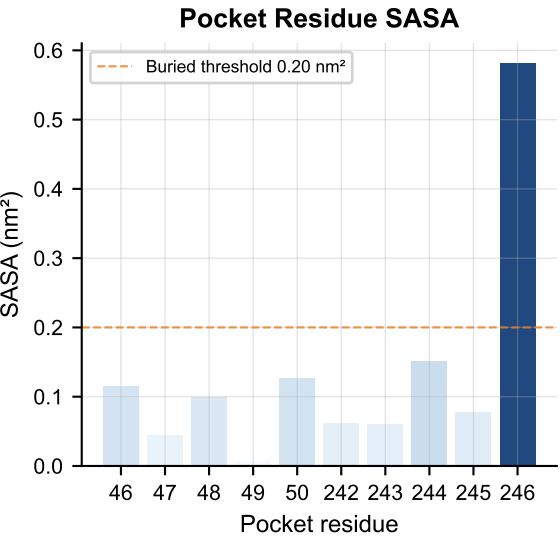
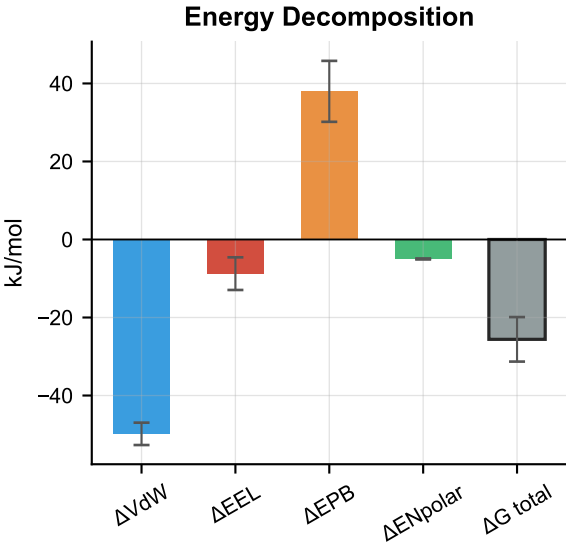
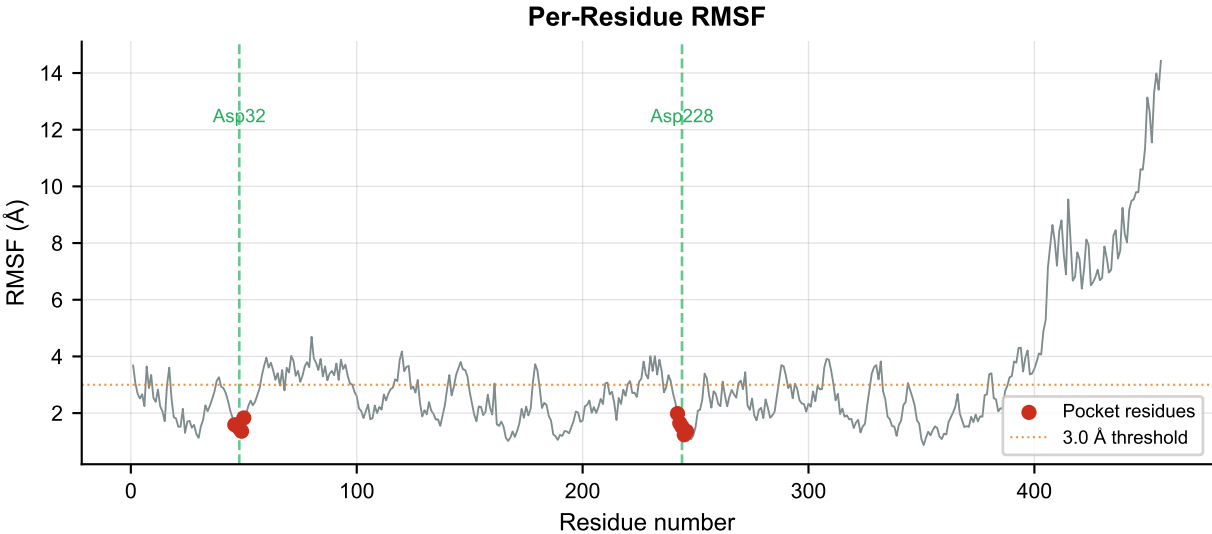




Simulation Summary

H-bonds (mean):	0.89 ± 0.83
H-bond pairs ≤3.5Å:	2.44
H-bonds unique:	22
Max H-bond occupancy:	0.284
Mean H-bond occupancy:	0.040
Min P-L distance:	1.93 Å
Rg (mean):	3.1540 ± 0.1054 nm
SASA protein (mean):	243.37 nm ²
RMSD ligand (mean):	5.61 ± 1.71 Å
RMSD protein (mean):	7.19 ± 2.09 Å
RMSF pocket (mean):	1.554 ± 0.214 Å

Classification

Marginal

$\Delta G = -25.60$ kJ/mol
RMSD lig = 5.61 Å
H-bonds = 0.89