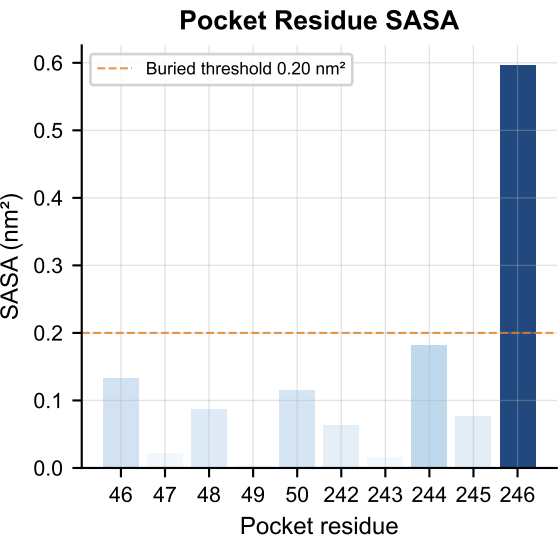
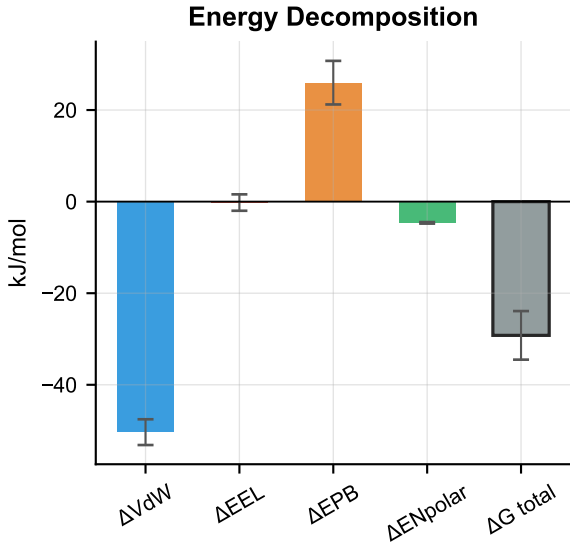
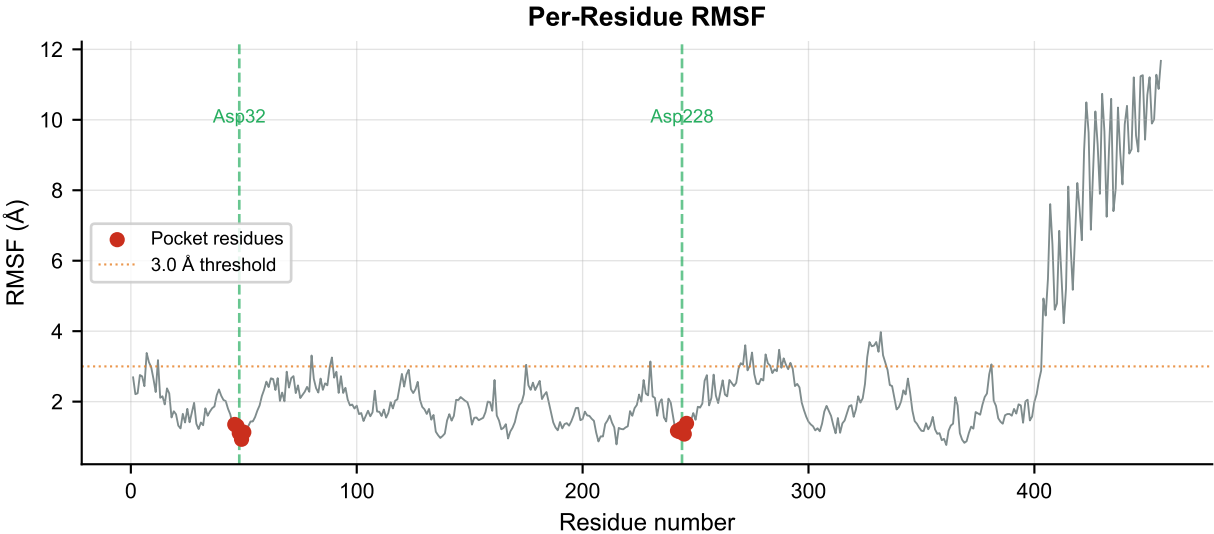




Simulation Summary

H-bonds (mean):	0.01 ± 0.12
H-bond pairs ≤3.5Å:	0.06
H-bonds unique:	1
Max H-bond occupancy:	0.015
Mean H-bond occupancy:	0.015
Min P-L distance:	1.95 Å
Rg (mean):	2.6423 ± 0.1282 nm
SASA protein (mean):	240.33 nm ²
RMSD ligand (mean):	3.92 ± 0.58 Å
RMSD protein (mean):	5.64 ± 1.73 Å
RMSF pocket (mean):	1.185 ± 0.131 Å

Classification

Marginal

$\Delta G = -29.21$ kJ/mol
RMSD lig = 3.92 Å
H-bonds = 0.01