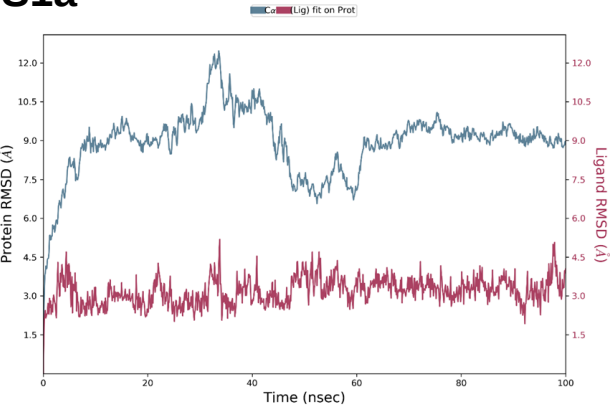
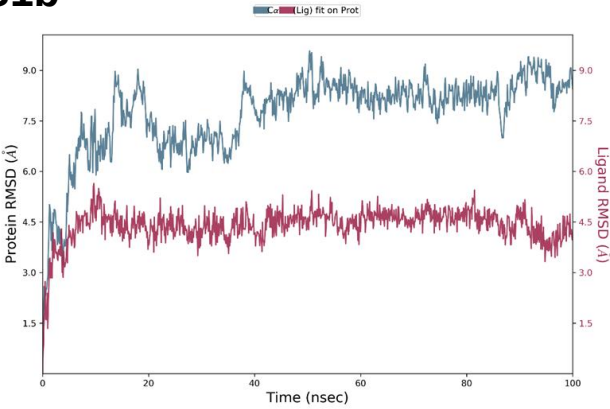


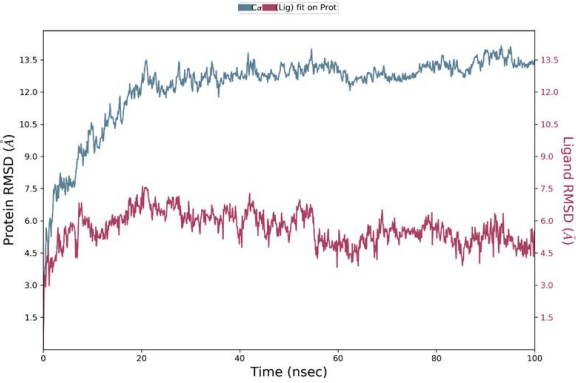
S1a



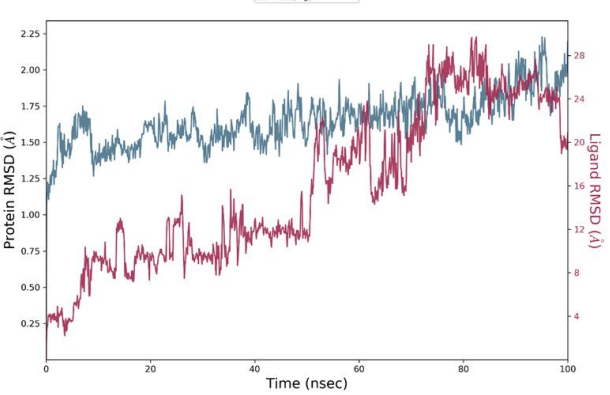
S1b



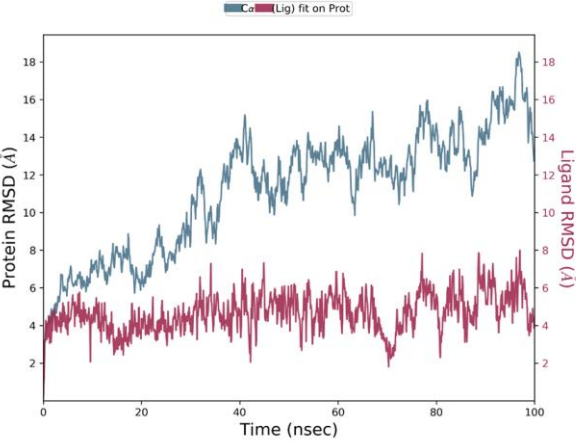
S1c



S1d



S1e



S1f

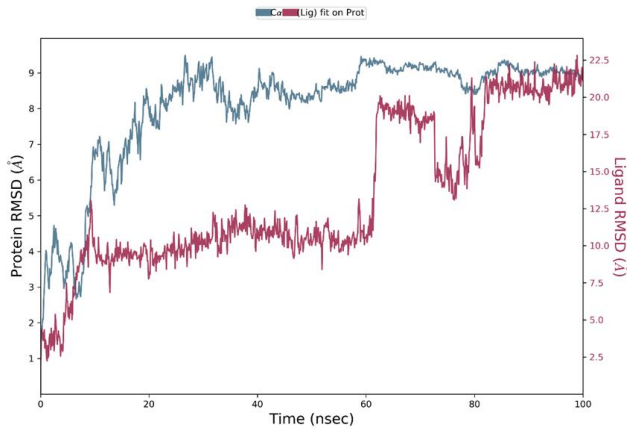


Figure S1. Protein substrate RMSD (a) P5-CLUH (b) P5-CYP51A1 (c) P5-GLUD1 (d) P5-LSS. (e) P5-P4HB. (f) P5-PITRM1

