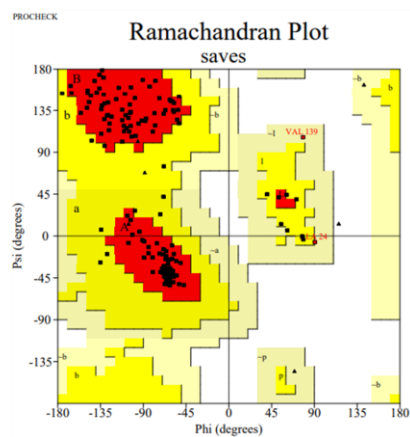


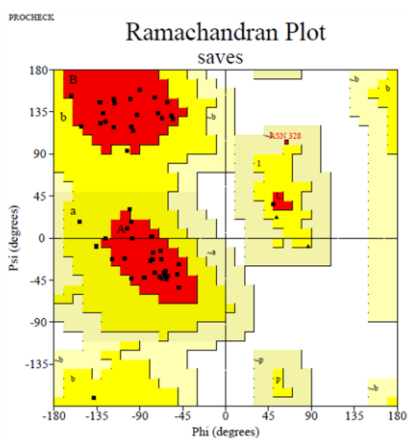
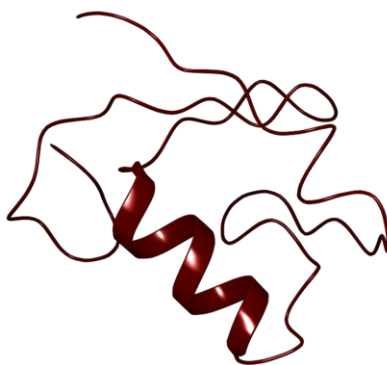
Supplementary material

Figure S1. 3D structures of target proteins of Ermp1 from *S. pombe*. Homology modeling in Phyre2 and Ramachandran plot. Model validation by using PROCHECK-SAVES v6.0 server. Editing the model in UCSF Chimera 1.17.1.

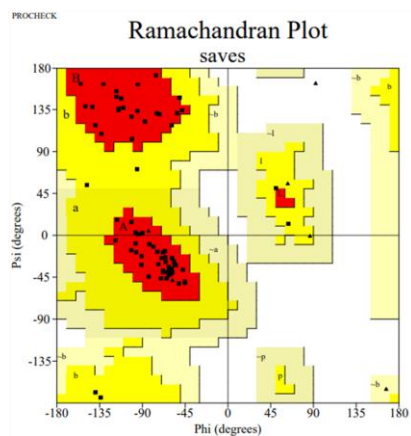
Ypt5



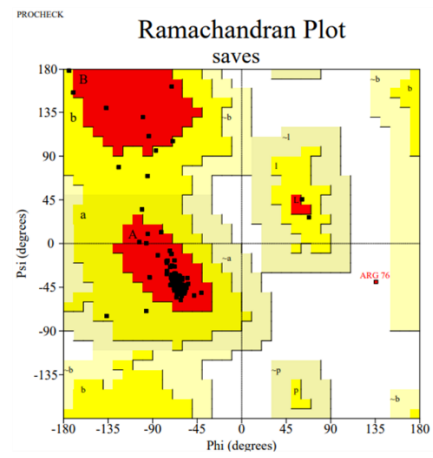
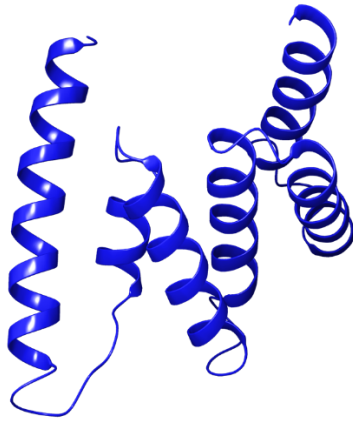
Pex12



Oca8



Fis1



Pmc1

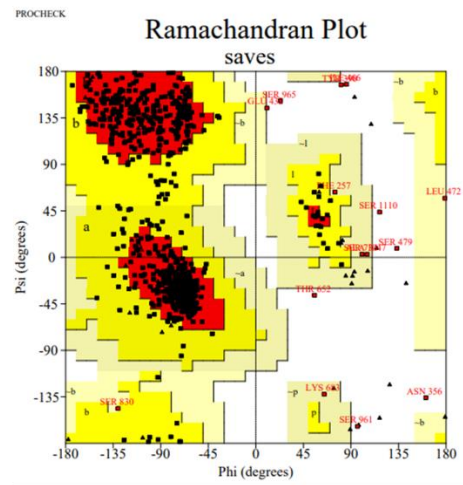


Figure S2. AlphaFold prediction and Ramachandran Plot of the 3D structure of Amk2 from *S. pombe*.

