

Simulation Interactions Diagram Report

Simulation Details

Jobname: desmond_md_job_Myricetin
Entry title: Myricetin - minimized

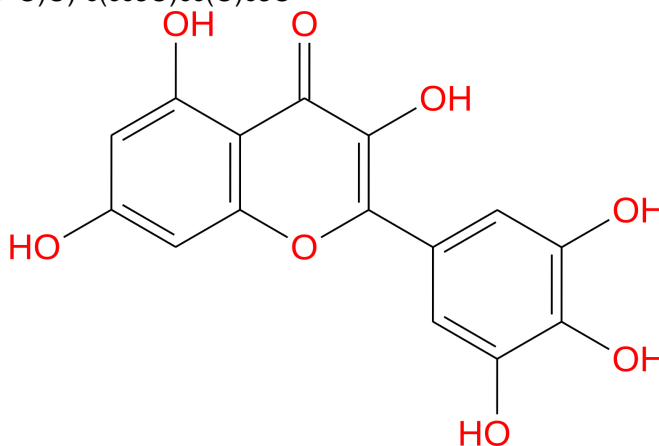
CPU #	Job Type	Ensemble	Temp. [K]	Sim. Time [ns]	# Atoms	# Waters	Charge
1	mdsim	NPT	300.0	100.102	48229	13484	0

Protein Information

	Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	# Atoms	# Heavy Atoms	Charge
	496	'A'	ict_values([496])	7667	3946	-1
- A SSA	1		5 10 15 20 25 30 35 40 45 50 55 60 65 70			
			EYSPNTQQGRTSIVHLFEWRWVDIALECEERYLAPKGFQVSPNENVAIYNPFRPWERYQPVSYKLC			
- A SSA	71		75 80 85 90 95 100 105 110 115 120 125 130 135 140			
			TRSGNEDEFNRNMVTRCANNVGVRIYVDVINHMCNAVSAAGTSSTCGSYFNPGRDFPAVPYSGWDFNDGK			
- A SSA	141		145 150 155 160 165 170 175 180 185 190 195 200 205 210			
			CKTGSGDIENYNDATQVRDCRLTGLLDLALEKDYVRSKIAEYMNHLIDIGVAGFRDLASKHMWPGDIKAI			
- A SSA	211		215 220 225 230 235 240 245 250 255 260 265 270 275 280			
			LDKLHNLNSNWFPAGSKPFIYQEVIDLGGEPKSSDYFGNGRVTEFKYGAQLGTIVIRKWNGEKMSYLNW			
- A SSA	281		285 290 295 300 305 310 315 320 325 330 335 340 345 350			
			GEGWGFVPSDRALVFVDNHDNQRGHGAGGASILTFWDARLYKMAVGFMALHPYGFTRVMSSYRWPRQFQN			
- A SSA	351		355 360 365 370 375 380 385 390 395 400 405 410 415 420			
			GNDVNDWVGPPNNNGVIKEVTINPDTCGNDWVCEHRWRQIRNMVIFRNVDGQPFNTWYDNGSNQVAFG			
- A SSA	421		425 430 435 440 445 450 455 460 465 470 475 480 485 490			
			RGNRGFIVFNDDWSFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIYVSDDGKAHFSISNSAEDPFIAT			
- A SSA	491		491 496			
			HAESKI			

Ligand Information

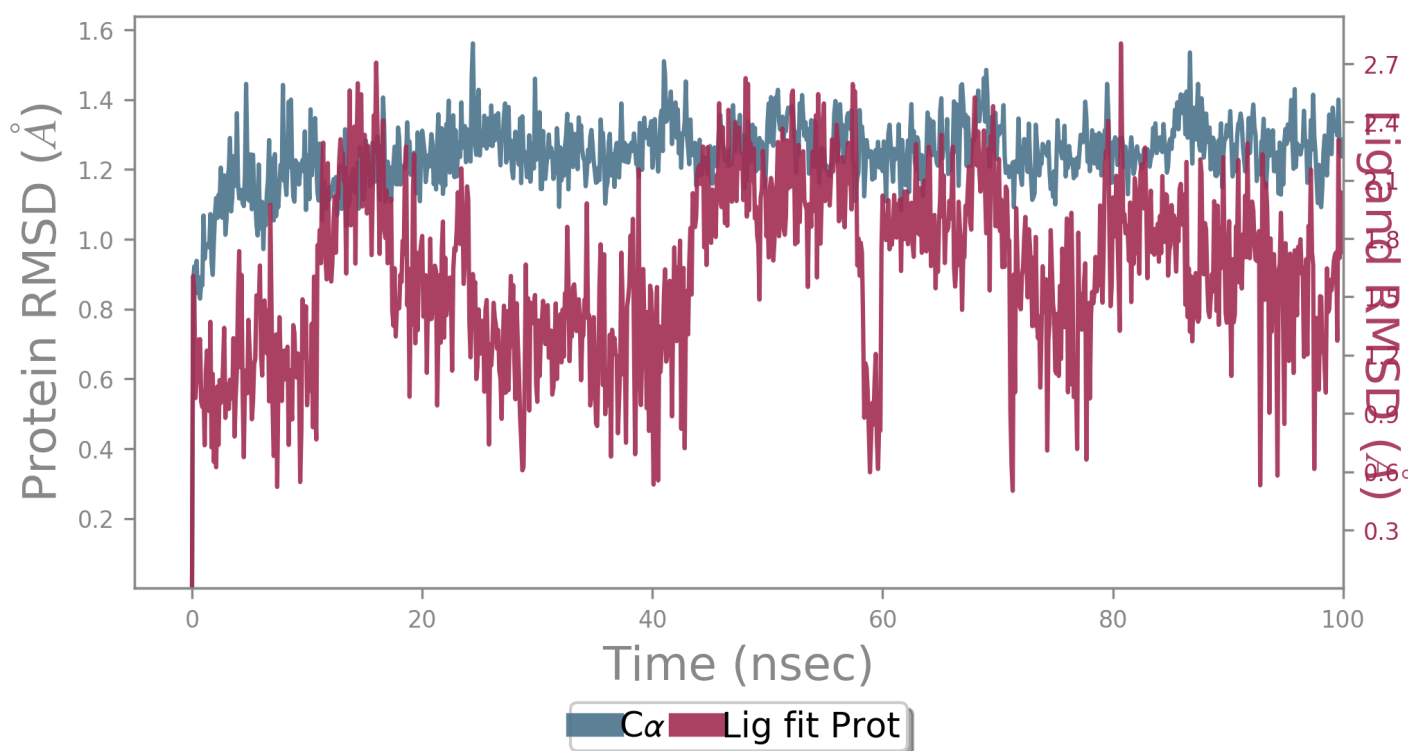
SMILES	Oc1cc(O)cc(c12)oc(c(c2=O)O)-c(cc3O)cc(O)c3O
PDB Name	'UNK'
Num. of Atoms	33 (total) 23 (heavy)
Atomic Mass	318.242 au
Charge	0
Mol. Formula	C15H10O8
Num. of Fragments	2
Num. of Rot. Bonds	7



Counter Ion/Salt Information

Type	Num.	Concentration [mM]	Total Charge
Na	39	52.588	+39

Protein-Ligand RMSD



The Root Mean Square Deviation (RMSD) is used to measure the average change in displacement of a selection of atoms for a particular frame with respect to a reference frame. It is calculated for all frames in the trajectory. The RMSD for frame x is:

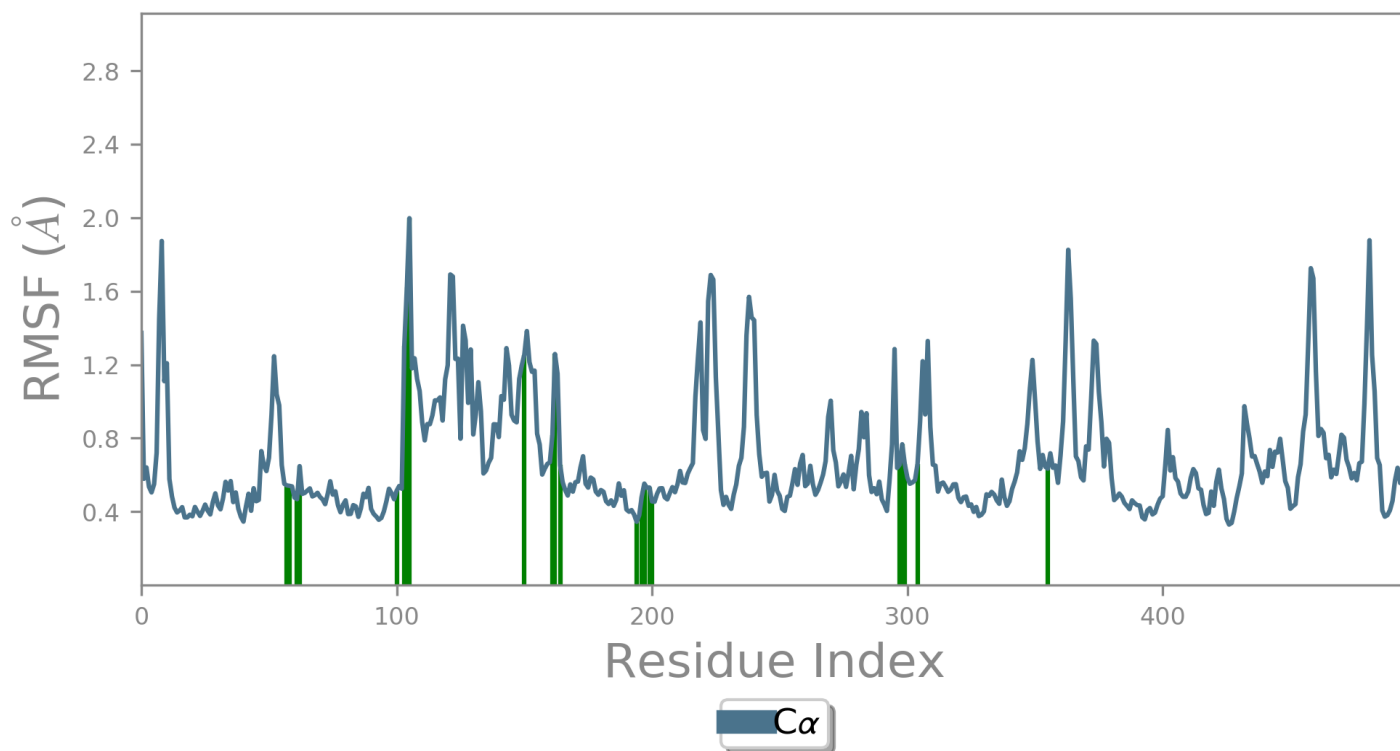
$$RMSD_x = \sqrt{\frac{1}{N} \sum_{i=1}^N (r'_i(t_x) - r_i(t_{ref}))^2}$$

where N is the number of atoms in the atom selection; t_{ref} is the reference time, (typically the first frame is used as the reference and it is regarded as time $t=0$); and r' is the position of the selected atoms in frame x after superimposing on the reference frame, where frame x is recorded at time t_x . The procedure is repeated for every frame in the simulation trajectory.

Protein RMSD: The above plot shows the RMSD evolution of a protein (left Y-axis). All protein frames are first aligned on the reference frame backbone, and then the RMSD is calculated based on the atom selection. Monitoring the RMSD of the protein can give insights into its structural conformation throughout the simulation. RMSD analysis can indicate if the simulation has equilibrated — its fluctuations towards the end of the simulation are around some thermal average structure. Changes of the order of 1-3 Å are perfectly acceptable for small, globular proteins. Changes much larger than that, however, indicate that the protein is undergoing a large conformational change during the simulation. It is also important that your simulation converges — the RMSD values stabilize around a fixed value. If the RMSD of the protein is still increasing or decreasing on average at the end of the simulation, then your system has not equilibrated, and your simulation may not be long enough for rigorous analysis.

Ligand RMSD: Ligand RMSD (right Y-axis) indicates how stable the ligand is with respect to the protein and its binding pocket. In the above plot, 'Lig fit Prot' shows the RMSD of a ligand when the protein-ligand complex is first aligned on the protein backbone of the reference and then the RMSD of the ligand heavy atoms is measured. If the values observed are significantly larger than the RMSD of the protein, then it is likely that the ligand has diffused away from its initial binding site.

Protein RMSF



The Root Mean Square Fluctuation (RMSF) is useful for characterizing local changes along the protein chain. The RMSF for residue i is:

$$RMSF_i = \sqrt{\frac{1}{T} \sum_{t=1}^T \langle (r'_i(t)) - r_i(t_{ref})^2 \rangle}$$

where T is the trajectory time over which the RMSF is calculated, t_{ref} is the reference time, r_i is the position of residue i ; r' is the position of atoms in residue i after superposition on the reference, and the angle brackets indicate that the average of the square distance is taken over the selection of atoms in the residue.

On this plot, peaks indicate areas of the protein that fluctuate the most during the simulation. 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.

Ligand Contacts: Protein residues that interact with the ligand are marked with green-colored vertical bars.

