

## Simulation Interactions Diagram Report

## Simulation Details

Jobname: full  
Entry title: Converted file

CPU #	Job Type	Ensemble	Temp. [K]	Sim. Time [ns]	# Atoms	# Waters	Charge
Unknown*	Unknown*	Unknown*	300.0	501.000	391440	107770	831

\* The configuration file (-out.cfg) was not found. Keep it in same directory as .aef file.

## Protein Information

Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	# Atoms	# Heavy Atoms	Charge
1860	'NoChainId'	ict_values([1860])	19416	15166	0

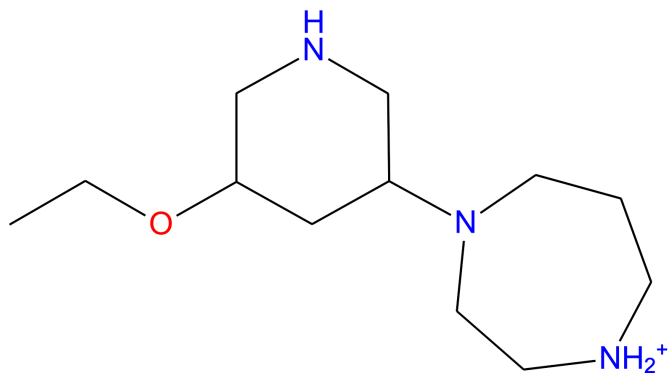
SSA	0	0	5	10	15	20	25	30	35	40	45	50	55	60	65	69
SSA	70	75	80	85	90	95	100	105	110	115	120	125	130	135	139	
SSA	140	145	150	155	160	165	170	175	180	185	190	195	200	205	209	
SSA	210	215	220	225	230	235	240	245	250	255	260	265	270	275	279	
SSA	280	285	290	295	300	305	310	315	320	325	330	335	340	345	349	
SSA	350	355	360	365	370	375	380	385	390	395	400	405	410	415	420	
SSA	421	425	430	435	440	445	450	455	460	465	470	475	480	485	490	
SSA	491	495	500	505	510	515	520	525	530	535	540	545	550	555	560	
SSA	561	565	570	575	580	585	590	595	600	605	610	615	620	625	630	
SSA	631	635	640	645	650	655	660	665	670	675	680	685	690	695	700	
SSA	701	705	710	715	720	725	730	735	740	745	750	755	760	765	771	
SSA	772	775	780	785	790	795	800	805	810	815	820	825	830	835	841	
SSA	842	845	850	855	860	865	870	875	880	885	890	895	900	905	911	
SSA	912	915	920	925	930	935	940	945	950	955	960	965	970	975	981	
SSA	982	985	990	995	1000	1005	1010	1015	1020	1025	1030	1035	1040	1045	1051	
SSA	1052	1055	1060	1065	1070	1075	1080	1085	1090	1095	1100	1105	1110	1115	1122	
SSA	1123	1125	1130	1135	1140	1145	1150	1155	1160	1165	1170	1175	1180	1185	1192	
SSA	1193	1195	1200	1205	1210	1215	1220	1225	1230	1235	1240	1245	1250	1255	1262	
SSA	1263	1265	1270	1275	1280	1285	1290	1295	1300	1305	1310	1315	1320	1325	1332	
SSA	1333	1335	1340	1345	1350	1355	1360	1365	1370	1375	1380	1385	1390	1395	1402	
SSA	1403	1405	1410	1415	1420	1425	1430	1435	1440	1445	1450	1455	1460	1465	1472	
SSA	1473	1475	1480	1485	1490	1495	1500	1505	1510	1515	1520	1525	1530	1535	1543	
SSA	1544	1545	1550	1555	1560	1565	1570	1575	1580	1585	1590	1595	1600	1605	1613	
SSA	1614	1615	1620	1625	1630	1635	1640	1645	1650	1655	1660	1665	1670	1675	1683	
SSA	1684	1685	1690	1695	1700	1705	1710	1715	1720	1725	1730	1735	1740	1745	1753	
SSA	1754	1755	1760	1765	1770	1775	1780	1785	1790	1795	1800	1805	1810	1815	1823	
SSA	1824	1825	1830	1835	1840	1845	1850	1855	1860	1865	1870	1875	1880	1885	1893	