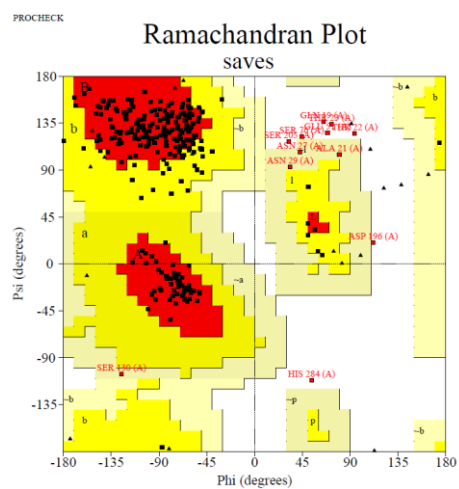
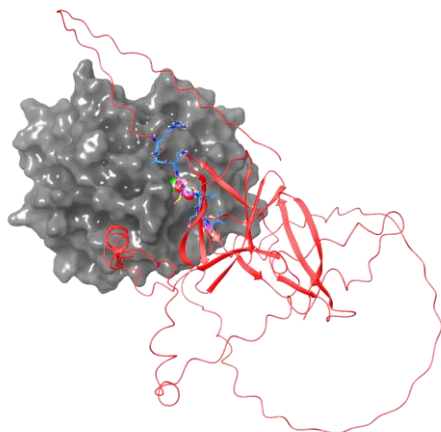
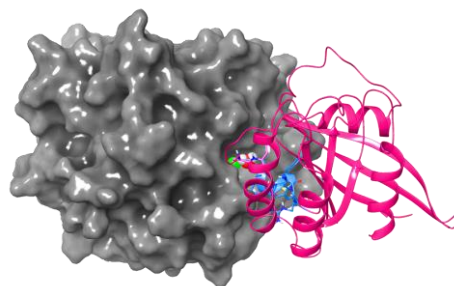


Figure S3. Molecular docking of the M28 domain of Ermp1 with protein targets. Ligand cleavage segment is shown in blue. Cleavage residues are shown in pink. Solvation performed in the WaterMap tool. Editing the models in Maestro 13.0.

