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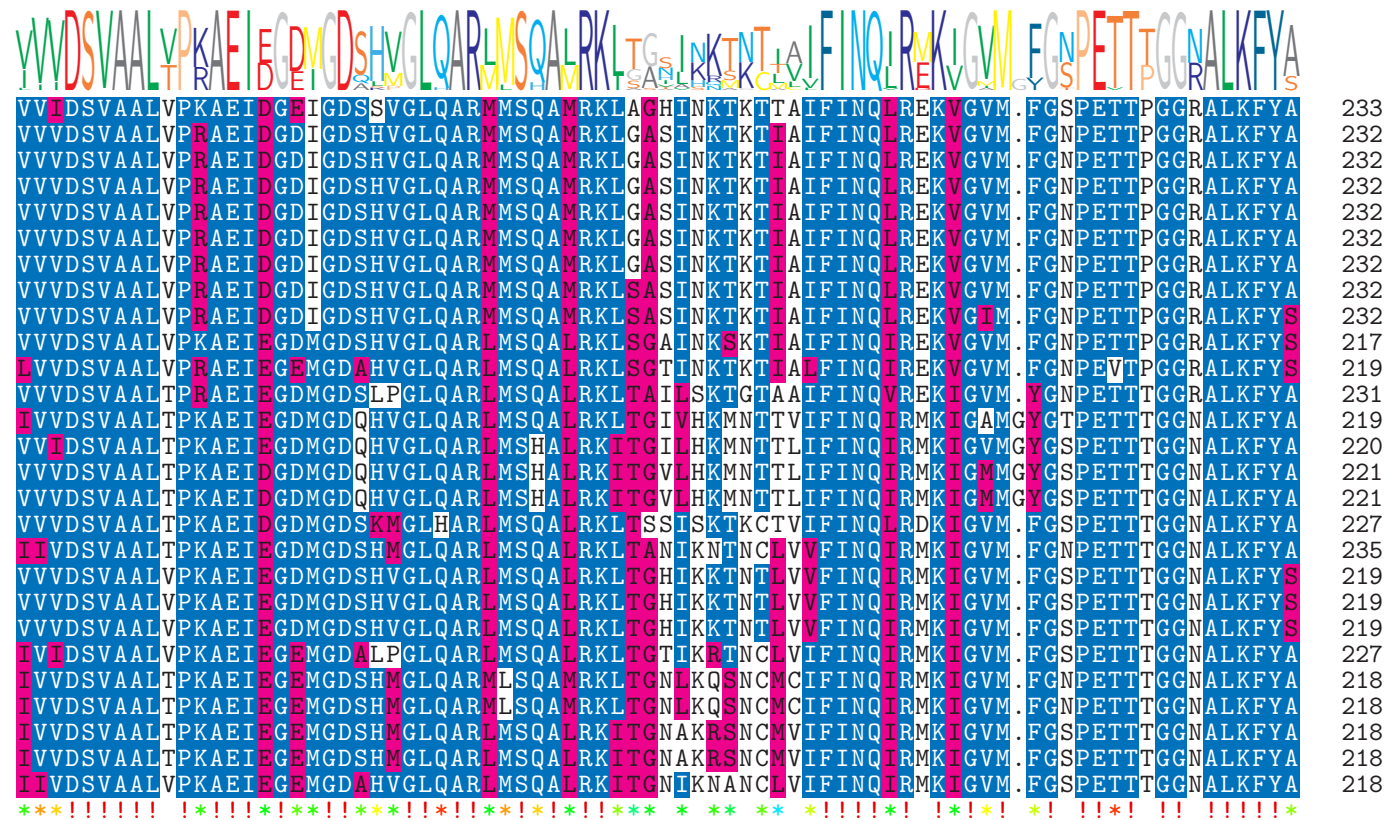
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|-------|------|----|----|-----|----|----|-----|----|----|----|-----|-----|-----|-----|---|-----|---|----|----|----|---|---|----|---|----|---|----|----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MATKK | ...  | KT | NF | DD  | IT | KY | GA  | ER | D  | K  | A   | L   | A   | D   | A | L   | I | E  | K  | D  | F | G | K  | S | I  | M | R  | L  | G | E | A | . | A | N | Q | K | V | S | V | S | S | G | S | L | A | L | D | I | A | L | G | A | G | G | Y | P | K | G | R |   |   |   |   |   |   |   |   |   |   |   |   |
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NTDB id 1074 ABD1 RS10195 WP 000344167.1  
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consensus

| Sequence                                                                                                                                                          | Position |
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| 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      |
| 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 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 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 E V Q K Q G G T A A Y I D A E H A L D P K Y A T A L G V N I D E L L S Q P D T G E Q G L E I A D A L V R S G A V D I     | 140      |
| I T E I Y G P E S S G K T T L A L A I V A Q A Q K A G G T C A F I D A E H A L D P Y A R A L G V N I D E L L 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      |
| I I E I Y G P E S S G K T T L T L H I I A E C Q K A G G V C A F I D A E H A L D V K Y A K N L G V N I D E L L Y V S Q P D F G E Q A L E I V E T I A R S G A V D L | 139      |
