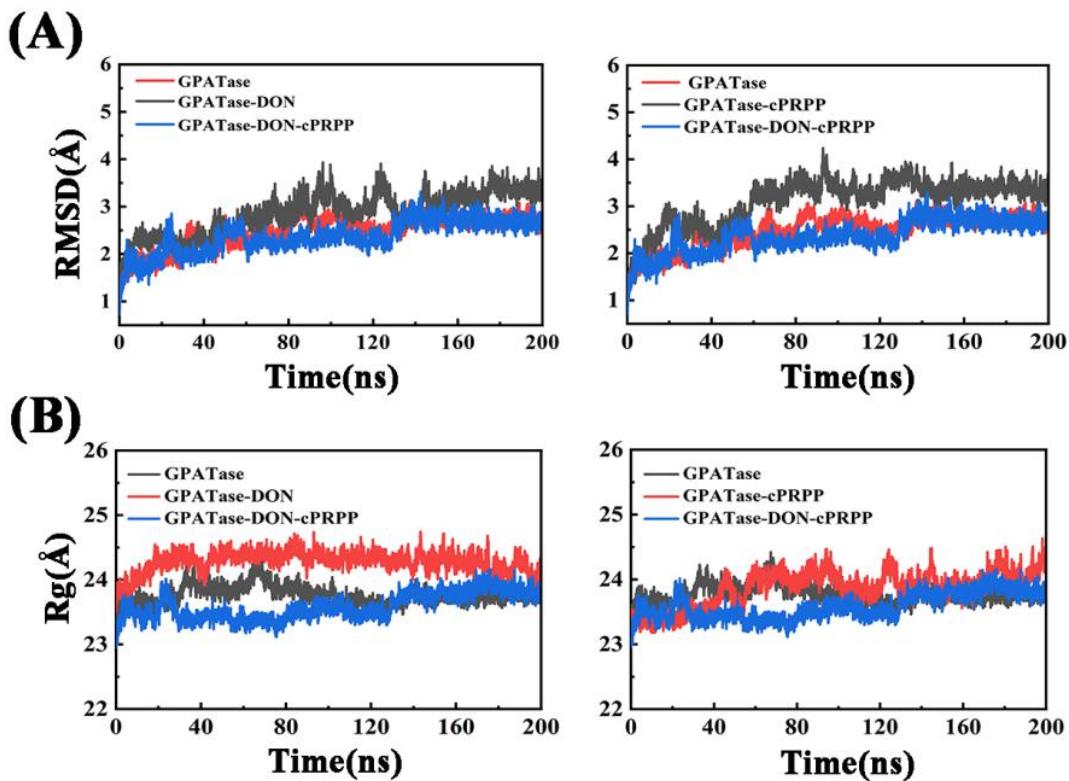
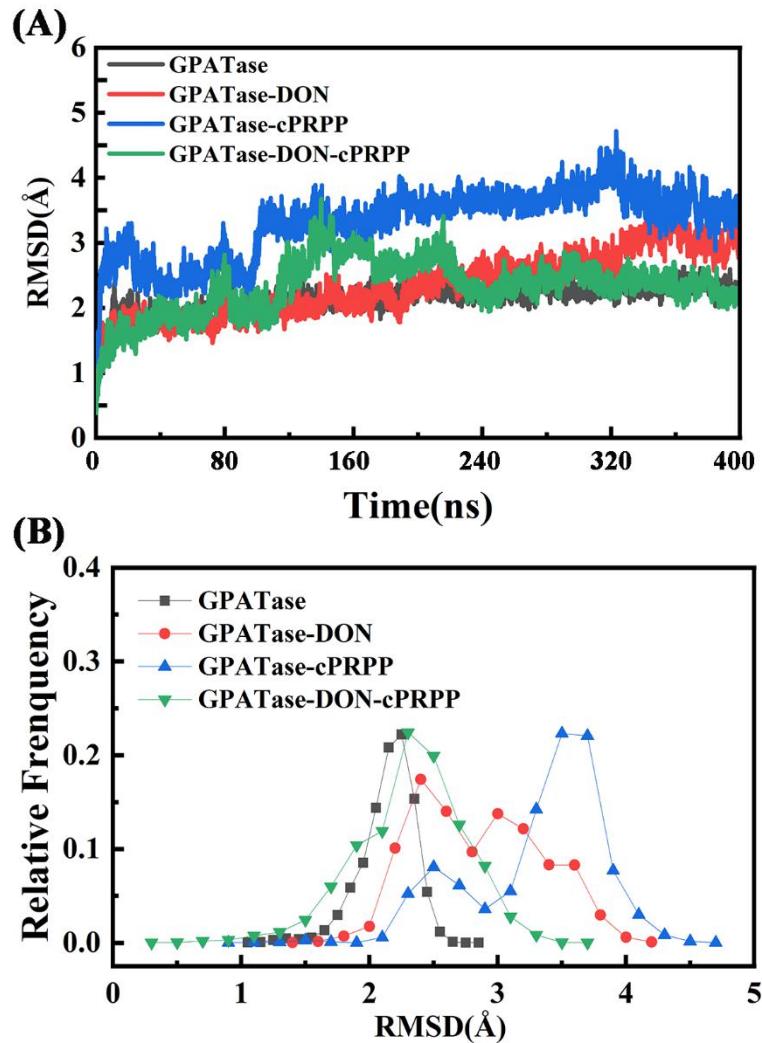