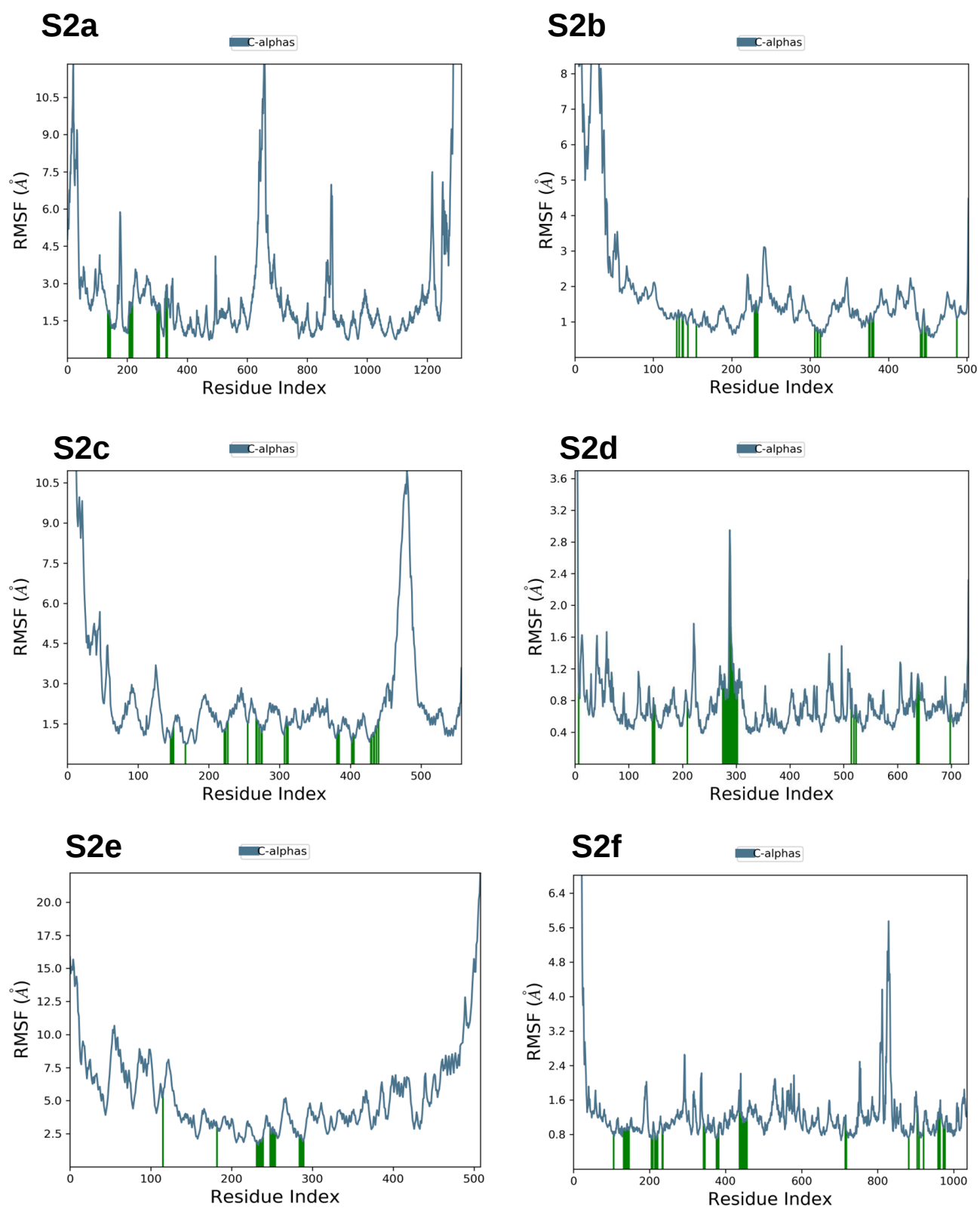


Figure S2. Protein RMSF (a) CLUH (b) CYP51A1 (c) GLUD1 (d) LSS. (e) P4HB. (f) PITRM1

