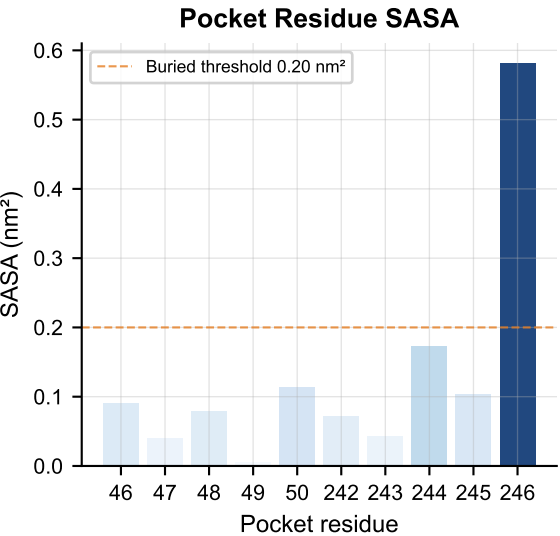
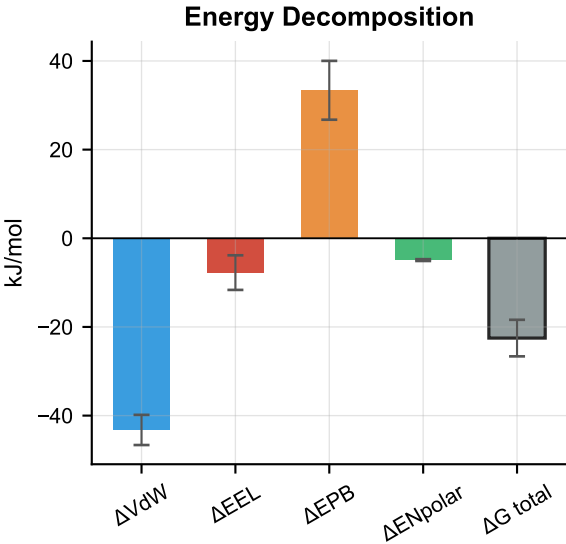
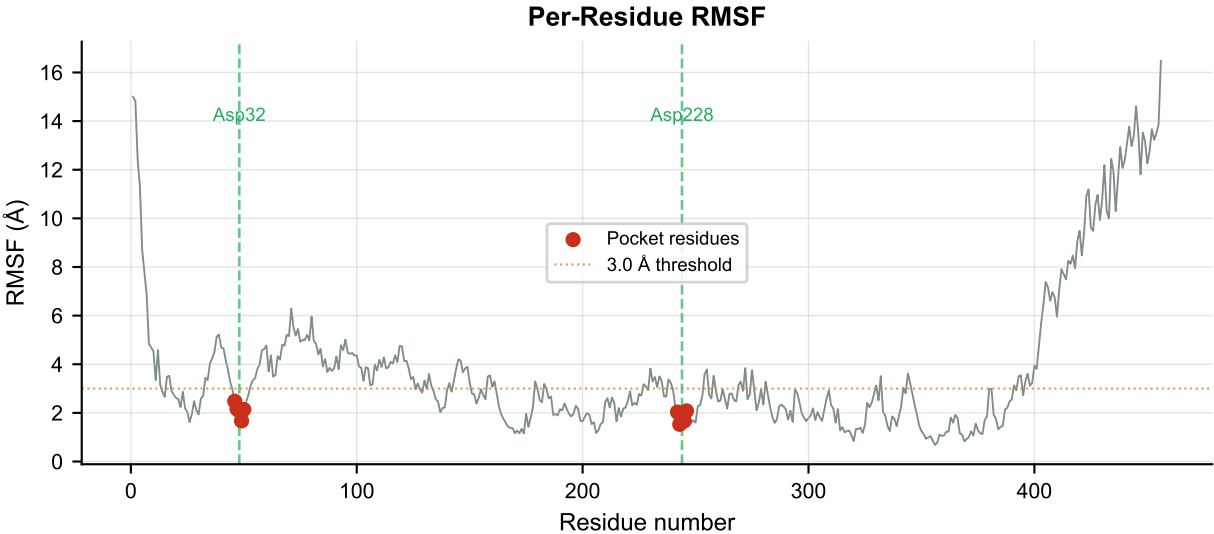




Simulation Summary

H-bonds (mean):	0.48 ± 0.67
H-bond pairs ≤3.5Å:	2.85
H-bonds unique:	14
Max H-bond occupancy:	0.165
Mean H-bond occupancy:	0.034
Min P-L distance:	2.05 Å
Rg (mean):	2.9961 ± 0.1426 nm
SASA protein (mean):	251.00 nm ²
RMSD ligand (mean):	4.69 ± 2.18 Å
RMSD protein (mean):	5.41 ± 2.79 Å
RMSF pocket (mean):	1.960 ± 0.279 Å

Classification

Marginal

$\Delta G = -22.51$ kJ/mol
RMSD lig = 4.69 Å
H-bonds = 0.48