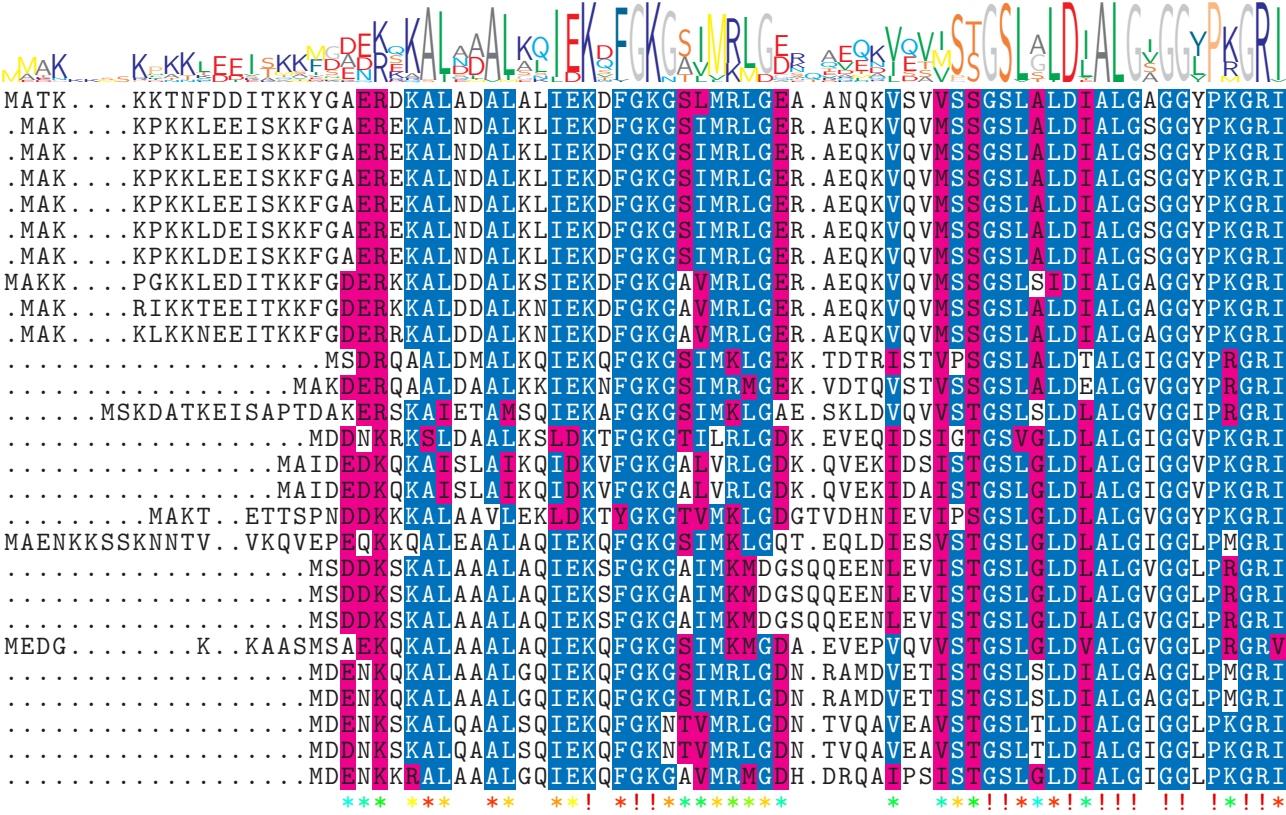


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