Protein Secondary Structure

% Helix

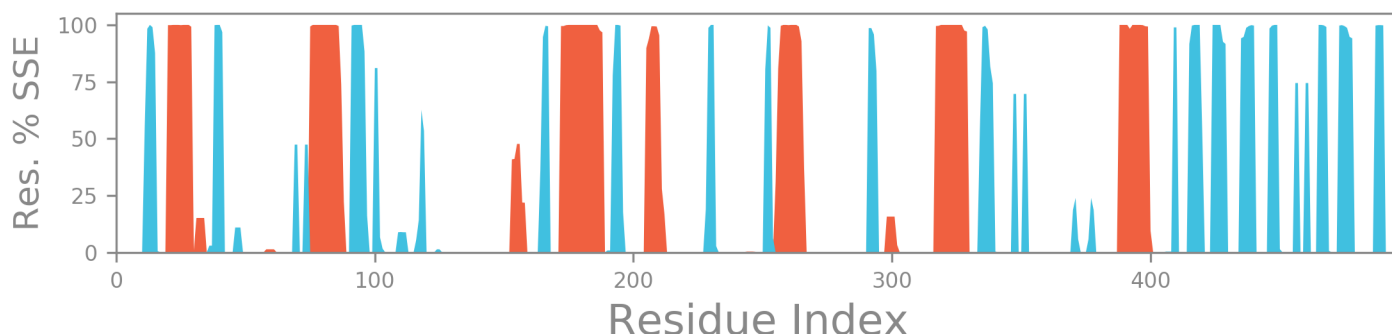
17.14

% Strand

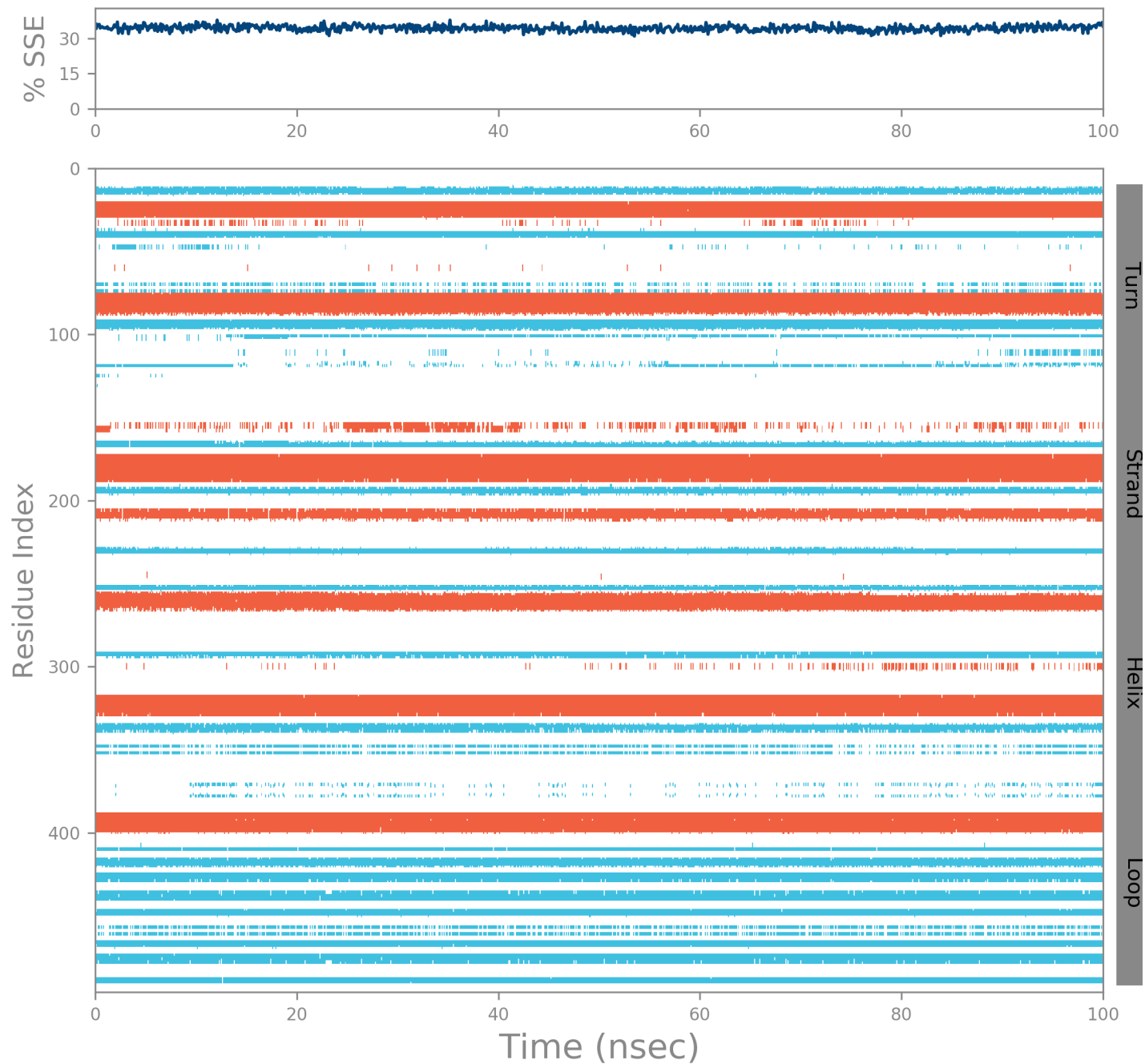
17.33

% Total SSE

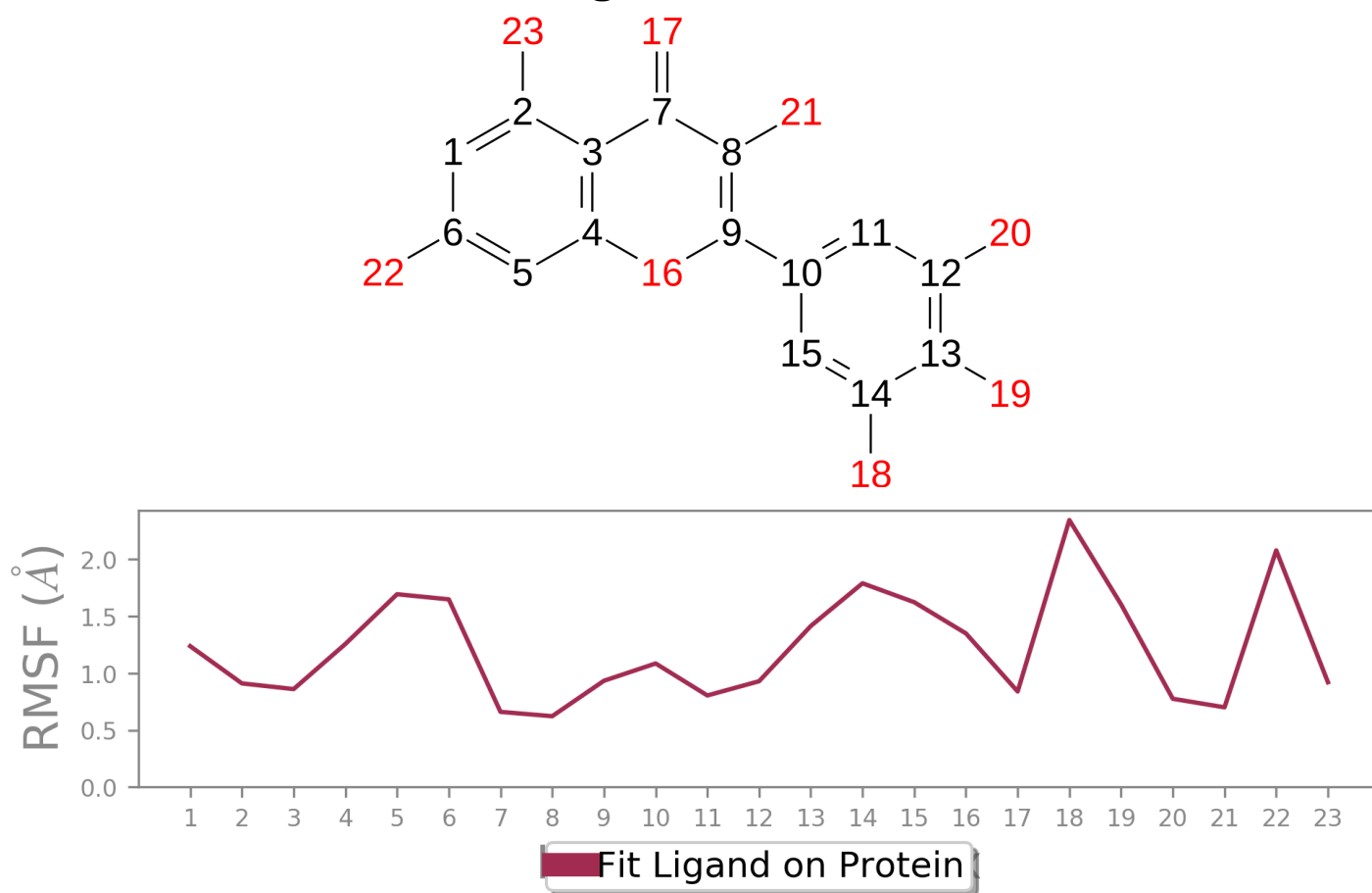
34.47



Protein secondary structure elements (SSE) like **alpha-helices** and **beta-strands** are monitored throughout the simulation. The plot above reports SSE distribution by residue index throughout the protein structure. The plot below summarizes the SSE composition for each trajectory frame over the course of the simulation, and the plot at the bottom monitors each residue and its SSE assignment over time.



Ligand RMSF



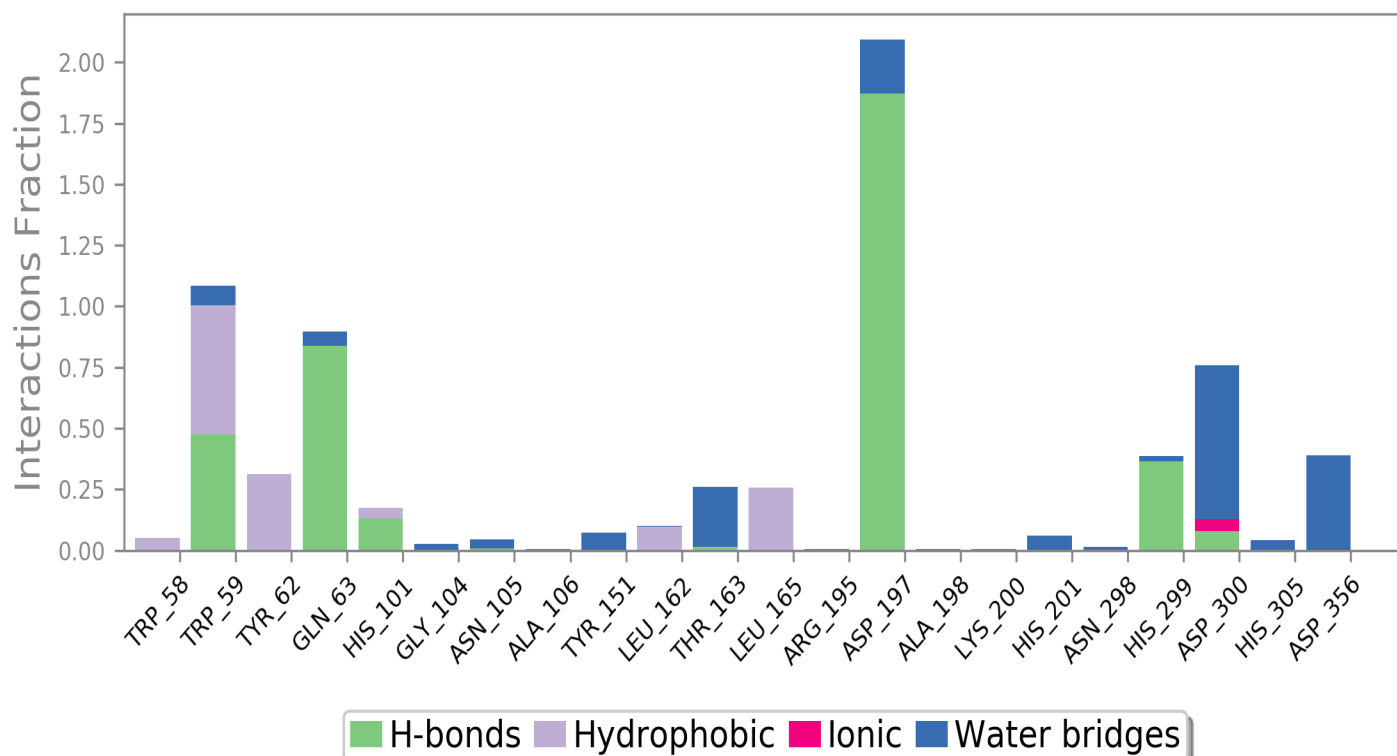
The Ligand Root Mean Square Fluctuation (L-RMSF) is useful for characterizing changes in the ligand atom positions. The RMSF for atom i is:

$$RMSF_i = \sqrt{\frac{1}{T} \sum_{t=1}^T (r'_i(t) - r_i(t_{ref}))^2}$$

where T is the trajectory time over which the RMSF is calculated, t_{ref} is the reference time (usually for the first frame, and is regarded as the zero of time); r is the position of atom i in the reference at time t_{ref} and r' is the position of atom i at time t after superposition on the reference frame.

Ligand RMSF shows the ligand's fluctuations broken down by atom, corresponding to the 2D structure in the top panel. The ligand RMSF may give you insights on how ligand fragments interact with the protein and their entropic role in the binding event. In the bottom panel, the 'Fit Ligand on Protein' line shows the ligand fluctuations, with respect to the protein. The protein-ligand complex is first aligned on the protein backbone and then the ligand RMSF is measured on the ligand heavy atoms.

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: π -Cation; π - π ; 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 π -Cation interactions.

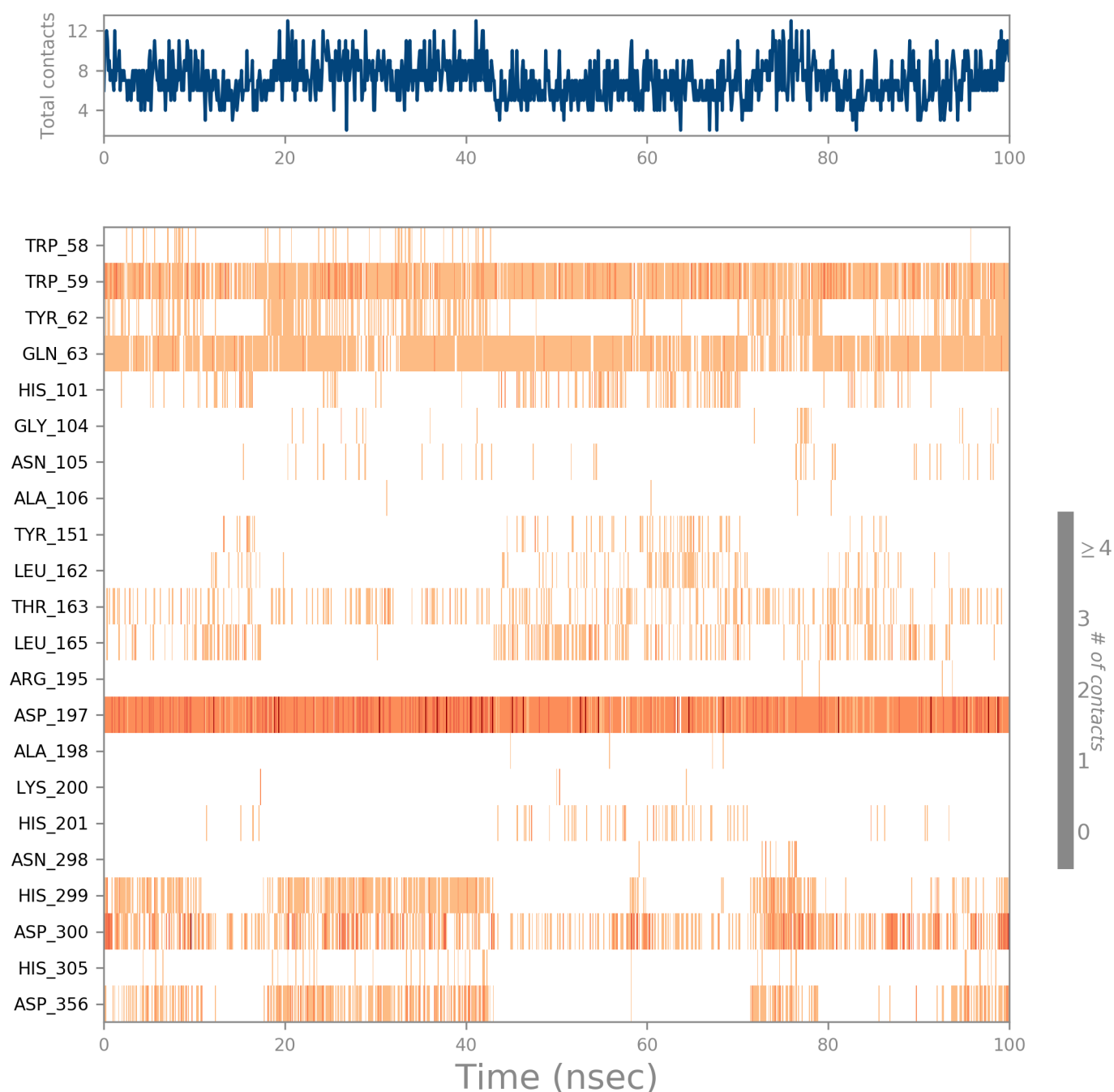
The current geometric criteria for hydrophobic interactions is as follows: π -Cation — Aromatic and charged groups within 4.5 Å; π - π — Two aromatic groups stacked face-to-face or face-to-edge; Other — A non-specific hydrophobic sidechain within 3.6 Å of a ligand's aromatic or aliphatic carbons.

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.

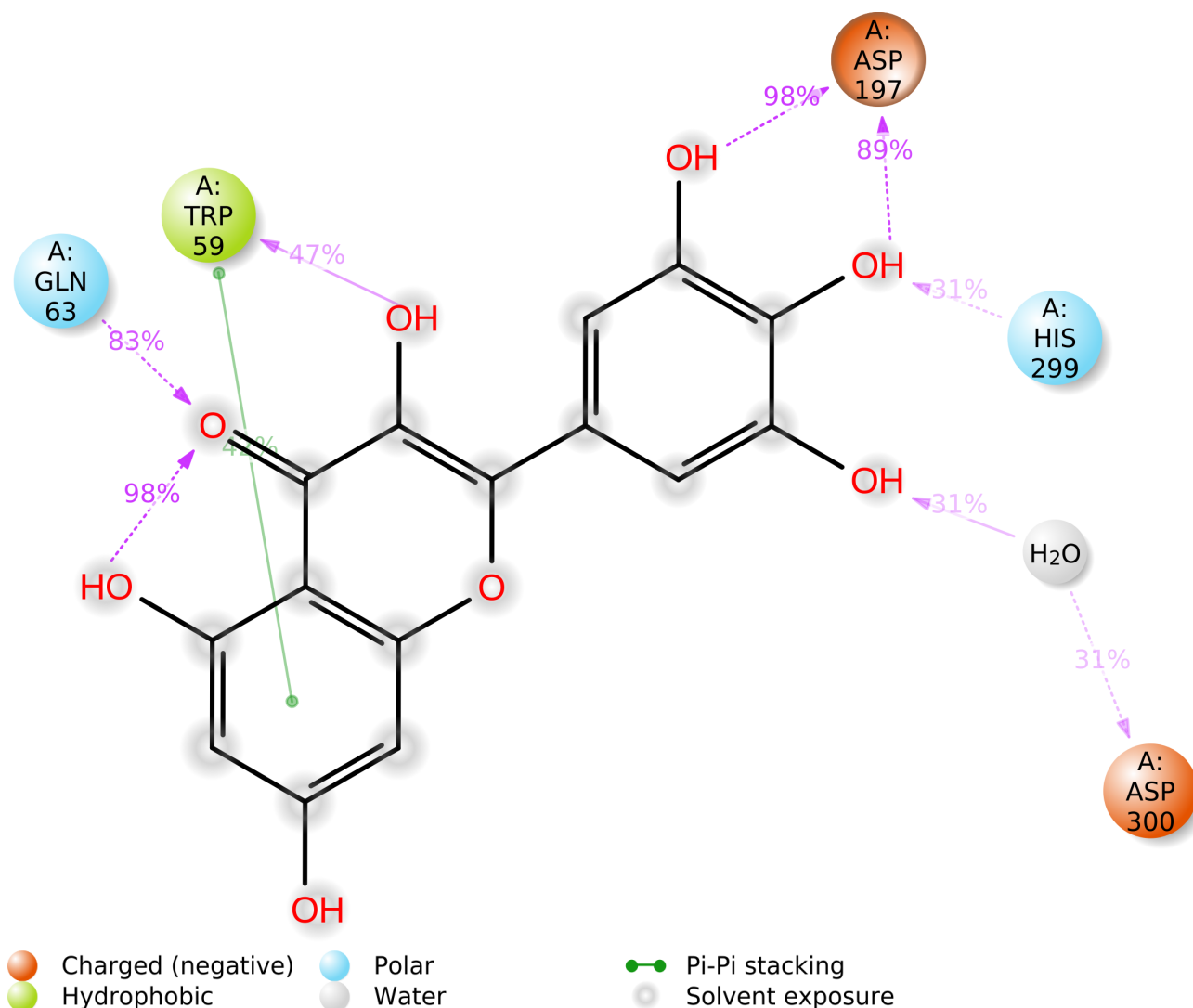
The current geometric criteria for a protein-water or water-ligand H-bond are: a distance of 2.8 Å between the donor and acceptor atoms (D—H...A); a donor angle of $\geq 110^\circ$ between the donor-hydrogen-acceptor atoms (D—H...A); and an acceptor angle of $\geq 90^\circ$ between the hydrogen-acceptor-bonded_atom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

