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NTDB id 1205 PSJM300 05545 AFN77183.1
consensus

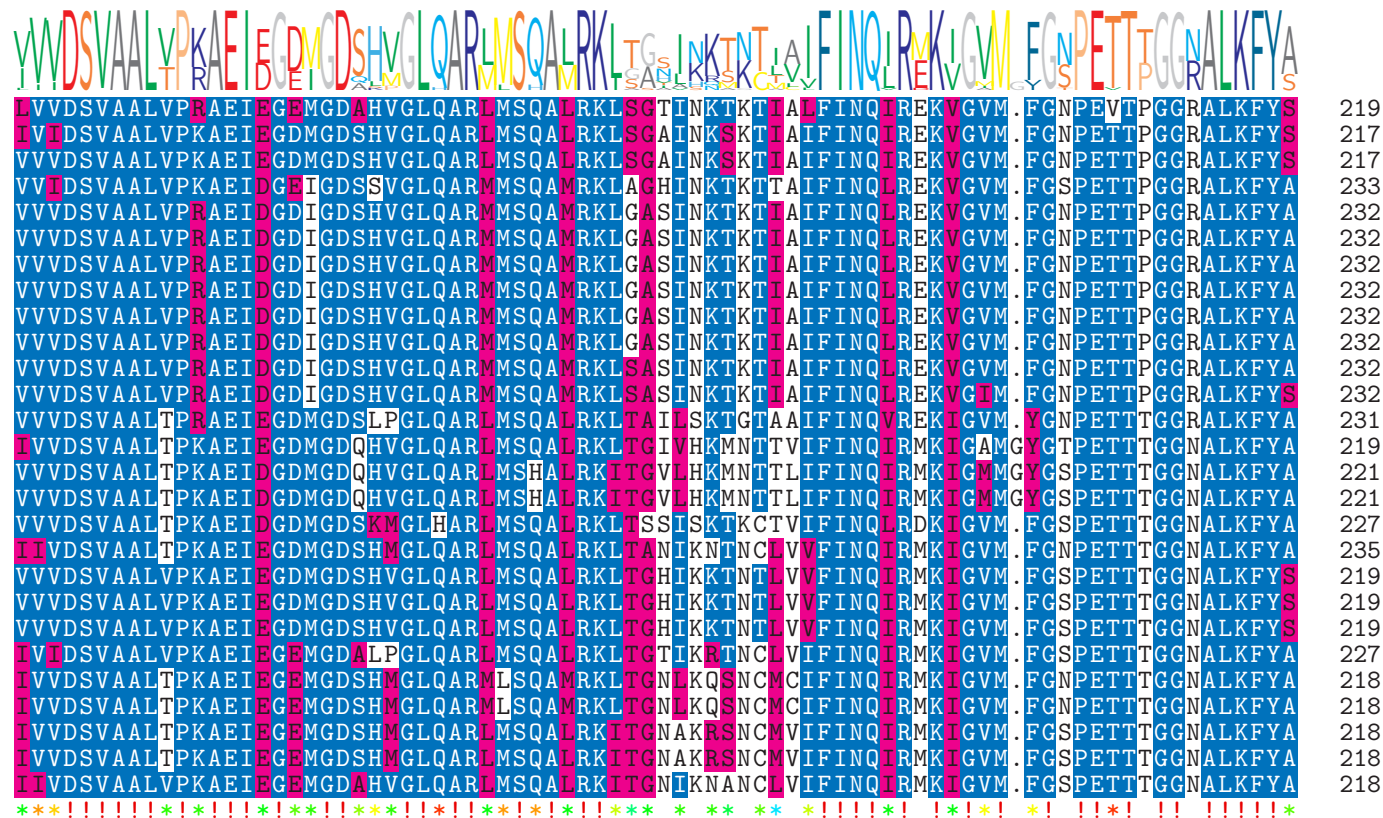
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I I E I Y G P E S S G K T T V S I L H A I A E V Q R Q G G Q A A F I D A E H A L D P V Y A Q K L G V N I D E L L S Q P D T G E Q G L E I A E A L V R S G A V D I	138
I I E V Y G P E S S G K T T V A L H A I A E V Q Q Q G G Q A A F I D A E H A L D P V Y A Q K L G V N I E L L L S Q P D T G E Q A L E I A E A L V R S G A V D I	138
I V E I Y G P E S S G K T T V A L H A V A A V Q K E G G I A A F I D A E N A L D P E Y A K A L G V N I D E L L S Q P D Y G E Q G L Q I A E K L I T S G A V D L	154
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
I I E I Y G P E S S G K T T V A L H A V A Q A Q K E G G I A A F I D A E H A L D P A Y A A A L G V N I D E L L S Q P D S G E Q G L E I A G K L I D S G A V D L	153
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I T E I Y G P E S G K G K T T L A L A T V A A Q A Q K A G G T C A F I D A E H A L D P V Y A R L G V N T D E L L V S Q P D N G E Q A L E I M E L L V R S G A I D V	152
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V V E I Y G P E S S G K T T L T L Q V V A E M Q K L G C T A F I D A E H A L D V T Y A D K L G V K V P D L L I S Q P D T G E Q A L E I A D A L V R S G S V D L	148
I V E I F G P E S S G K T T L T L E L I A A A Q R E G K T C A F I D A E H A L D P V Y A K K L G V N I D E L L V S Q P D T G E Q A L E I C D A L A R S G A V D V	139
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I I E I Y G P E S S G K T T M T L Q A I A Q C Q K S G G T C A F I D A E H A L D P Q Y A R K L G V D I D N L L V S Q P D N G E Q A L E I A D M L V R S G A I D L	139
I V E I Y G P E S S G K T T M T L Q A I A Q C Q K A G C T C A F I D A E H A L D P Q Y A R K L G V D I D N L L V S Q P D H G E Q A L E I A D M L V R S G A I D L	139
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NTDB id 1334 RAOC RS04870 WP 004918236.1	SVRIIDIRRLSDTGKIKDKSGEV	IGNRTKVVKNKVAPPFKSAEF	DIMYGEGVSKVGEILDVATDL	DIQKSGSWFSYQ	307
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consensus