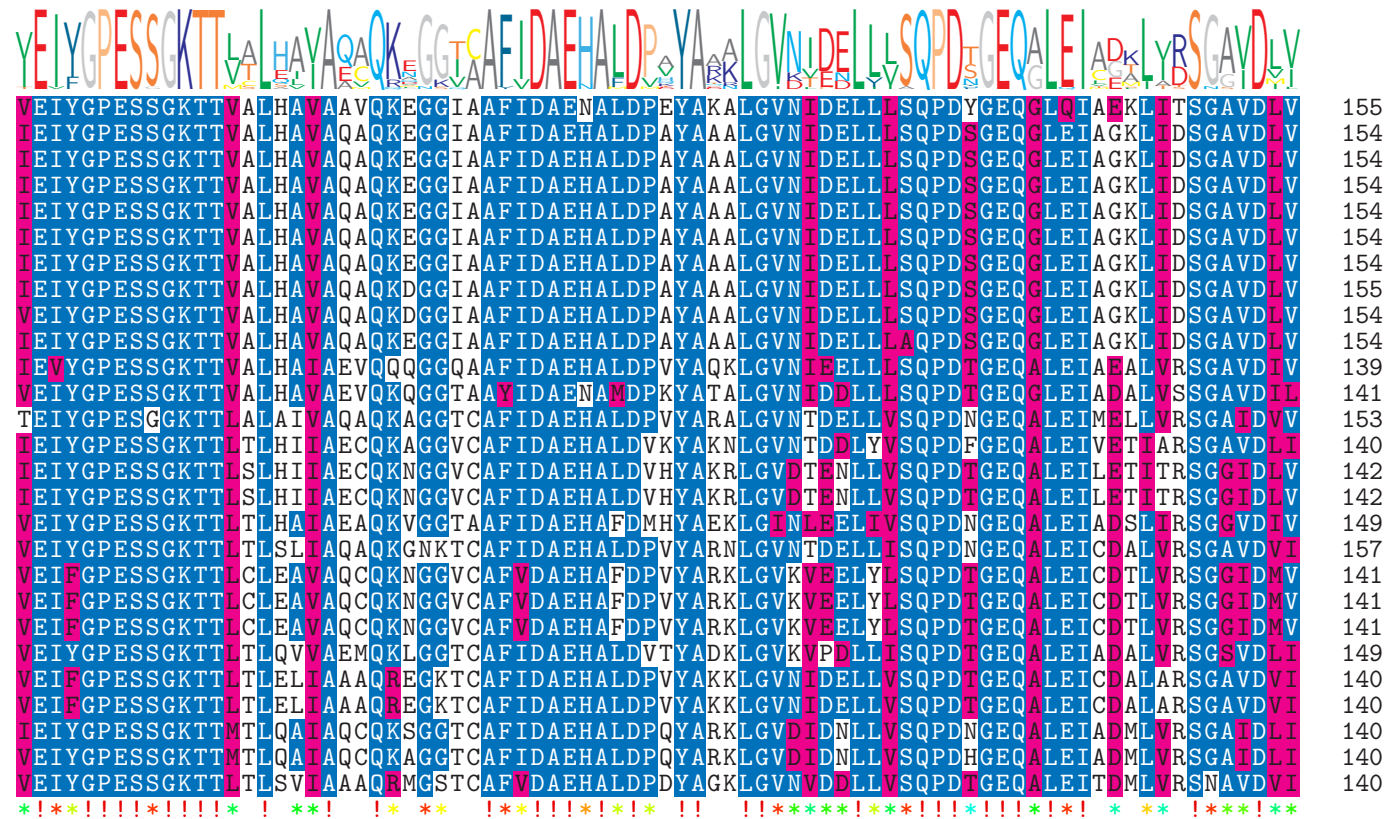


