T0457.t2k str4

Sequence logo / multiple sequence alignment profile.

Row 1 (positions 1–100):
`MVEIFNEIMQRVKEAETIIHRHVRPDPDAYGSQLGLKLYLERKFPEKNIYATGEAEPSLSFIGDLDEIDDSVYSDALVIVCDTANAPRIDDQRYLNGQS`

Secondary structure annotation row 1:
`H          GUTRP    RQVSVSH              G  USGRQRP  QVSV SGS GS VSH  S  VSGP    QSVSG S  H  SGTR`

Row 2 (positions 101–200):
`LIKIDHHPATDQYGDVNFVNTEASSTSEIIFDFISHFNDLSIIDEHVARVLYLGIVGDTGRFLFSNTSPHTMEVASQLLAYPFNHNAELNKMSEKDPKLM`

Secondary structure annotation row 2:
`P   QVSGS G VE  EQVSGSH        G T UV SH       SES G E VSGV SH     G TV SH     SGSUSGH`

Row 3 (positions 201–300):
`PFQGYVLQNFELSDSHEYCQIKITNDVLKQFDIQPNEASQFVNTVADISGLKIWMFGVGEDGQIRCRIRSKGITINDVANQFGGGGHPNASGVSVYSWDE`

Secondary structure annotation row 3:
`GT  EDEGE B AB  ESH  G TV SH       GUSGRQB    ADG EAB   QG V SH   G TV  SGSGE EQV   S`

Row 4 (positions 301–317):
`FEELAQALRQKLLEHHHHHH`

Secondary structure annotation row 4:
`H        SG SV`