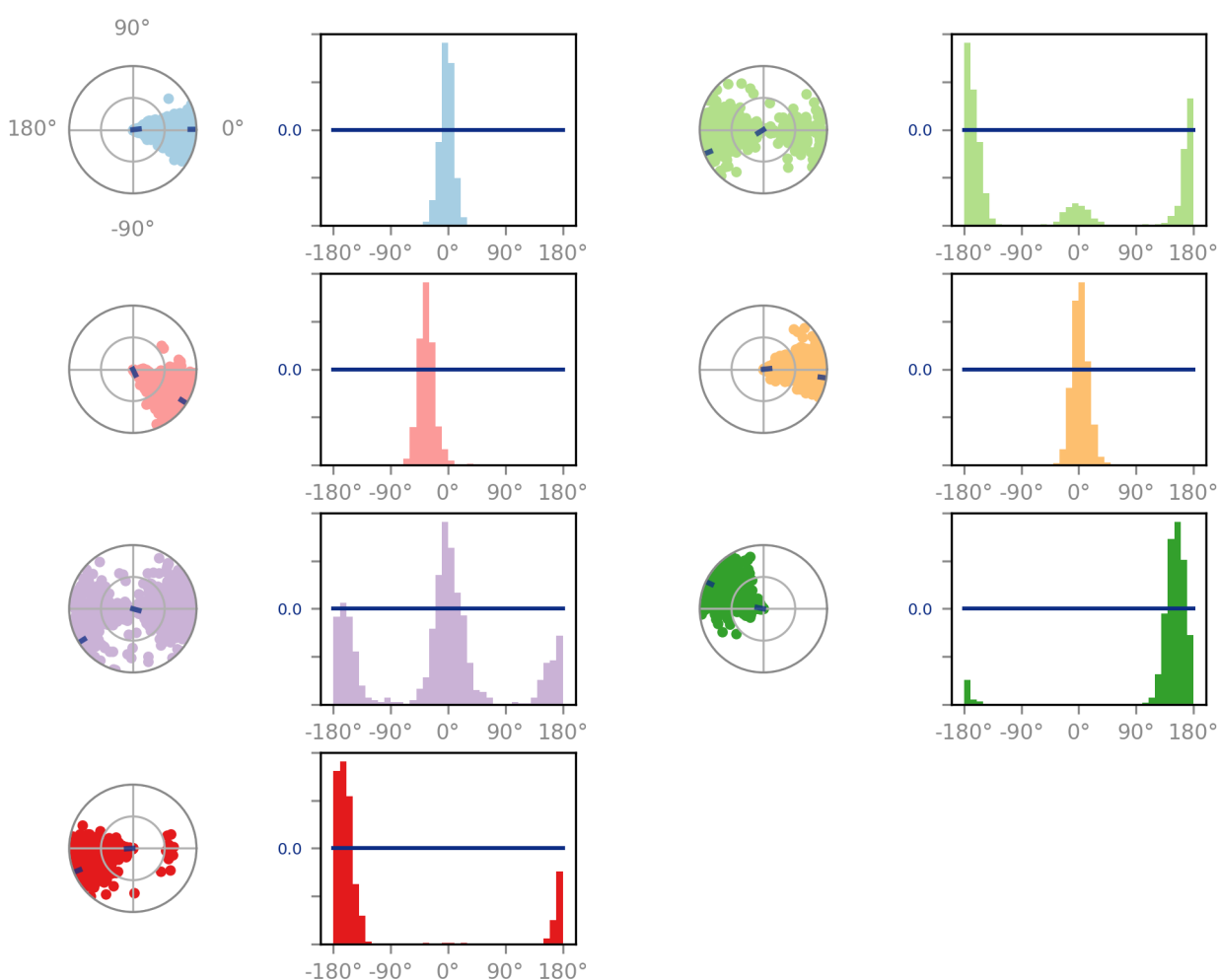
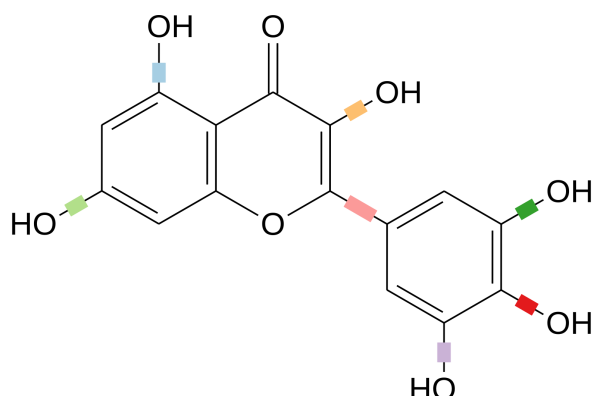
Ligand-Protein Contacts



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 100.00 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.

Ligand Torsion Profile



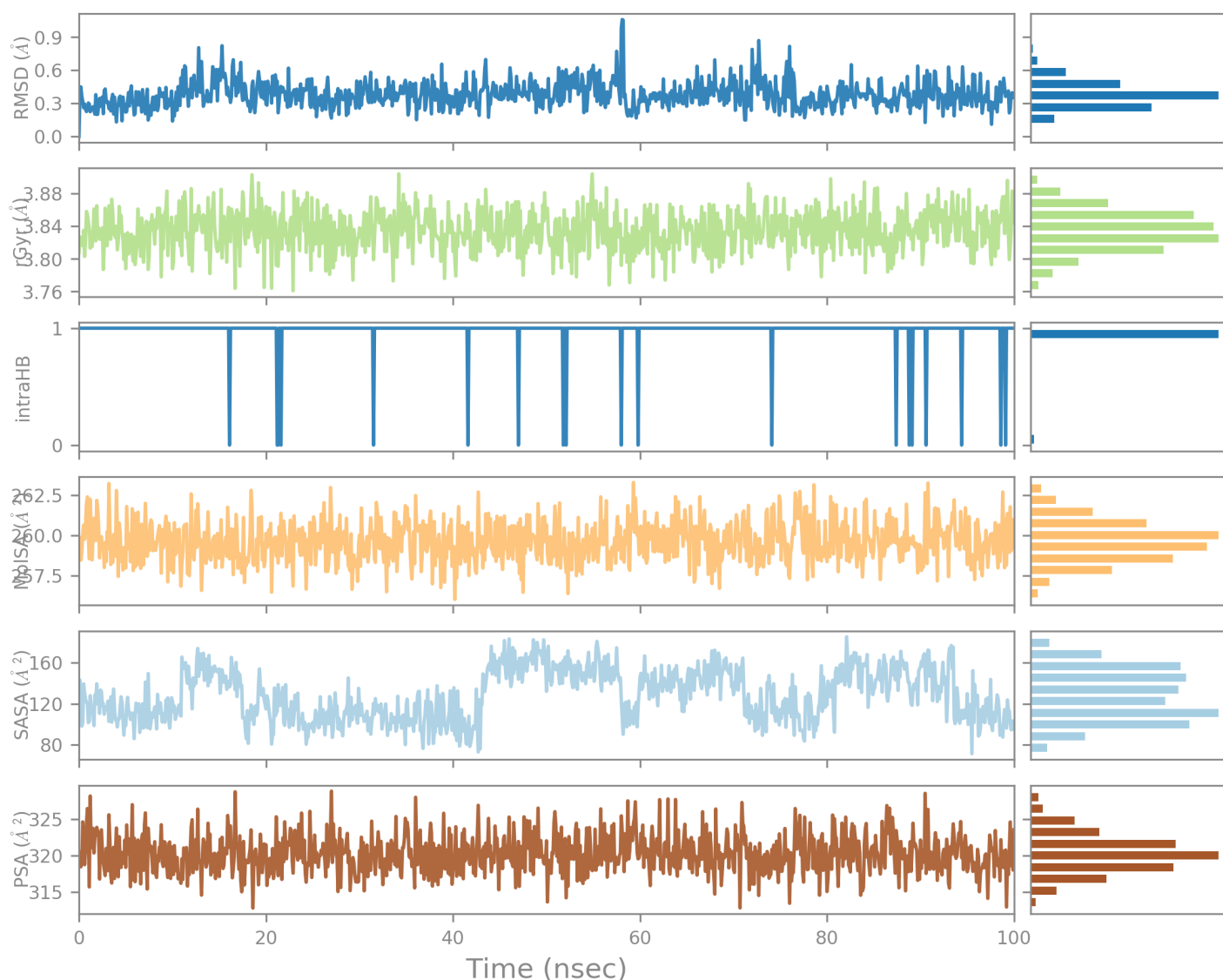
The ligand torsions plot summarizes the conformational evolution of every rotatable bond (RB) in the ligand throughout the simulation trajectory (0.00 through 100.00 nsec). The top panel shows the 2d schematic of a ligand with color-coded rotatable bonds. Each rotatable bond torsion is accompanied by a dial plot and bar plots of the same color.

Dial (or radial) plots describe the conformation of the torsion throughout the course of the simulation. The beginning of the simulation is in the center of the radial plot and the time evolution is plotted radially outwards.

The bar plots summarize the data on the dial plots, by showing the probability density of the torsion. If torsional potential information is available, the plot also shows the potential of the rotatable bond (by summing the potential of the related torsions). The values of the potential are on the left Y-axis of the chart, and are expressed in *kcal/mol*. Looking at the histogram and torsion potential relationships may give insights into the

conformational strain the ligand undergoes to maintain a protein-bound conformation.

Ligand Properties



Ligand RMSD: Root mean square deviation of a ligand with respect to the reference conformation (typically the first frame is used as the reference and it is regarded as time $t=0$).

Radius of Gyration (rGyr): Measures the 'extendedness' of a ligand, and is equivalent to its principal moment of inertia.

Intramolecular Hydrogen Bonds (intraHB): Number of internal hydrogen bonds (HB) within a ligand molecule.

Molecular Surface Area (MolSA): Molecular surface calculation with 1.4 Å probe radius. This value is equivalent to a van der Waals surface area.

Solvent Accessible Surface Area (SASA): Surface area of a molecule accessible by a water molecule.

Polar Surface Area (PSA): Solvent accessible surface area in a molecule contributed only by oxygen and nitrogen atoms.

Simulation Interactions Diagram Report

Simulation Details

Jobname: desmond_md_job_HighScore

Entry title: 6-O-b-D-Glucopyranosyl-2,4,6,3',4',6'-hexahydroxybenzophenone - minimized

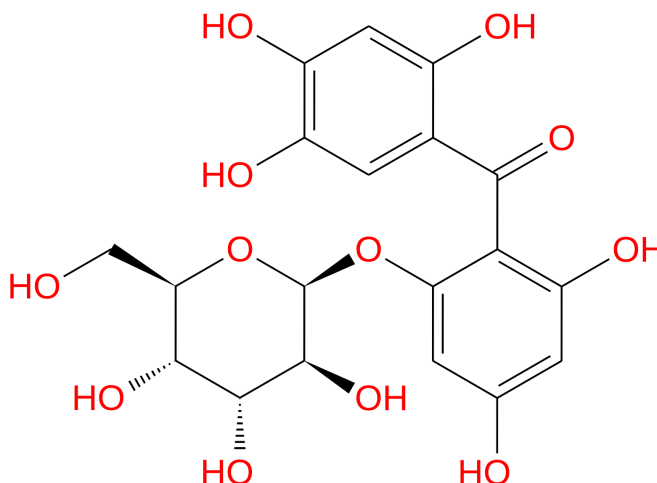
CPU #	Job Type	Ensemble	Temp. [K]	Sim. Time [ns]	# Atoms	# Waters	Charge
1	mdsim	NPT	300.0	100.102	48243	13482	0

Protein Information

	Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	# Atoms	# Heavy Atoms	Charge									
	496	'A'	ict_values([496])	7669	3946	+1									
- A	1	5	10	15	20	25	30	35	40	45	50	55	60	65	70
SSA		EYSPNTQQGR	TSIVHLFEWR	VDIALE	CERYLAP	KGF	GGVQV	SPNEN	VAIYN	PF	RP	WWE	RYQ	PV	SYKLC
- A	71	75	80	85	90	95	100	105	110	115	120	125	130	135	140
SSA		TRSGNEDE	FRNMVTR	CNNVGV	RIYVDA	VINHM	CGNAV	SAGT	SSTCG	SYFNP	GS	SRD	FP	PAV	PYSGWDFNDGK
- A	141	145	150	155	160	165	170	175	180	185	190	195	200	205	210
SSA		CKTGSGDI	ENYNDAT	QVRDC	RLTGL	LDL	ALEKDY	VRSKIA	EYMNHL	IDIG	VAGF	RLD	ASKH	MWPG	DIKAI
- A	211	215	220	225	230	235	240	245	250	255	260	265	270	275	280
SSA		LDKLHNL	NSNWFP	PAGSK	PFYQ	EV	IDL	GGEP	IKSSD	YFG	NR	VT	EK	YGA	KLGT
- A	281	285	290	295	300	305	310	315	320	325	330	335	340	345	350
SSA		GEGWGF	VPSDR	ALVF	VDN	HDN	QR	GH	GAG	GAS	IL	T	F	D	A
- A	351	355	360	365	370	375	380	385	390	395	400	405	410	415	420
SSA		GNDVND	WVG	PPN	NG	V	I	K	E	V	T	I	N	P	D
- A	421	425	430	435	440	445	450	455	460	465	470	475	480	485	490
SSA		RGNRG	FIV	F	N	N	D	D	W	S	F	S	L	T	L
- A	491	495	496												
SSA		HAESKI													

Ligand Information

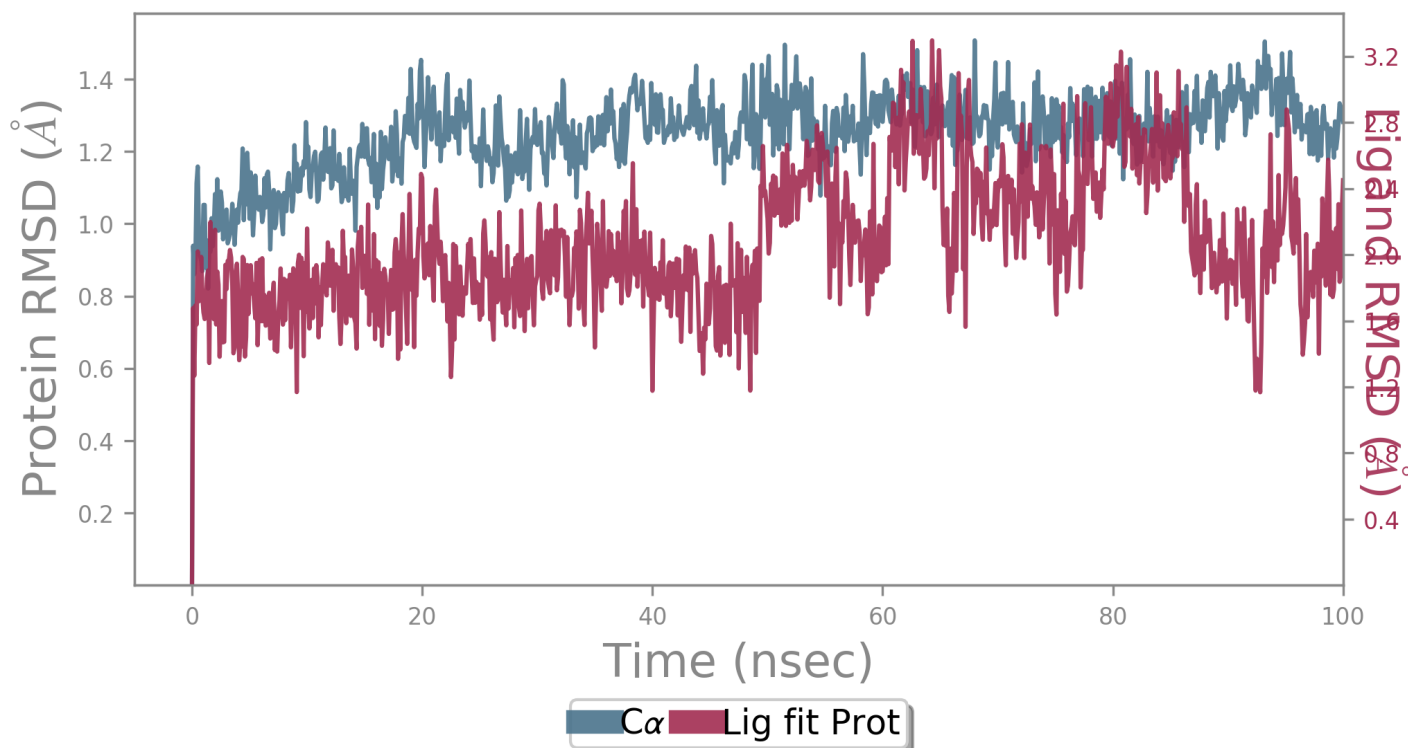
SMILES	c1c(O)c(O)cc(O)c1C(=O)c2c(cc(O)cc2O)O[C@H](O3)[C@@H](O)[C@H](O)[C@H](O)[C@H]3O)[C@H]3CO
PDB Name	'UNK'
Num. of Atoms	51 (total) 31 (heavy)
Atomic Mass	440.364 au
Charge	0
Mol. Formula	C19H20O12
Num. of Fragments	3
Num. of Rot. Bonds	14



Counter Ion/Salt Information

Type	Num.	Concentration [mM]	Total Charge
Cl	39	52.595	-39
Na	38	51.247	+38

Protein-Ligand RMSD



The Root Mean Square Deviation (RMSD) is used to measure the average change in displacement of a selection of atoms for a particular frame with respect to a reference frame. It is calculated for all frames in the trajectory. The RMSD for frame x is:

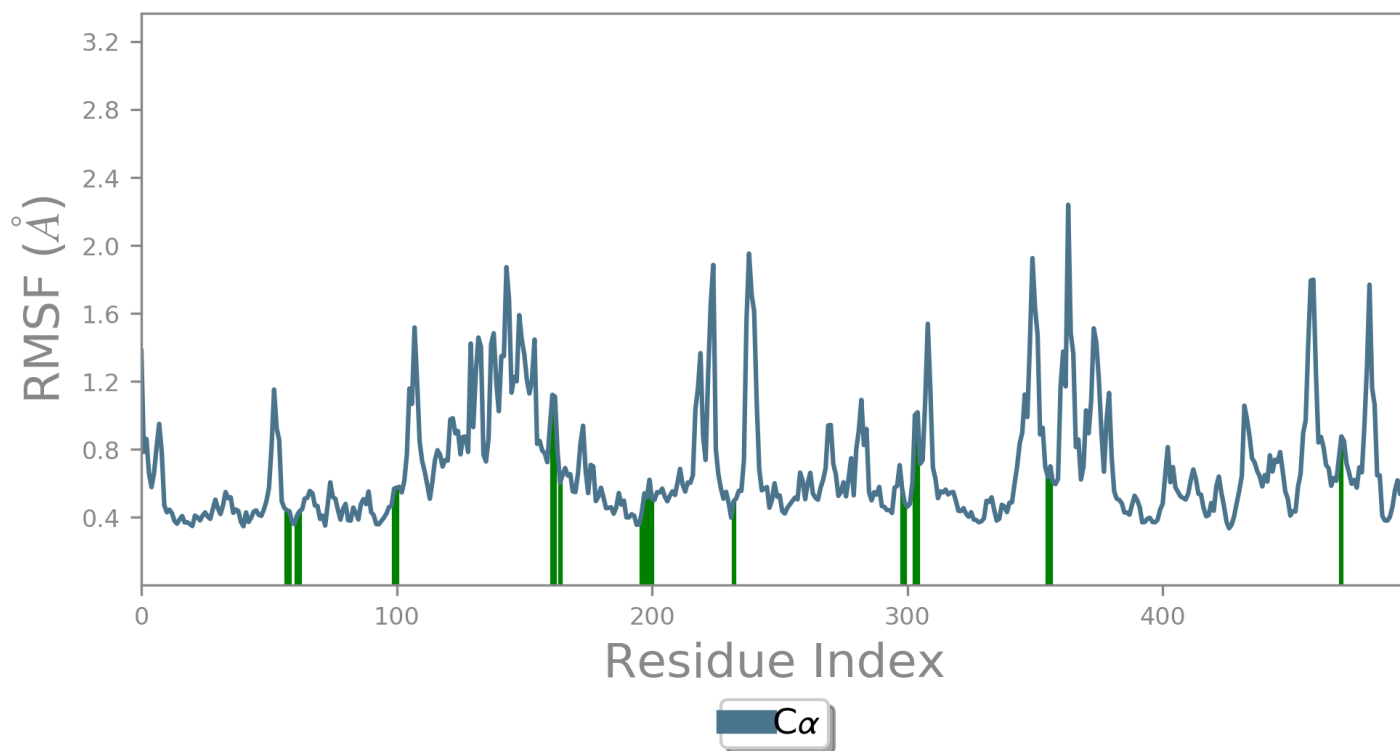
$$RMSD_x = \sqrt{\frac{1}{N} \sum_{i=1}^N (r'_i(t_x) - r_i(t_{ref}))^2}$$

where N is the number of atoms in the atom selection; t_{ref} is the reference time, (typically the first frame is used as the reference and it is regarded as time $t=0$); and r' is the position of the selected atoms in frame x after superimposing on the reference frame, where frame x is recorded at time t_x . The procedure is repeated for every frame in the simulation trajectory.

Protein RMSD: The above plot shows the RMSD evolution of a protein (left Y-axis). All protein frames are first aligned on the reference frame backbone, and then the RMSD is calculated based on the atom selection. Monitoring the RMSD of the protein can give insights into its structural conformation throughout the simulation. RMSD analysis can indicate if the simulation has equilibrated — its fluctuations towards the end of the simulation are around some thermal average structure. Changes of the order of 1-3 Å are perfectly acceptable for small, globular proteins. Changes much larger than that, however, indicate that the protein is undergoing a large conformational change during the simulation. It is also important that your simulation converges — the RMSD values stabilize around a fixed value. If the RMSD of the protein is still increasing or decreasing on average at the end of the simulation, then your system has not equilibrated, and your simulation may not be long enough for rigorous analysis.

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Protein Secondary Structure

% Helix

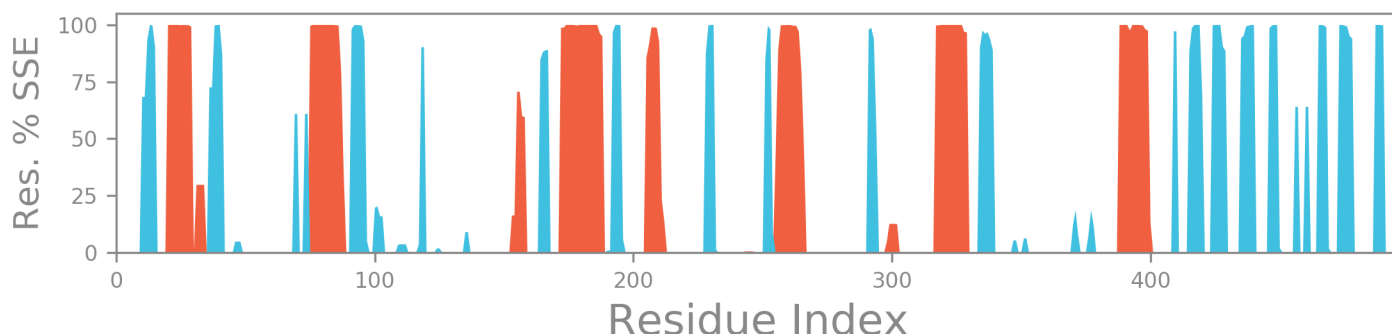
17.38

% Strand

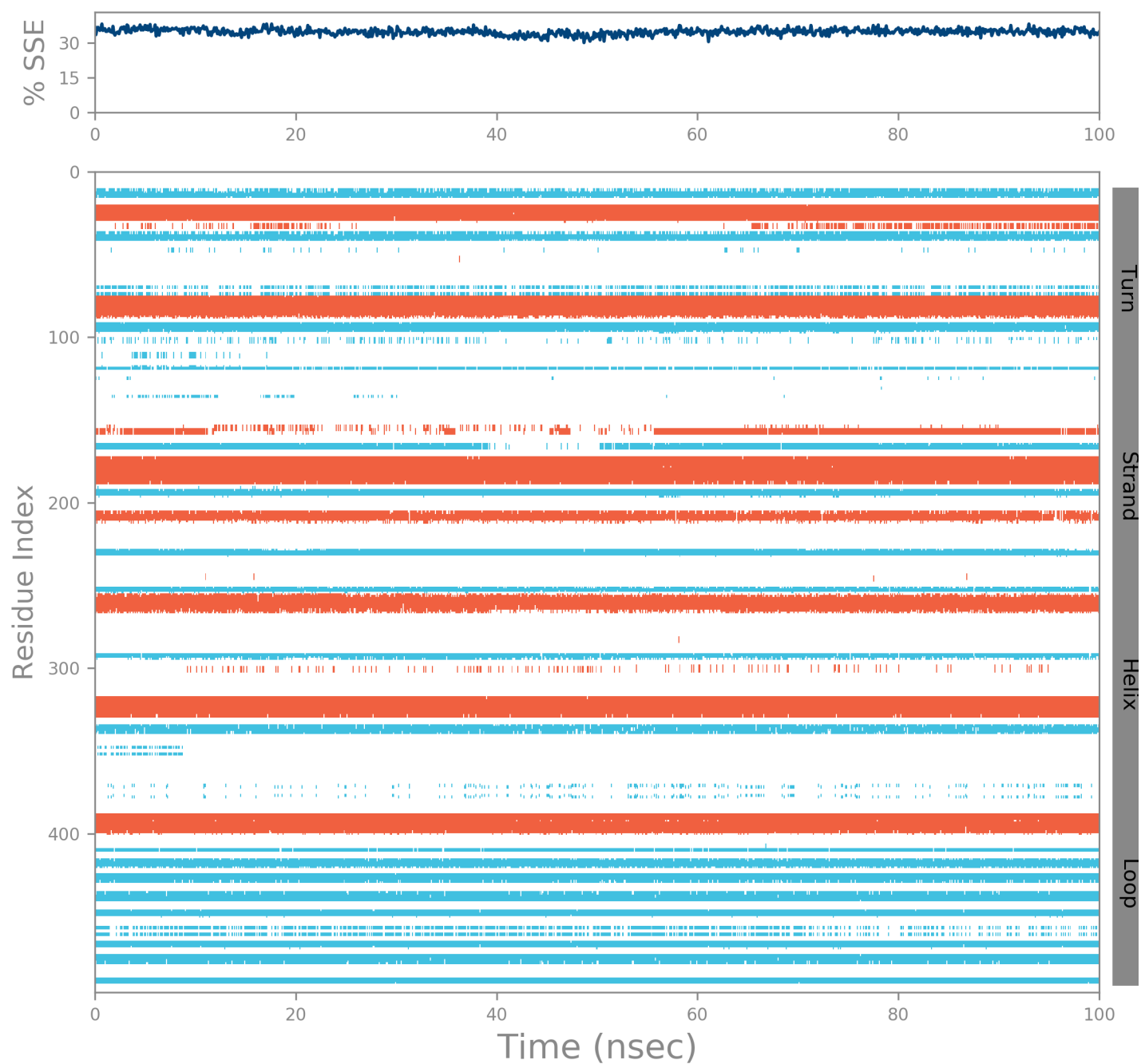
17.33

% Total SSE

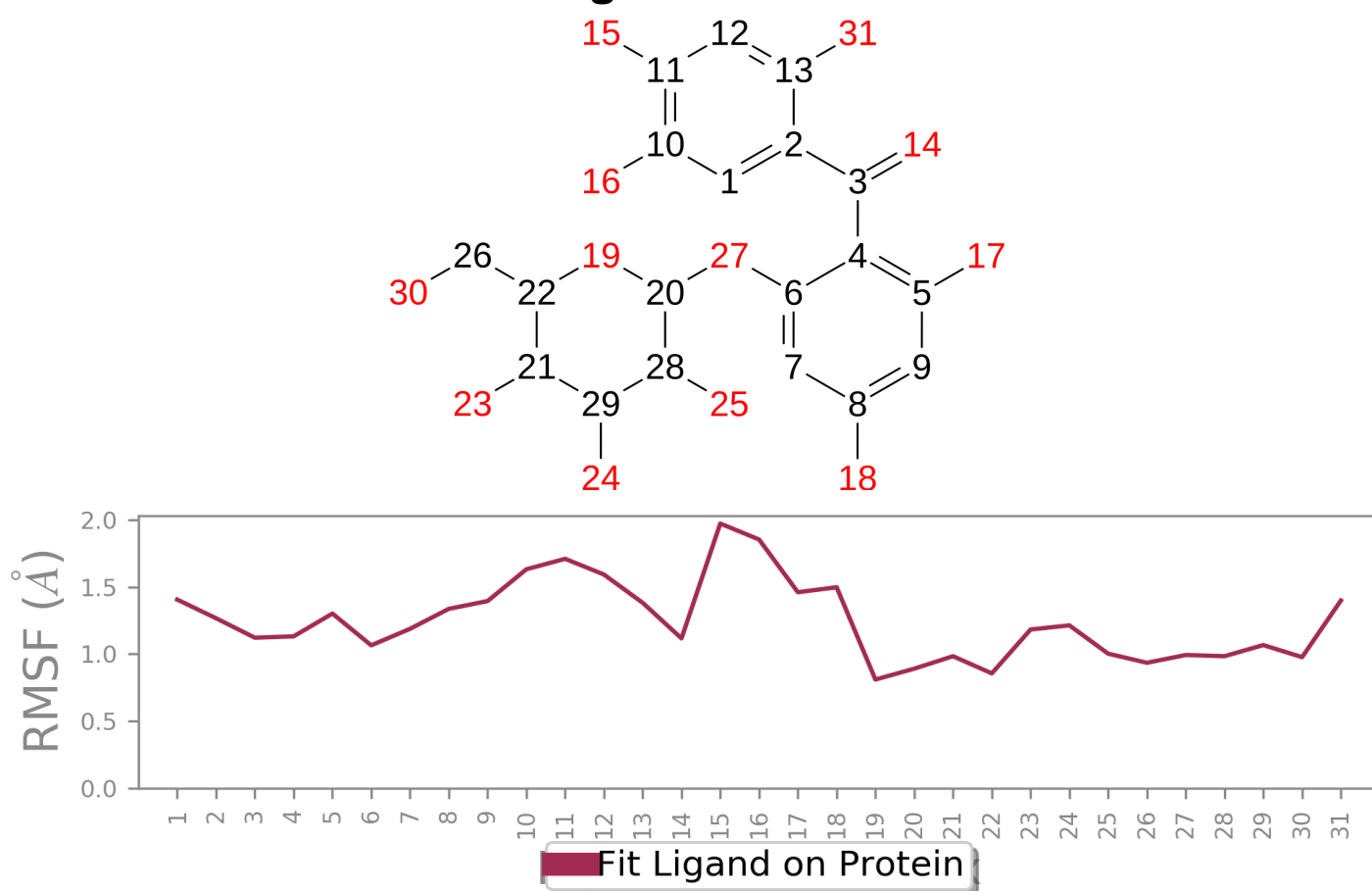
34.71



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Ligand RMSF



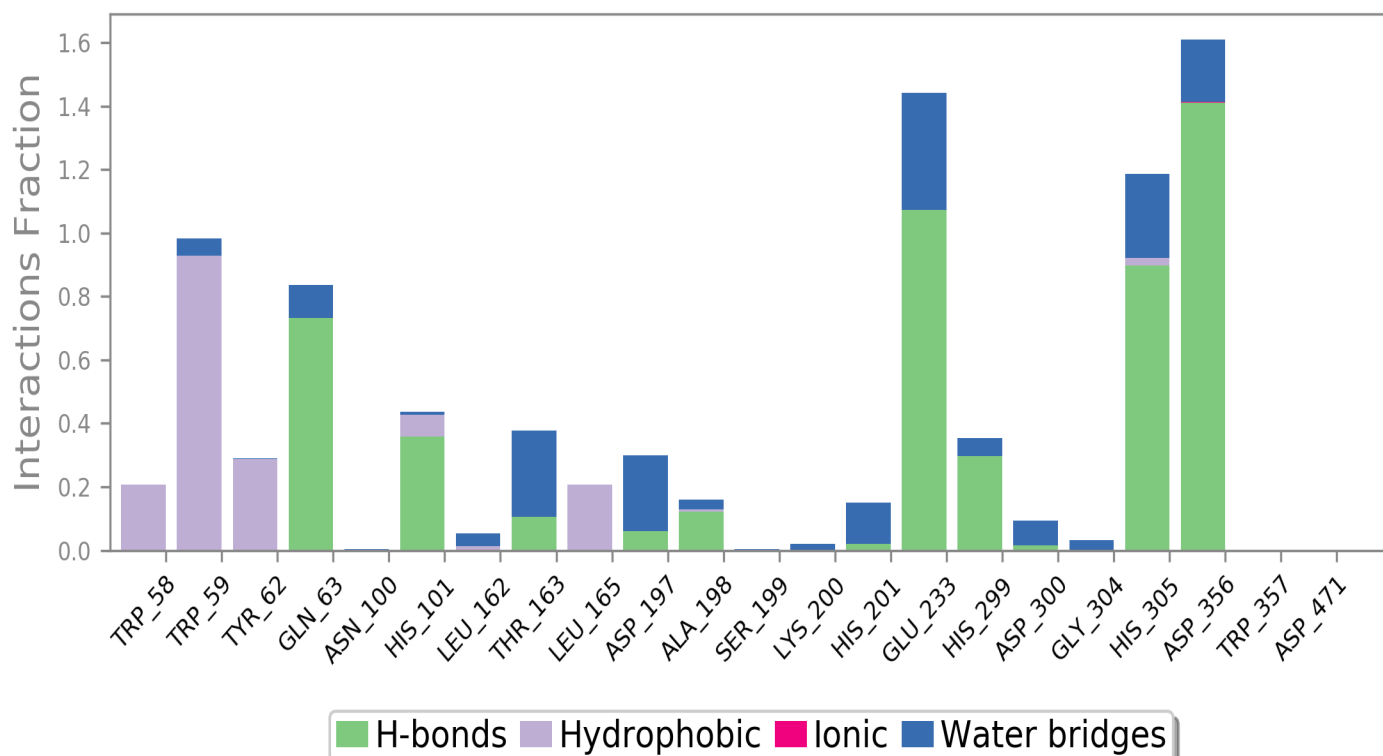
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Protein interactions with the ligand can be monitored throughout the simulation. These interactions can be categorized by type and summarized, as shown in the plot above. Protein-ligand interactions (or 'contacts') are categorized into four types: 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.

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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).