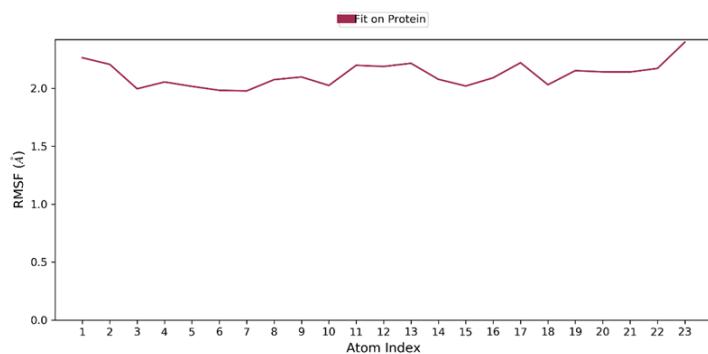
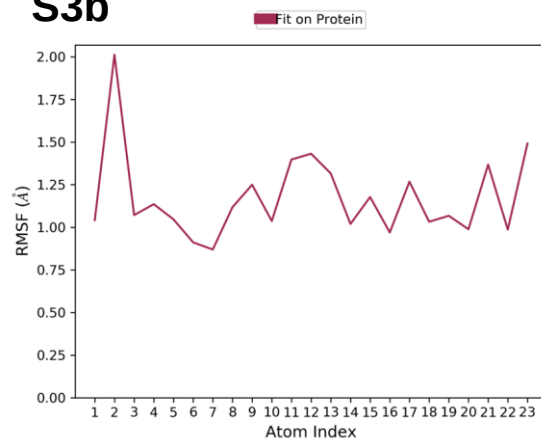
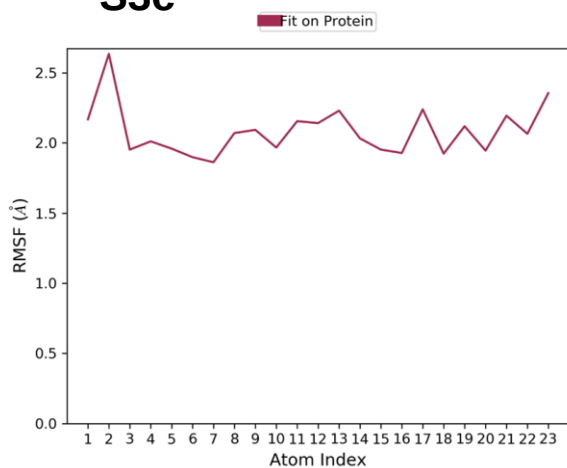
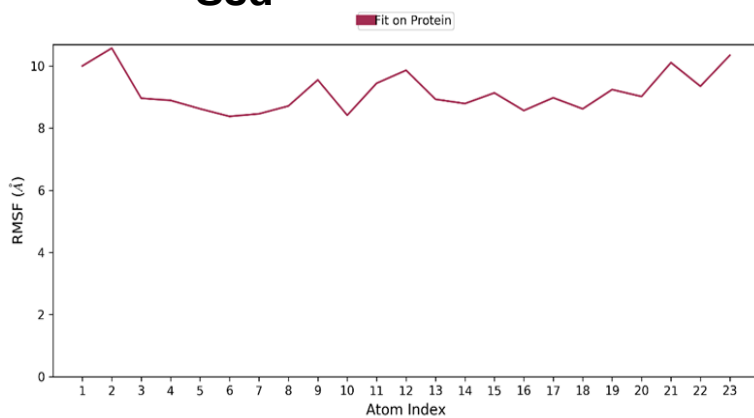
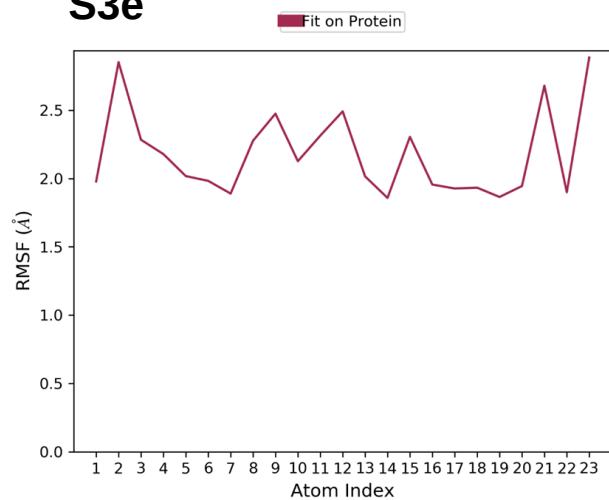
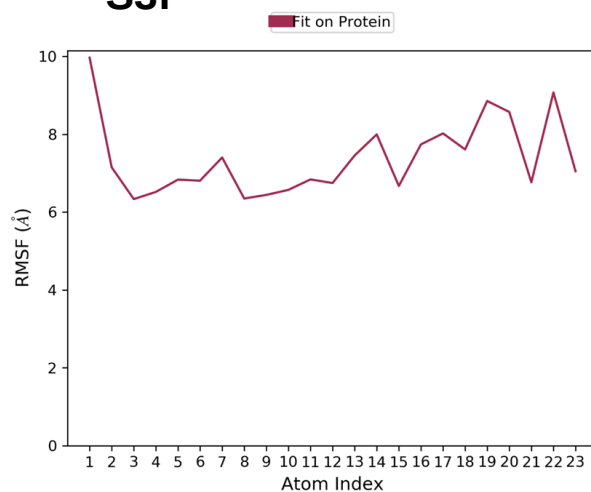
S3a**S3b****S3c****S3d****S3e****S3f**

