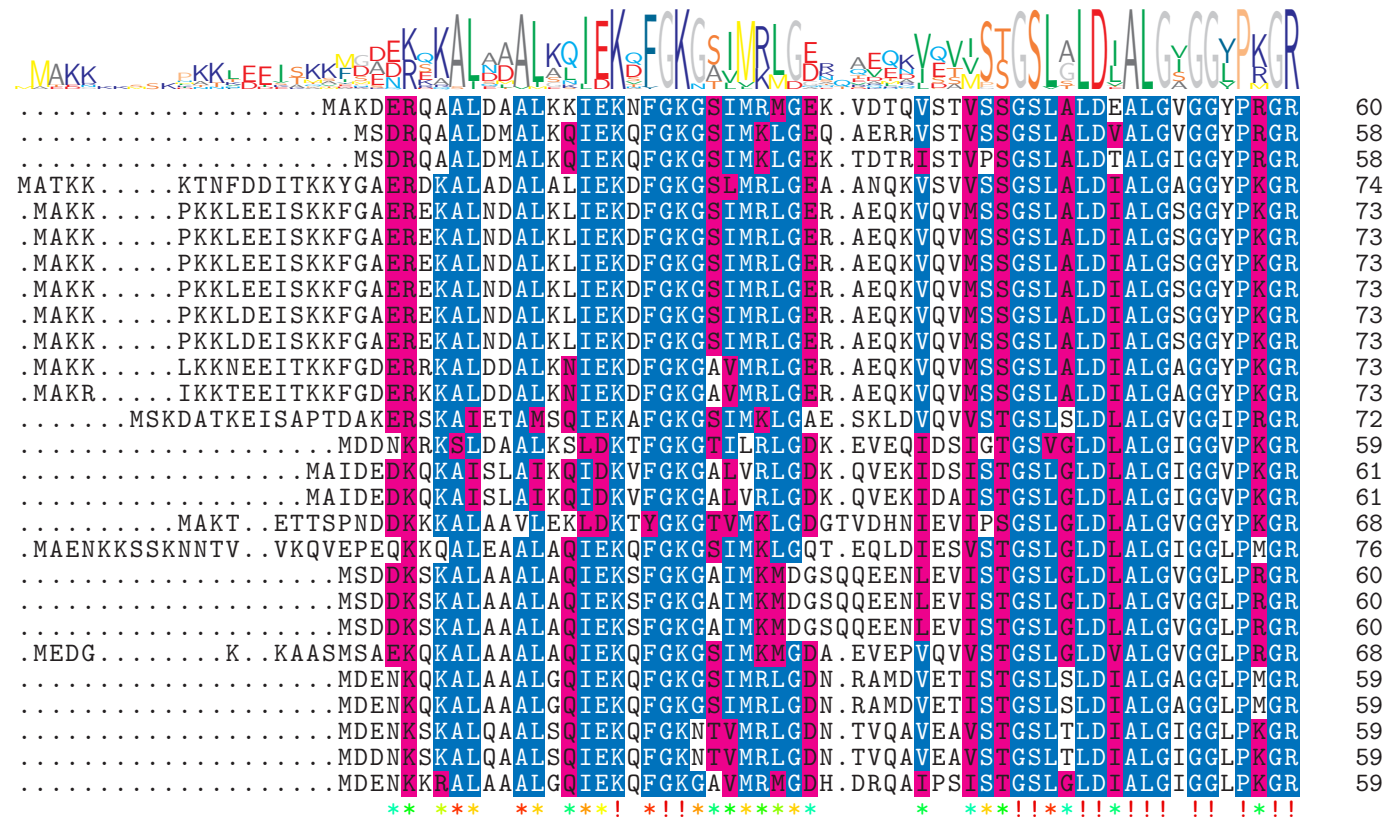


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consensus