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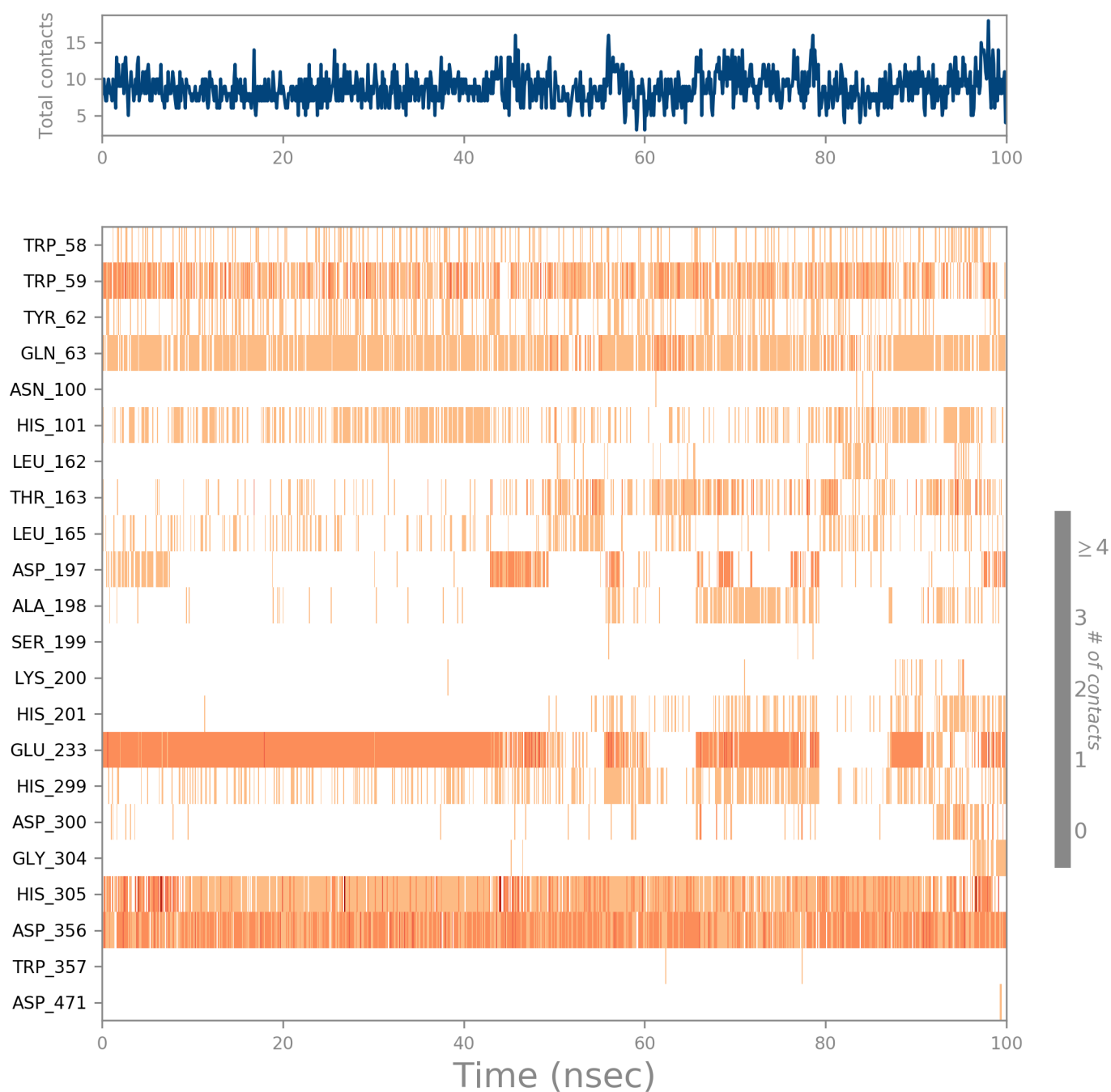
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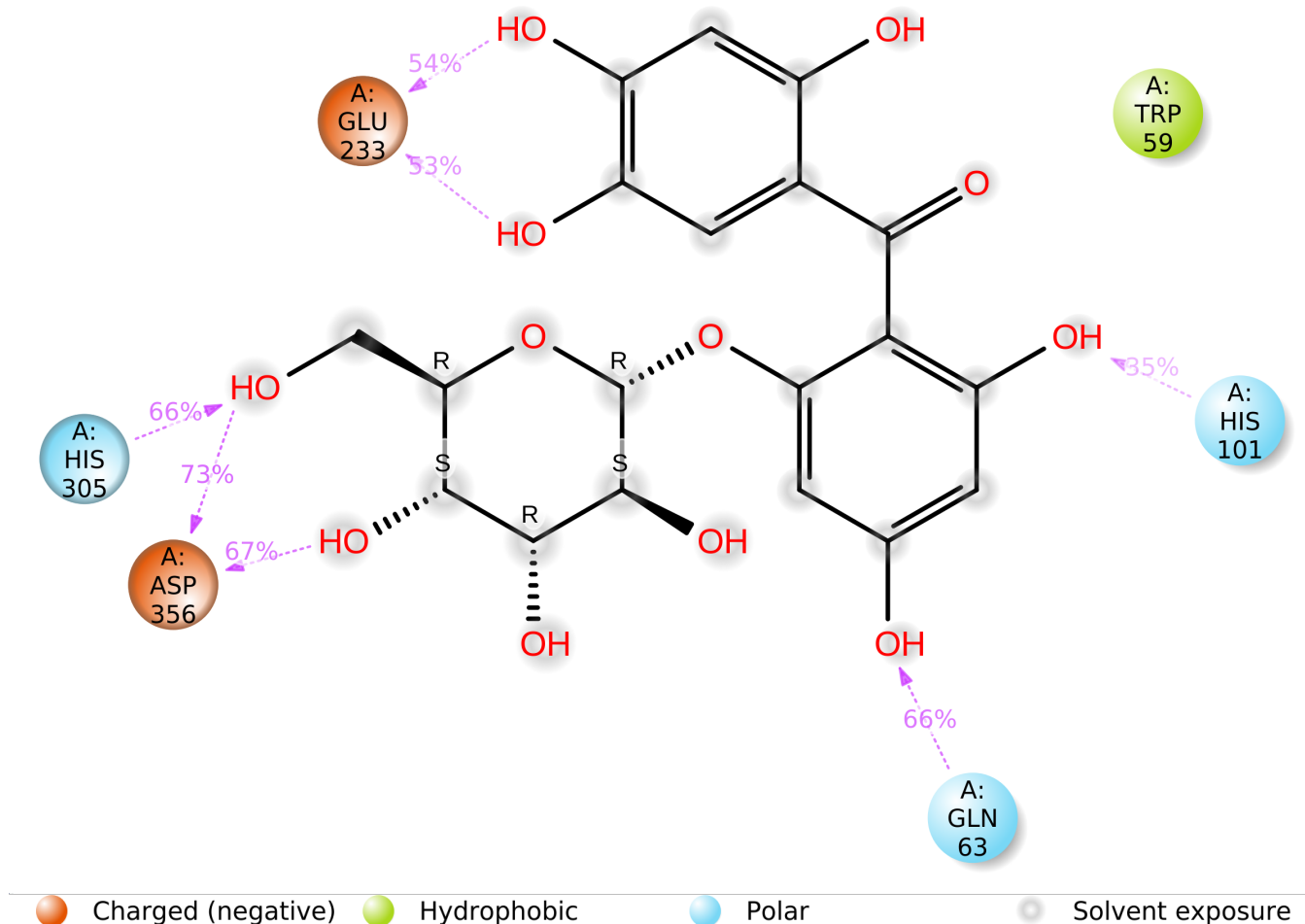
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Protein-Ligand Contacts (cont.)



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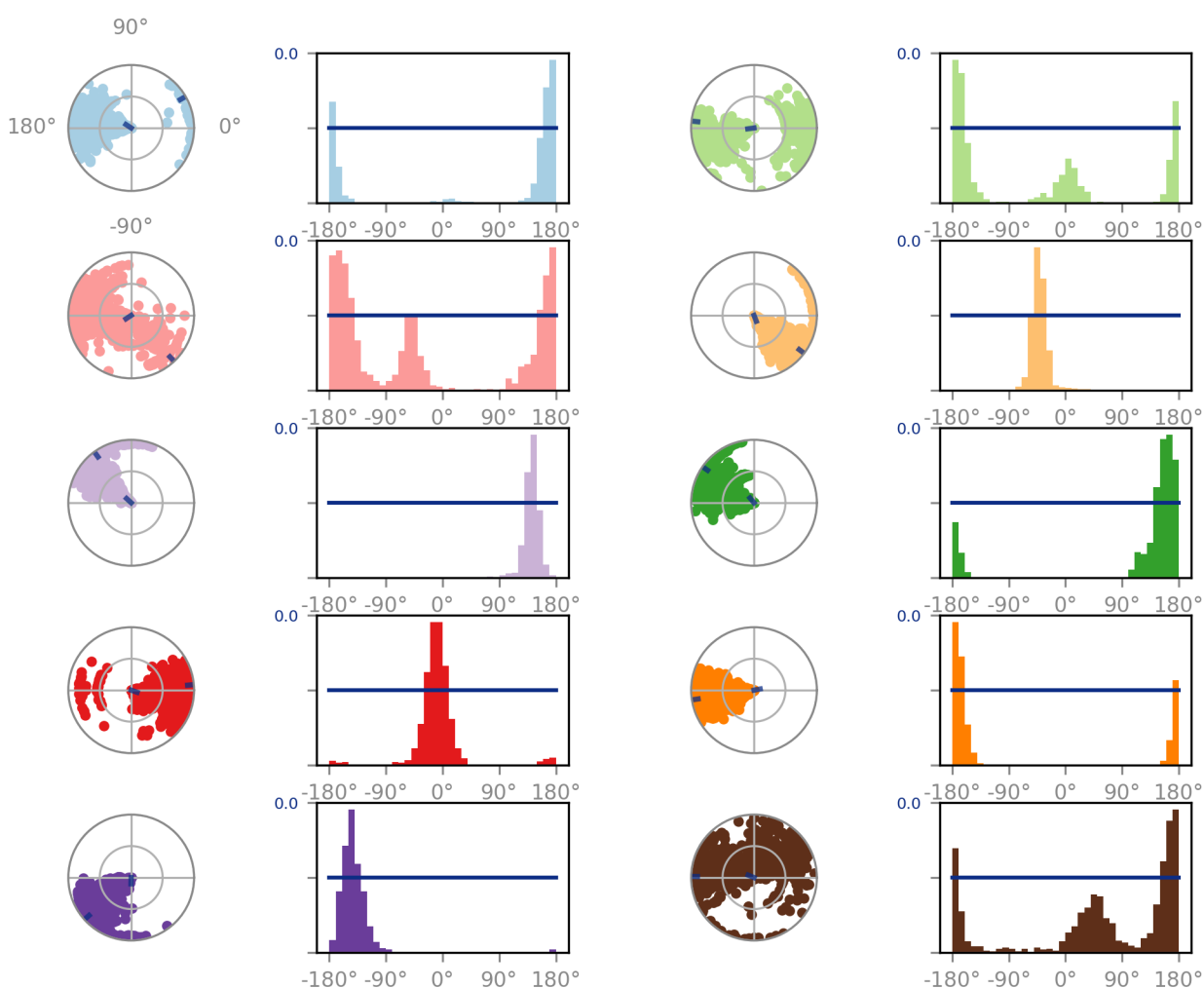
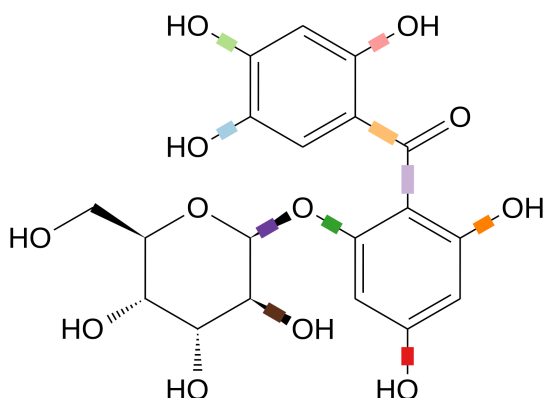
Ligand-Protein Contacts



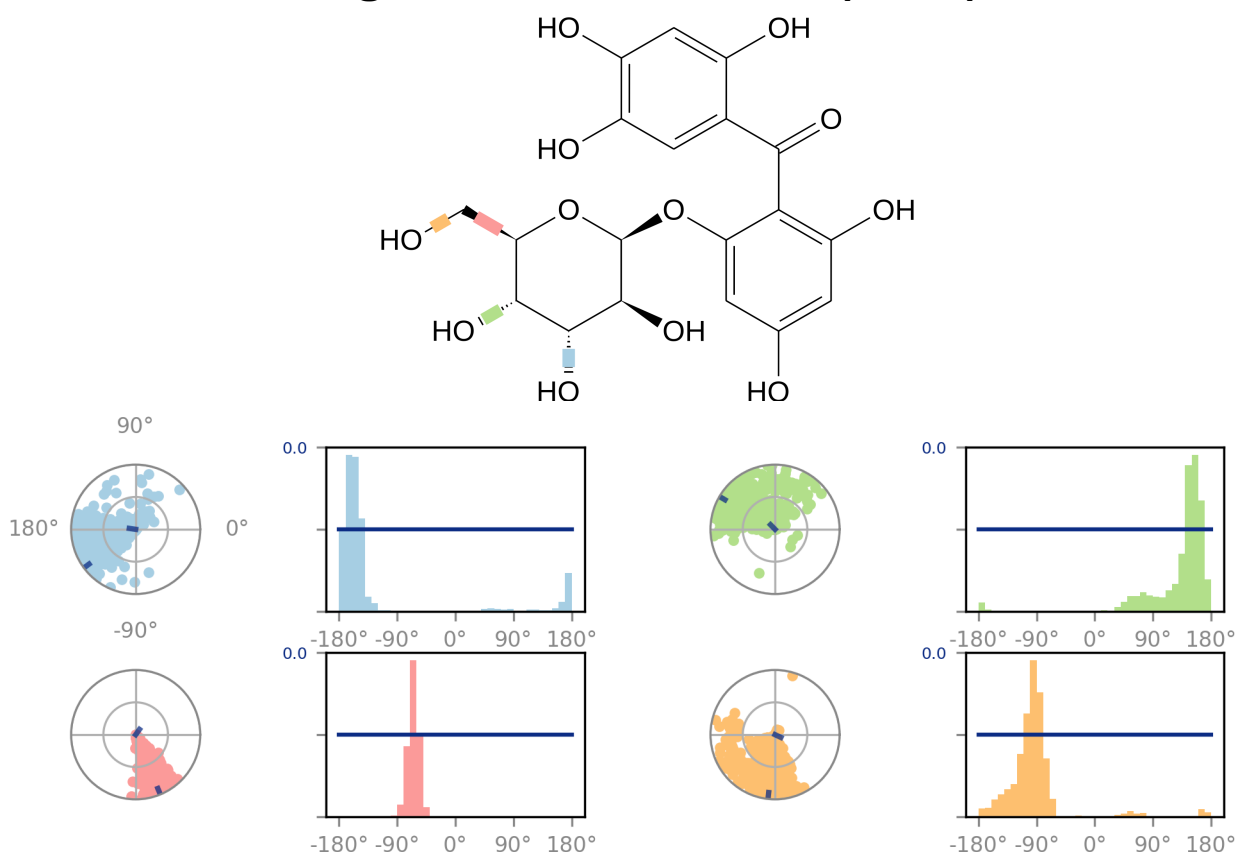
A schematic of detailed ligand atom interactions with the protein residues. Interactions that occur more than **30.0%** of the simulation time in the selected trajectory (0.00 through 100.00 nsec), are shown.

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.

Ligand Torsion Profile



Ligand Torsion Profile (cont.)

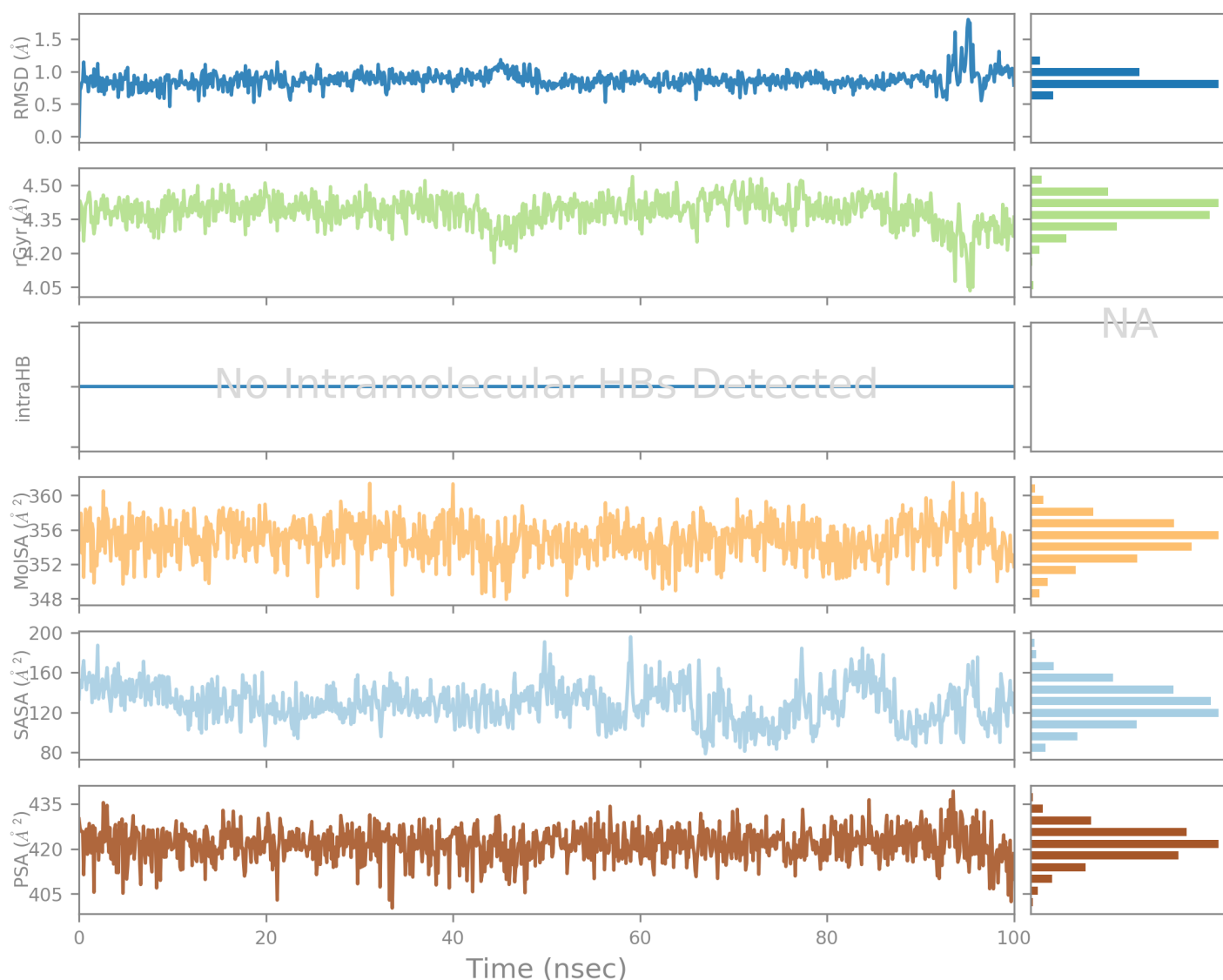


The ligand torsions plot summarizes the conformational evolution of every rotatable bond (RB) in the ligand throughout the simulation trajectory (0.00 through 100.00 nsec). The top panel shows the 2d schematic of a ligand with color-coded rotatable bonds. Each rotatable bond torsion is accompanied by a dial plot and bar plots of the same color.

