



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 16, 2026 – 10:36 AM UTC

PDB ID : 3U8N / pdb_00003u8n
Title : Crystal structure of the acetylcholine binding protein (AChBP) from *Lymnaea stagnalis* in complex with NS3950 (1-(6-bromo-5-ethoxypyridin-3-yl)-1,4-diazepane)
Authors : Rohde, L.A.H.; Ahring, P.K.; Jensen, M.L.; Nielsen, E.O.; Peters, D.; Helgstrand, C.; Krintel, C.; Harpsoe, K.; Gajhede, M.; Kastrop, J.S.; Balle, T.
Deposited on : 2011-10-17
Resolution : 2.35 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

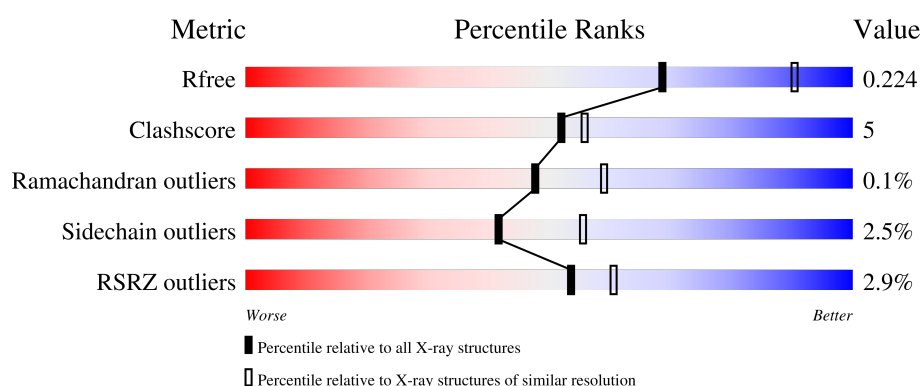
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



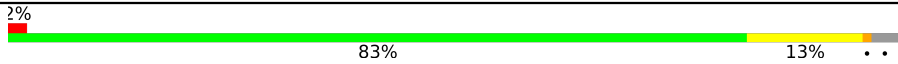
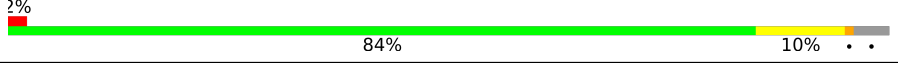
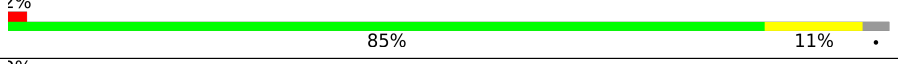
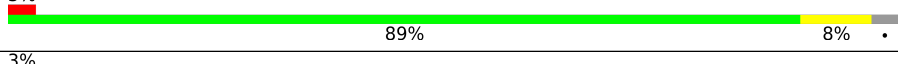
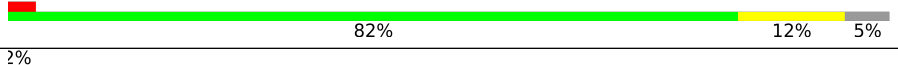
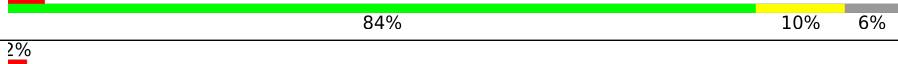
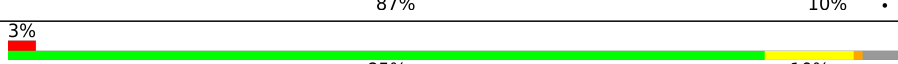
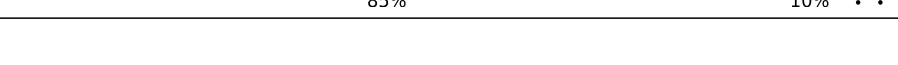
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	210	3% 86% 10% .
1	B	210	5% 83% 14% .
1	C	210	2% 87% 10% .
1	D	210	2% 85% 12% .
1	E	210	3% 80% 15% ..

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Mol	Chain	Length	Quality of chain
1	F	210	
1	G	210	
1	H	210	
1	I	210	
1	J	210	
1	K	210	
1	L	210	
1	M	210	
1	N	210	
1	O	210	
1	P	210	
1	Q	210	
1	R	210	
1	S	210	
1	T	210	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 34660 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Acetylcholine-binding protein.

