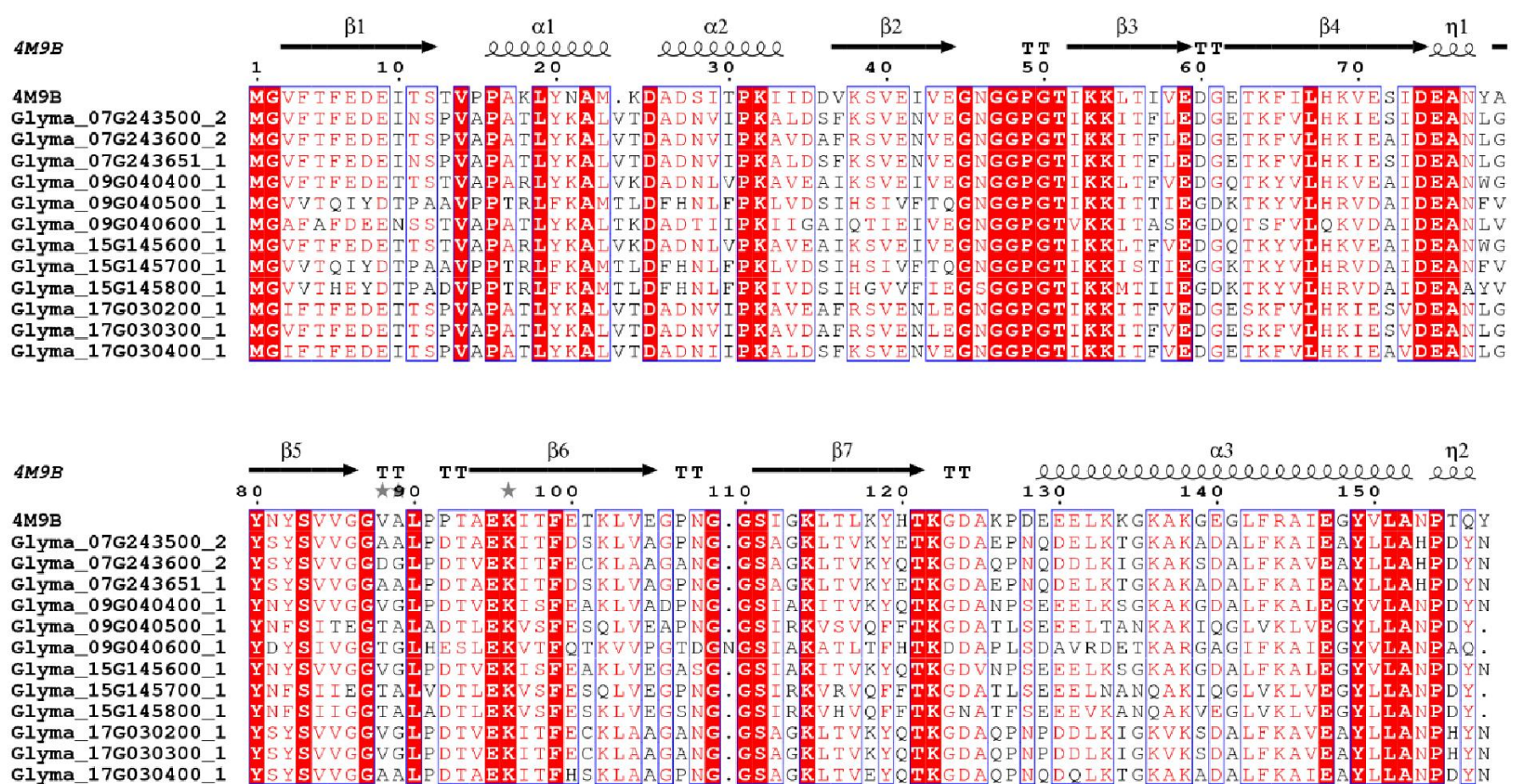


a



b

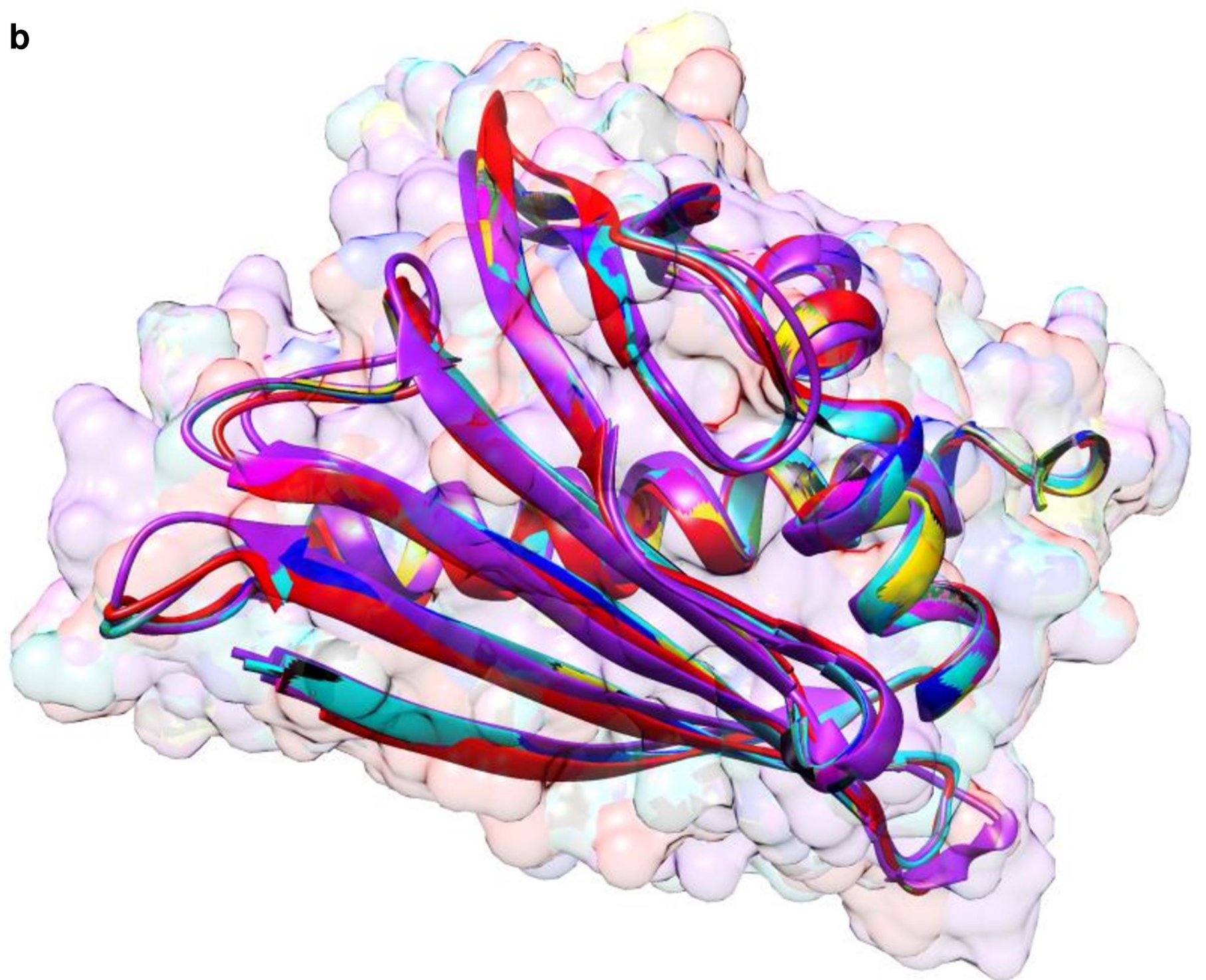


Figure S6. *In silico* analysis of soybean GmPR10 protein and its paralogs. **(a)** Protein alignment with all 11 paralogs of GmPR10 (Glyma.17G030400.1) selected in the Wm82.a2.v1 reference genome assembly of *Glycine max* in Phytozome v.13 database. The graphical representation of the alignment was made with ESPrpt version 3 online software (<https://esprpt.ibcp.fr/>) using as a model for the secondary structure representation (top on the alignment) the structure of the panallergen Ara h 8 from peanuts (*Arachis hypogaea*; PDB ID: 4M9B), used to generate structural model, as follows. **(b)** Superposition of the structural models of the GmPR10 protein and its 11 paralogs, obtained by similarity. Parameters analyzed to choose the best model: *GMQE* (Global Model Quality Estimate) – 0.81-0.86; *Coverage* – greater than 0.93; *QMEAN DisCO* (Qualitative Model Energy Analysis) – 0.86 ± 0.07 . **Color Legend** (structural models): Glyma.07G243500.2 – hot pink; Glyma.07G243600.2 – yellow; Glyma.07G243651.1 – green; Glyma.09G040400.1 – cyan; Glyma.09G040500.1 – blue; Glyma.09G040600.1 – medium blue; Glyma.15G145600.1 – purple; Glyma.15G145700.1 – red; Glyma.15G145800.1 – light green; Glyma.17G030200.1 – dark gray; Glyma.17G030300.1 – magenta; Glyma.17G030400.1 – black.