

# FEP+ Simulation Details and Results

## System Details

Job name: absolute\_binding\_chosen\_hits

Job type: absolute\_binding

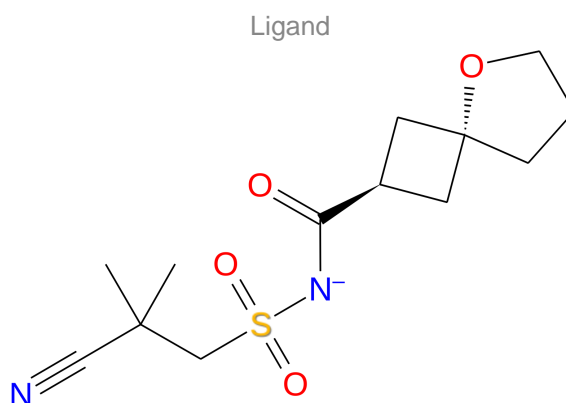
Perturbation: (Z3357096556 ↔ None)

	Ensemble	Force Field	Temp. [K]	Sim Time [ns]	No. Atoms / Waters	$\Delta G$ [kcal/mol]
Solvent:	NPT	S-OPLS*	300.0	5.0	3260 / 1071	279.54 $\pm$ 0.06
Complex:	muVT	S-OPLS*	300.0	5.0	41432 / 10057	294.29 $\pm$ 0.11
Corr. Term:						-8.86 $\pm$ 0.00

**Absolute binding free energy ( $\Delta\Delta G$ ) is: -5.90 kcal/mol**

## Ligand Information

Name	HexID	No. Atoms / Heavy	Atomic Mass	Charge	Mol. Formula
Z3357096556	dab1ad8	39 / 20	299.4 au	-1	C13H19N2O4S



## Protein Information

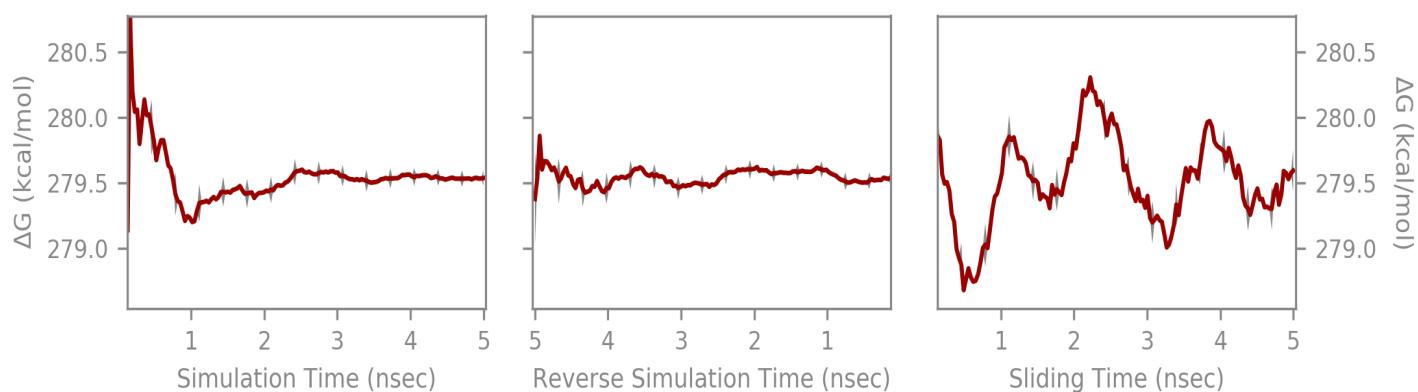
Name	Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	No. Atoms	No. Heavy Atoms	Charge
1L2S_prepared_A_apo_...	358	'A'	358	5582	2800	+4

