

logo

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NTDB id 601 KW2 RS02615 WP 021036805.1
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NTDB id 287 SP RS11210 WP 001109712.1
NTDB id 377 SMU RS09275 WP 002262344.1
NTDB id 297 STER RS00545 WP 011680614.1
NTDB id 329 STU RS10020 WP 011225298.1
consensus

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logo

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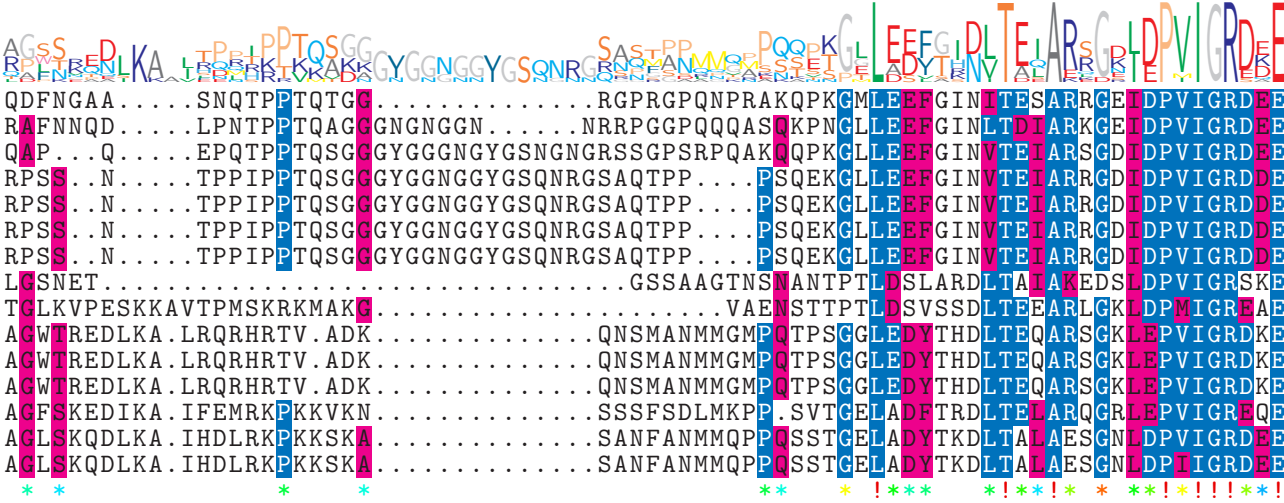
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consensus

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Sequence	Position
...ITHLYTSVNGKQKKQIDLCNCYQ...IMKSGGQEALEFGAGNASNGNSDEPFNPF...NDIFSALQG...	71
...IHLIYANVNGKQKKQIDLCNCYQ...IMKTDPENGPLNHSQQNSSSINPF...F...DDFFGDLLNNF	70
...IHLTYNVNGHQKKQVLDLCNCYQ...IMKTDPNNSLLAGLNQQNRGGRDPF...EDFFNQLGNF	69
...IHLTYNLNGKQKKQIDLCNCYK...IITKTDPNNSLFGKMTDLNNRDFDPF...GDDFNDLNNF	69
...IHLTYNLNGKQKKQIDLCNCYK...IITKTDPNNSLFGKMTDLNNRDFDPF...GDDFNDLNNF	69
...IHLTYNLNGKQKKQIDLCNCYK...IITKTDPNNSLFGKMTDLNNRDFDPF...GDDFNDLNNF	69
...IHLTYNLNGKQKKQIDLCNCYK...IITKTDPNNSLFGKMTDLNNRDFDPF...GDDFNDLNNF	69
GQEMSQTIHYTPRAKKVIELSMDEARKLGHSYVGTETHILLGLIREGEGVAARVLNNLGVSLNKARQQVLQL.....	141
VKVKRSTLRFSPRAFEVMTAASFIAIHNNSEAVGTETHELLYALLQVEDGFGQLLLKL.....QKINIVSLRKETLEKR	143
QDETFTLELPFSRRLQILFDEAEYVASVVHAKVLGTETHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
QDETFTLELPFSRRLQILFDEAEYVASVVHAKVLGTETHVLYAILHDGNALATRILERAGFSYEDKKDQVKIAALRRNLEER	150
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N..DTIMLLERQSHALKRTLAEEAAISQVTHAKEVGTETHVLFAMLLNPNLLATRILELVGFHAKDDGESIRLLDLRKVTERY	154
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ESDIIDLRAQSPALEAMLEAQEIASVTGAVEVGESEHVLMAFLHKLDMVCRLLLEVAGFYQKDDSDKPRIIDLRRSLERN	156

logo

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NTDB id	245	SPD	RS03860	WP	000882517.1
NTDB id	243	SPR	RS03635	WP	000882517.1
NTDB id	241	SP	RS04015	WP	000882523.1
NTDB id	85	BSU	00860	NP	387967.1
NTDB id	610	V4T04	RS10165	WP	012897346.1
NTDB id	290	KZH43	RS10025	WP	001109677.1
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NTDB id	377	SMU	RS09275	WP	002262344.1
NTDB id	297	STER	RS00545	WP	011680614.1
NTDB id	329	STU	RS10020	WP	011225298.1
consensus					



