diversity

MDPI

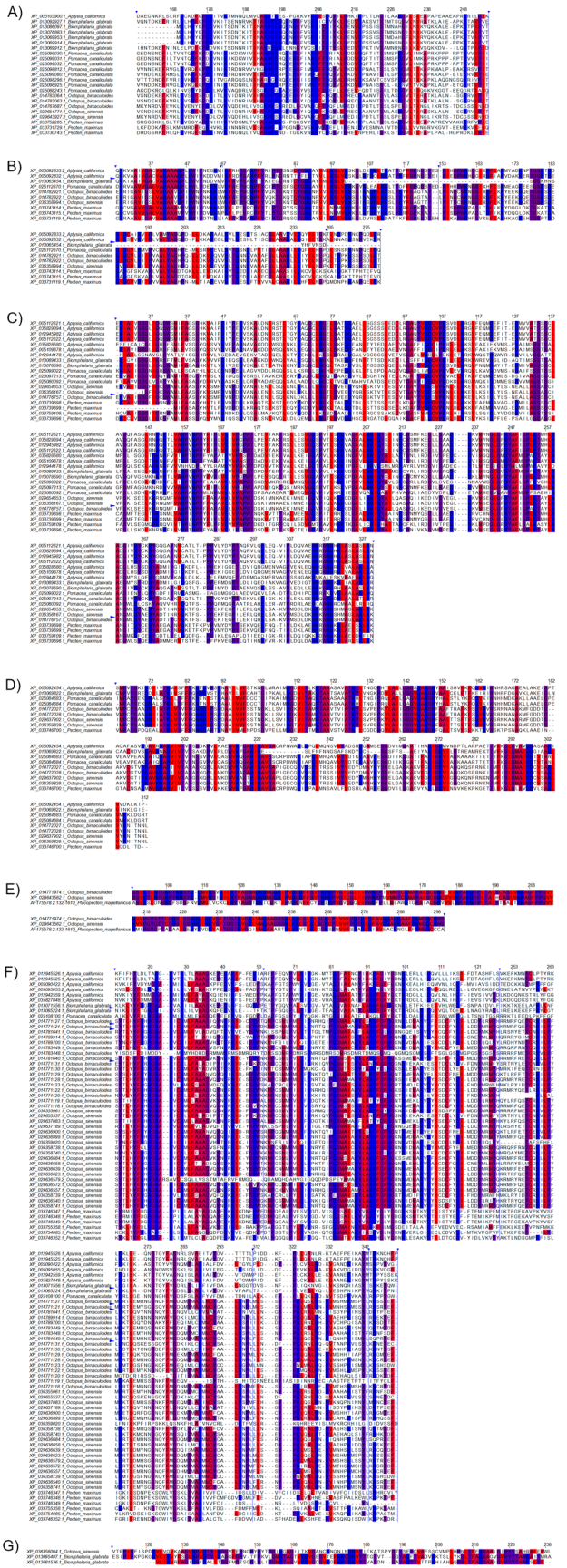

Figure S1. Alignment of amino acid sequences of molluscan crystallins. The most conserved regions for each crystalline family are presented: a) α-crystallins, the region from 159 to 255 alignment position is shown; (b) J1A-crystallins, the regions from 28 to 56, 67 to 126, 153 to 242, 265 to 278 alignment positions are shown; (c) λ-crystallins, the region from 18 to 329 alignment position is shown; (d) μ-crystallins, the region from 63 to 313 alignment position is shown; (e) Ω-crystallines, shown section from 99 to 300 alignment position; (f) S-crystallines, the regions from 11 to 51, 63 to 127, 250 to 302, 312 to 343 and 451 to 458 alignment positions are shown; (g) ζ-crystallines, the region from 119 to 305 alignment position is shown. Multiple sequence alignments were performed by the Clustal Omega algorithm and improved by the MUSCLE algorithm. Amino acid residues with >60% identity were highlighted in color. The most hydrophobic residues are colored red and the most hydrophilic residues are colored blue according to the amino acid hydrophobicity table [1]. The sign ▼ above the sequences indicates the excised regions. The single-letter amino acid designations correspond to the commonly used ones.

References

1. Kyte, J.; Doolittle, R.F. A simple method for displaying the hydropathic character of a protein. *J Mol Biol* **1982**, *157*, 105–132, doi: 10.1016/0022-2836(82)90515-0.