## Salt Information

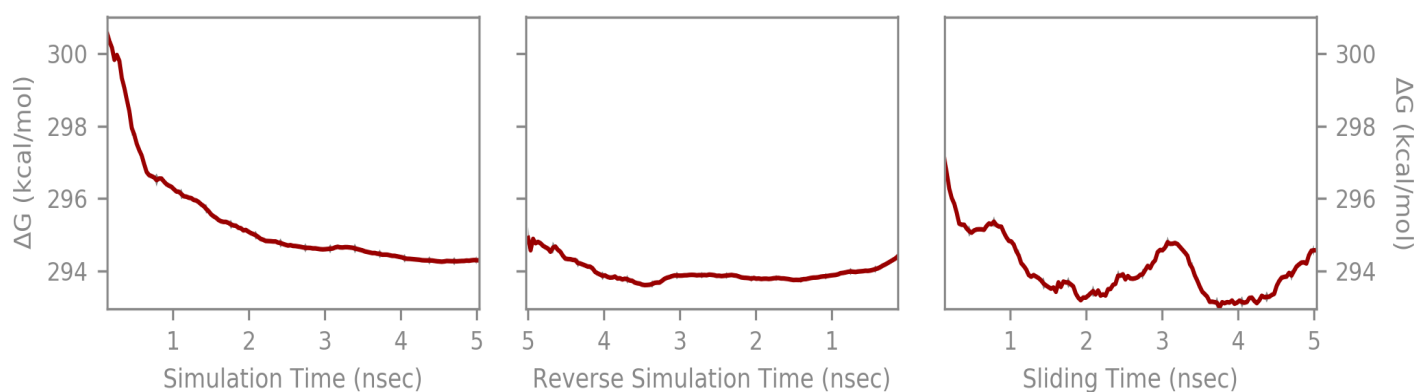
Ion Type	Concentration in Complex	Concentration in Solvent
Na	50.9 mM	47.0 mM
Cl	50.9 mM	54.2 mM