Dial (or radial) plots describe the conformation of the torsion throughout the course of the simulation. The beginning of the simulation is in the center of the radial plot and the time evolution is plotted radially outwards.

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Ligand Properties



Ligand RMSD: Root mean square deviation of a ligand with respect to the reference conformation (typically the first frame is used as the reference and it is regarded as time $t=0$).

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Solvent Accessible Surface Area (SASA): Surface area of a molecule accessible by a water molecule.

Polar Surface Area (PSA): Solvent accessible surface area in a molecule contributed only by oxygen and nitrogen atoms.

Simulation Interactions Diagram Report

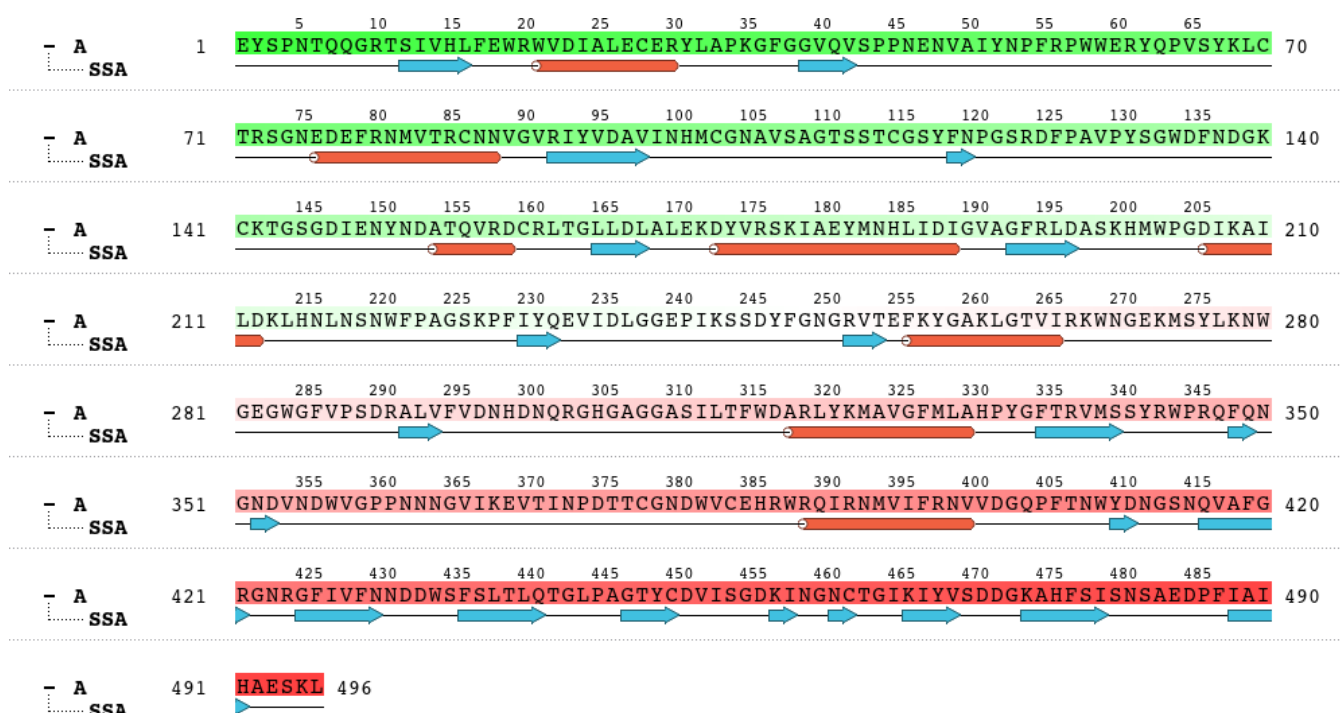
Simulation Details

Jobname: desmond_md_job_Acarbose
Entry title: Acarbose - minimized

CPU #	Job Type	Ensemble	Temp. [K]	Sim. Time [ns]	# Atoms	# Waters	Charge
1	mdsim	NPT	300.0	100.102	48455	13533	0

Protein Information

Tot. Residues	Prot. Chain(s)	Res. in Chain(s)	# Atoms	# Heavy Atoms	Charge
496	'A'	ict_values([496])	7669	3946	+1



Ligand Information

SMILES: O[C@@H]1[C@@H](O)[C@@H](O)O[C@H](C)[C@H]1[NH2+].[C@@H](C=C2CO)[C@H](O)[C@@H](O)[C@@H]2O[C@@H](O3[C@H](O)[C@@H](O)[C@@H](C[C@H]3CO)O[C@@H](O4[C@H](O)[C@@H](O)[C@@H](C[C@H]4CO)O[C@H](O5[C@@H](O)[C@@H](O)[C@@H](O)[C@@H]5CO

PDB Name: 'UNK'

Num. of Atoms: 109 (total) 55 (heavy)

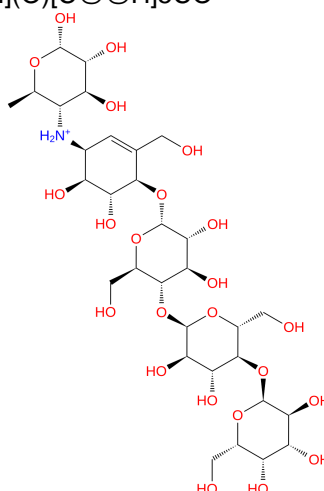
Atomic Mass: 808.769 au

Charge: +1

Mol. Formula: C31H54NO23

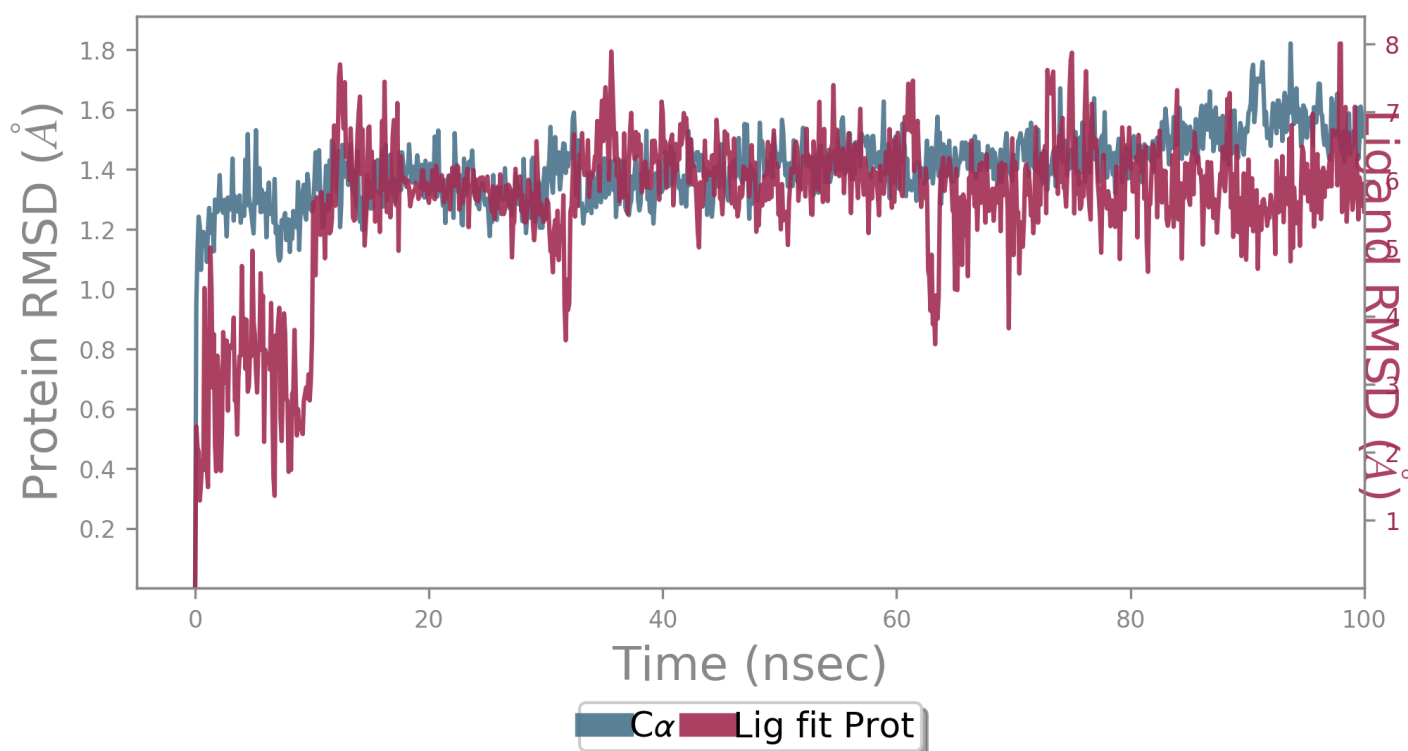
Num. of Fragments: 9

Num. of Rot. Bonds: 28



Type	Num.	Concentration [mM]	Total Charge
Cl	40	53.741	-40
Na	38	51.054	+38

Protein-Ligand RMSD



The Root Mean Square Deviation (RMSD) is used to measure the average change in displacement of a selection of atoms for a particular frame with respect to a reference frame. It is calculated for all frames in the trajectory. The RMSD for frame x is:

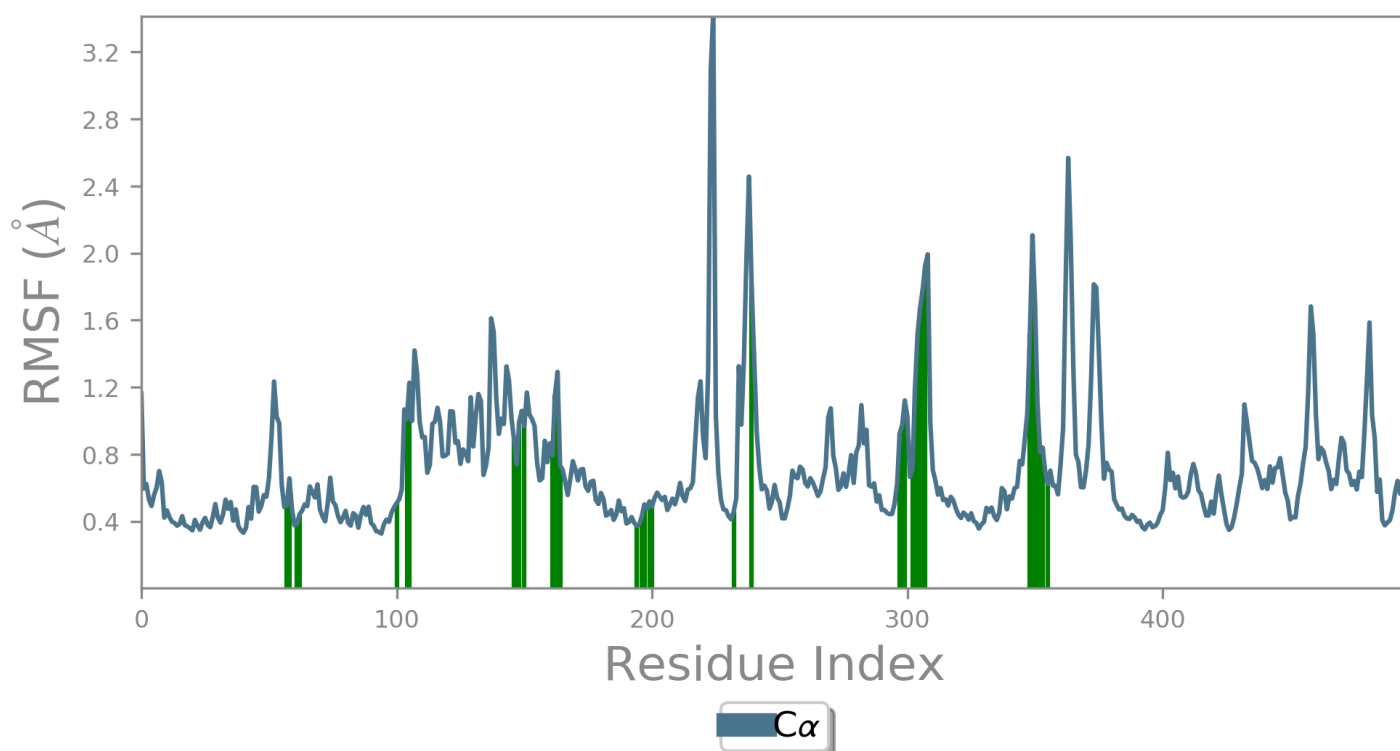
$$RMSD_x = \sqrt{\frac{1}{N} \sum_{i=1}^N (r'_i(t_x) - r_i(t_{ref}))^2}$$

where N is the number of atoms in the atom selection; t_{ref} is the reference time, (typically the first frame is used as the reference and it is regarded as time $t=0$); and r' is the position of the selected atoms in frame x after superimposing on the reference frame, where frame x is recorded at time t_x . The procedure is repeated for every frame in the simulation trajectory.

Protein RMSD: The above plot shows the RMSD evolution of a protein (left Y-axis). All protein frames are first aligned on the reference frame backbone, and then the RMSD is calculated based on the atom selection. Monitoring the RMSD of the protein can give insights into its structural conformation throughout the simulation. RMSD analysis can indicate if the simulation has equilibrated — its fluctuations towards the end of the simulation are around some thermal average structure. Changes of the order of 1-3 Å are perfectly acceptable for small, globular proteins. Changes much larger than that, however, indicate that the protein is undergoing a large conformational change during the simulation. It is also important that your simulation converges — the RMSD values stabilize around a fixed value. If the RMSD of the protein is still increasing or decreasing on average at the end of the simulation, then your system has not equilibrated, and your simulation may not be long enough for rigorous analysis.

Ligand RMSD: Ligand RMSD (right Y-axis) indicates how stable the ligand is with respect to the protein and its binding pocket. In the above plot, 'Lig fit Prot' shows the RMSD of a ligand when the protein-ligand complex is first aligned on the protein backbone of the reference and then the RMSD of the ligand heavy atoms is measured. If the values observed are significantly larger than the RMSD of the protein, then it is likely that the ligand has diffused away from its initial binding site.

Protein RMSF



The Root Mean Square Fluctuation (RMSF) is useful for characterizing local changes along the protein chain. The RMSF for residue i is:

$$RMSF_i = \sqrt{\frac{1}{T} \sum_{t=1}^T \langle (r'_i(t)) - r_i(t_{ref})^2 \rangle}$$

where T is the trajectory time over which the RMSF is calculated, t_{ref} is the reference time, r_i is the position of residue i ; r' is the position of atoms in residue i after superposition on the reference, and the angle brackets indicate that the average of the square distance is taken over the selection of atoms in the residue.

On this plot, peaks indicate areas of the protein that fluctuate the most during the simulation. 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.

Ligand Contacts: Protein residues that interact with the ligand are marked with green-colored vertical bars.

