

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the first motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is MKKYILLRRLRSLLSIFVVTALTYTIIYTMVPRRLIFRQDPNPNYKIAKTADSKANYENTIYERMGYIDYYDTKELQEKASSLDKS.

85

85

85

85

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the second motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is VTTKPTKENKAIYQKYVDSLGRGWRLHQFKQSKQFYATRDPVPLERVFGEFYTHLFEFDNTGWVKDKTNPNLKRYIRIENDPAIGW.

170

170

170

170

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the third motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is SVVSGSGTKHKYLLYFNQFPFVHQNFVKMNLGTSYPTYAEQGVLDVITQGGQQTQSSEVNFPTGK.

255

254

254

254

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the fourth motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is ARDRSYYGNDPYTATKSRYQPSMTSSAIALGIGLVISYALAIPLGSYMARFKNTLFDVSTGVLTFLLSLPTIALVYIIRLI.

340

338

338

338

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the fifth motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is GSEIGLPDSFPILGAGDWRSYVLPVILGGLSTPGLAIWIRRYMIDLQSQDFVRFARAKGLSEQEISNKHIFKNAMVSLVSGIPA.

425

423

423

423

logo

NTDB id 27844 SPYM RS01330 WP 011017334.1

NTDB id 476 HSISS4 RS06995 WP 013990225.1

NTDB id 293 STER RS06925 WP 011681416.1

NTDB id 325 STU RS16125 WP 002946410.1

consensus

Sequence logo for the sixth motif. The y-axis represents information content. The x-axis shows amino acid positions. The consensus sequence is SIIVGVTGATLTETIFAYPGMGKMLIDSVRASNNAMVGLVFIFTALSFSLVGDILMTIDPRIKLTSGKGGK.

500

497

497

497

 non conserved
 similar
 $\geq 50\%$ conserved