Figure S3. Substrate (P5) RMSF (a) CLUH (b) CYP51A1 (c) GLUD1 (d) LSS. (e) P4HB. (f) PITRM1

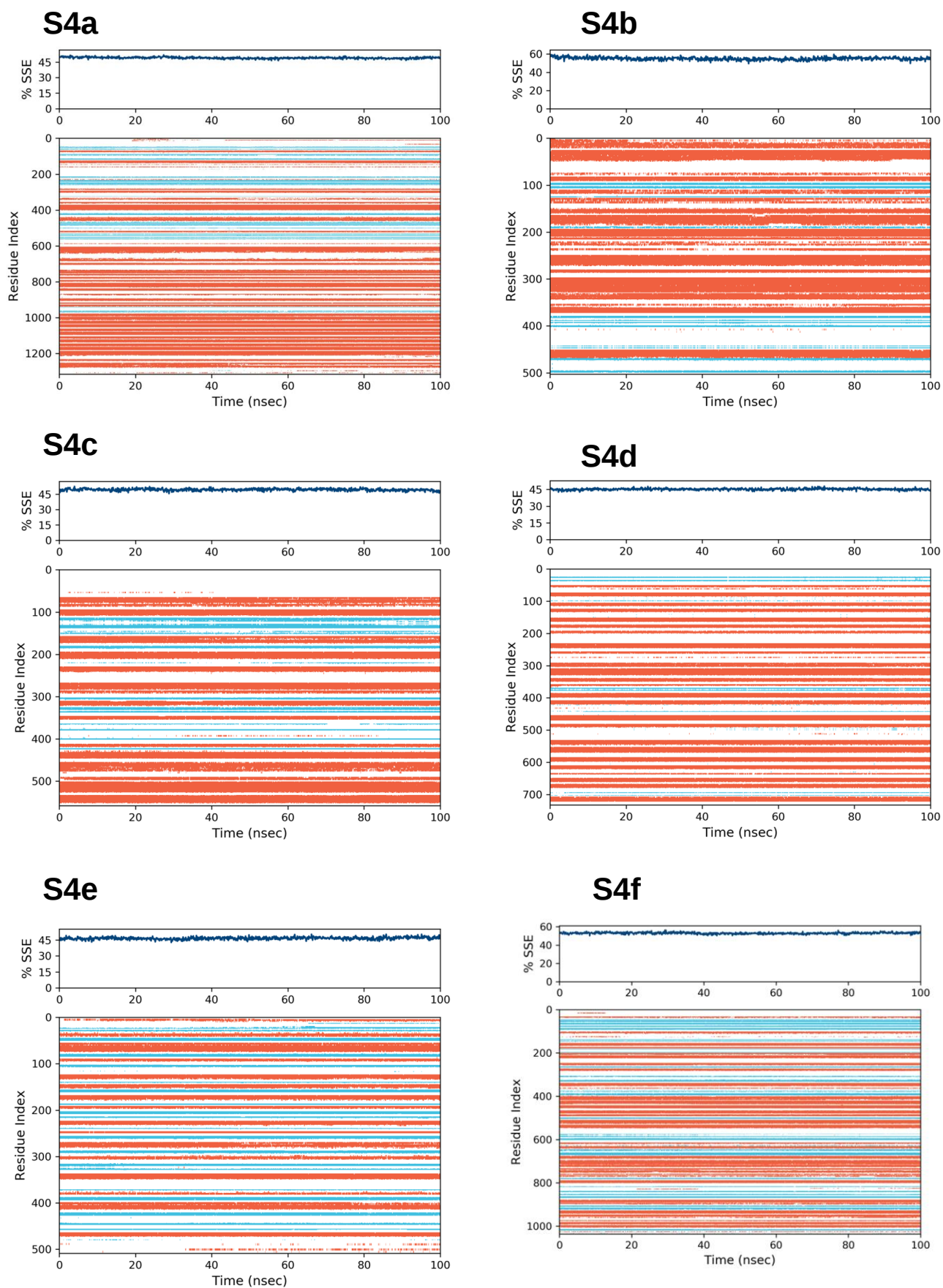


Figure S4. Secondary structure elements [SSE] (a) CLUH (b) CYP51A1 (c) GLUD1 (d) LSS. (e) P4HB. (f) PITRM1