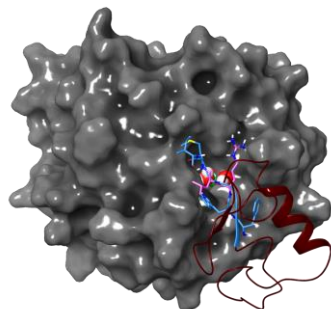
Ermp1-Amk2



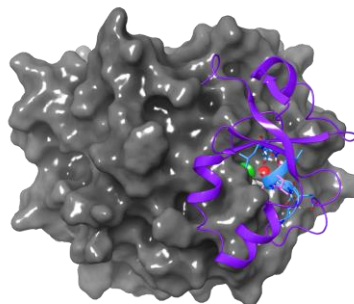
Ermp1-Ypt5



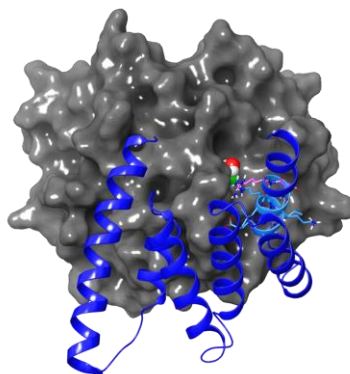
Ermp1-Pex12



Ermp1-Oca8



Ermp1-Fis1



Ermp1-Pmc1

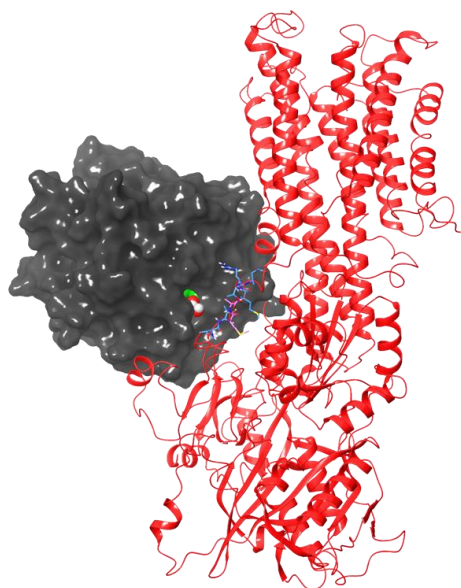
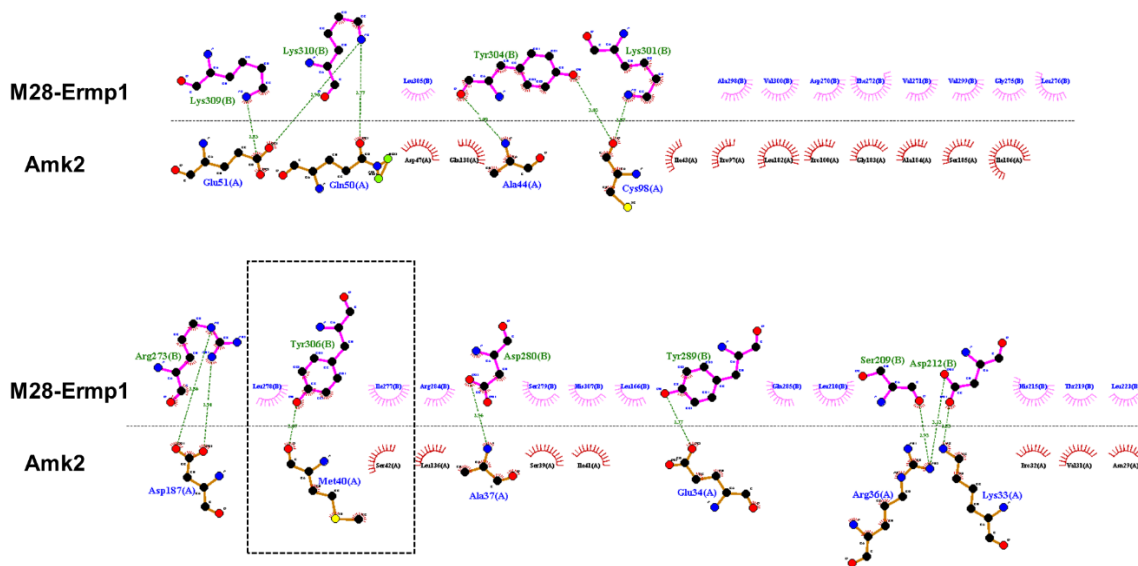
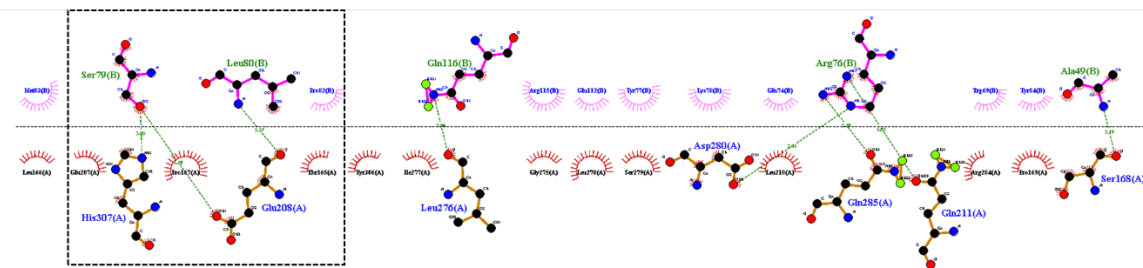


Figure S4. DIMPLOT 2D-interaction plot of M28 domain of Ermp1 with protein targets (A-F). The horizontal dashed line represents the interface. The green dotted line represents the hydrogen bond length, while the arc represents the hydrophobic interaction. The dotted boxes delineate the identified interactions between the residues of Ermp1's catalytic cavity and the potential cleavage residues within the target proteins.



A) Ermp1-Amk2

Ypt5



M28-Ermp1

B) Ermp1-Ypt5

C) Ermp1-Pex12

D) Ermp1-Oca8

M28-Ermp1

E) Ermp1-Fis1

F) Ermp1-Pmc1

Figure S5. Representation of the solvation of the interaction complexes of the M28 domain of Ermp1 and cleavage sites of protein targets (A-F). Binding sites Zn^{2+} are shown in orange. Catalytic site is shown in purple. Catalytic stabilizer is shown in magenta. Cleavage residues are shown in pink. Solvation performed in the WaterMap tool. Editing the models in Maestro 13.0.