## Free Energy Convergence

### Solvent Leg



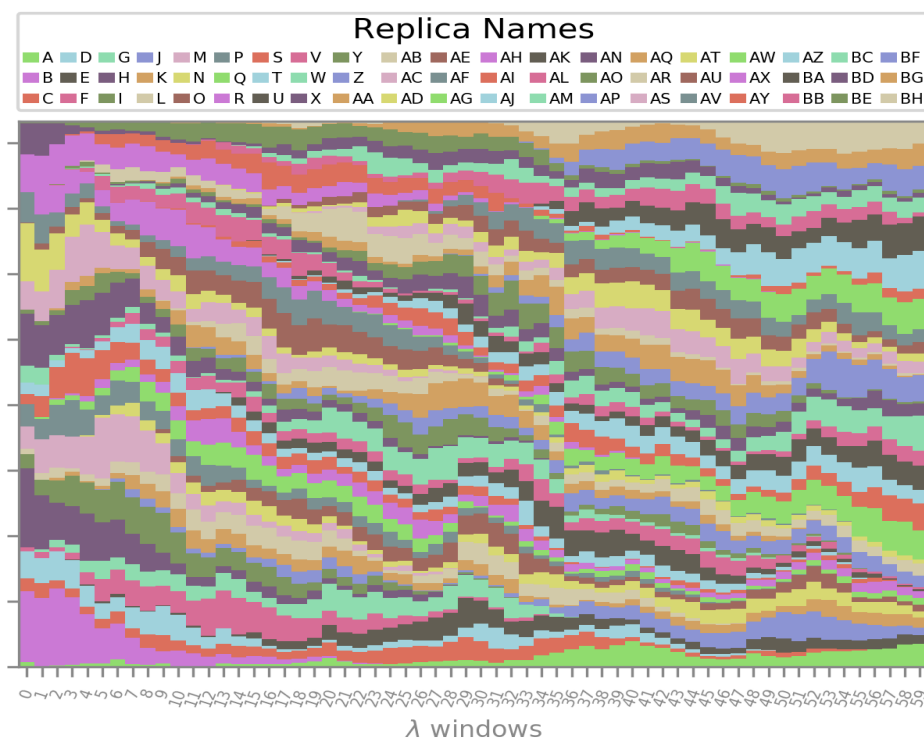
### Complex Leg



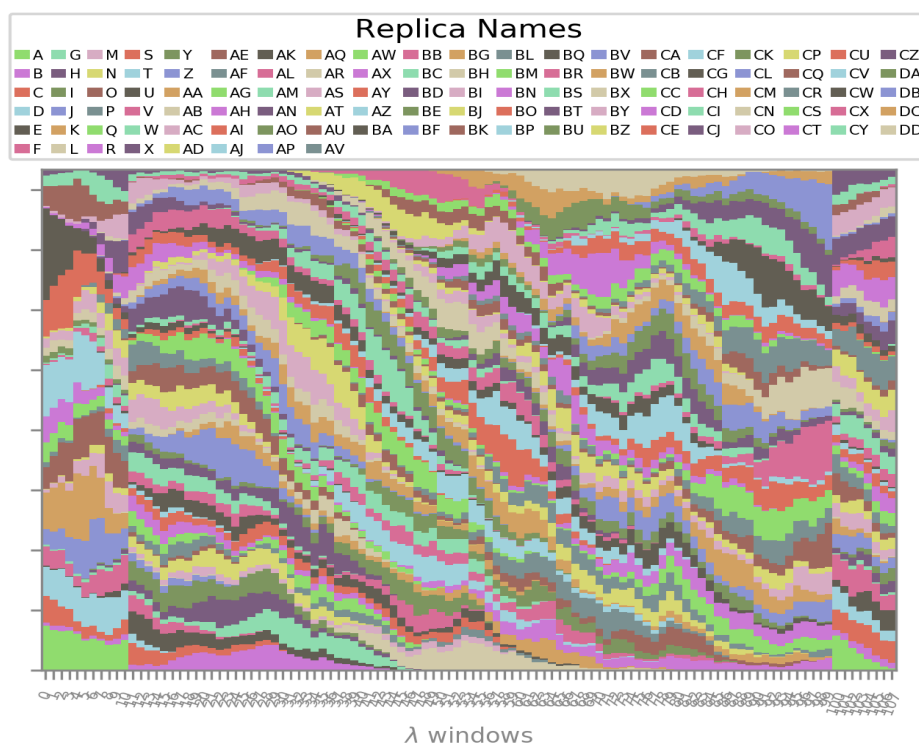
The total free energy differences between the two ligands ( $\Delta G$  in kcal/mol) in solvent and complex legs are plotted as a function of time. Three plots for each leg show the accumulated data during different time window schemes: forward; reverse; and sliding window.

# Exchange Density of FEP Replicas Over $\lambda$ -Windows

## Solvent Leg



## Complex Leg



For both legs of the FEP simulation, each replica is color coded and the plot shows how it occupies different lambda windows during the course of the simulation. Ideally each replica will sample all lambda windows uniformly, however non-uniform sampling is sufficient in most instances.

# Protein Analysis for End-Point $\lambda$ -Replicas

## Protein Information

Name	Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	No. Atoms	No. Heavy Atoms	Charge
1L2S_prepared_A_apo_...	358	'A'	358	5582	2800	+4

- A	4	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	93
SSA	APQOINDIVHRTITPLIEQQKIPGMMAVAVIYQGKPYFTWGYADIAKKQPVTTQOTLFELGSVSKTFTGVLGGDAIARGEIKLSDPTTKYW																			

- A	94	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	183
SSA	PELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSDLLRFYQNWQPAWAPGTQRLYANSSIGLFGALAVKPSGLSFEQAMQTRVFQPLK																			

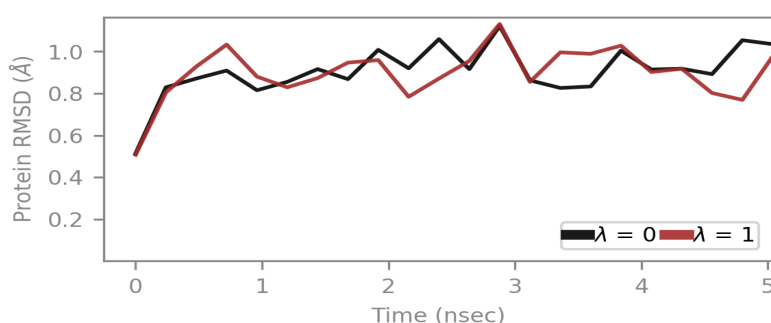
  

- A	184	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	273
SSA	LNHTWINVPPAEKKNYAWGYREGKAVHVSPGALDAEAYGVKSTIEDMARVQSNLKPLDINEKTLQGGIQLAQSRYWQTGDMYQGLGWEM																			

