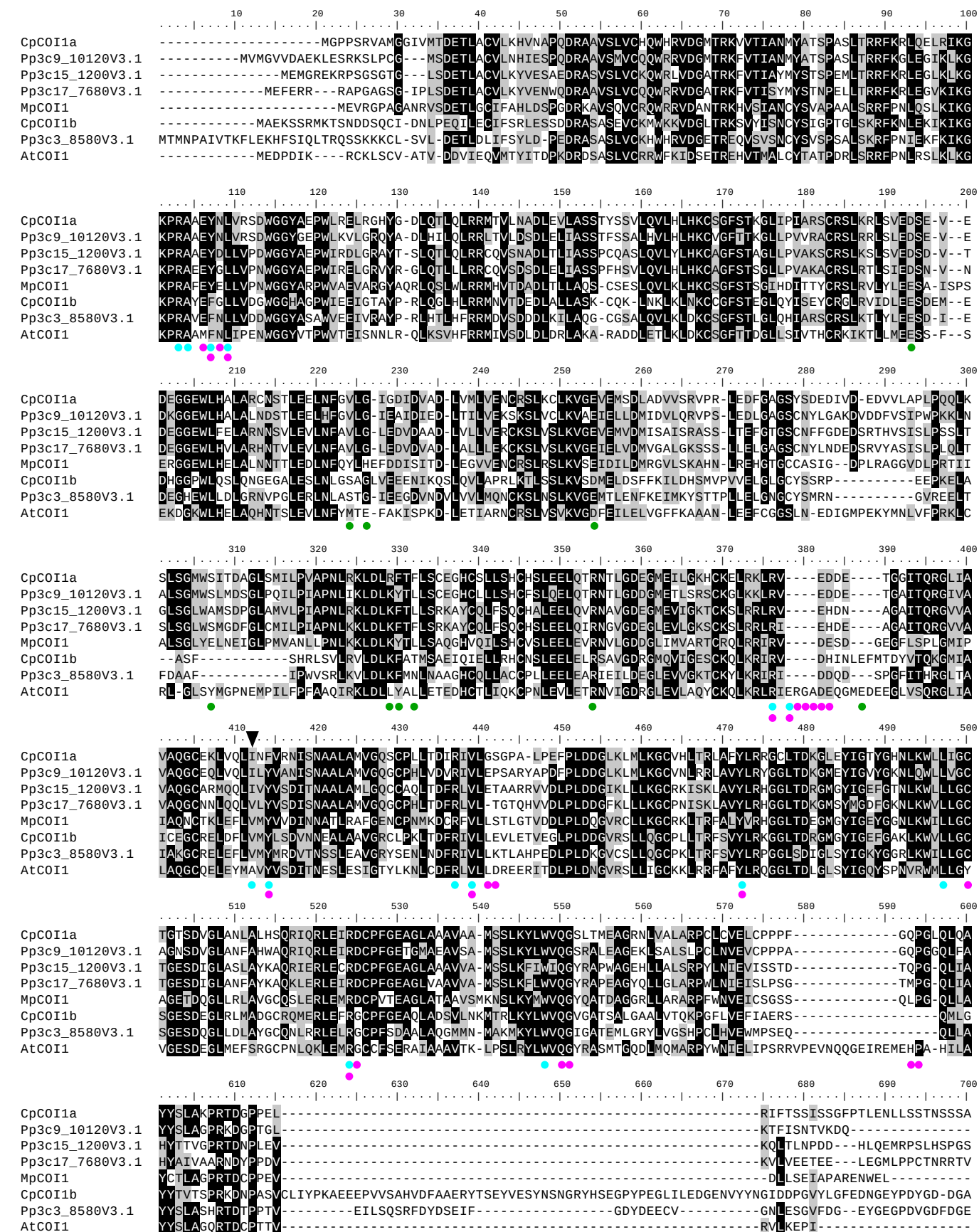




Supplementary Figure 3. Sequence alignment of COI1

Sequences of COI1 homologs were aligned by MEGA version X using Muscle. Sequence alignments were drawn using BioEdit software version 7.2.5. The Shading thresholds of identical or similar residues were 60%. Identical and similar residues were highlighted by black and gray, respectively. Ligand-, JAZ1 degron helix-, and JAZ1 degron loop- contacting residues in AtCOI1 were indicated by blue, green, and magenta dots, respectively. The residue essential for the recognition of dr-OPDA in MpCOI1 were indicated by a triangle.