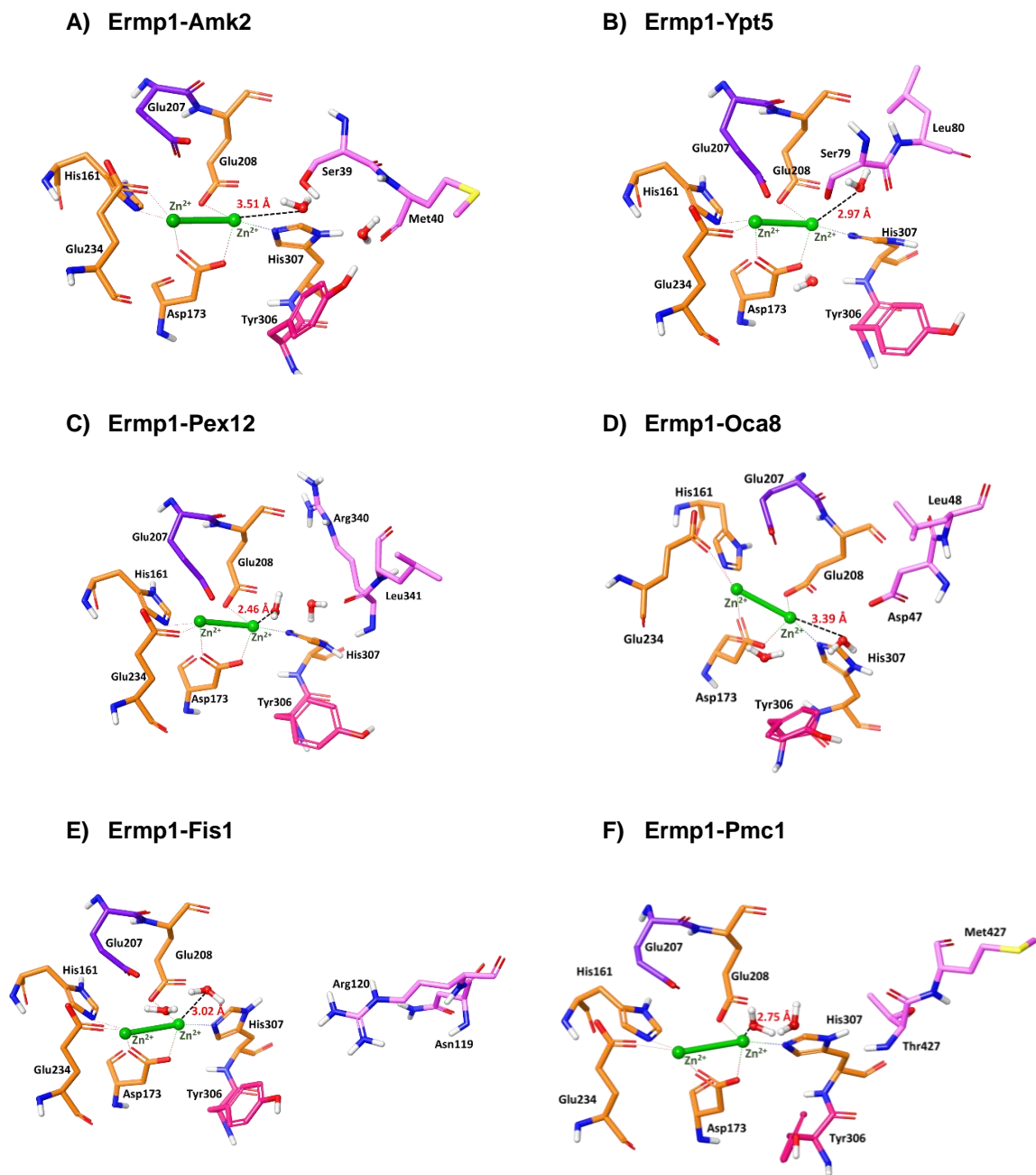


Figure S6. Analysis of RMSF trajectories of residues of the protein-protein complexes. The Root Mean Square Fluctuation (RMSF) was calculated to examine residual fluctuations throughout the simulation time for Ermp1-Amk2, Ermp1-Pex12, and Ermp1-Ypt5 (A-C respectively). Each simulation was conducted for 120 ns in the Desmond Molecular Dynamics System to assess the stability of protein-protein interaction.