## Ligand Information

SMILES

CCOC(CNC1)CC1N2CCC[NH2+]  
CC2

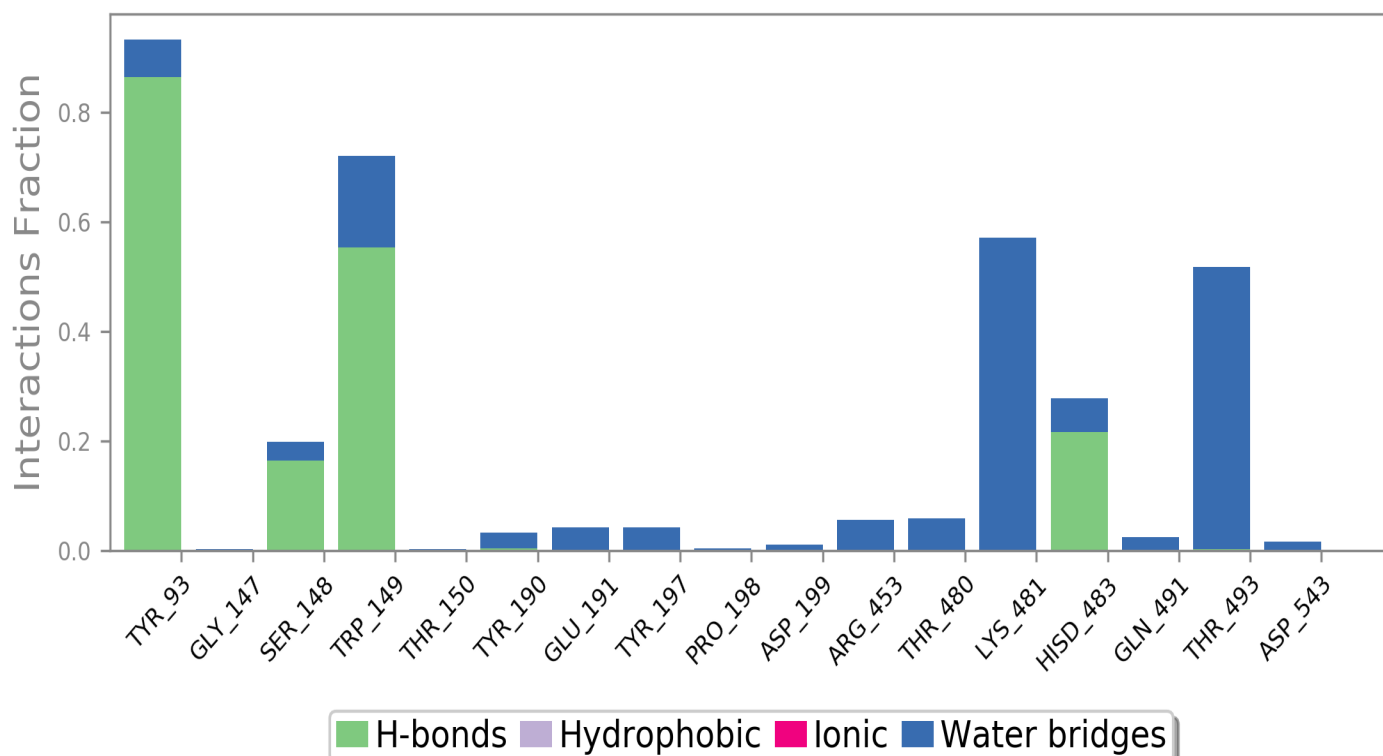
PDB Name '09P'  
Num. of Atoms 21 (total) 16 (heavy)  
Atomic Mass 252.234 au  
Charge 0  
Mol. Formula C<sub>12</sub>H<sub>5</sub>N<sub>3</sub>O  
Num. of Fragments 4  
Num. of Rot. Bonds 3