Protein Secondary Structure

% Helix

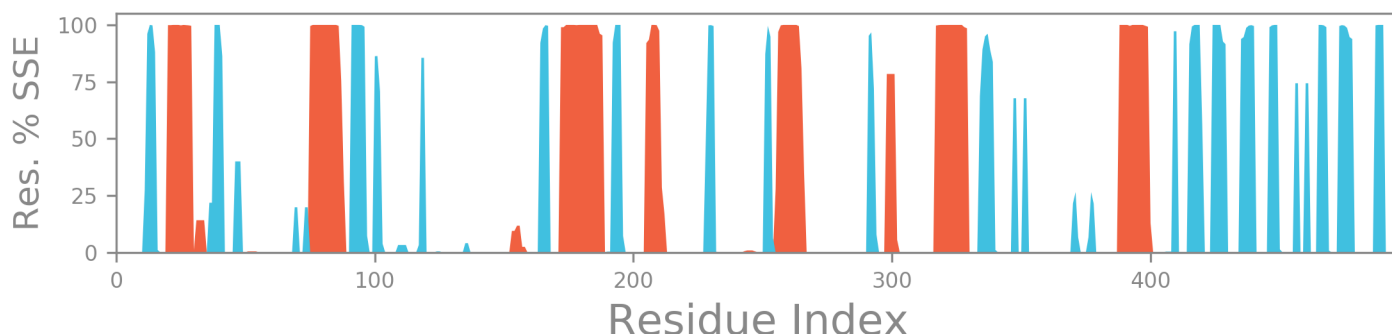
17.34

% Strand

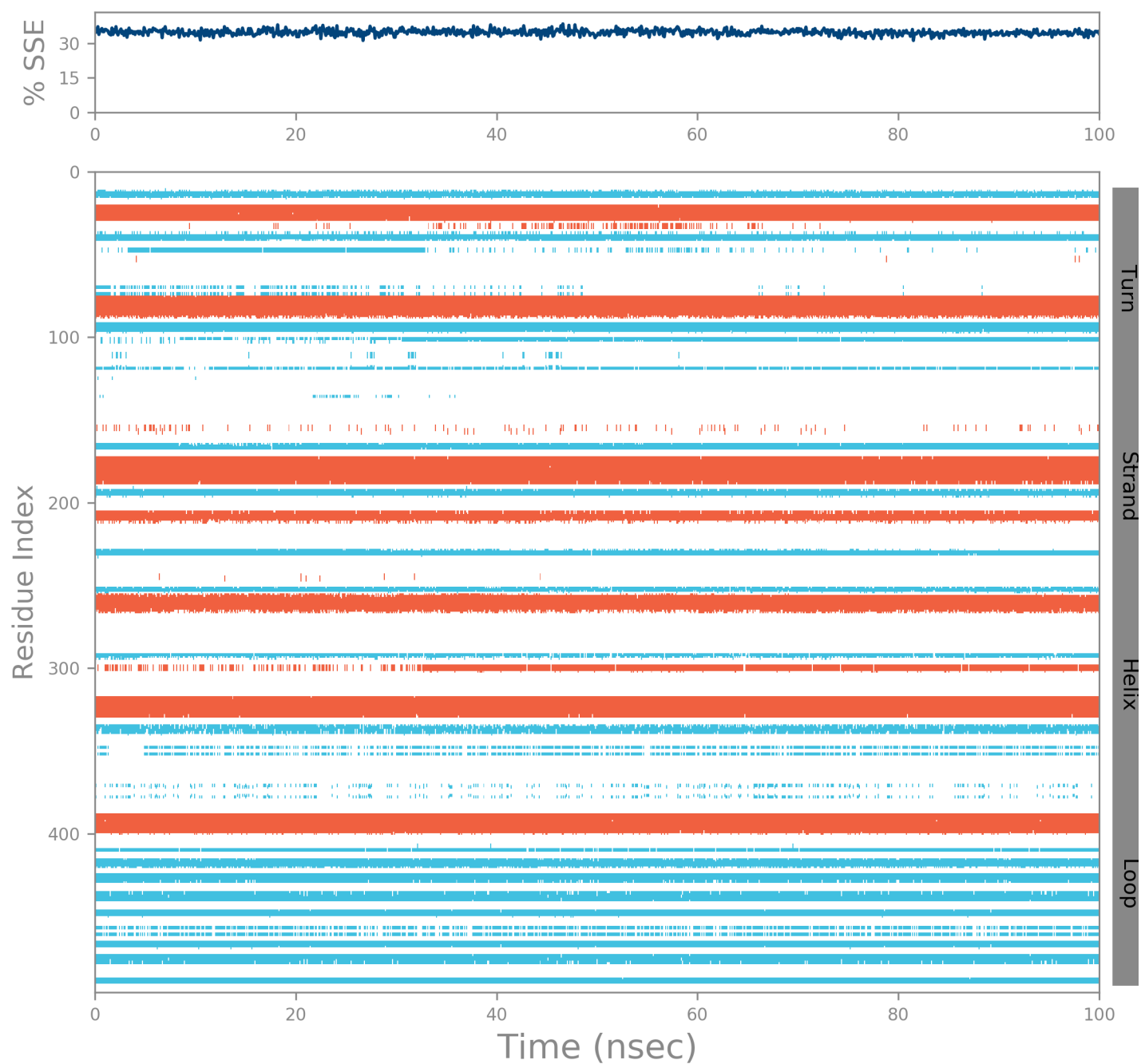
17.51

% Total SSE

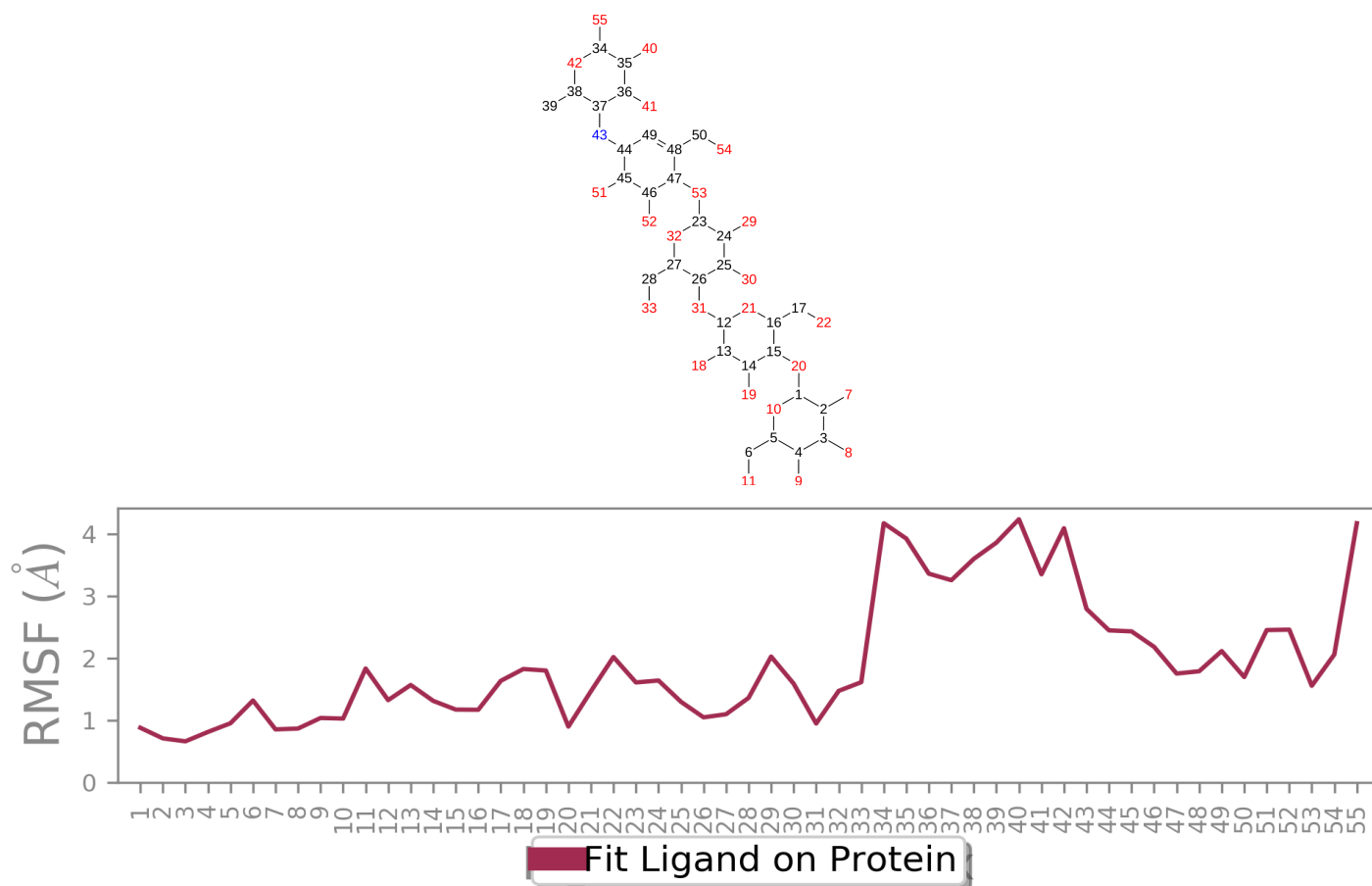
34.85



Protein secondary structure elements (SSE) like **alpha-helices** and **beta-strands** are monitored throughout the simulation. The plot above reports SSE distribution by residue index throughout the protein structure. The plot below summarizes the SSE composition for each trajectory frame over the course of the simulation, and the plot at the bottom monitors each residue and its SSE assignment over time.



Ligand RMSF



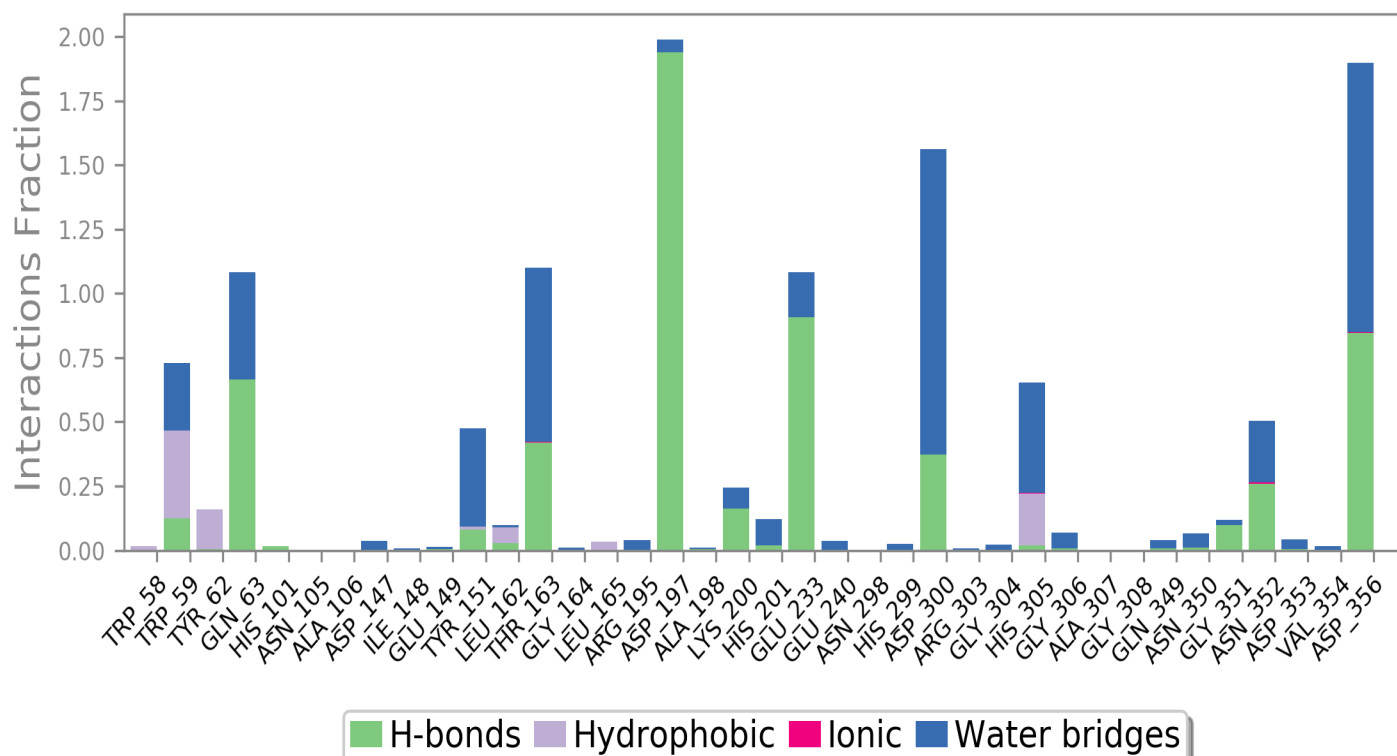
The Ligand Root Mean Square Fluctuation (L-RMSF) is useful for characterizing changes in the ligand atom positions. The RMSF for atom i is:

$$RMSF_i = \sqrt{\frac{1}{T} \sum_{t=1}^T (r'_i(t) - r_i(t_{ref}))^2}$$

where T is the trajectory time over which the RMSF is calculated, t_{ref} is the reference time (usually for the first frame, and is regarded as the zero of time); r is the position of atom i in the reference at time t_{ref} and r' is the position of atom i at time t after superposition on the reference frame.

Ligand RMSF shows the ligand's fluctuations broken down by atom, corresponding to the 2D structure in the top panel. The ligand RMSF may give you insights on how ligand fragments interact with the protein and their entropic role in the binding event. In the bottom panel, the 'Fit Ligand on Protein' line shows the ligand fluctuations, with respect to the protein. The protein-ligand complex is first aligned on the protein backbone and then the ligand RMSF is measured on the ligand heavy atoms.

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: π -Cation; π - π ; 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 π -Cation interactions.

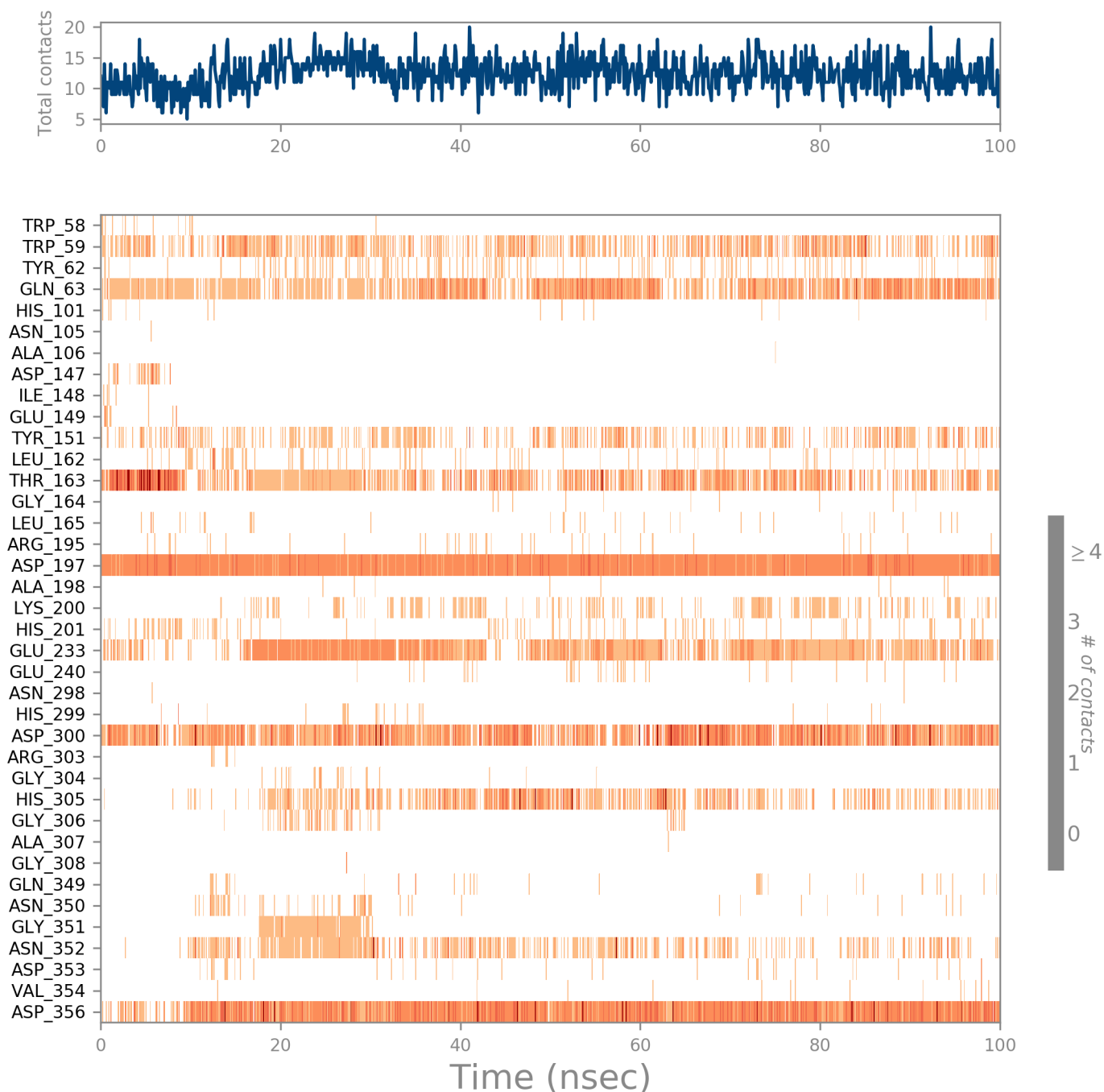
The current geometric criteria for hydrophobic interactions is as follows: π -Cation — Aromatic and charged groups within 4.5 Å; π - π — Two aromatic groups stacked face-to-face or face-to-edge; Other — A non-specific hydrophobic sidechain within 3.6 Å of a ligand's aromatic or aliphatic carbons.

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.