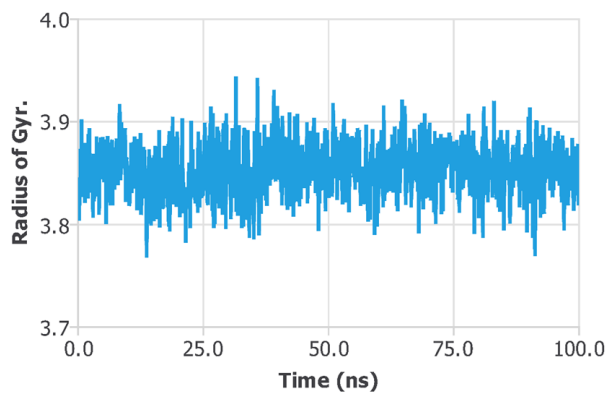
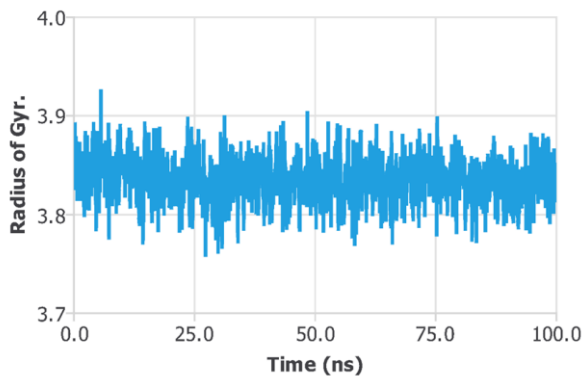
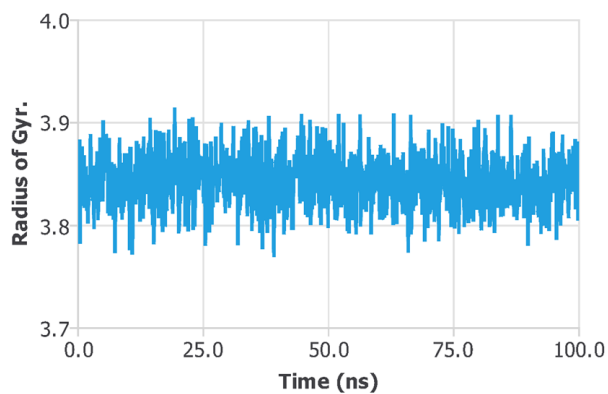
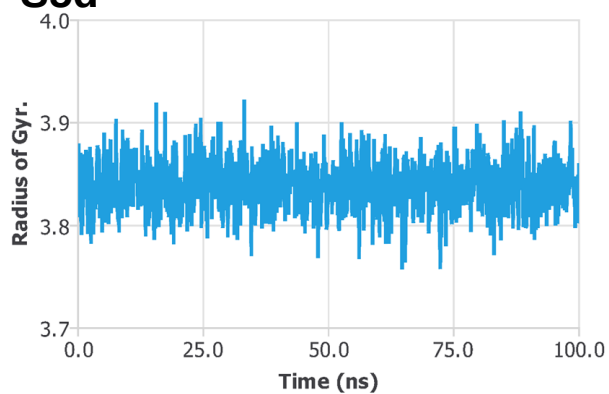
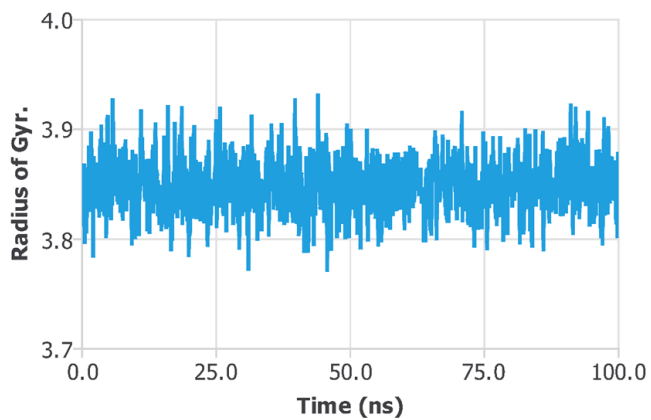
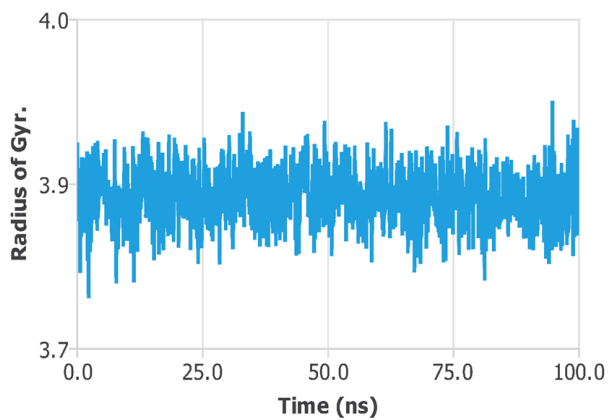
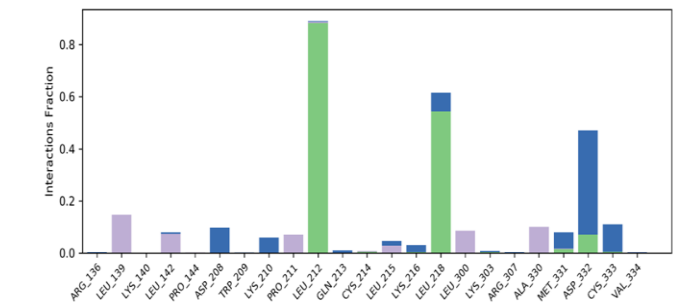
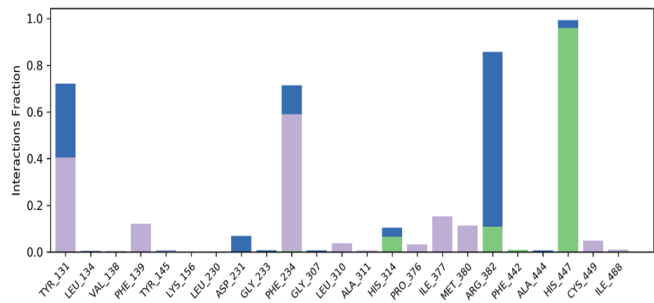
S5a**S5b****S5c****S5d****S5e****S5f**