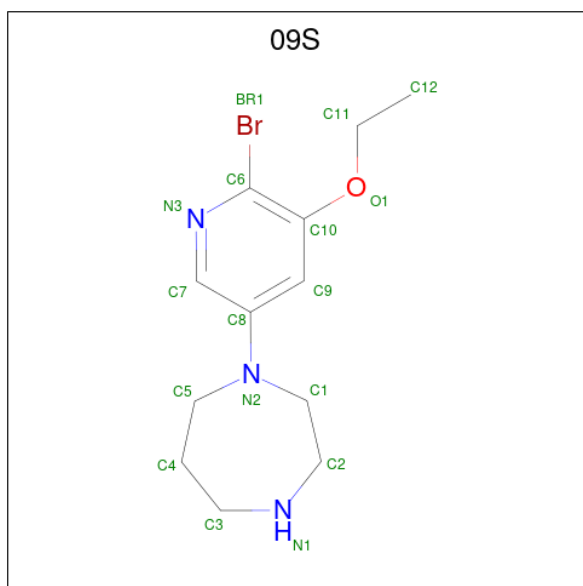
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	1	0
			1616	1013	276	321	6			
1	B	203	Total	C	N	O	S	0	2	0
			1626	1018	278	323	7			
1	C	204	Total	C	N	O	S	0	1	0
			1635	1023	279	327	6			
1	D	205	Total	C	N	O	S	0	2	0
			1642	1027	280	328	7			
1	E	201	Total	C	N	O	S	0	4	0
			1625	1019	278	321	7			
1	F	204	Total	C	N	O	S	0	2	0
			1641	1027	284	324	6			
1	G	201	Total	C	N	O	S	0	1	0
			1609	1009	275	319	6			
1	H	201	Total	C	N	O	S	0	1	0
			1609	1009	275	319	6			
1	I	203	Total	C	N	O	S	0	3	0
			1637	1025	283	322	7			
1	J	201	Total	C	N	O	S	0	1	0
			1609	1009	275	319	6			
1	K	204	Total	C	N	O	S	0	1	0
			1633	1022	281	324	6			
1	L	200	Total	C	N	O	S	0	2	0
			1608	1009	274	318	7			
1	M	202	Total	C	N	O	S	0	2	0
			1628	1020	282	320	6			
1	N	198	Total	C	N	O	S	0	2	0
			1590	1000	272	311	7			
1	O	201	Total	C	N	O	S	0	1	0
			1609	1009	275	319	6			
1	P	203	Total	C	N	O	S	0	1	0
			1626	1018	280	322	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	203	Total	C	N	O	S	0	1	0
			1626	1018	280	322	6			
1	R	200	Total	C	N	O	S	0	1	0
			1605	1007	274	318	6			
1	S	203	Total	C	N	O	S	0	2	0
			1629	1020	280	322	7			
1	T	201	Total	C	N	O	S	0	3	0
			1620	1016	278	319	7			

- Molecule 2 is 1-(6-bromo-5-ethoxypyridin-3-yl)-1,4-diazepane (CCD ID: 09S) (formula: C₁₂H₁₈BrN₃O).



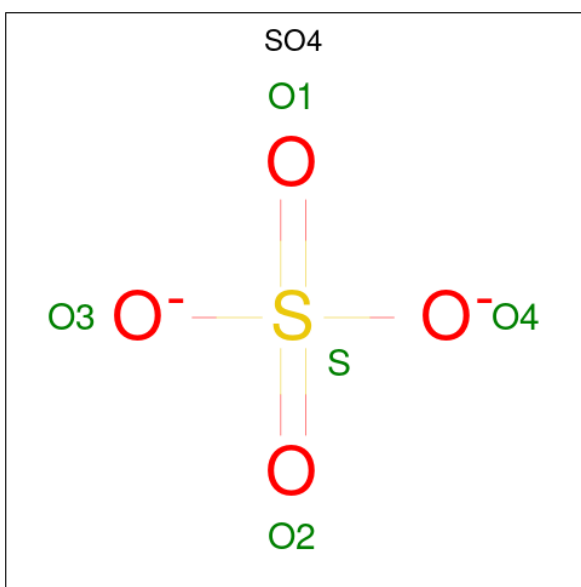
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	B	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	C	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	D	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	E	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	F	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	G	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		

