

logo

NTDB id 1144289 C7S08 RS00695 WP 003687350.1

NTDB id 1115 OK783 RS00485 WP 003698035.1

NTDB id 1100 NMB RS09455 WP 002225652.1

NTDB id 1092 CAD91899.1 1..2286()

consensus



Sequence logo for the first motif, showing high conservation of MNTKLTKIISGLFVATAAFQTASAGNITDIKVSSLPNKQKIVKVSFDKEIVNPTGFVTSSPARIALDFEQTGISMDQQVL.

80

80

80

80

logo

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consensus



Sequence logo for the second motif, showing high conservation of EYADPLLISKISAAQNSSRARLVNLNKPQQYNTTEVRGNKVMIFINESDDTVSAPARPAVKAAPAAPAKQQAAAA PSTKSAV.

150

150

160

160

logo

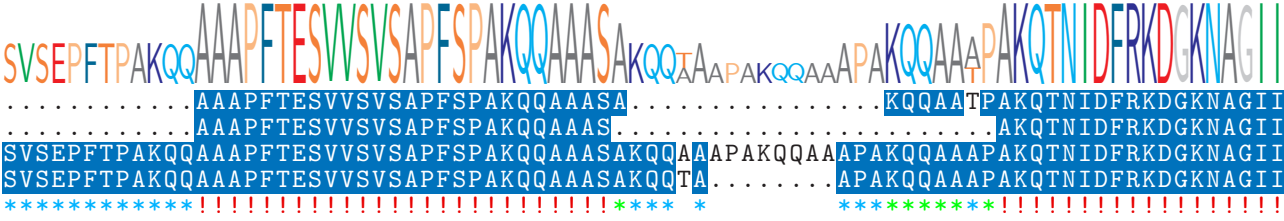
NTDB id 1144289 C7S08 RS00695 WP 003687350.1

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consensus



Sequence logo for the third motif, showing high conservation of SVSEPFPAKQQAAAPFTESVSVSAPFSPAQQAAA SAKQQAAPAKQQAAAPAKQTVIDFRKDGNAGII.

202

194

240

232

logo

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consensus



Sequence logo for the fourth motif, showing high conservation of ELAALGFAGQPDISQQHDHIIIVTLKNHTLPTTLQRSLDVADF KTPVQKVT LKRLNNDTQLIITTTGNWELVNKSAAPGYF.

282

274

320

312

logo

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consensus



Sequence logo for the fifth motif, showing high conservation of TFQVLPKKQNLES GGVNNA PKTFTGRKISLDFQDVEIR TILQILAKESGMNIVASDSVNGKMTLSLKDV PWDQALD LVMQ.

362

354

400

392

logo

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consensus



Sequence logo for the sixth motif, showing high conservation of ARNLDMRQQGNIVNIAPRDELLAKDKAFLQAEKD IADLGALYSQNFQLKYKNVEEFRSILRLDNADTTGNRNTLVSGRGS.

442

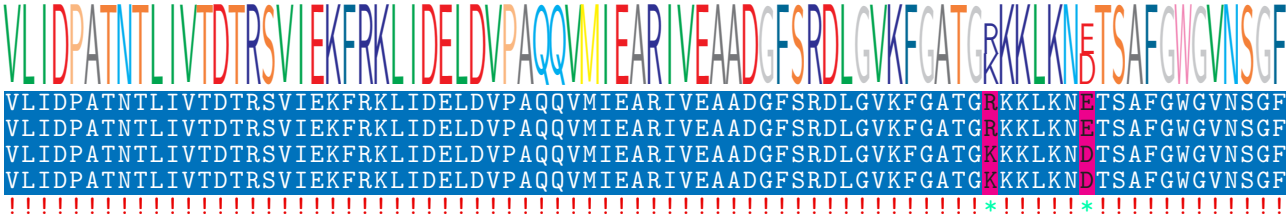
434

480

472

logo

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consensus



522
514
560
552

logo

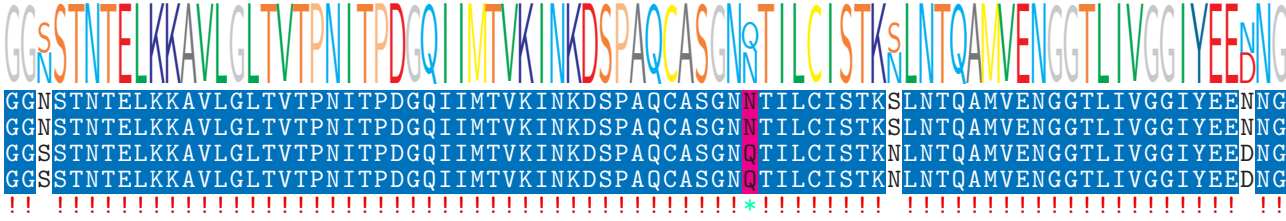
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consensus



602
594
640
632

logo

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consensus



682
674
720
712

<0

logo

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consensus



731
723
769
761

☒ non conserved
☒ similar
☒ ≥ 50% conserved