Figure S5. Radius of gyration (a) CLUH (b) CYP51A1 (c) GLUD1 (d) LSS. (e) P4HB. (f) PITRM1

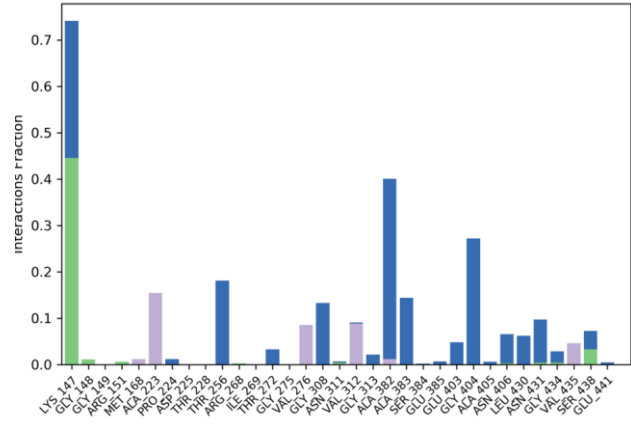
S6a



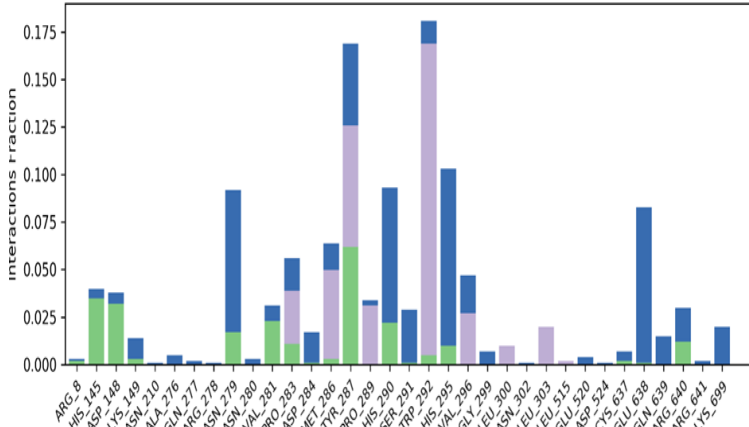
S6b



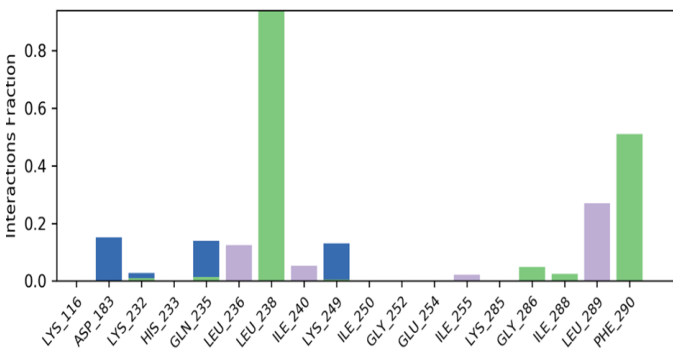
