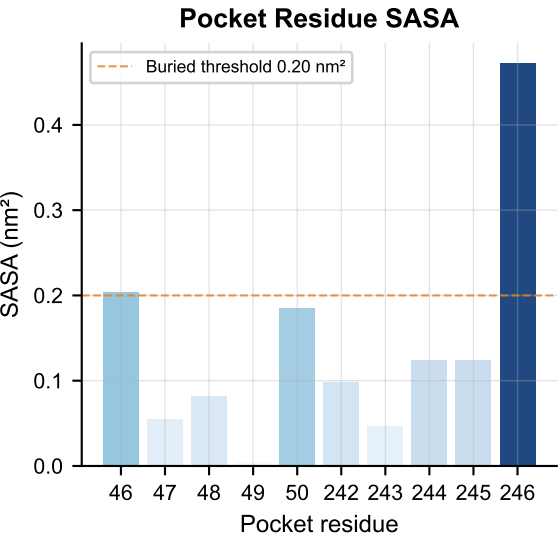
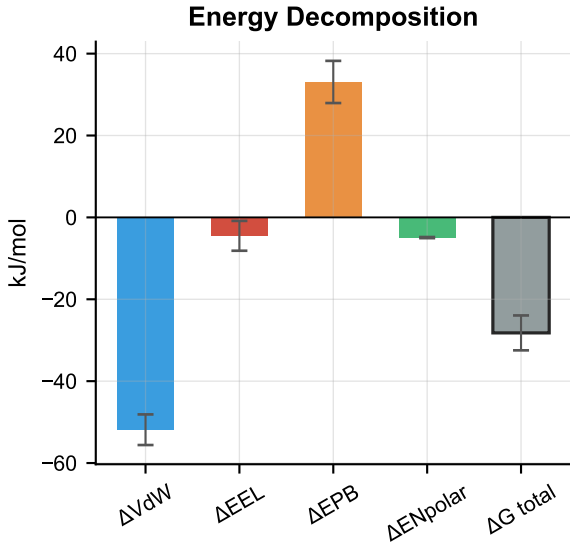
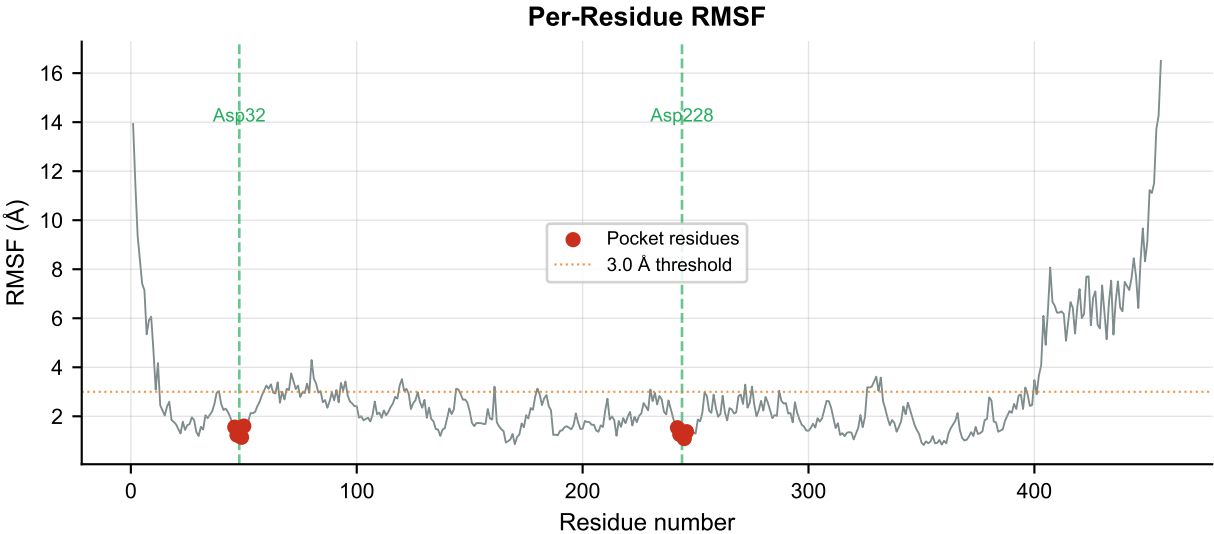




Simulation Summary

H-bonds (mean):	1.92 ± 1.08
H-bond pairs ≤3.5Å:	5.41
H-bonds unique:	23
Max H-bond occupancy:	0.570
Mean H-bond occupancy:	0.083
Min P-L distance:	1.95 Å
Rg (mean):	2.9041 ± 0.0520 nm
SASA protein (mean):	246.85 nm ²
RMSD ligand (mean):	3.20 ± 0.64 Å
RMSD protein (mean):	5.00 ± 1.72 Å
RMSF pocket (mean):	1.339 ± 0.166 Å

Classification

Stable

$\Delta G = -28.21$ kJ/mol
RMSD lig = 3.20 Å
H-bonds = 1.92