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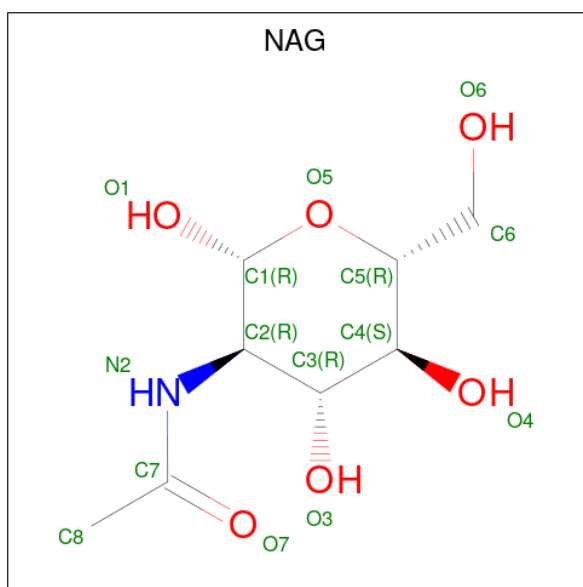
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	H	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	I	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	J	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	K	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	L	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	M	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	N	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	O	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	P	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	Q	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	R	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	S	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		
2	T	1	Total	Br	C	N	O	0	0
			17	1	12	3	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	N	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	P	1	Total	O	S	0	0
			5	4	1		
3	S	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		
4	T	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	116	Total	O	0	0
			116	116		
5	B	130	Total	O	0	0
			130	130		
5	C	112	Total	O	0	0
			112	112		
5	D	118	Total	O	0	0
			118	118		
5	E	110	Total	O	0	0
			110	110		
5	F	79	Total	O	0	0
			79	79		
5	G	91	Total	O	0	0
			91	91		
5	H	77	Total	O	0	0
			77	77		
5	I	77	Total	O	0	0
			77	77		

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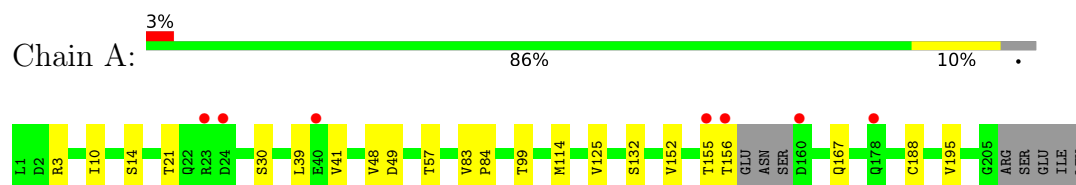
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	J	77	Total 77	O 77	0	0
5	K	102	Total 102	O 102	0	0
5	L	88	Total 88	O 88	0	0
5	M	99	Total 99	O 99	0	0
5	N	96	Total 96	O 96	0	0
5	O	95	Total 95	O 95	0	0
5	P	83	Total 83	O 83	0	0
5	Q	69	Total 69	O 69	0	0
5	R	80	Total 80	O 80	0	0
5	S	68	Total 68	O 68	0	0
5	T	58	Total 58	O 58	0	0

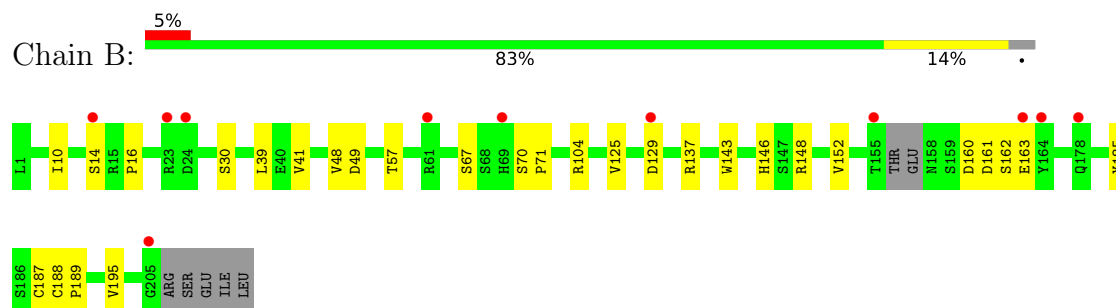
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

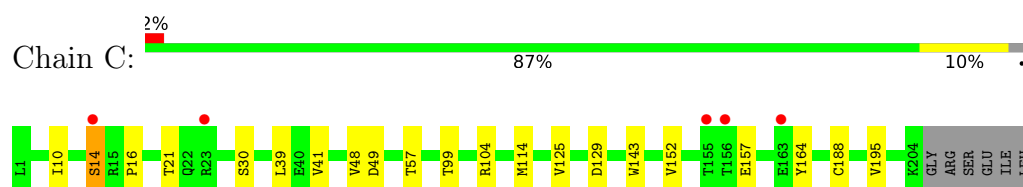
- Molecule 1: Acetylcholine-binding protein