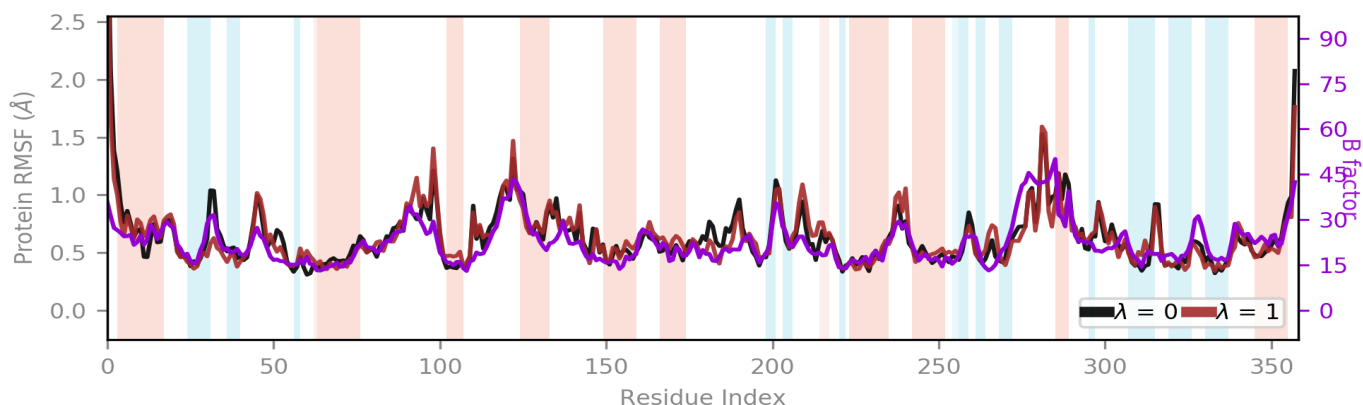
- A	274	275	280	285	290	295	300	305	310	315	320	325	330	335	340	345	350	355	361	
SSA	LDWFPVNPDSIINGSNDNKIALAARPVKAITPTTPAVRASWVHKGTGATGGFGSYVAFIPEKELGIVMLANKNYPNPARVDAAWQILNALQ																			

## Protein RMSD



The Root Mean Square Deviation (RMSD) of a protein is measured here over the backbone atoms. Monitoring protein RMSD for two end-points in the FEP simulation may give insights of its structural stability. Values of the order of 1-3 Å are perfectly acceptable for medium-size, globular proteins. Changes much larger than that, however, indicate that the protein is undergoing a larger than expected conformational changes for an equilibrated system, during the simulation.

## Protein RMSF



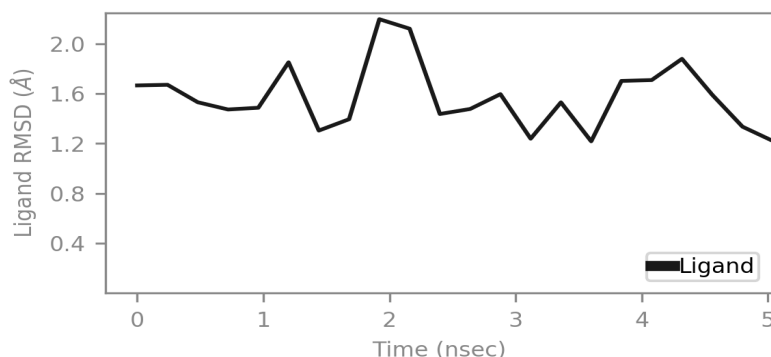
The Root Mean Square Fluctuation (RMSF) is useful for characterizing local changes along the protein chain. Protein backbone RMSF is shown in this plot. Typically you will observe that the tails (N- and C-terminal) fluctuate more than any other part of the protein. Secondary structure elements like alpha helices and beta strands are usually more rigid than the unstructured part of the protein, and thus fluctuate less than the loop regions. Experimental B factors extracted from PDB is overlaid alongside with RMSF values. RMSF and B factors fluctuations should correlate, but not necessarily follow each other.