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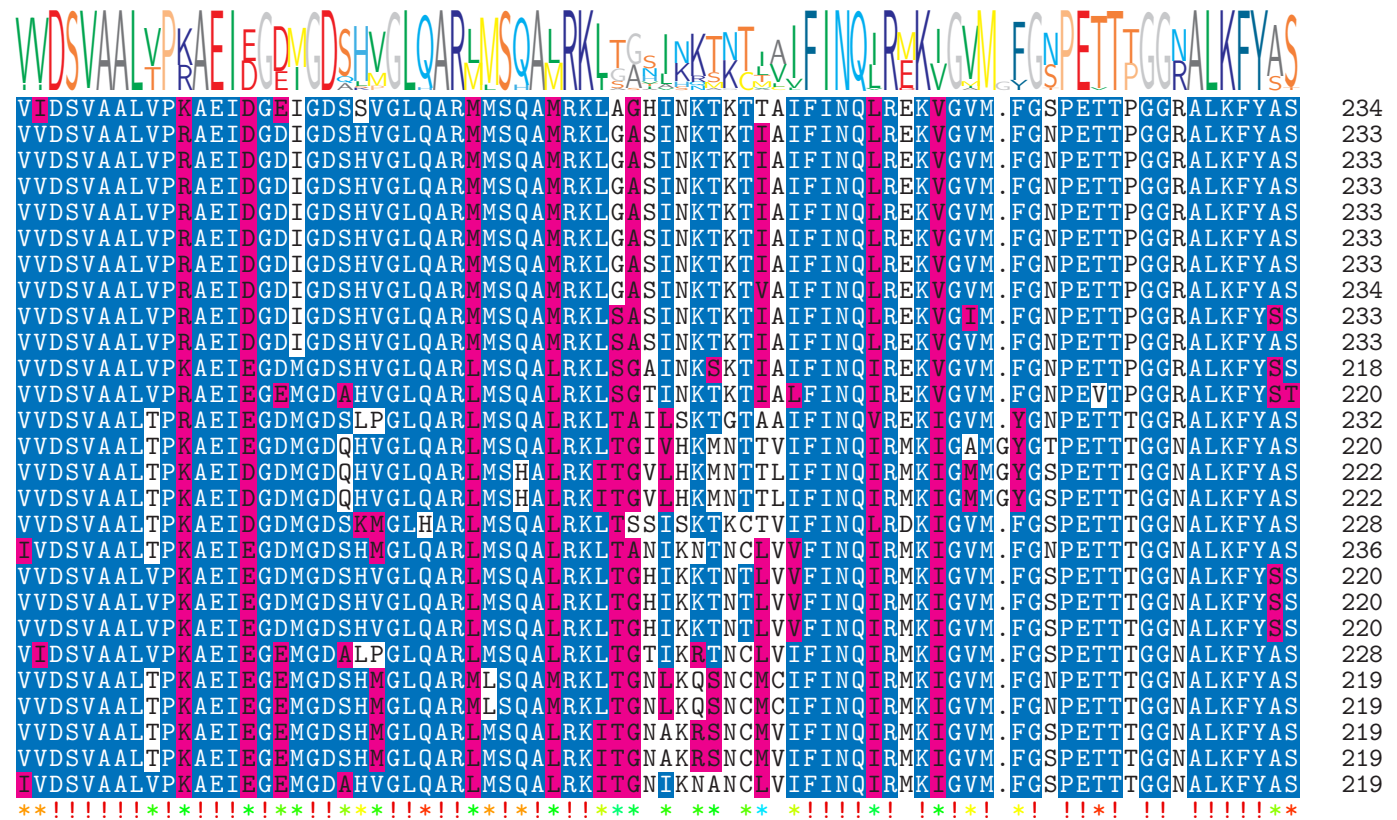
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consensus