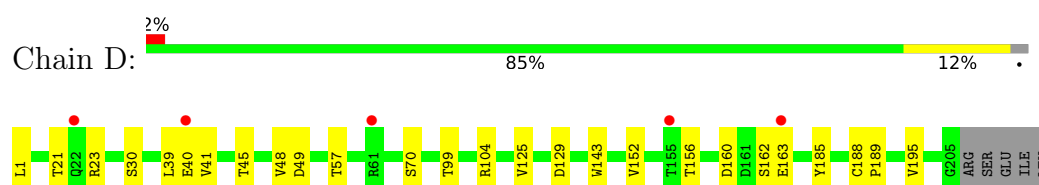
- Molecule 1: Acetylcholine-binding protein



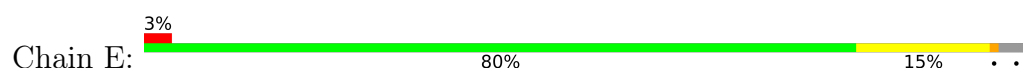
- Molecule 1: Acetylcholine-binding protein

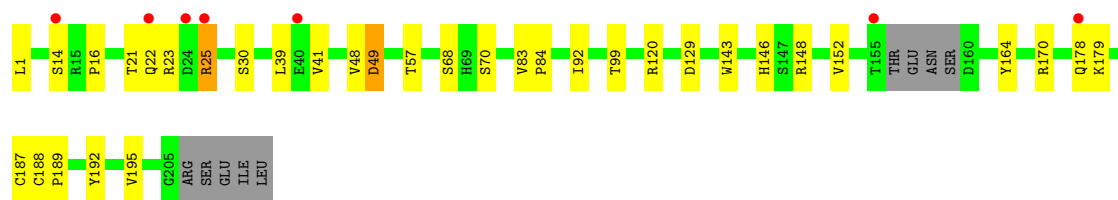


- Molecule 1: Acetylcholine-binding protein

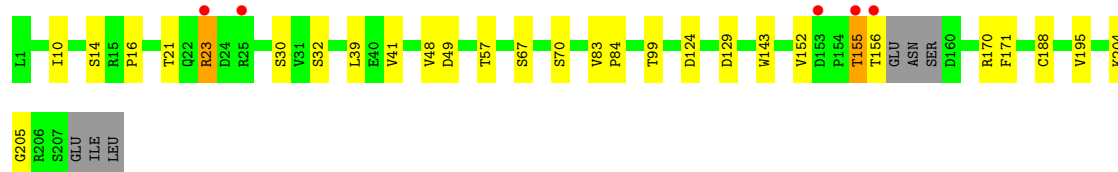
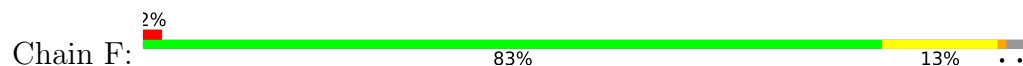


- Molecule 1: Acetylcholine-binding protein

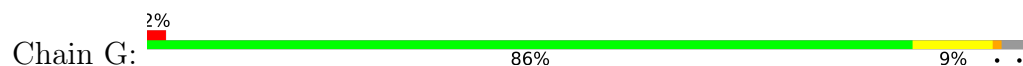




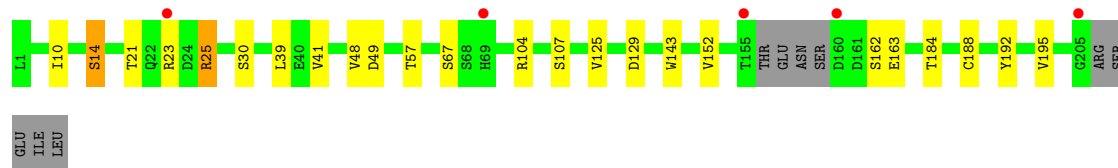
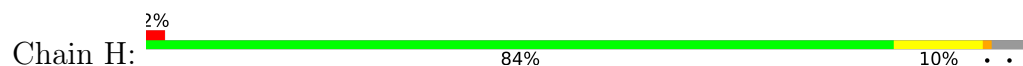
- Molecule 1: Acetylcholine-binding protein