| I I E I Y G P E S S G K T T L S L Q I V A E C Q K N G G I C A F I D A E H A L D V Y A K N L G V D T E N L L V S Q P D T G E Q A L E I L E T I T R S G A V D L     | 140      |
| I I E I Y G P E S S G K T T L S L H I I A E C Q K N G G V C A F I D A E H A L D V H Y A K R L G V D T E N L L V S Q P D T G E Q A L E I L E T I T R S G G I D L   | 141      |
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| I V E I F G P E S S G K T T L C L E A V A Q C Q K N G G V C A F V D A E H A F D P V Y A R K L G V K V E E L Y L S Q P D T G E Q A L E I C D T L V R S G G I D M   | 140      |
| I V E I F G P E S S G K T T L C L E A V A Q C Q K N G G V C A F V D A E H A F D P V Y A R K L G V K V E E L Y L S Q P D T G E Q A L E I C D T L V R S G G I D M   | 140      |
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| 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 Y A K K L G V N I D E L L 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      |
| 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 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      |
| 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 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 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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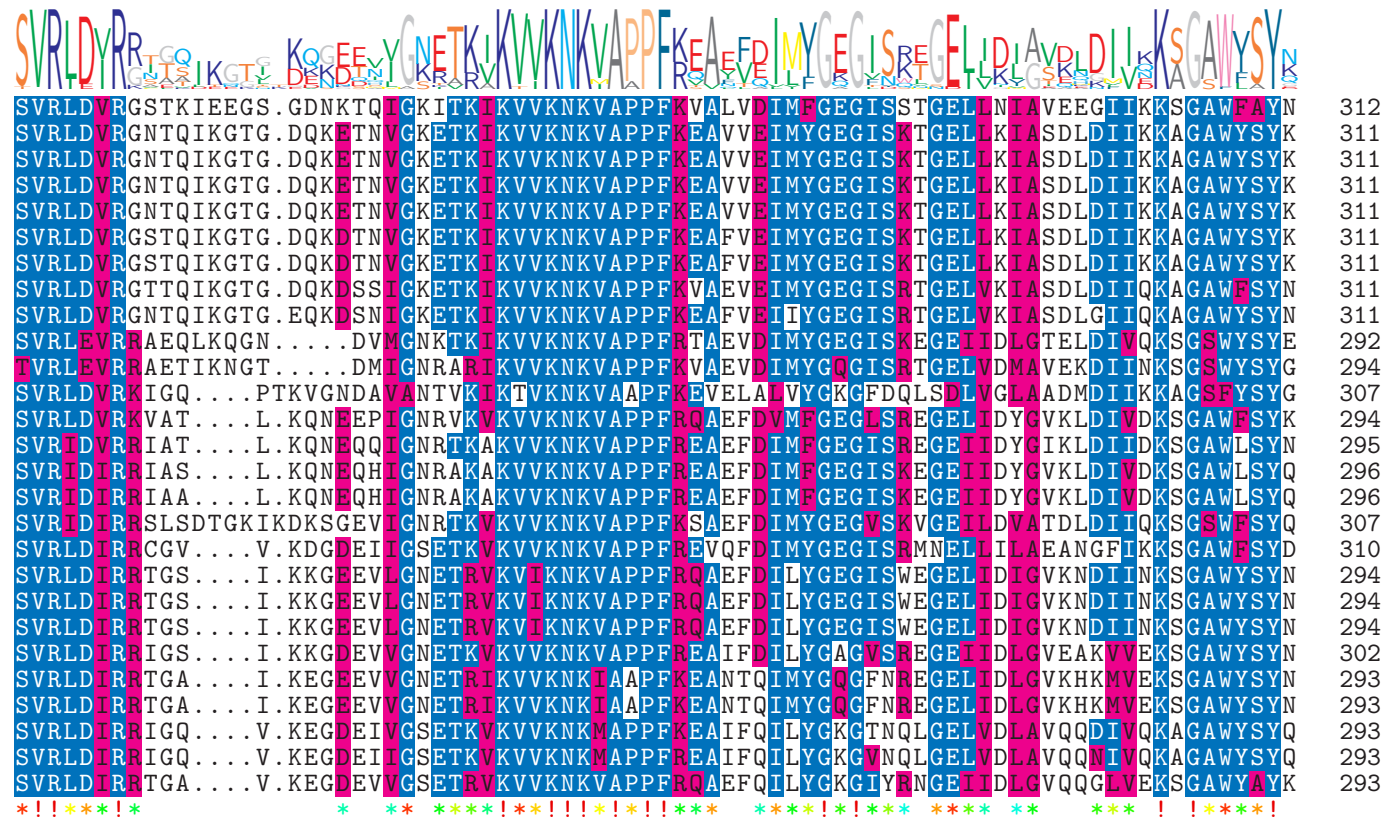
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| NTDB id 1165 A1552VC RS01565 WP 000344154.1 | ... | 354 |  |
| NTDB id 1142 GTF74 RS11550 WP 000344154.1   | ... | 354 |  |
| NTDB id 1074 ABD1 RS10195 WP 000344167.1    | ... | 349 |  |
| NTDB id 1022 ACIAD RS06390 WP 004925639.1   | ... | 349 |  |
| NTDB id 1205 PSJM300 05545 AFN77183.1       | ... | 347 |  |
| consensus                                   |     |     |  |

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