#### Counter Ion/Salt Information

Type	Num.	Concentration [mM]	Total Charge
Na	496	83.680	+496
Cl	465	78.450	-465

## Protein-Ligand Contacts



Protein interactions with the ligand can be monitored throughout the simulation. These interactions can be categorized by type and summarized, as shown in the plot above. Protein-ligand interactions (or 'contacts') are categorized into four types: Hydrogen Bonds, Hydrophobic, Ionic and Water Bridges. Each interaction type contains more specific subtypes, which can be explored through the 'Simulation Interactions Diagram' panel. The stacked bar charts are normalized over the course of the trajectory: for example, a value of 0.7 suggests that 70% of the simulation time the specific interaction is maintained. Values over 1.0 are possible as some protein residue may make multiple contacts of same subtype with the ligand.

**Hydrogen Bonds:** (H-bonds) play a significant role in ligand binding. Consideration of hydrogen-bonding properties in drug design is important because of their strong influence on drug specificity, metabolism and adsorption. Hydrogen bonds between a protein and a ligand can be further broken down into four subtypes: backbone acceptor; backbone donor; side-chain acceptor; side-chain donor.

The current geometric criteria for protein-ligand H-bond is: distance of 2.5 Å between the donor and acceptor atoms (D—H...A); a donor angle of  $\geq 120^\circ$  between the donor-hydrogen-acceptor atoms (D—H...A); and an acceptor angle of  $\geq 90^\circ$  between the hydrogen-acceptor-bonded\_atom atoms (H...A—X).

**Hydrophobic contacts:** fall into three subtypes:  $\pi$ -Cation;  $\pi$ - $\pi$ ; and Other, non-specific interactions. Generally these type of interactions involve a hydrophobic amino acid and an aromatic or aliphatic group on the ligand, but we have extended this category to also include  $\pi$ -Cation interactions.