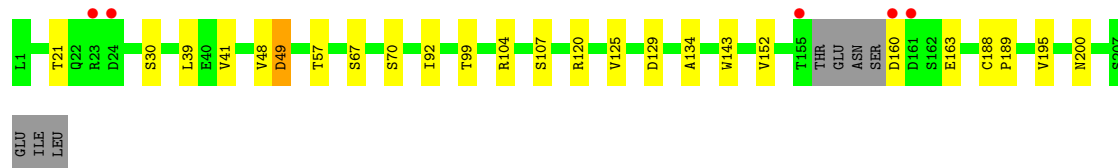
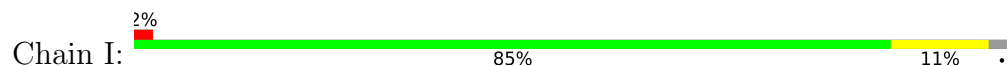
- Molecule 1: Acetylcholine-binding protein



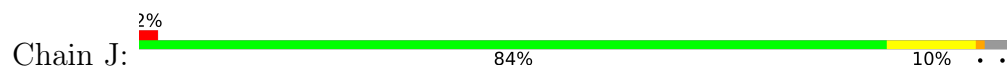
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein

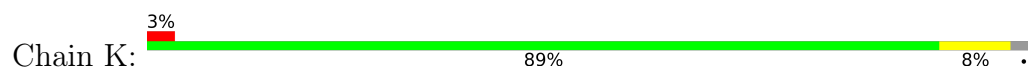


- Molecule 1: Acetylcholine-binding protein

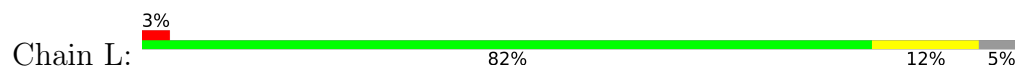




- Molecule 1: Acetylcholine-binding protein

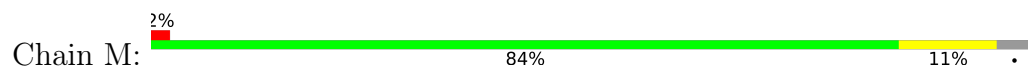


- Molecule 1: Acetylcholine-binding protein

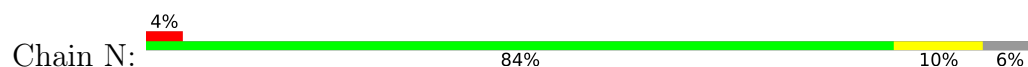


LEU

- Molecule 1: Acetylcholine-binding protein

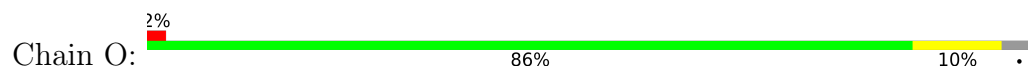


- Molecule 1: Acetylcholine-binding protein

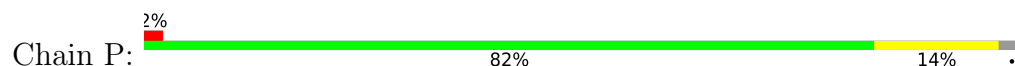


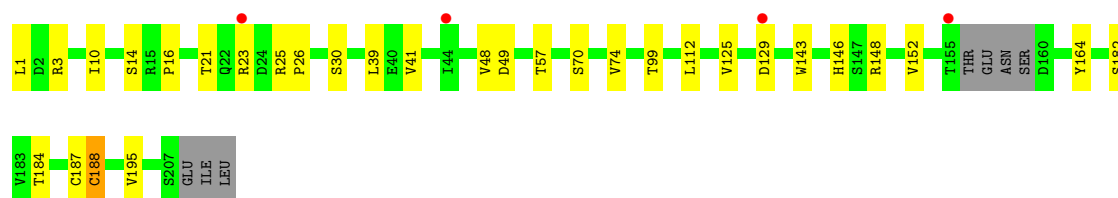
ILE
LEU

- Molecule 1: Acetylcholine-binding protein

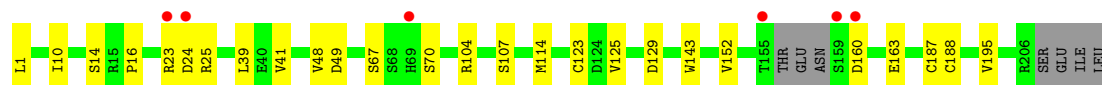
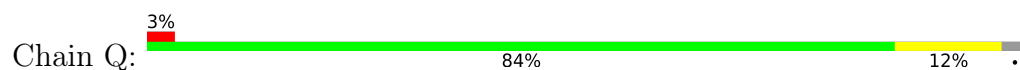