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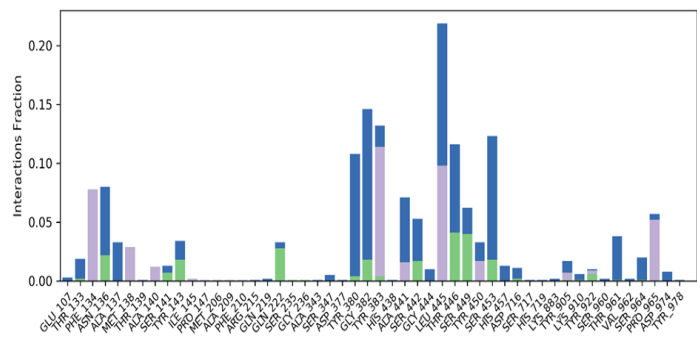
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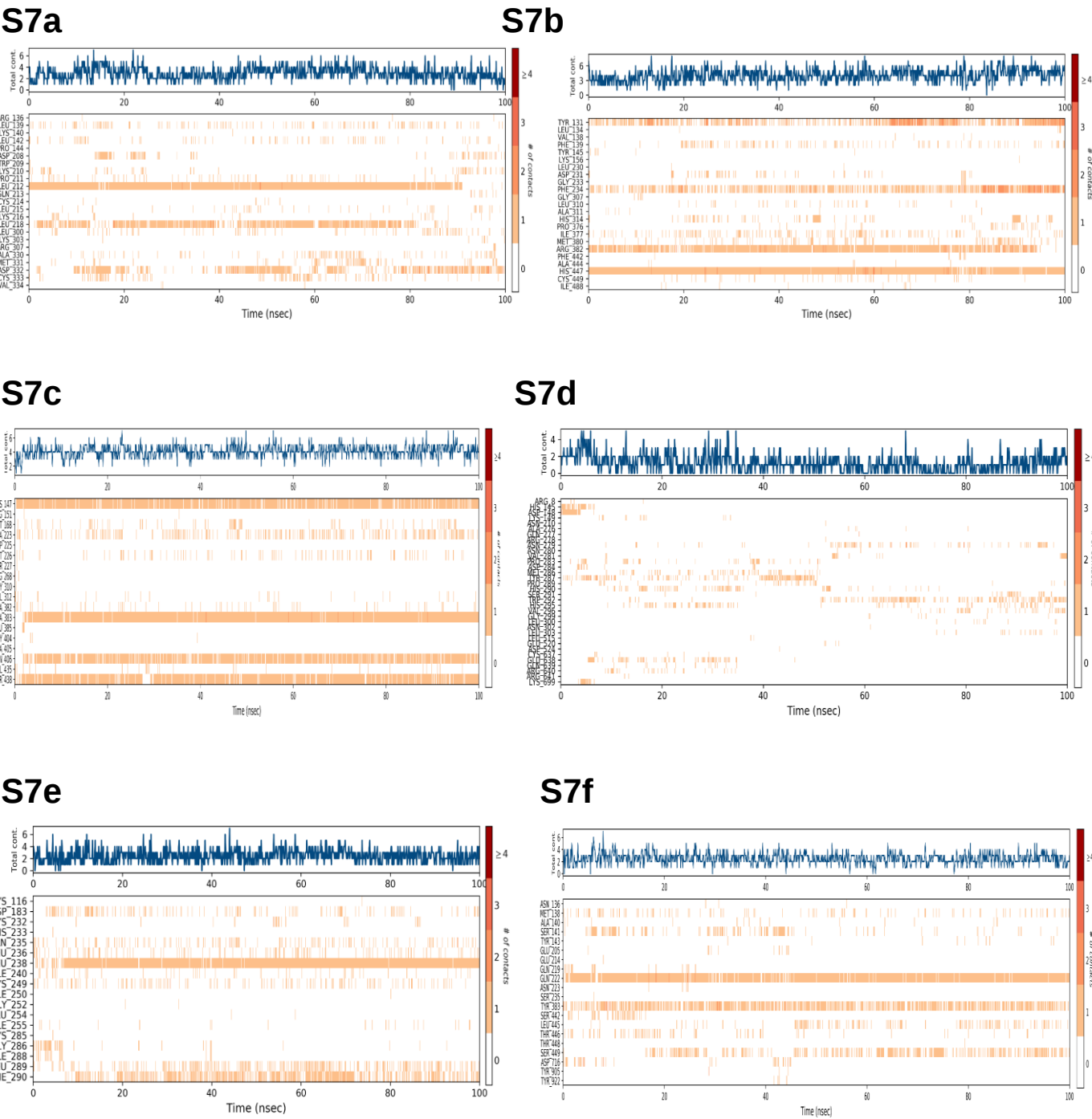


