLDPRNTLIINDTSQKIDQIRKMIDLIDIPVKQMIEARIVR	456	
NTDB id	1052	ABD1	RS15850	WP	001017033.1	GLQHTSGGGTSTSTNLNTGVDSLGNVGSLLSPRGITITQDDRTNTLIINDTAQSIDIQIRKMIDLIDVQVKQVMVEARIVR	464	
NTDB id	1039	HON27	RS01460	WP	031993779.1	GLQHTSGGGTSTSTNLNTGVDSLGNVGSLLSPRGITITQDDRTNTLIINDTAQSIDIQIRKMIDLIDVQVKQVMVEARIVR	464	
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NTDB id	1257	GCO85	RS04855	WP	163621000.1		.DKQNSSLSDRGKISVDARTNTIIWIQDTGTKIEEVRELIKQLDIPVKQVLIEARIVE	442
NTDB id	1186	GTF74	RS01320	WP	000788426.1		.GEGNVNMLSERGSISIDERTNSLLIRELPDNIAVIREIIIESLDIPVKQVQIEARIVT	329
NTDB id	1175	A1552VC	RS12105	WP	000788426.1		.GEGNVNMLSERGSISIDERTNSLLIRELPDNIAVIREIIIESLDIPVKQVQIEARIVT	329
NTDB id	1408	DSB67	RS13980	WP	010643500.1		.GEGNISMLSDRGSMITIDERTNSLLIRELPENIEVIREIIIESLDIPVKQVQIEARIVT	330
NTDB id	357191	E5221	RS26365	WP	082044629.1		...DDGILTGRGSLSVDERTNTLVVHQPADRLAELRRQLVAQLDVVPVRQVAIEARIVE	199
NTDB id	1193	PAKAF	RS26665	WP	003161249.1		DGGQEKGEGGRGSITVDDRNTNSIIAYQQPERLDELRRIVSQLDIPVRQVMIEARIVE	458
consensus							* * * * *	

NTDB	id	1115	OK783	RS00485	WP	003698035.1	AADGFSRD	LGVKFG	CATGRKKLKN	ETSAF		GWGVNS		GFGGGDK	WEAQT	..K	INLP	VA	...	531				
NTDB	id	1100	NMB	RS09455	WP	002225652.1	AADGFSRD	LGVKFG	CATGKKKLKN	DTSAF		GWGVNS		GFGGDDK	WGAET	..K	INLP	PIT	...	577				
NTDB	id	1092	CAD91899.1	1..2286()			AADGFSRD	LGVKFG	CATGKKKLKN	DTSAF		GWGVNS		GFGGDDK	WGAET	..K	INLP	PTT	...	569				
NTDB	id	1009	ACIAD	RS15175	WP	004923730.1	ATTSFSKEM	GKVKWG	ILSQGINQNS	NLLVGS		ETTLW	NLRNPDSN		GTYYT	IERPDN	LNV	DLG	...	516				
NTDB	id	1052	ABD1	RS15850	WP	001017033.1	ASTSF	TKELGVK	WG	ILSQGITNNNN	LVLVGS		ETTLW	NLRPEPKDET	..T...	GGYKYT	IERPDN	LNV	DLG	...	529			
NTDB	id	1039	HON27	RS01460	WP	031993779.1	ASTSF	TKELGVK	WG	ILSQGITNNNN	LVLVGS		ETTLW	NLRPEPKDET	..T...	GGYKYT	IERPDN	LNV	DLG	...	529			
NTDB	id	1284	ACE17W	RS12370	WP	010946666.1	VTKDFSQD	ICIRW	CVSRP	THL	S...	G.....		TLEGANELARGT	PANV	PLER	..RLN	LDL	AAAP	...	497			
NTDB	id	1257	GC075	RS04855	WP	163621000.1	VTKDFSQD	ICIRW	CVSRP	THL	S...	G.....		TLEGANELARGT	PANV	PLER	..RLN	LDL	AAAP	...	497			
NTDB	id	1186	GTF74	RS01320	WP	000788426.1	VKEGNLE	ELGVR	WGMSTNGS	...	HSVG	GSIES		NLWQKGL	LAD		DEFP	VDE	..FLNV	NLA	...	383		
NTDB	id	1175	A1552VC	RS12105	WP	000788426.1	VKEGNLE	ELGVR	WGMSTNGS	...	HSVG	GSIES		NLWQKGL	LAD		DEFP	VDE	..FLNV	NLA	...	383		
NTDB	id	1408	DSB67	RS13980	WP	010643500.1	INEGNMDE	LGVR	WGFTS	SINGS	...	HTVG	GSIE		NLATIGLYD	GGGEGDDG	...	GSSV	GID	..FLNV	NLA	...	392	
NTDB	id	357191	E5221	RS26365	WP	082044629.1	ANVDY	EKSLGVR	WGPLYVES					PRPGK	DL	..FV	DLG	VE	...	234				
NTDB	id	1193	PAKAF	RS26665	WP	003161249.1	ANVGDK	SLGVR	WGGAYH	KGN	...WSGY	GK	DGNIGIK	DE	GMNCGPI	AGSCTF	PTT	...GTSK	SPSP	..FV	DLG	AK	...	526
consensus																								
							*	*****	!*	***!		*		*			*							