- Molecule 1: Acetylcholine-binding protein

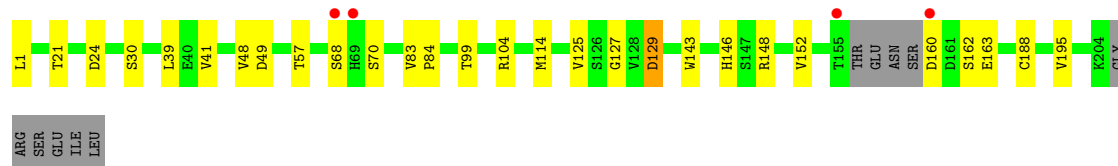
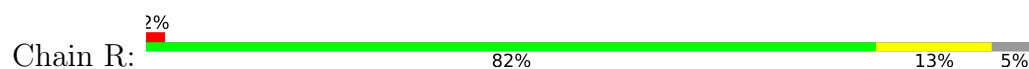




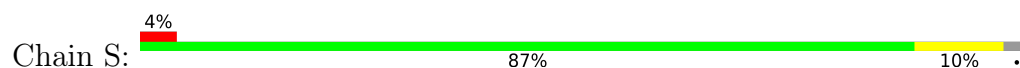
- Molecule 1: Acetylcholine-binding protein



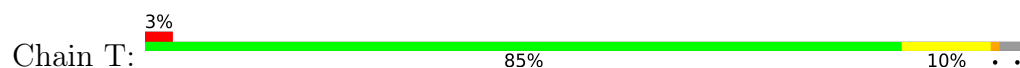
- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



- Molecule 1: Acetylcholine-binding protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	239.12Å 73.11Å 271.84Å 90.00° 97.45° 90.00°	Depositor
Resolution (Å)	33.05 – 2.35 33.05 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.3 (33.05-2.35) 95.1 (33.05-2.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.72 (at 2.34Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.197 , 0.230 0.190 , 0.224	Depositor DCC
R_{free} test set	3743 reflections (1.92%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	34660	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, 09S, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.50	0/1654	0.75	0/2256
1	B	0.51	0/1667	0.76	0/2274
1	C	0.50	0/1674	0.78	1/2285 (0.0%)
1	D	0.50	0/1684	0.75	1/2299 (0.0%)
1	E	0.49	0/1672	0.73	0/2280
1	F	0.48	0/1682	0.77	0/2292
1	G	0.47	0/1647	0.79	1/2246 (0.0%)
1	H	0.47	0/1647	0.74	0/2246
1	I	0.46	0/1681	0.75	1/2291 (0.0%)
1	J	0.45	0/1647	0.74	2/2246 (0.1%)
1	K	0.48	0/1671	0.76	0/2278
1	L	0.47	0/1649	0.74	0/2250
1	M	0.50	0/1669	0.76	0/2274
1	N	0.49	0/1631	0.73	0/2225
1	O	0.47	0/1647	0.75	1/2246 (0.0%)
1	P	0.48	0/1664	0.78	2/2268 (0.1%)
1	Q	0.48	0/1664	0.75	0/2268
1	R	0.45	0/1643	0.73	0/2241
1	S	0.45	0/1670	0.73	0/2277
1	T	0.46	0/1664	0.76	0/2269
All	All	0.48	0/33227	0.75	9/45311 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	1

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	25	ARG	N-CA-C	-6.68	101.64	110.40
1	P	188	CYS	CA-C-N	6.02	125.72	119.64
1	P	188	CYS	C-N-CA	6.02	125.72	119.64
1	J	15	ARG	CA-C-N	5.72	125.40	119.56
1	J	15	ARG	C-N-CA	5.72	125.40	119.56