Alpha-helical and beta-strand regions are highlighted in red and blue backgrounds, respectively. These regions are defined by helices or strands that persist over 70% of the entire simulation. One should expect secondary structure elements to be in the low-fluctuating RMSF region.

# Ligand Analysis for End-Point $\lambda$ -Replicas

Title	PDB Name	No. Atoms	No. Heavy	No. Hot Atoms	Rot. Bonds	Atomic Mass	Charge
Z3357096556	'UNK'	39	20	39	5	299.4 au	-1

## Ligand RMSD in complex

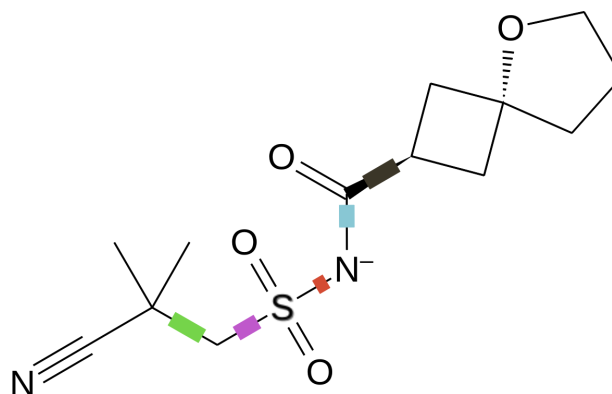


The Root Mean Square Deviation (RMSD) of a ligand is measured with respect to the input ligand pose by first aligning the complex on the protein. If the values observed are significantly larger than the RMSD of the protein (See the *Protein Analysis Report*), then it is likely that the ligand has diffused away from its initial binding site. Remember that since the FEP calculation is in the 'REST' mode, the fluctuations may be larger than observed for typical MD jobs.

