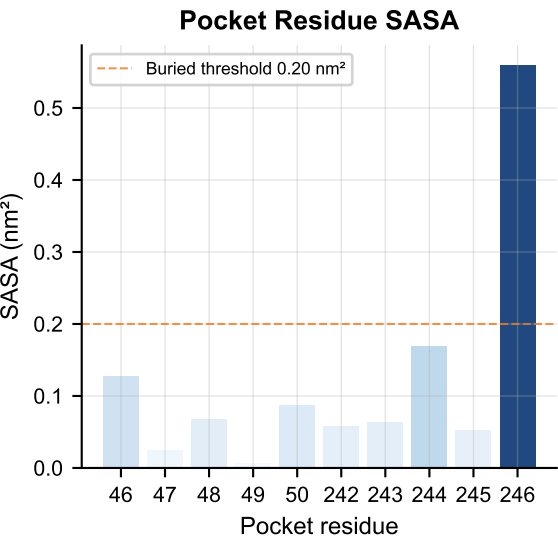
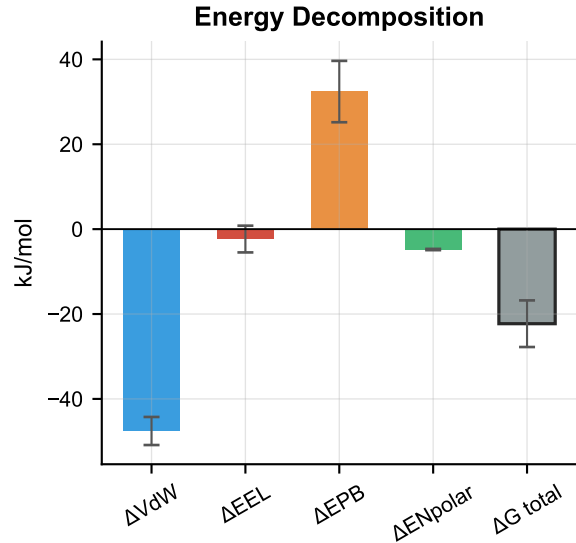
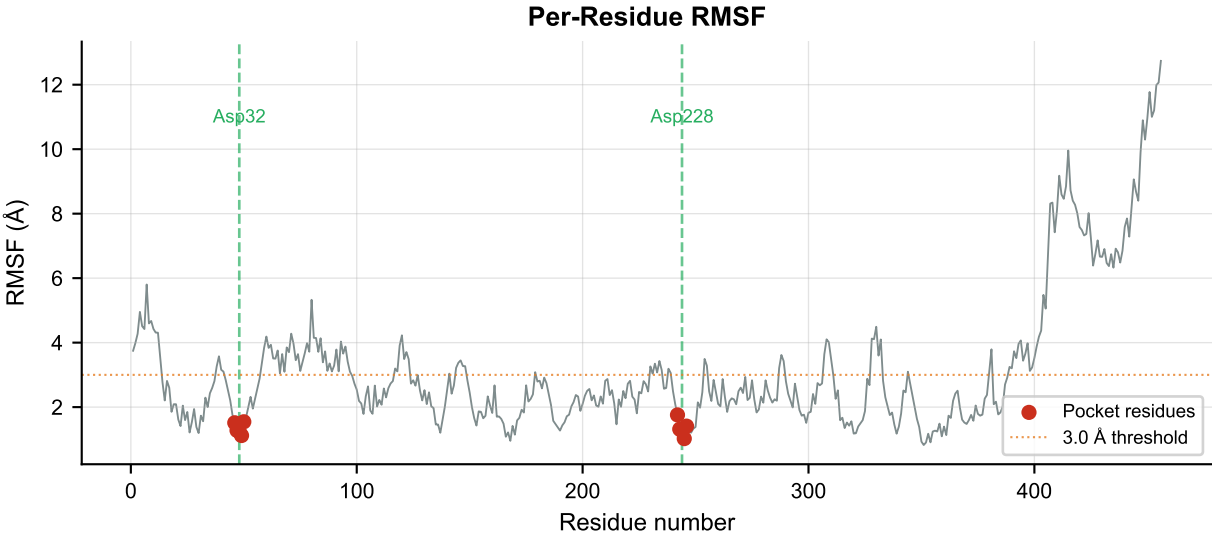




Simulation Summary

H-bonds (mean):	1.15 ± 0.79
H-bond pairs ≤3.5Å:	2.38
H-bonds unique:	13
Max H-bond occupancy:	0.567
Mean H-bond occupancy:	0.088
Min P-L distance:	2.05 Å
Rg (mean):	3.1142 ± 0.0699 nm
SASA protein (mean):	242.32 nm ²
RMSD ligand (mean):	6.55 ± 1.59 Å
RMSD protein (mean):	8.30 ± 2.31 Å
RMSF pocket (mean):	1.347 ± 0.205 Å

Classification

Marginal

$\Delta G = -22.28$ kJ/mol
RMSD lig = 6.55 Å
H-bonds = 1.15