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	155	THR	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1616	0	1568	16	0
1	B	1626	0	1577	21	0
1	C	1635	0	1582	14	0
1	D	1642	0	1591	18	0
1	E	1625	0	1583	29	0
1	F	1641	0	1599	25	1
1	G	1609	0	1560	15	0
1	H	1609	0	1561	15	1
1	I	1637	0	1597	13	0
1	J	1609	0	1561	16	0
1	K	1633	0	1586	15	0
1	L	1608	0	1563	21	0
1	M	1628	0	1587	18	0
1	N	1590	0	1553	16	0
1	O	1609	0	1561	16	0
1	P	1626	0	1579	27	0
1	Q	1626	0	1579	17	0
1	R	1605	0	1558	18	0
1	S	1629	0	1584	14	0
1	T	1620	0	1577	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	17	0	18	1	0
2	B	17	0	18	2	0
2	C	17	0	18	2	0
2	D	17	0	18	4	0
2	E	17	0	18	2	0
2	F	17	0	18	5	0
2	G	17	0	18	1	0
2	H	17	0	18	2	0
2	I	17	0	18	0	0
2	J	17	0	18	0	0
2	K	17	0	18	3	0
2	L	17	0	18	1	0
2	M	17	0	18	2	0
2	N	17	0	18	1	0
2	O	17	0	18	0	0
2	P	17	0	18	4	0
2	Q	17	0	18	1	0
2	R	17	0	18	3	0
2	S	17	0	18	0	0
2	T	17	0	18	5	0
3	A	5	0	0	1	0
3	H	5	0	0	0	0
3	N	5	0	0	0	0
3	P	10	0	0	0	0
3	S	5	0	0	0	0
4	C	14	0	13	0	0
4	G	14	0	13	0	0
4	T	14	0	13	2	0
5	A	116	0	0	3	0
5	B	130	0	0	2	0
5	C	112	0	0	0	0
5	D	118	0	0	2	0
5	E	110	0	0	2	0
5	F	79	0	0	3	0
5	G	91	0	0	3	0
5	H	77	0	0	2	0
5	I	77	0	0	0	0
5	J	77	0	0	2	0
5	K	102	0	0	3	0
5	L	88	0	0	1	0
5	M	99	0	0	1	0
5	N	96	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	O	95	0	0	3	0
5	P	83	0	0	3	0
5	Q	69	0	0	2	0
5	R	80	0	0	1	0
5	S	68	0	0	0	0
5	T	58	0	0	0	0
All	All	34660	0	31905	329	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 329 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:ASP:OD1	1:E:120[B]:ARG:HG2	1.52	1.07
1:T:49:ASP:OD1	1:T:120[B]:ARG:HG3	1.53	1.06
1:M:49:ASP:OD1	1:M:120[B]:ARG:HG2	1.58	1.04
1:I:49:ASP:OD1	1:I:120[B]:ARG:HG2	1.59	1.02
1:F:152:VAL:HG12	1:F:195:VAL:HG23	1.46	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:156:THR:OG1	1:H:184:THR:OG1[1_565]	2.05	0.15

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	199/210 (95%)	198 (100%)	1 (0%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	201/210 (96%)	197 (98%)	2 (1%)	2 (1%)	12	12
1	C	203/210 (97%)	202 (100%)	1 (0%)	0	100	100
1	D	205/210 (98%)	205 (100%)	0	0	100	100
1	E	201/210 (96%)	201 (100%)	0	0	100	100
1	F	202/210 (96%)	200 (99%)	2 (1%)	0	100	100
1	G	198/210 (94%)	198 (100%)	0	0	100	100
1	H	198/210 (94%)	198 (100%)	0	0	100	100
1	I	202/210 (96%)	201 (100%)	1 (0%)	0	100	100
1	J	198/210 (94%)	194 (98%)	4 (2%)	0	100	100
1	K	201/210 (96%)	200 (100%)	1 (0%)	0	100	100
1	L	198/210 (94%)	197 (100%)	1 (0%)	0	100	100
1	M	200/210 (95%)	199 (100%)	1 (0%)	0	100	100
1	N	196/210 (93%)	195 (100%)	1 (0%)	0	100	100
1	O	198/210 (94%)	197 (100%)	1 (0%)	0	100	100
1	P	200/210 (95%)	199 (100%)	1 (0%)	0	100	100
1	Q	200/210 (95%)	197 (98%)	3 (2%)	0	100	100
1	R	197/210 (94%)	196 (100%)	1 (0%)	0	100	100
1	S	201/210 (96%)	200 (100%)	1 (0%)	0	100	100
1	T	200/210 (95%)	200 (100%)	0	0	100	100
All	All	3998/4200 (95%)	3974 (99%)	22 (1%)	2 (0%)	48	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	163	GLU
1	B	161	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/196 (96%)	185 (98%)	4 (2%)	47	61
1	B	191/196 (97%)	188 (98%)	3 (2%)	55	70
1	C	192/196 (98%)	186 (97%)	6 (3%)	35	47
1	D	193/196 (98%)	188 (97%)	5 (3%)	40	54
1	E	191/196 (97%)	185 (97%)	6 (3%)	35	47
1	F	192/196 (98%)	187 (97%)	5 (3%)	40	54
1	G	188/196 (96%)	183 (97%)	5 (3%)	39	52
1	H	188/196 (96%)	181 (96%)	7 (4%)	30	40
1	I	192/196 (98%)	188 (98%)	4 (2%)	47	61
1	J	188/196 (96%)	183 (97%)	5 (3%)	39	52
1	K	191/196 (97%)	185 (97%)	6 (3%)	35	47
1	L	189/196 (96%)	183 (97%)	6 (3%)	34	46
1	M	190/196 (97%)	187 (98%)	3 (2%)	55	70
1	N	186/196 (95%)	182 (98%)	4 (2%)	45	59
1	O	188/196 (96%)	185 (98%)	3 (2%)	55	70
1	P	190/196 (97%)	184 (97%)	6 (3%)	34	46
1	Q	190/196 (97%)	185 (97%)	5 (3%)	40	54
1	R	188/196 (96%)	182 (97%)	6 (3%)	34	46
1	S	191/196 (97%)	188 (98%)	3 (2%)	55	70
1	T	190/196 (97%)	186 (98%)	4 (2%)	47	61
All	All	3797/3920 (97%)	3701 (98%)	96 (2%)	42	55