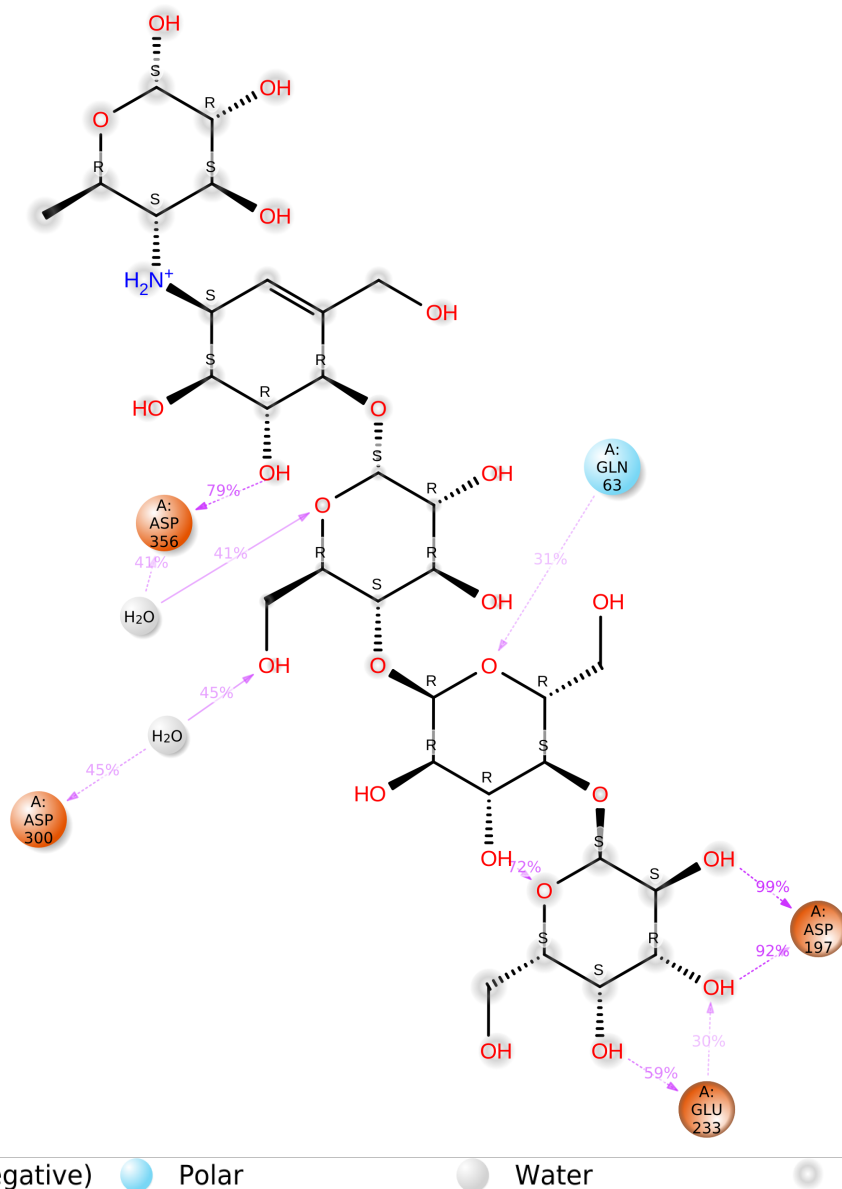
The current geometric criteria for a protein-water or water-ligand H-bond are: a distance of 2.8 Å between the donor and acceptor atoms (D—H...A); a donor angle of $\geq 110^\circ$ between the donor-hydrogen-acceptor atoms (D—H...A); and an acceptor angle of $\geq 90^\circ$ between the hydrogen-acceptor-bonded_atom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

Protein-Ligand Contacts (cont.)



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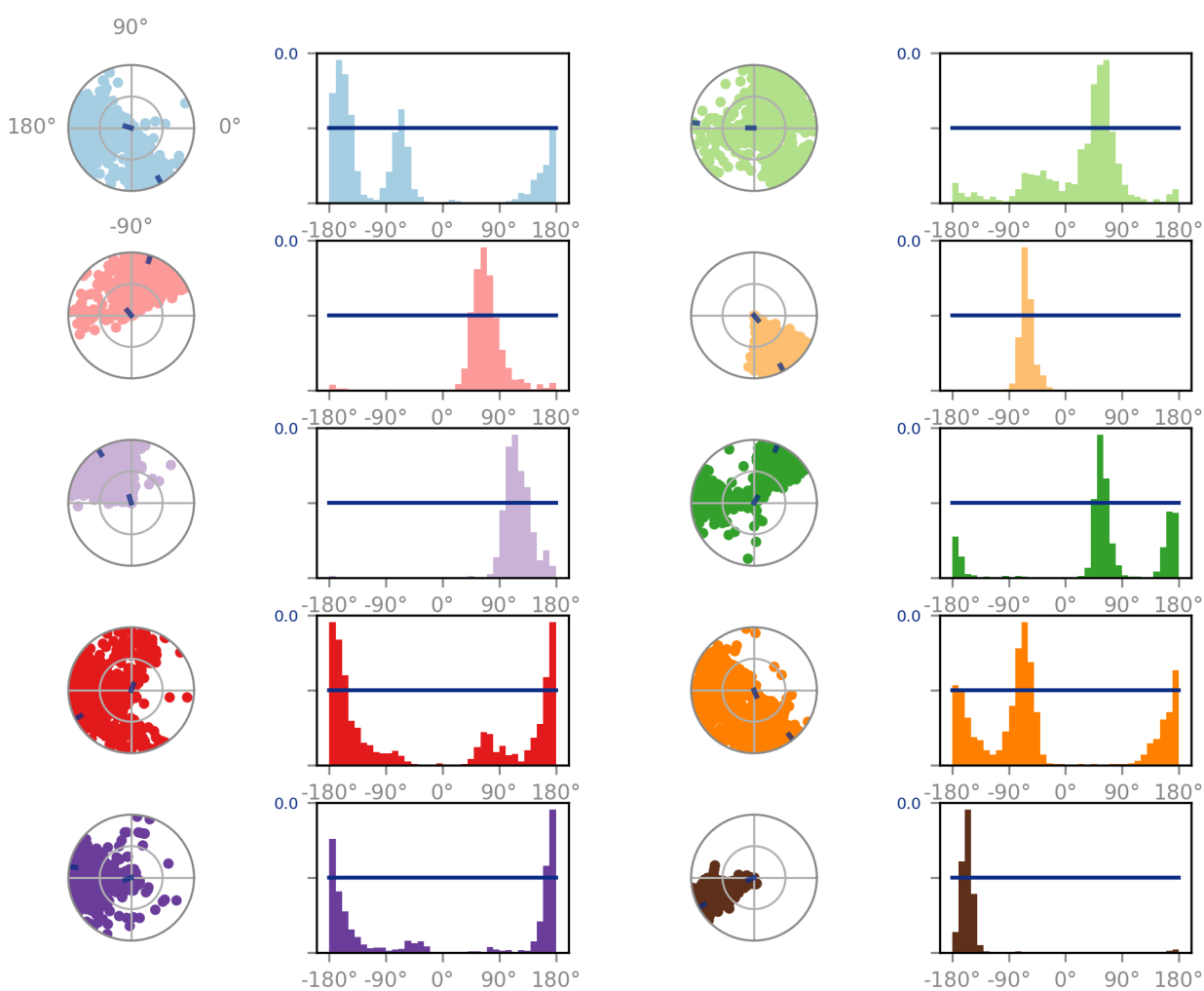
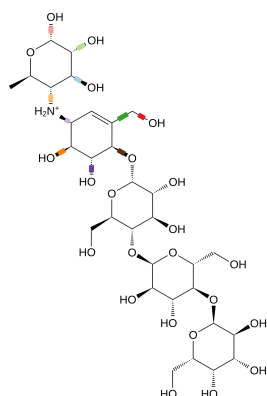
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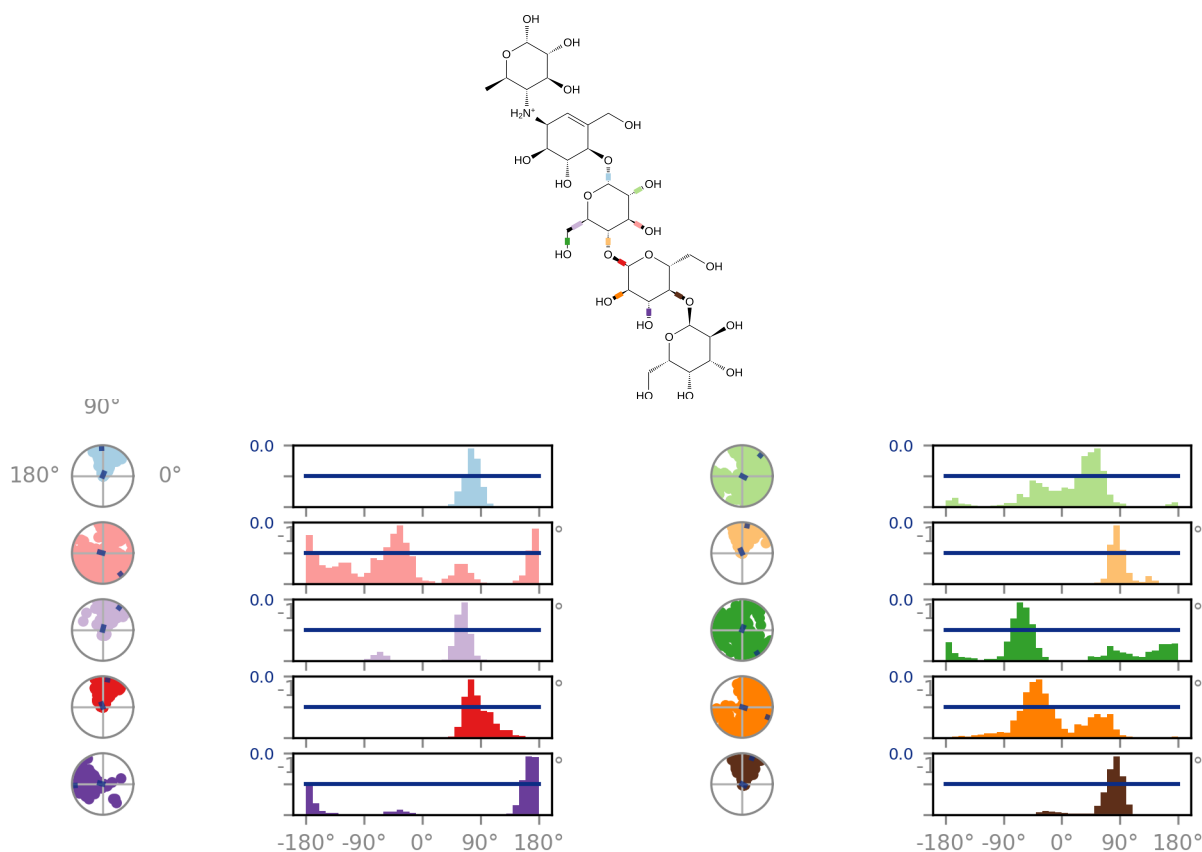
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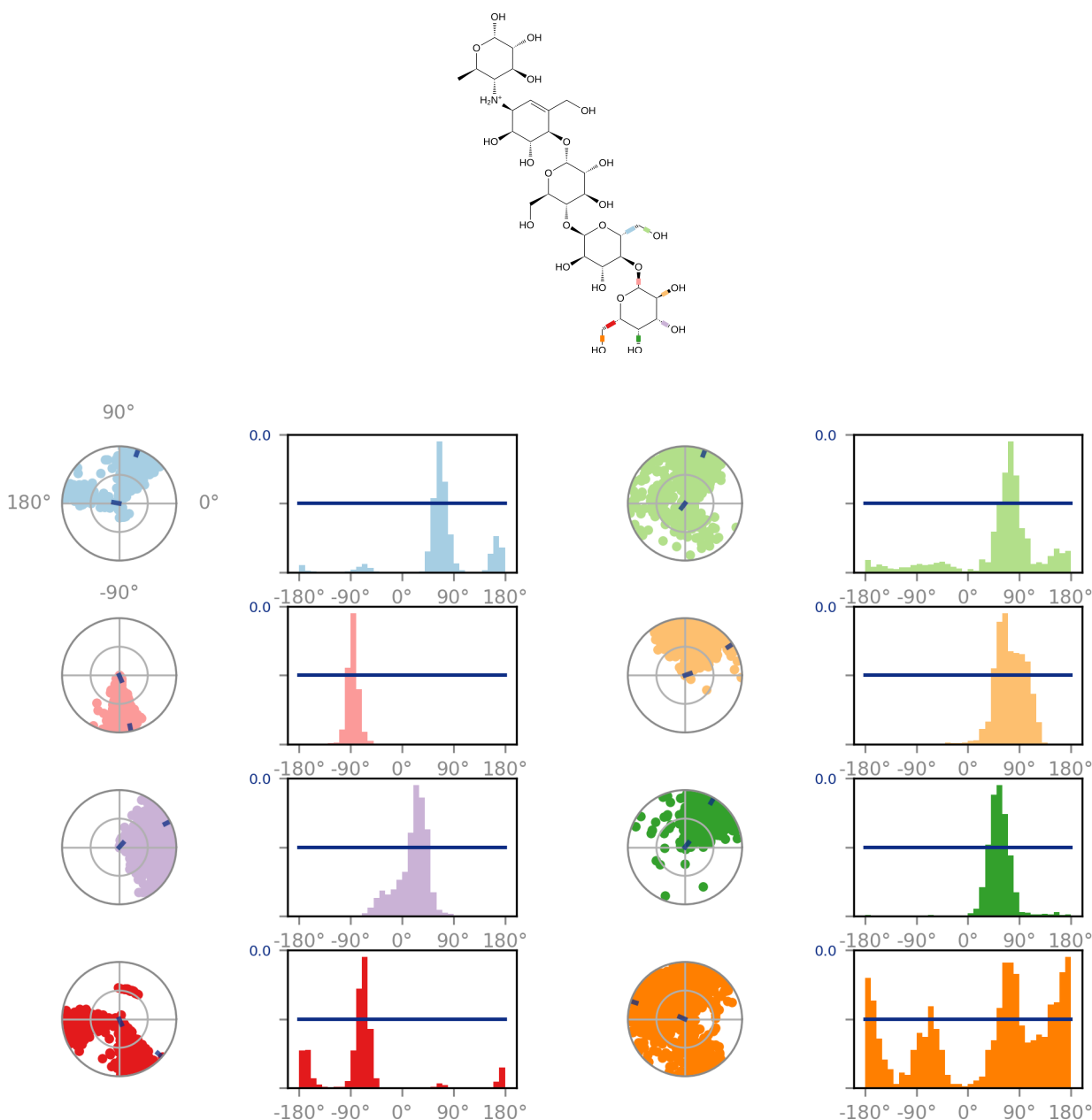
Ligand Torsion Profile



Ligand Torsion Profile (cont.)



Ligand Torsion Profile (cont.)

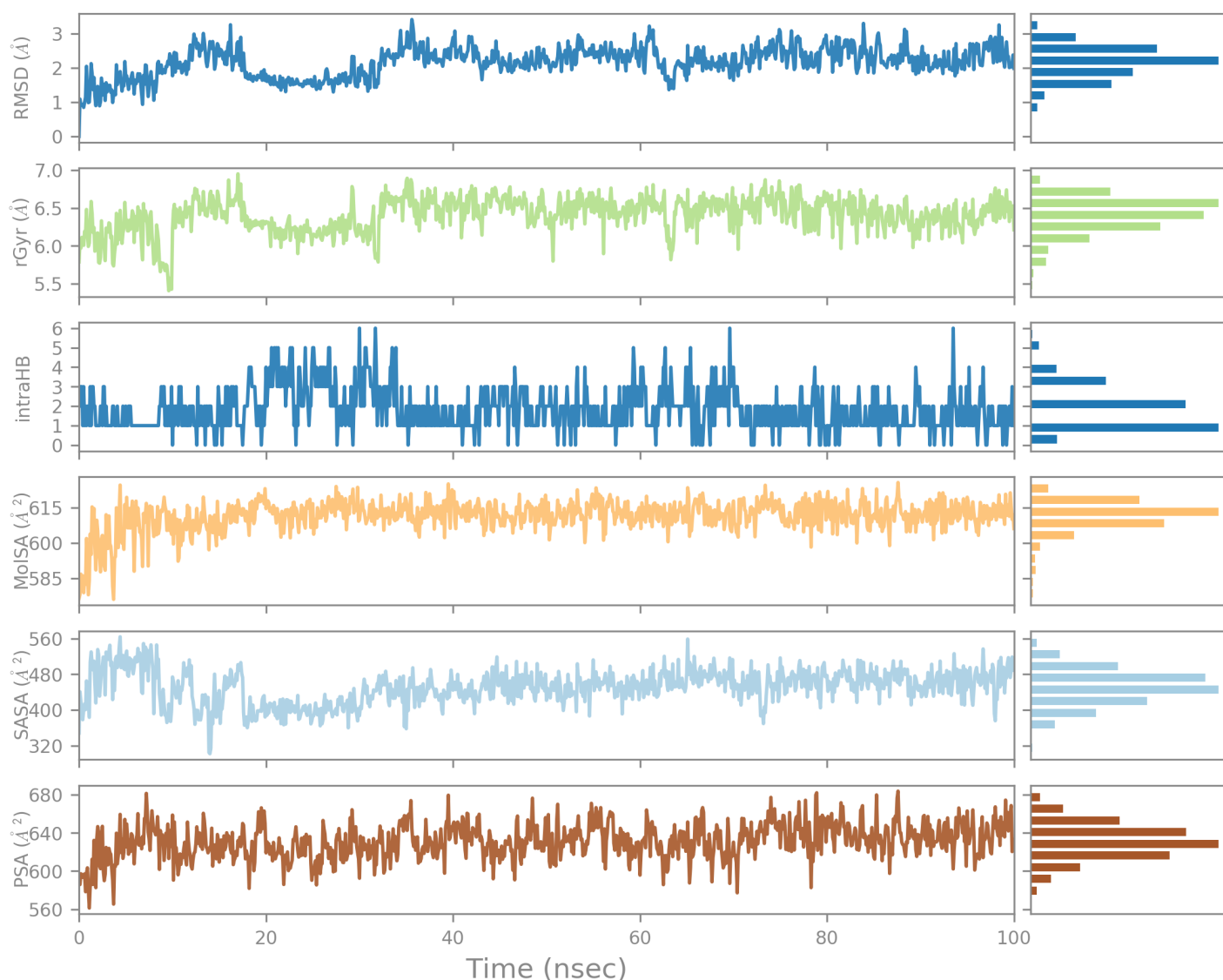


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