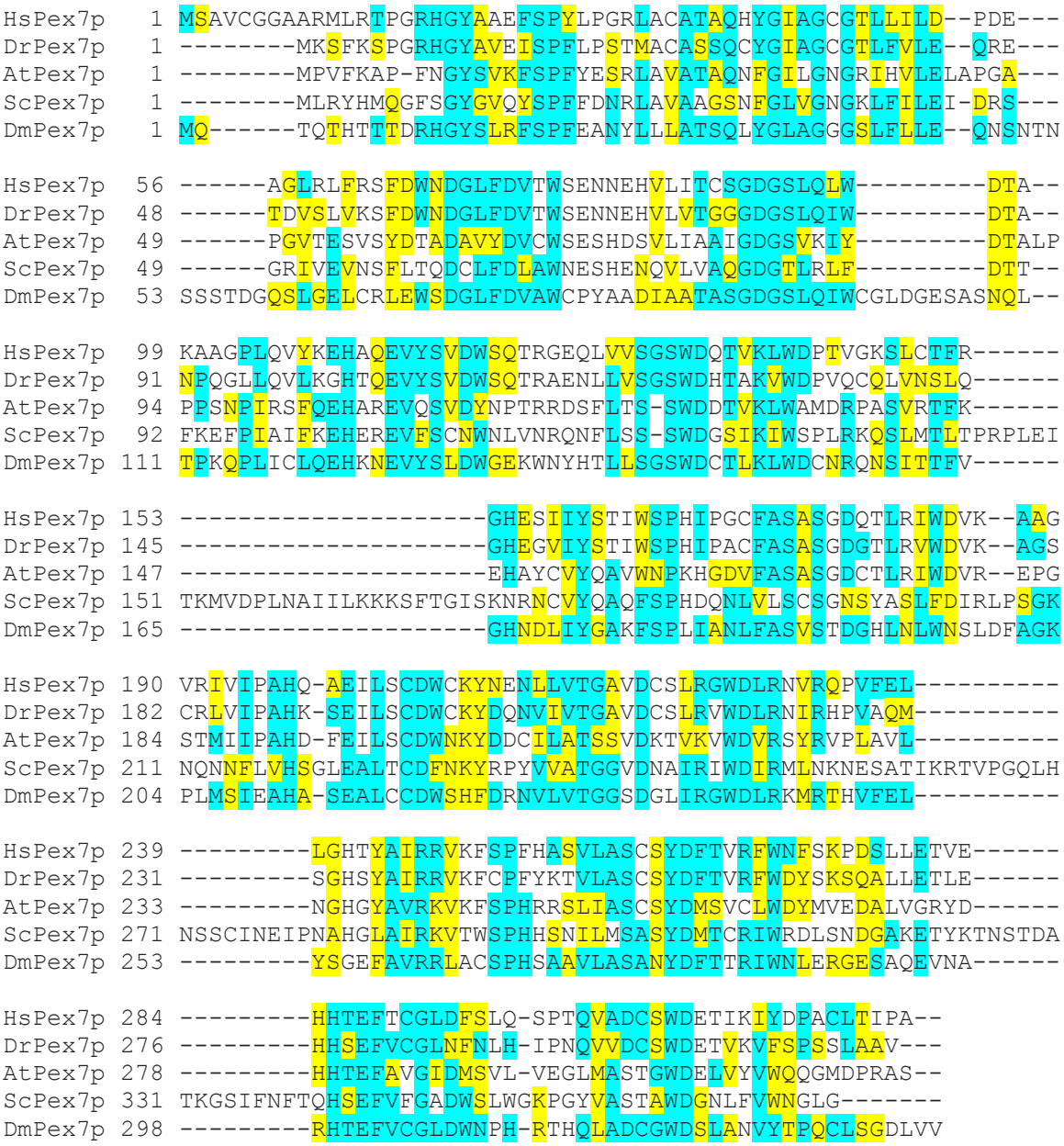


Figure S2. Sequence alignment of Pex7 protein homologues. Sequence alignment of human (HsPex7p, CAG46851.1), zebrafish (DrPex7p, AAI64338.1), plant (AtPex7p, OAP16388.1), yeast (ScPex7p, KZV12380.1) and fruit fly (DmPex7p, NP_001137914.1) Pex7 proteins. Amino acid sequences were aligned with use of the Kalign program (https://www.ebi.ac.uk/Tools/msa/kalign). Residues that are identical (blue) or similar (yellow) to residues in *Drosophila* Pex7 are shaded. Similarity rules: G = A = S; A = V; V = I = L = M; I = L = M = F = Y = W; K = R = H; D = E = Q = N; and S = T = Q = N. Dashes represent gaps. Sequence accession numbers are given within brackets.