## *Supplementary Material*

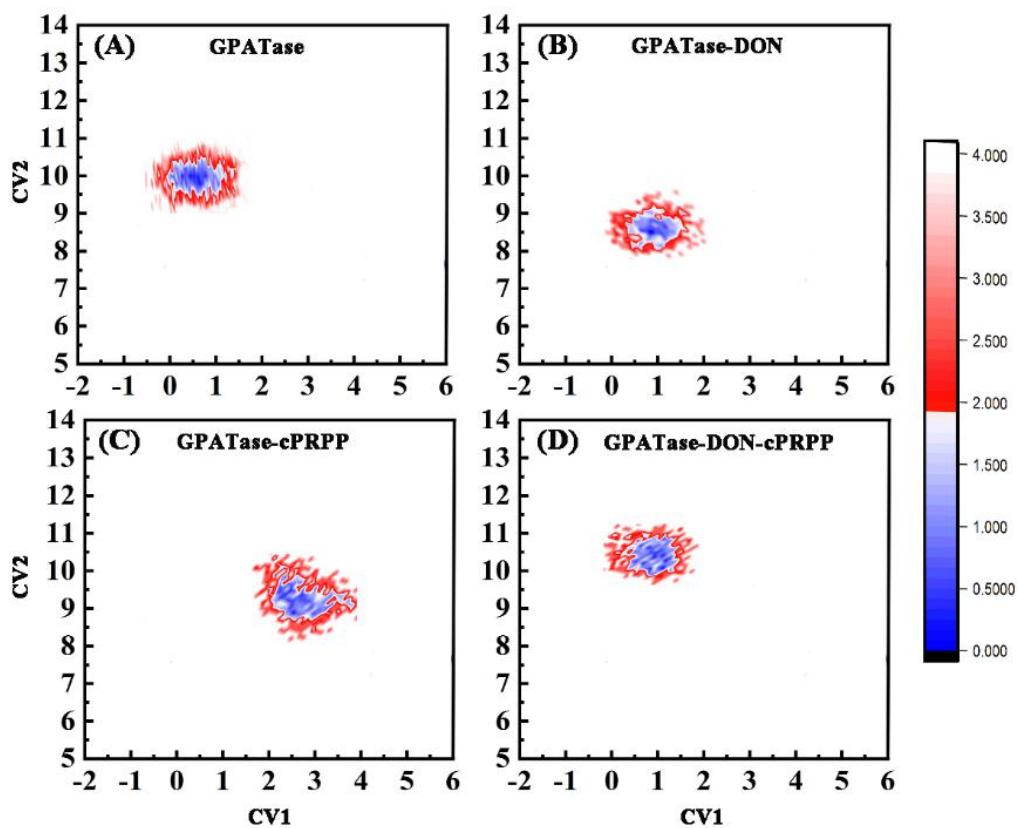
### Supplementary Figures and Tables



**Figure S1.** Stability analysis during 200ns cMD simulations for four systems. **(A)** The RMSD plot and **(B)** Radius of gyration( $R_g$ ) plot.