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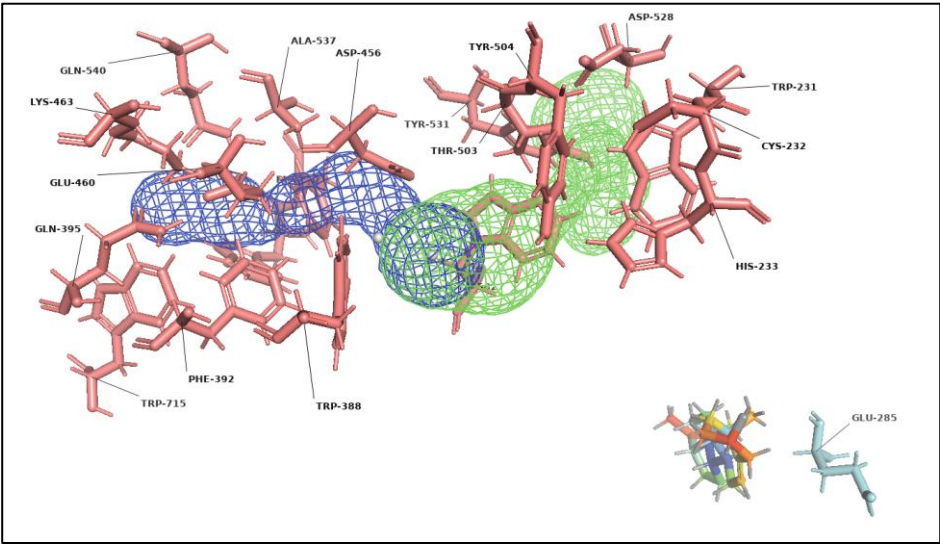


S6f

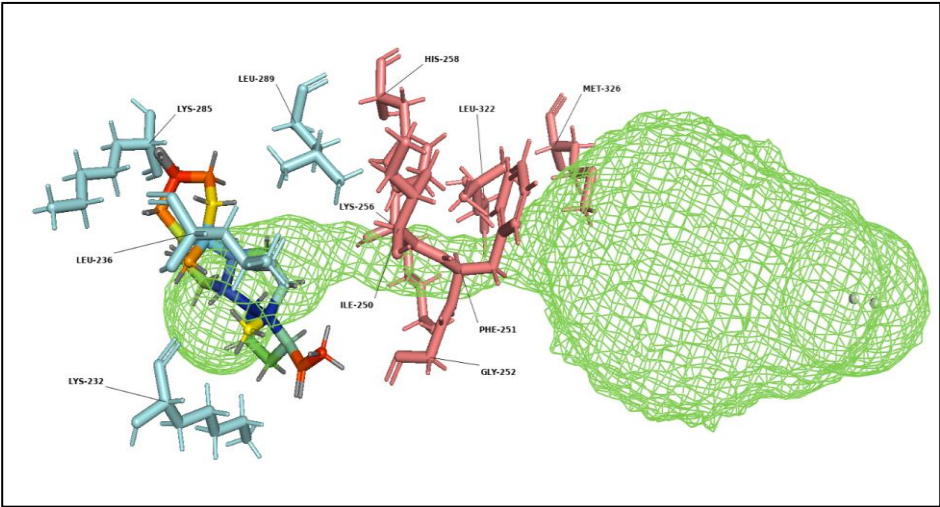




S8a



S8b



S8c

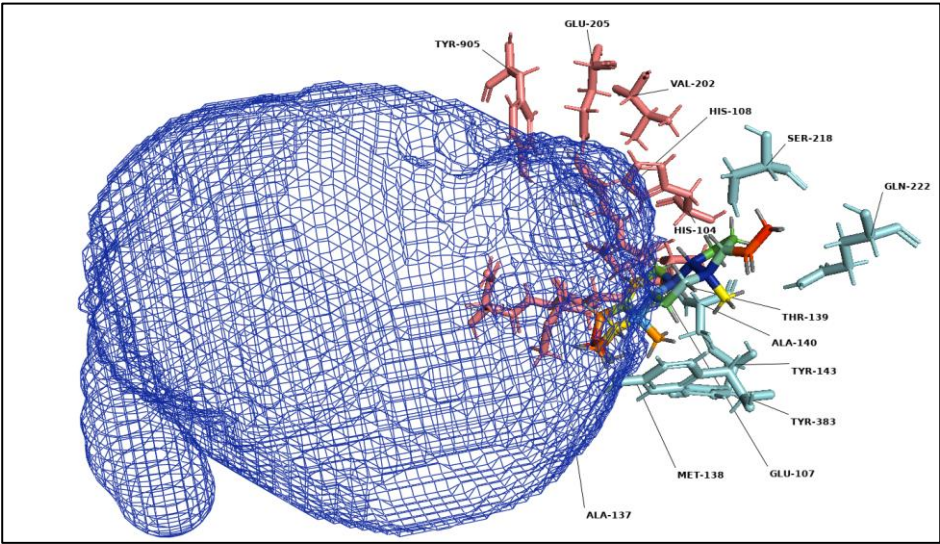


Figure S8. Non-involvement of tunnels for P5 transport. (a) LSS protein, Cyan color denotes hydrogen and hydrophobic interactions; Red Salmon color denotes other amino acids surrounding the tunnel. (b) P4HB protein, Cyan color denotes hydrogen and hydrophobic interactions; Red Salmon color denotes other amino acids surrounding the tunnel. (C) PITRM1 protein, Cyan color denotes hydrogen and hydrophobic interactions; Red Salmon color denotes other amino acids surrounding the tunnel. (b)