132
139
141
138
138
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188
201
214
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214
218
221
221

logo

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consensus					



212
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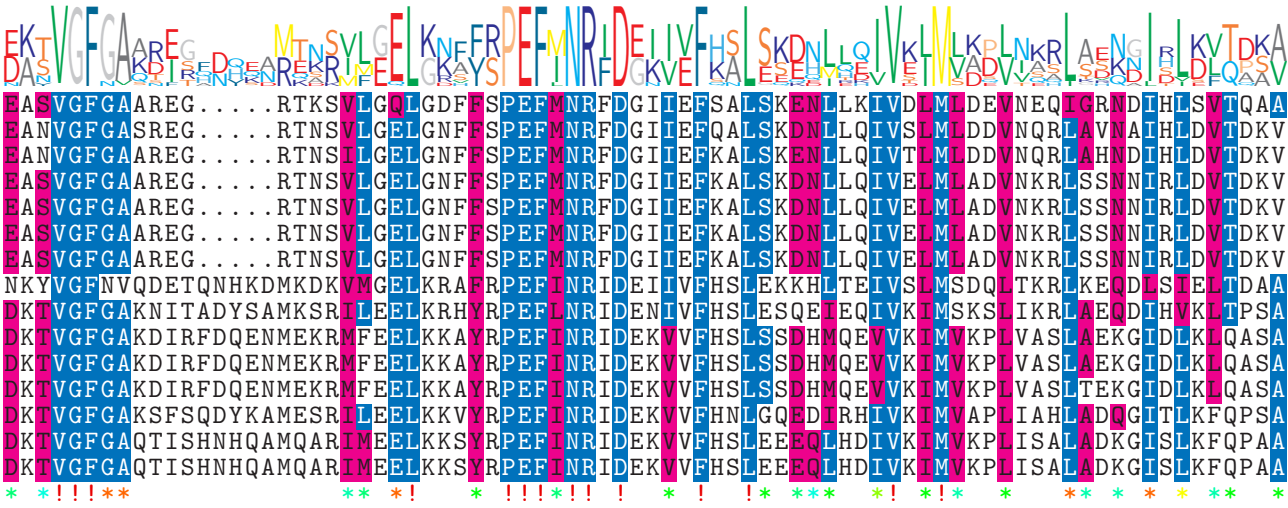
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consensus



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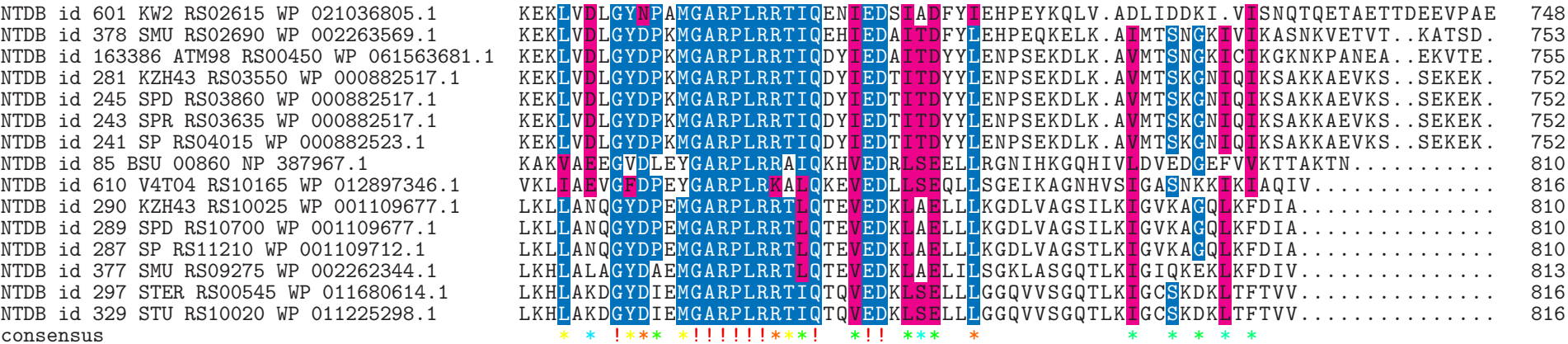
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consensus



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685
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756
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logo



 non conserved
 similar
 ≥ 50% conserved