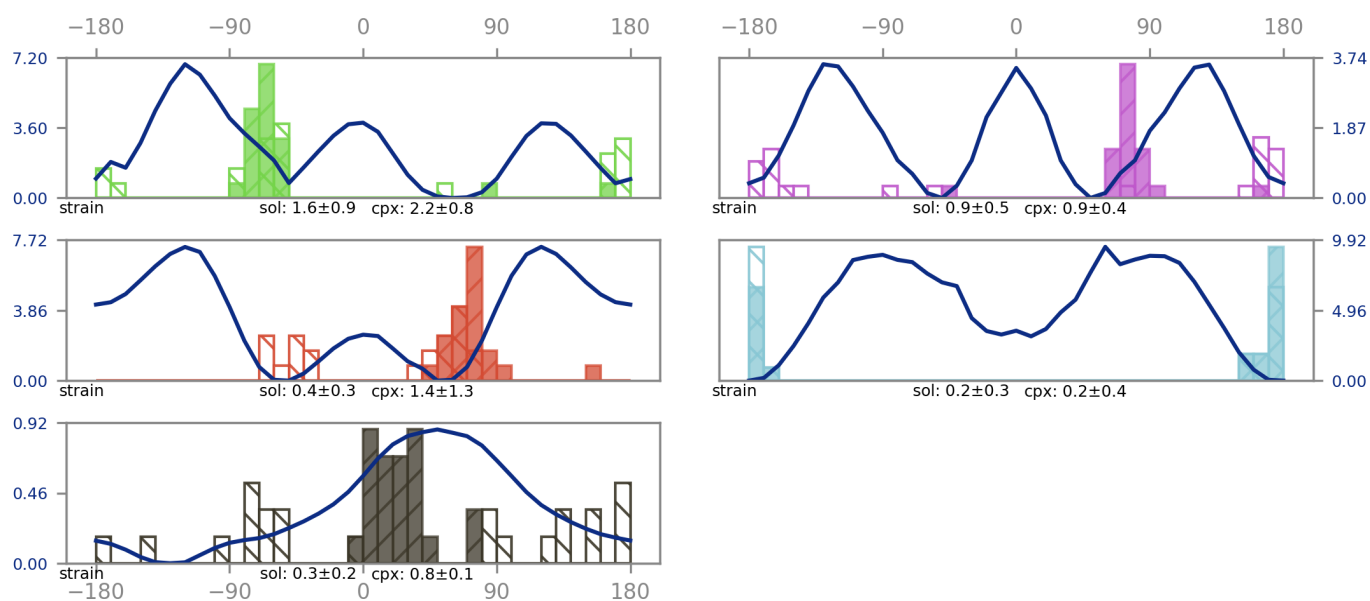
## Ligand Misc. Properties

	Units	Solvent Leg	Complex Leg
RMSD	Å	1.6 ± 0.25	1.6 ± 0.27
Radius of gyration	Å	3.7 ± 0.16	3.6 ± 0.07
Molecular SA	Å <sup>2</sup>	277.3 ± 3.70	276.4 ± 2.56
Solvent-accessible SA	Å <sup>2</sup>	518.0 ± 9.28	90.3 ± 11.72
Polar SA	Å <sup>2</sup>	152.7 ± 5.07	159.9 ± 4.14
Intramolecular HB	#	0.0 ± 0.00	0.0 ± 0.00
Number of waters	#	N/A	10.9 ± 2.42
Ligand strain	kcal/mol	3.2 ± 1.10	5.4 ± 1.66

# Ligand Conformation Analysis

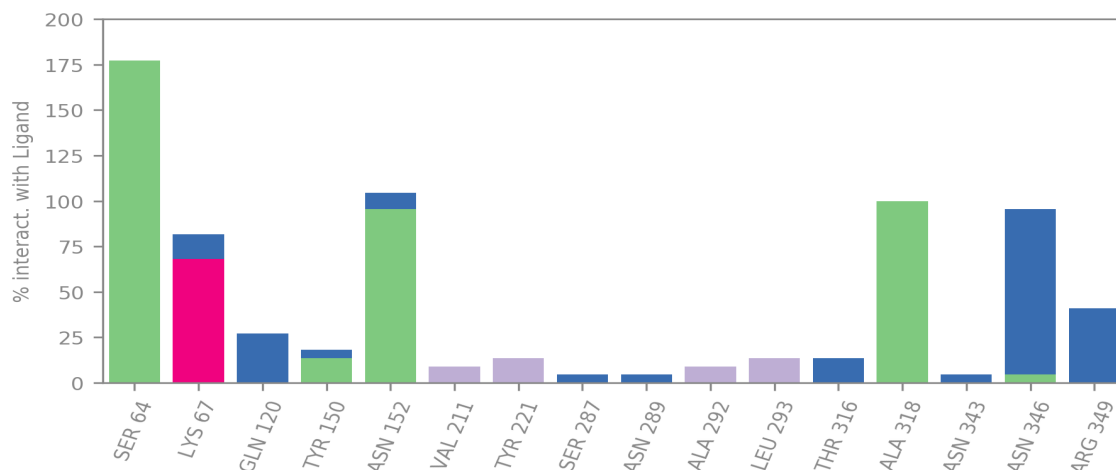


Z3357096556



Rotatable bonds (Rb) in both ligands are enumerated and color-coded. For each Rb, a representative dihedral angle is monitored throughout the complex and solvent simulation legs, their distributions are then plotted. Hollow bars show **solvent** and filled bars show **complex** leg distributions. Input starting conformation is marked as a gray vertical line. Potential energy around each Rb overlays the plot with the dark-blue curve and corresponding labels on the Y-axis. Local strain energies are shown below the plot. The units are in *kcal/mol*.

## Protein-Ligand Interactions



Above bar chart illustrates the type of interactions the protein residues make with the ligand. Multiple types of specific interactions are monitored throughout the simulation and provide a way to examine and compare how the protein interacts with the ligand. The specific interactions types monitored and displayed are: **hydrogen bond**, **hydrophobic**, **ionic** and **water bridges**. The stacked bar charts are normalized over the course of the trajectory. More information about the geometry and the different interaction subtype categories can be found in the Schrödinger's *Desmond User Manual*, under 'Simulation Interactions Diagram' (SID) section. **Note:** The values may exceed 100% as the residue can make multiple contacts of the same type with the ligand.