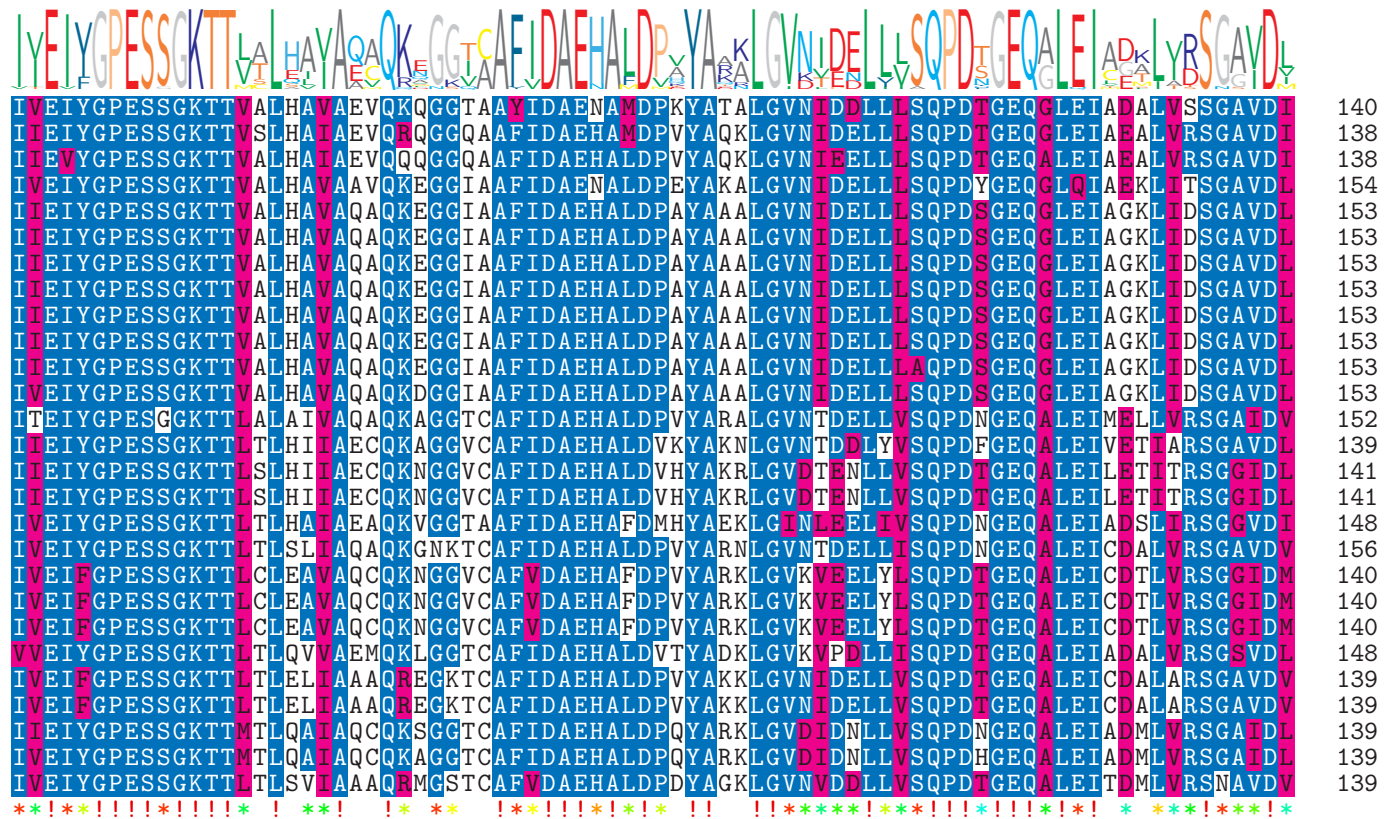
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consensus

