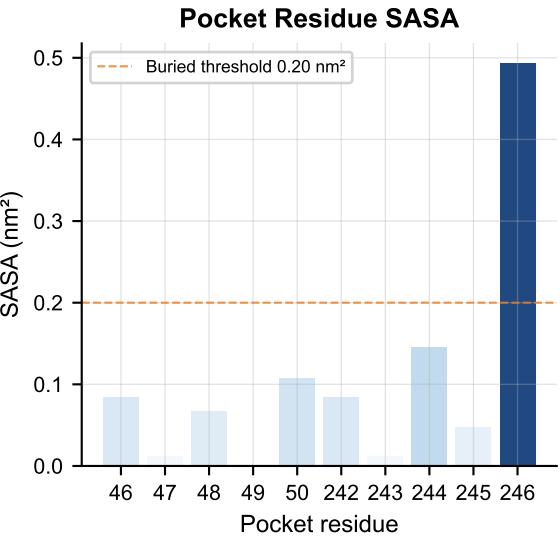
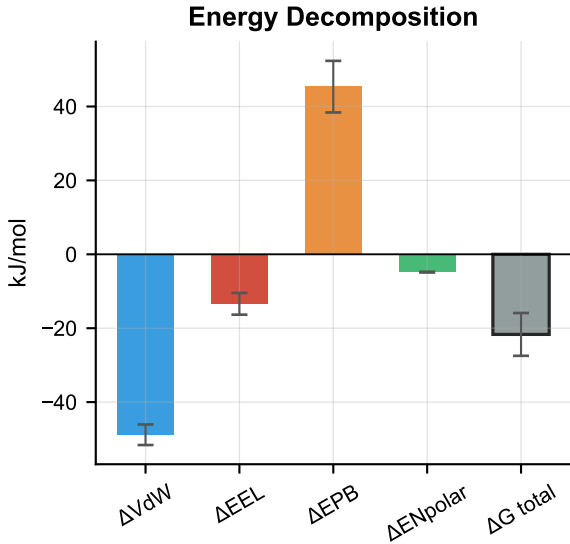
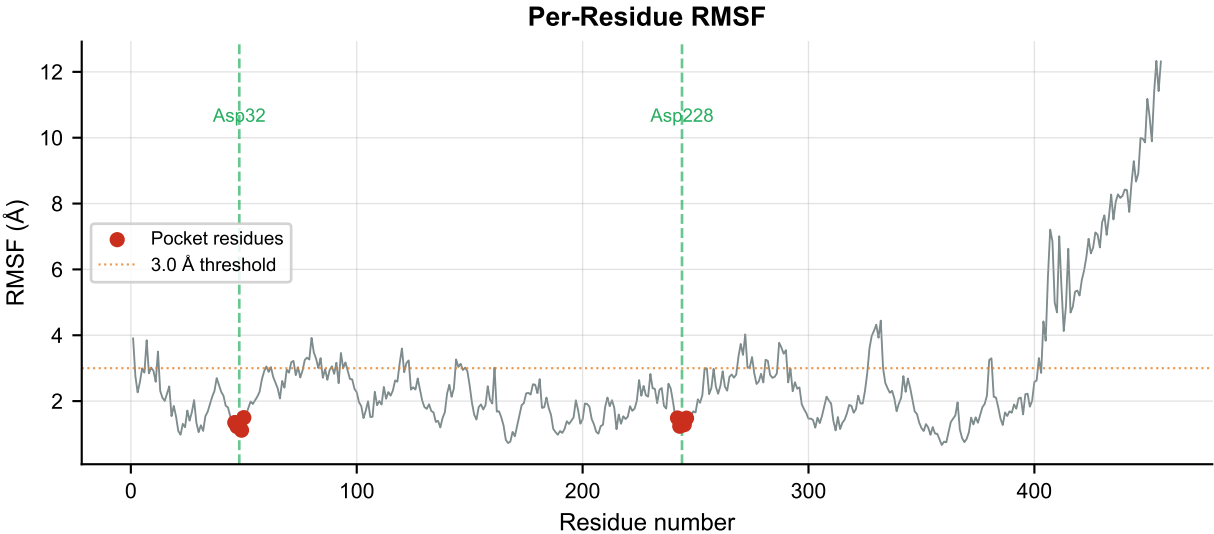




Simulation Summary

H-bonds (mean):	1.17 ± 0.78
H-bond pairs ≤3.5Å:	1.57
H-bonds unique:	10
Max H-bond occupancy:	0.626
Mean H-bond occupancy:	0.117
Min P-L distance:	2.04 Å
Rg (mean):	2.8174 ± 0.0769 nm
SASA protein (mean):	246.22 nm ²
RMSD ligand (mean):	3.02 ± 0.87 Å
RMSD protein (mean):	4.22 ± 1.56 Å
RMSF pocket (mean):	1.329 ± 0.123 Å

Classification

Marginal

$\Delta G = -21.68$ kJ/mol
RMSD lig = 3.02 Å
H-bonds = 1.17