NTDB id 1115	OK783	RS00485	WP 003698035.1	AAANSISLVRAISSGALNLELSASESLSKTTKTLANPRVLTQNRKEAKIESGYEIPFTVTTASGGNSTNTELKKA	606							
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NTDB id 1284	ACE17W	RS12370	WP 010946666.1	LTGATPASVGIALAKLNDNILLDLELSALESEGRAELISSPRLITTNQQAAVIESGEEIPYQEATSSGAT...AVAFKKA	574							
NTDB id 1257	GC085	RS04855	WP 163621000.1	LTGATPASVGIALAKLNDNILLDLELSALESEGRAELISSPRLITTNQQAAVIESGEEIPYQEATSSGAT...AVAFKKA	574							
NTDB id 1186	GTF74	RS01320	WP 000788426.1	STSANASSIAFQVAKLGSCTLDDLELSALQNESKAEIISSPRLITTNKKPAYIEQGTEIPYLESSSSGAS...TVAFKKA	460							
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NTDB id 357191	E5221	RS26365	WP 082044629.1	RVGGSIGLGLLRGDVILLDLELSAMEKSGNGEIIISQPKVVTTADKETARILKGEVVPYQETS KSGAT...SVAFREAE	306							
NTDB id 1193	PAKAF	RS26665	WP 003161249.1	DATSGIGLGFITDNILLDLQLSAMKEKTGNCEIVSQPKVVTTADKETARILKGEVVPYQEASSGAT...STSFKEA	598							
consensus				* * * * *	* * * *	* ! * ! * ! * ! *	* * * * *	* * * * *	* ! * * * ! * ! * *	* * * * *	* * * * *	* * * * *


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NTDB id 1115 OK783 RS00485 WP 003698035.1
NTDB id 1100 NMB RS09455 WP 002225652.1
NTDB id 1092 CAD91899.1 1..2286( )
NTDB id 1009 ACIAD RS15175 WP 004923730.1
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NTDB id 1408 DSB67 RS13980 WP 010643500.1
NTDB id 357191 ES221 RS26365 WP 082044629.1
NTDB id 1193 PAKAF RS26665 WP 003161249.1
consensus

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logo

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NTDB id 1115 OK783 RS00485 WP 003698035.1
NTDB id 1100 NMB RS09455 WP 002225652.1
NTDB id 1092 CAD91899.1 1..2286( )
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NTDB id 357191 ES221 RS26365 WP 082044629.1
NTDB id 1193 PAKAF RS26665 WP 003161249.1
consensus

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LLSLNVTPSITPDGKIIMKLDISKDSVAGA...APNGELIILNKNNTINTNVLVDNGETVLGGVFEQTTMNSQTKVPFFGD	684
VLSLKVTPQITPDGKIIMDLQINQDTPSPQTFLL..GVPAIITKEIQTNVLVNNGQITVLGGIYKQDKNKVINRIPFFGE	651
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VLSLKVTPQITPDNRLVLDLSVTQDRPGQVVKGTGEAVSIDTQRIGTQVLVNNGETVLGGIFQHSITNSVDKVPPLIGD	549
SLSLEVTNPITPDNKVIIMTVRVTKDEPDYVNAL..NNVPPIRKNEVNAKVRVTGGETIVIGGVYSTSQNNVVDKVPFFGD	384
ALSLEVTNPITPDNRIIVEVKVTKDAPDYQNMML..NGVPPILNKNEVNAKILVNDGETIVIGGVFSTSEQSKSVEKVPFFLGE	676



Sequence	Score
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IPVIGNLFXTRGKKTDRELLIFITPRIMGTAGNSLRY.....	769
IPVIGNLFXTRGKKTDRELLIFITPRIMGTAGNSLRY*.....	761
LPYVGRLFKKTAKSEAKNELLIFVTPRIVNDTIVGNH.....	709
IPVVGRLFRKDKVKSDDKQELLIFVTPRIVNDTLARNH.....	721
IPVVGRLFRKDKVKSDDKQELLIFVTPRIVNDTLARNH.....	721
LPVVGILFSNRQITLKNELLIFITPRIITNALSITTIEGREKDVKYK	698
LPVVGILFSNRQITLKNELLIFITPRIITNALSITTIEGREKDVKYK	698
LPVLGALFRRETYEQMGKSELLIFVTPKVVIQ.....	571
LPVLGALFRRETYEQMGKSELLIFVTPKVVIQ.....	571
LPVLGALFRRETYEQMGKSELLIFVTPKVVIQ.....	580
LPYVGRLFRREDALQEKKSELLVFLTPRIMSDQAIIVSR.....	422
LPYLGRLFREDTVDTRKNELLVFLTPRIMNNQAIAIGR.....	714

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- X non conserved
- X similar
- X > 50% conserved