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		MSXLIIGDRRLGALLDQGYLIDRDLQRALERHREVGGRLAELVLYDQYYSERRIASXIEBDFGIPLVQLHAEVETBPXXK	
NTDB id 1028	TT RS08215 WP 011173991.1	MSVLTIGDKRLGAAALLDAGLLTDEELQRALERHREVGGS LAEVLVDMGLLSERRIAQTIEDRFGIPLVELHRVEIPPVK	80
NTDB id 1306	DR RS10060 WP 027479822.1	.MALSIGDRRLGAILLDQGYLGDNDLQRALERHSEVGGRLADVLDIDSGMVGEKRIARAIEEALGIPLVNLAVQPDPAAAL	79
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NTDB id 1251	GCO85 RS07725 WP 011946523.1	.....	0
NTDB id 1112609	KH007 RS04260 WP 150734768.1	.....	0
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NTDB id 1018	ACIAD RS01685 WP 004920473.1	.....	0
consensus			

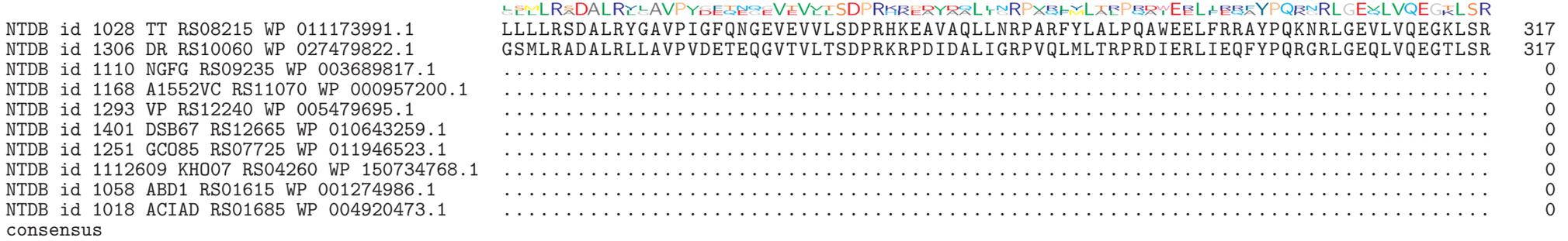
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NTDB id 1306	DR RS10060 WP 027479822.1	RSIRPQTALNLQAFPPFALE..GDRLRVALVDPLSSFSIETLEDDSGFDIEPYQALREEVMWAIATHYPELGLEIVVPSGA	157
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NTDB id 1112609	KH007 RS04260 WP 150734768.1	.....	0
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NTDB id 1018	ACIAD RS01685 WP 004920473.1	.....	0
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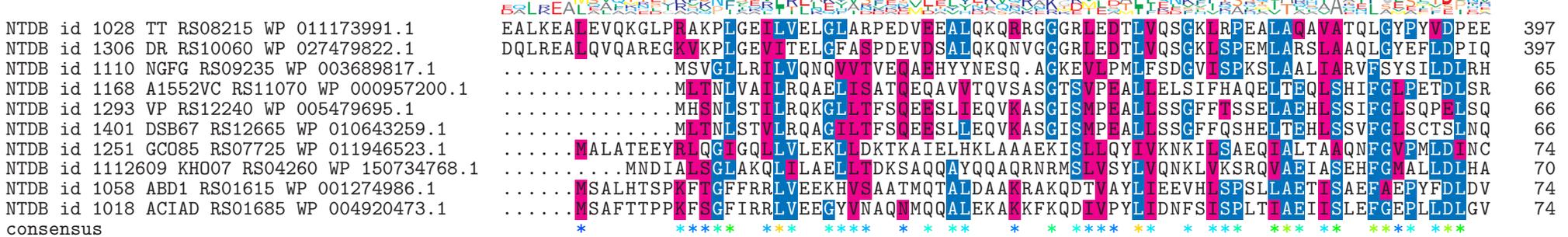
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		SXGSKKLCERLTHGYIIRKLYALYQRTGELCRTLYSRXTREBLYEXLAEQEGTFLFLESTEGIVPDPSSAA	
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NTDB id 1018	ACIAD RS01685 WP 004920473.1	.....	0
consensus			

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