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Sequence	Score
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GAKIGGQKDNVRVWLKENPEISDEIDAKIRALNGVEMHI....TEGTQDET.....GERPEE.....	348
GERIGGGRDNCREFLRENAELARIENKVRREHLGVTPMG....AV.TLAEVEED.....	352
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GDKIGGQKANACKYLKENPEIAKTLDKKLREMLLNPNEM....QLIAETSSAADDVEF..GAVPEEF.....	354
GNKIGGQKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEEEDPD...LLES.....	349
GNKIGGQKNNVIRYFEENNQIAEEIERNIREQLLTGTN....GAVQ.I.EDEEEDPD...LLES.....	349
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		IEE	
NTDB id 625 LCA RS02525 WP 011374196.1	...	355	
NTDB id 332492 EKQ63 RS20140 WP 001976711.1	...	343	
NTDB id 115 BSU 16940 NP 389576.2	...	348	
NTDB id 600 KW2 RS01765 WP 011675413.1	...	387	
NTDB id 269 KZH43 RS08665 WP 001085462.1	IEE	388	
NTDB id 228 SPD RS09265 WP 001085462.1	IEE	388	
NTDB id 194 SPR RS08825 WP 001085462.1	IEE	388	
NTDB id 159 SP RS09750 WP 001085462.1	IEE	388	
NTDB id 499 SM12261 RS08315 WP 078228268.1	IEE	384	
NTDB id 527 SMSK321 RS11065 WP 001085454.1	IEE	384	
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NTDB id 408 SMU RS09530 WP 002262392.1	D..	383	
NTDB id 1313 DR RS12030 WP 010888966.1	...	363	
NTDB id 1245 Cj1673c YP 002345041.1	...	343	
NTDB id 1211 C694 RS00795 WP 000963128.1	...	347	
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NTDB id 1334 RAOC RS04870 WP 004918236.1	...	343	
NTDB id 1389 A4U84 RS07560 WP 021112712.1	...	372	
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NTDB id 1123 OK783 RS03845 WP 003688695.1	...	348	
NTDB id 1427 RS RS02760 WP 011000510.1	...	352	
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NTDB id 1074 ABD1 RS10195 WP 000344167.1	...	349	
NTDB id 1022 ACIAD RS06390 WP 004925639.1	...	349	
NTDB id 1205 PSJM300 05545 AFN77183.1	...	347	
consensus			

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