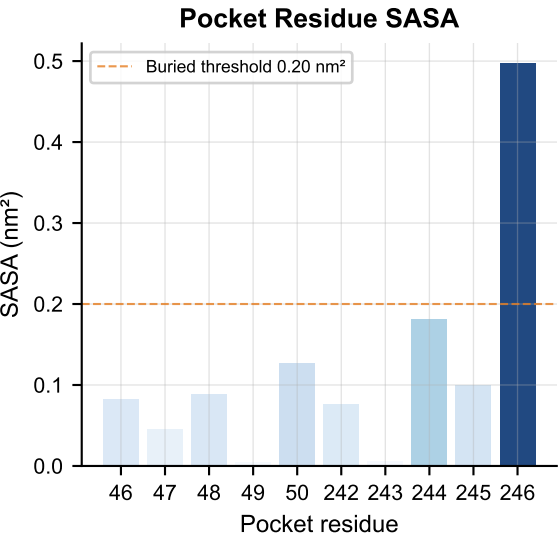
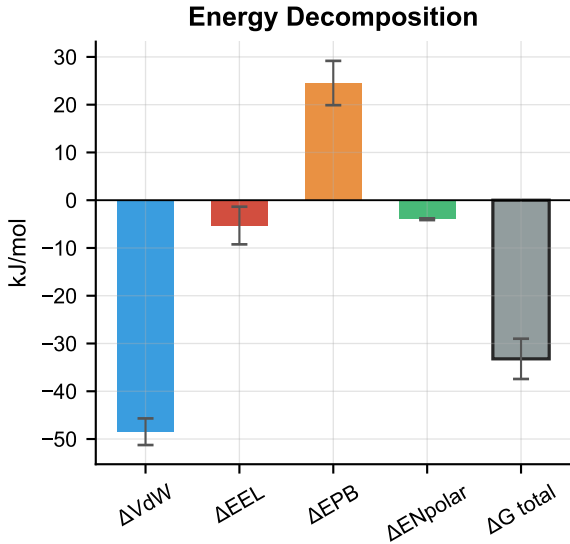
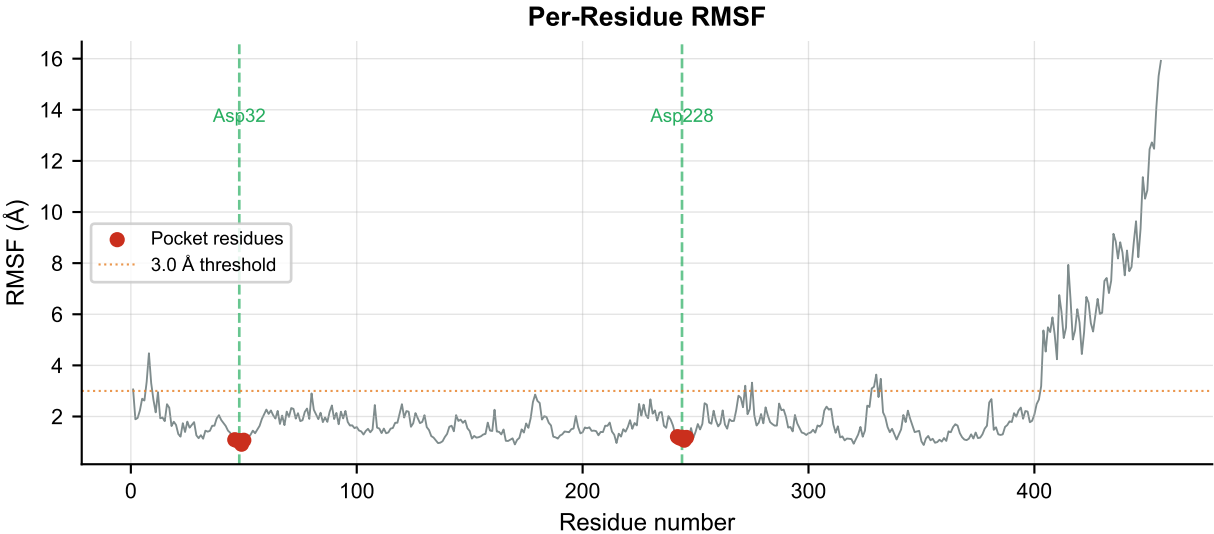




Simulation Summary

H-bonds (mean):	0.05 ± 0.24
H-bond pairs ≤3.5Å:	0.41
H-bonds unique:	5
Max H-bond occupancy:	0.028
Mean H-bond occupancy:	0.011
Min P-L distance:	2.49 Å
Rg (mean):	2.6907 ± 0.1003 nm
SASA protein (mean):	240.61 nm ²
RMSD ligand (mean):	4.38 ± 0.45 Å
RMSD protein (mean):	5.62 ± 1.36 Å
RMSF pocket (mean):	1.101 ± 0.083 Å

Classification

Marginal

$\Delta G = -33.21$ kJ/mol
RMSD lig = 4.38 Å
H-bonds = 0.05