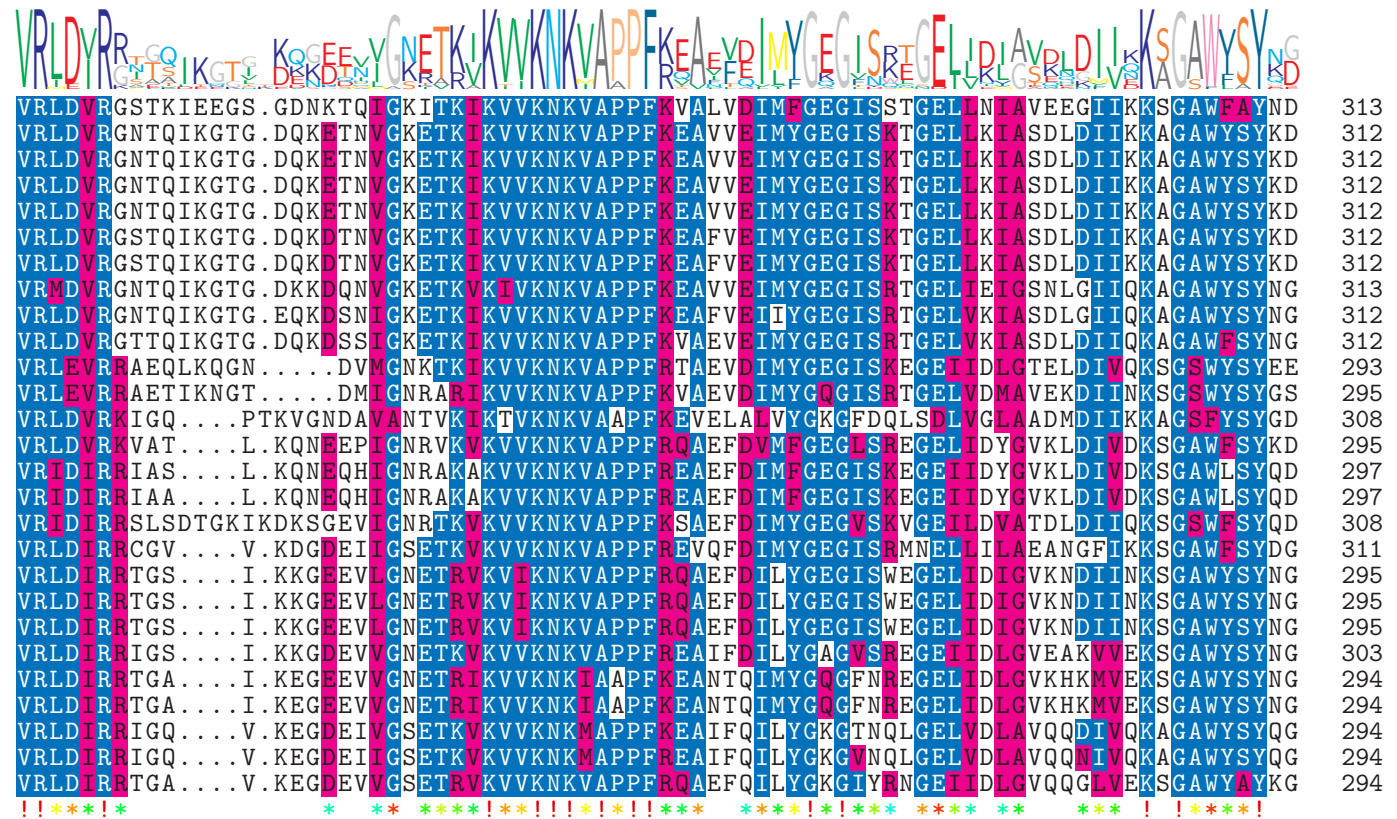
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consensus

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consensus

Sequence	Score
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EKIGQGSENAKKYLAEHPFIDEIDKQVRSKFGLDIGEEVSEQDT...ENKKDEP...KKEEA..VNEEVPLDLGDE	381
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EKIGQGSENAKKYLADNPEIFDEIDHQVRVQFGLDIGEEIAES...KKDEA...AQVDS..VNEEVPLDLGDE	377
EKIGQGSENAKKYLADNPEVFAIEDHQVRVQFGLDIGEEAAES...KKDEP...AQVDS..VNEEVPLDLGDE	377
EKIGQGSENAKKFLADNPATFDEIDRKIRVHYGLIEADGVEEVAT...EEA.PVV...AE..EIQDVILDLDGG	378
EKIGQGSENAKKFLADNPEIFDIDHKVRVQYGLIEEDNTEEEKQS...SKEKETD...EK..ADKNLVLELDDT	378
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ERIGGGRENAKQFLKENKDILMLIQEQIREHYGLDNGGVVQQQAE...ETQEELEFE.E	348
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ERIGGGRDNCREFLRNAAELAREIENKVRHGLVTPMG...AV.TLAEVEEED	352
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SKIGGGKANAAKYLEENPEIGQEIEQQIRAKLIVTSAN...TKATPVAEDLAD..I	347

logo

NTDB id 600 KW2 RS01765 WP 011675413.1		387
NTDB id 269 KZH43 RS08665 WP 001085462.1	LEIEIEE	388
NTDB id 228 SPD RS09265 WP 001085462.1	LEIEIEE	388
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consensus		

-  non conserved
-  similar
-  ≥ 50% conserved