

Sequence alignment showing conservation across multiple entries (2phk_A, 1kw_P_A, 1jkk_A, 20301962.m, 19526942.m, 38076166.m, SNRK.h, 24653592.f, 24653590.f, 24653588.f, 24653586.f, 31241799.i, 17511097.w, lia8_A, 19114316.y) from positions 610 to 80. Conserved regions are highlighted in red.

Sequence alignment of 10 homologous proteins. The proteins are numbered 810 to 10 at the top. The alignment shows conservation across 10 positions, with identical residues in green and similar residues in red. The proteins are numbered 810 to 10 at the top. The sequence starts with a signal peptide (SSP) and ends with a transmembrane domain (TMD).