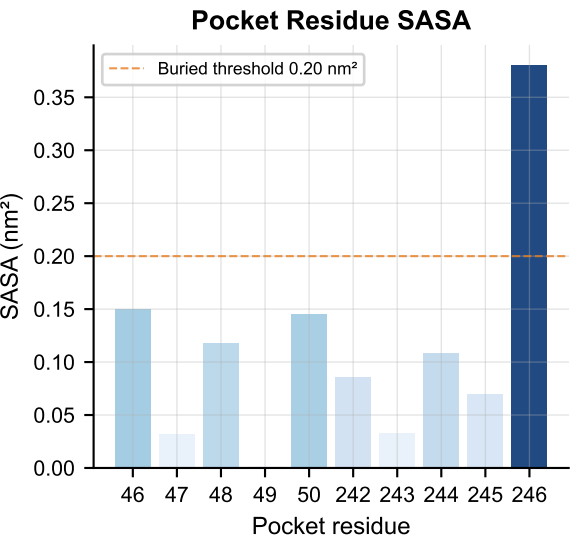
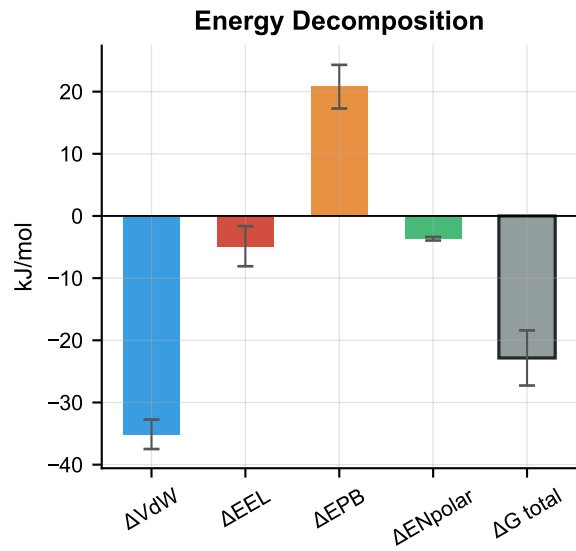
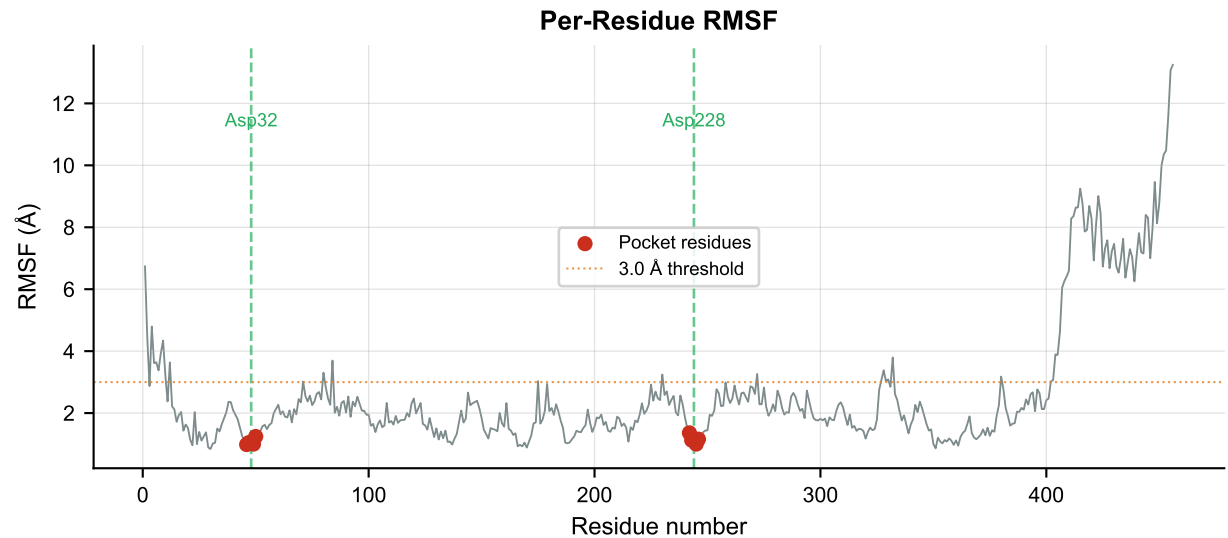




Simulation Summary

H-bonds (mean):	0.70 ± 0.51
H-bond pairs ≤3.5Å:	0.80
H-bonds unique:	15
Max H-bond occupancy:	0.552
Mean H-bond occupancy:	0.046
Min P-L distance:	1.95 Å
Rg (mean):	3.0224 ± 0.0829 nm
SASA protein (mean):	245.35 nm ²
RMSD ligand (mean):	6.37 ± 1.49 Å
RMSD protein (mean):	5.22 ± 1.54 Å
RMSF pocket (mean):	1.107 ± 0.116 Å

Classification

Marginal

$\Delta G = -22.84$ kJ/mol
RMSD lig = 6.37 Å
H-bonds = 0.70