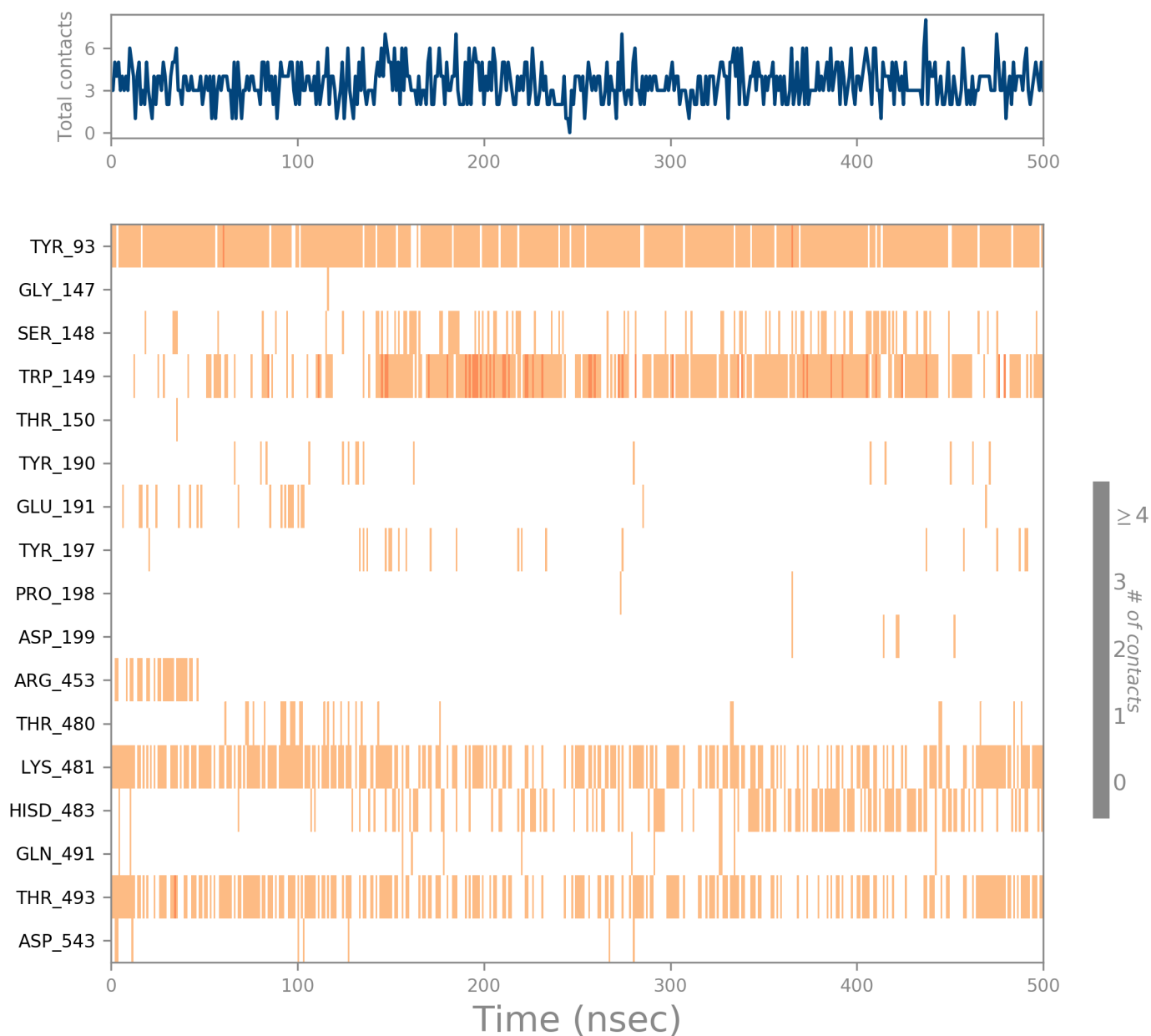
The current geometric criteria for hydrophobic interactions is as follows:  $\pi$ -Cation — Aromatic and charged groups within 4.5 Å;  $\pi$ - $\pi$  — Two aromatic groups stacked face-to-face or face-to-edge; Other — A non-specific hydrophobic sidechain within 3.6 Å of a ligand's aromatic or aliphatic carbons.

**Ionic interactions:** or polar interactions, are between two oppositely charged atoms that are within 3.7 Å of each other and do not involve a hydrogen bond. We also monitor Protein-Metal-Ligand interactions, which are defined by a metal ion coordinated within 3.4 Å of protein's and ligand's heavy atoms (except carbon). All ionic interactions are broken down into two subtypes: those mediated by a protein backbone or side chains.

**Water Bridges:** are hydrogen-bonded protein-ligand interactions mediated by a water molecule. The hydrogen-bond geometry is slightly relaxed from the standard H-bond definition.