**Figure S2.** Stability analysis during 400ns aMD simulations for four systems. (A) The RMSD plot of C $\alpha$  atoms. (B) The corresponding relative frequency RMSD values.



**Figure S3.** The free energy profile maps of flexible loops for (A) GPATase; (B) GPATase-DON; (C) GPATase-cPRPP; (D) GPATase-DON-cPRPP as a function of CV1 and CV2 in Å during cMD simulations.

**Table S1.** Clustering results for the top six clusters from GPATase model MD simulations trajectories with K-means clustering algorithm.

#Cluster	Frames	%	AvgDist <sup>a</sup>	Stdev <sup>b</sup>	Centroid <sup>c</sup>	AvgCDist <sup>d</sup>
0	6458	32.3	1.32	0.16	17321	2.12
1	3455	17.3	1.46	0.22	10827	1.95
2	2029	10.5	1.29	0.14	12286	1.95
3	1817	9.1	1.44	0.22	5837	1.69
4	1715	8.6	1.31	0.21	586	2.02
5	1277	6.4	1.30	0.20	2239	1.81

**Table S2.** Clustering results for the top six clusters from GPATase-DON model MD simulations trajectories with K-means clustering algorithm.

#Cluster	Frames	%	AvgDist <sup>a</sup>	Stdev <sup>b</sup>	Centroid <sup>c</sup>	AvgCDist <sup>d</sup>
0	3046	15.2	1.40	0.17	13644	1.32
1	2983	14.9	1.45	0.21	15864	1.41
2	2661	13.3	1.34	0.18	7767	1.53
3	2203	11.0	1.35	0.19	3133	1.78
4	2092	10.5	1.25	0.16	1500	2.14
5	1856	9.3	1.53	0.23	17478	1.58

**Table S3.** Clustering results for the top six clusters from GPATase-cPRPP model MD simulations trajectories with K-means clustering algorithm.

#Cluster	Frames	%	AvgDist <sup>a</sup>	Stdev <sup>b</sup>	Centroid <sup>c</sup>	AvgCDist <sup>d</sup>
0	4234	21.2	1.51	0.21	8412	2.06
1	3634	18.2	1.40	0.20	12680	2.00
2	2284	11.4	1.44	0.24	2355	2.16
3	2194	11.0	1.51	0.24	18376	2.19
4	1731	8.7	1.60	0.25	15455	1.79
5	1428	7.1	1.56	0.27	4250	1.99

**Table S4.** Clustering results for the top six clusters from GPATase-DON-cPRPP model MD simulations trajectories with K-means clustering algorithm.

#Cluster	Frames	%	AvgDist <sup>a</sup>	Stdev <sup>b</sup>	Centroid <sup>c</sup>	AvgCDist <sup>d</sup>
0	5109	25.5	1.36	0.19	11520	1.35
1	3248	16.2	1.49	0.23	7182	1.42
2	2854	14.3	1.32	0.16	17733	1.63
3	2579	12.9	1.37	0.20	14761	1.59
4	1721	8.6	1.40	0.20	16033	1.61
5	1372	6.9	1.35	0.23	1031	1.46

<sup>a</sup> AvgDist is the the average distance (Å) between all frames in the cluster

<sup>b</sup> Stdev is the standard deviation (Å) between all frames in the cluster.

<sup>c</sup> Centroid is the frame number of the lowest cumulative distance to any other frames.

<sup>d</sup> AvgCdist is the average distance (Å) of the cluster to any other cluster.