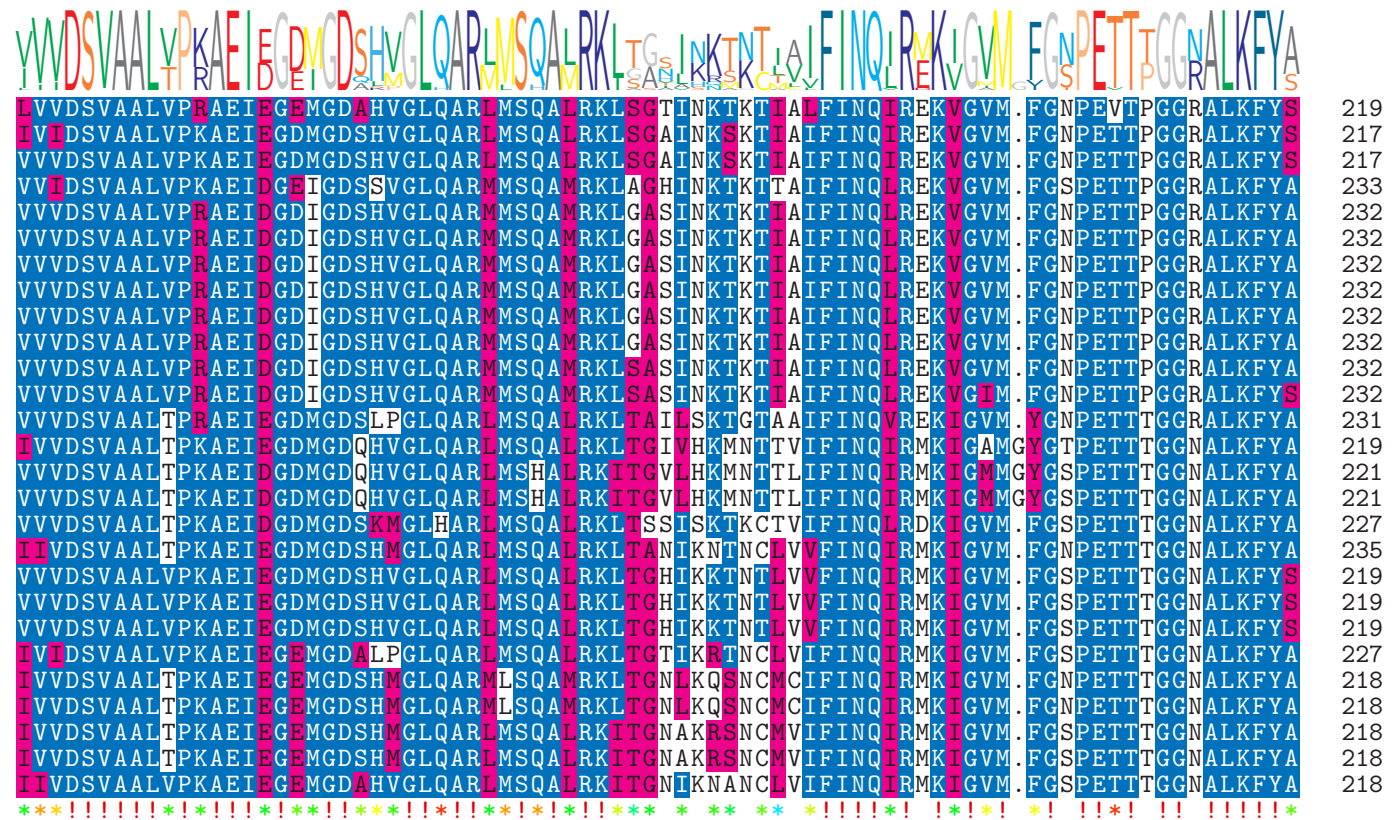
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consensus

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NTDB id 115 BSU 16940 NP 389576.2	SVRLEVRRAEQLKQGN.....DV	MGNKTKIKVVKNKVAPPFRTAEV	DIMYGEGISKEGEIIDLGTELDIV	QKSGSWYSYE	292	
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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIDIRRLSDTGKIKDKSGEV	IGNRTRKVVKNKVAPPFKSAEF	DIMYGEGVSKVGEILDVATDL	DI	IKKSGSWFSYQ	307
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NTDB id 1124 NGFG RS03960 WP 003688695.1	SVRLDIRRTGS....I.KKGEV	LGNETRVKVIKNKVAPPFRQAEF	DILYGEGISWEGELIDIGVKN	DI	INKSGAWYSYN	294
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consensus	*!!**!*~	*~**~*****!*****!!*!!*!!*~	*~*****!~!*****~*****~*	***~!~*****!		

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EERLGQGRENAKQFLKENKDITMLMIEQFIREHYGLDNNGVVQQAAEET.QEELEF....EE.....	348
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNNEEVPLDLGDLELEIE	385
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DEKIGQGSSENAKKYLAEHPEIFDEIDKQVRSKFGGLIDGEEVSEQDTENKKDE...PKKEEA..VNNEEVPLDLGDLELEIE	385
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DEKIGQGSSENAKKYLAADNPVFIAEIDHQRVVRVQFGLIDGEEIIAAS...KKDE...VAQVDS..VNNEVTLDLGDLELEIE	381
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GEKIGQGSSENAKKFLADNPFIIDDIDHKVRVQYGLIEEDNTEEKQSSEK.....ETDEK..ADKNLVLELDDTTIELE	382
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DKKLGGGRENAKALLKEDKALADEITLKIKESIGSNEEI....MPLPDEP..LEEME.....	347
DTKLGGGRDITVKELIKDNPELAEELEAKIREKLQAK.....	343
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GERPEE.....	348
GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GERPEE.....	348
GERIGGGRDNCREFLRENAELARENKVRHLGVTPMG.....AV.TLAEVEED.....	352
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPENM....QLIAETSSAADDFEF..GAVPEEF.....	354
GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPENM....QLIAETSSAADDFEF..GAVPEEF.....	354
GNKIGGQKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEEEPDP...LLES.....	349
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consensus			

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