The role of cosolvent–water interactions in effects of the media on functionality of enzymes: a case study of *Photobacterium leiognathi* luciferase

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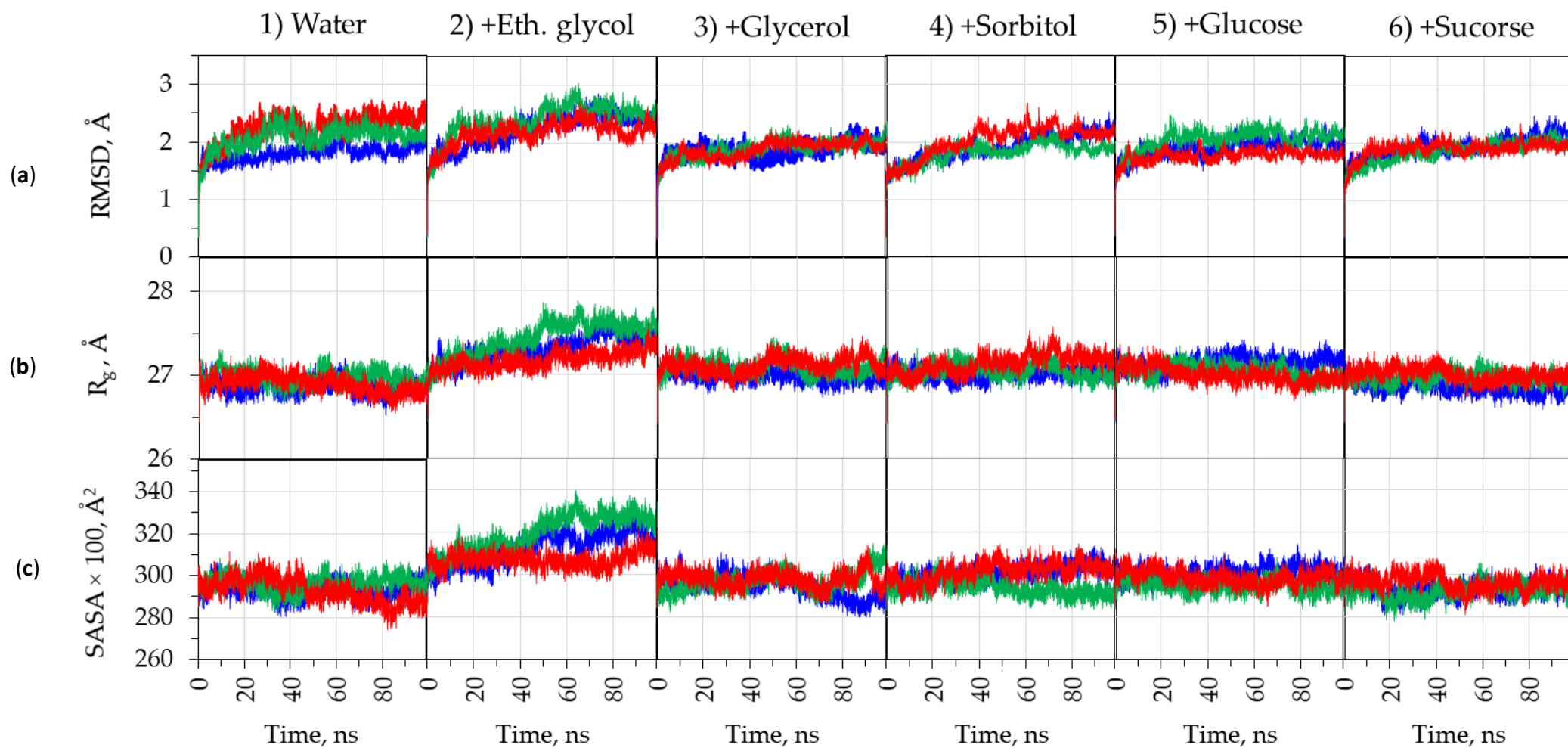
Supplementary Material

Figure S1. The structural parameters change of *P. leiognathi* luciferase obtained during 100-ns MD simulation using the models with water and the mixtures with 1) ethylene glycol (30 wt %), 2) glycerol (40 wt %), 3) sorbitol (40 wt %), 4) glucose (40 wt %), and 5) sucrose (40 wt %): (**a**) the root-mean-square-deviation of C_α-atoms (RMSD); (**b**) the gyration radius for all protein atoms (R_g); (**c**) the total solvent accessible surface area (SASA). Three independent runs are shown by blue, green and red curves.