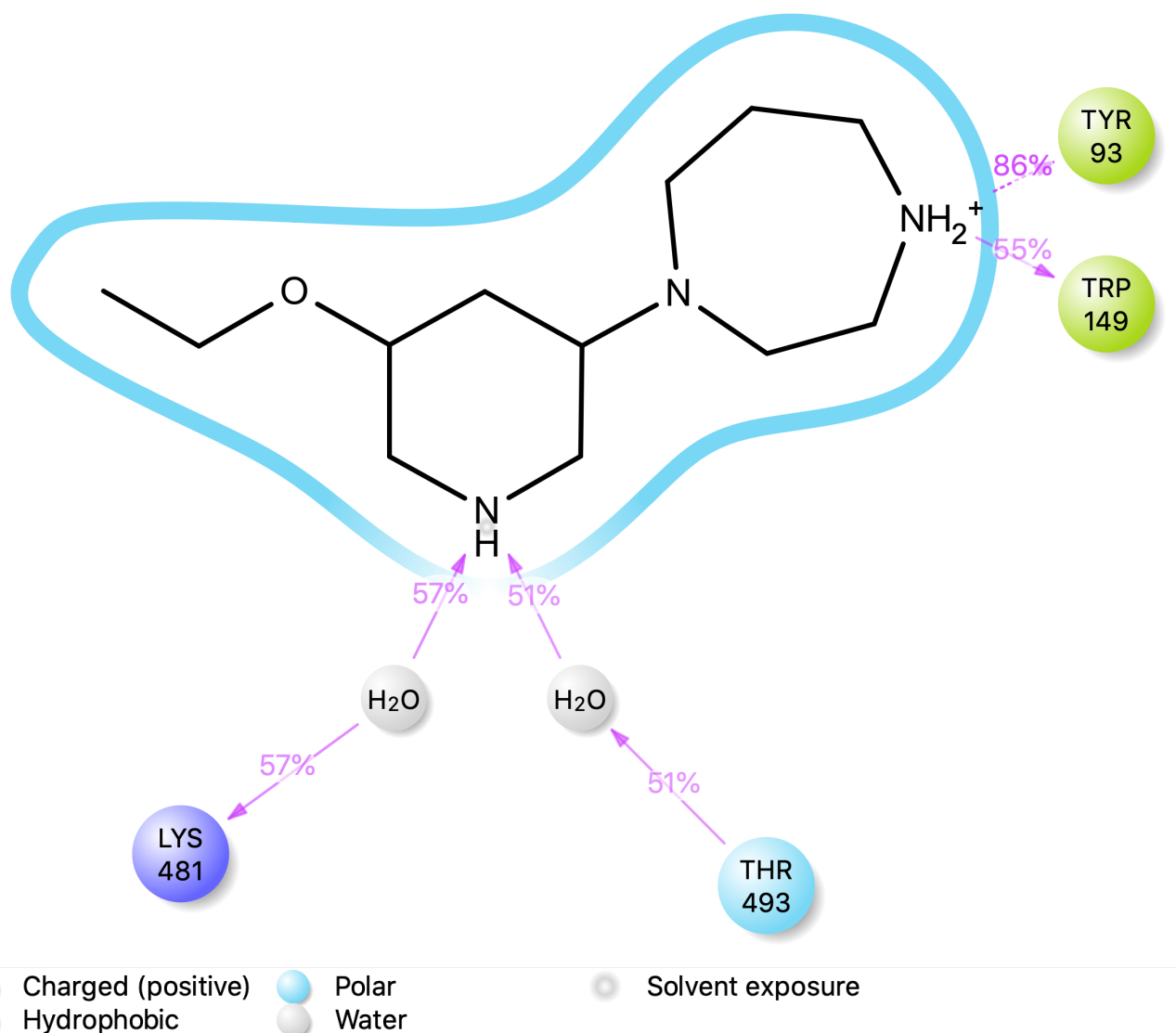
The current geometric criteria for a protein-water or water-ligand H-bond are: a distance of 2.8 Å between the donor and acceptor atoms (D—H...A); a donor angle of  $\geq 110^\circ$  between the donor-hydrogen-acceptor atoms (D—H...A); and an acceptor angle of  $\geq 90^\circ$  between the hydrogen-acceptor-bonded\_atom atoms (H...A—X).

## Protein-Ligand Contacts (cont.)



A timeline representation of the interactions and contacts (**H-bonds, Hydrophobic, Ionic, Water bridges**) summarized in the previous page. The top panel shows the total number of specific contacts the protein makes with the ligand over the course of the trajectory. The bottom panel shows which residues interact with the ligand in each trajectory frame. Some residues make more than one specific contact with the ligand, which is represented by a darker shade of orange, according to the scale to the right of the plot.

## Ligand-Protein Contacts



A schematic of detailed ligand atom interactions with the protein residues. Interactions that occur more than **30.0%** of the simulation time in the selected trajectory ( 0.00 through 500.00 nsec), are shown.

Note: it is possible to have interactions with >100% as some residues may have multiple interactions of a single type with the same ligand atom. For example, the ARG side chain has four H-bond donors that can all hydrogen-bond to a single H-bond acceptor.