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	39	LEU
1	O	129	ASP
1	L	129	ASP
1	N	14	SER
1	P	49	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	200	ASN

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Mol	Chain	Res	Type
1	M	55	GLN
1	S	69	HIS
1	L	200	ASN
1	O	22	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

29 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	P	213	-	4,4,4	0.26	0	6,6,6	0.12	0
3	SO4	N	212	-	4,4,4	0.23	0	6,6,6	0.33	0
2	09S	L	211	-	17,18,18	2.76	4 (23%)	15,23,23	1.48	4 (26%)
2	09S	C	211	-	17,18,18	2.87	3 (17%)	15,23,23	1.47	2 (13%)
3	SO4	H	212	-	4,4,4	0.25	0	6,6,6	0.14	0
2	09S	A	211	-	17,18,18	3.01	3 (17%)	15,23,23	1.46	3 (20%)
2	09S	I	211	-	17,18,18	2.88	4 (23%)	15,23,23	1.61	4 (26%)
3	SO4	P	212	-	4,4,4	0.26	0	6,6,6	0.06	0
2	09S	E	211	-	17,18,18	2.79	4 (23%)	15,23,23	1.75	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	09S	T	211	-	17,18,18	2.82	4 (23%)	15,23,23	2.21	4 (26%)
2	09S	Q	211	-	17,18,18	2.66	3 (17%)	15,23,23	1.79	4 (26%)
2	09S	R	211	-	17,18,18	2.84	4 (23%)	15,23,23	1.67	4 (26%)
3	SO4	A	212	-	4,4,4	0.20	0	6,6,6	0.22	0
3	SO4	S	212	-	4,4,4	0.22	0	6,6,6	0.13	0
2	09S	H	211	-	17,18,18	2.79	3 (17%)	15,23,23	1.78	2 (13%)
2	09S	O	211	-	17,18,18	2.93	2 (11%)	15,23,23	1.68	4 (26%)
2	09S	F	211	-	17,18,18	3.08	4 (23%)	15,23,23	1.48	3 (20%)
2	09S	P	211	-	17,18,18	2.94	3 (17%)	15,23,23	1.67	4 (26%)
2	09S	M	211	-	17,18,18	2.83	4 (23%)	15,23,23	1.66	3 (20%)
4	NAG	G	301	1	14,14,15	0.61	0	17,19,21	1.27	2 (11%)
4	NAG	C	300	1	14,14,15	0.49	0	17,19,21	1.90	6 (35%)
2	09S	G	211	-	17,18,18	2.89	4 (23%)	15,23,23	1.76	4 (26%)
2	09S	K	211	-	17,18,18	2.88	4 (23%)	15,23,23	1.60	2 (13%)
4	NAG	T	212	1	14,14,15	0.46	0	17,19,21	1.46	4 (23%)
2	09S	J	211	-	17,18,18	2.97	4 (23%)	15,23,23	1.41	4 (26%)
2	09S	S	211	-	17,18,18	2.87	5 (29%)	15,23,23	1.56	3 (20%)
2	09S	B	211	-	17,18,18	2.91	3 (17%)	15,23,23	1.43	2 (13%)
2	09S	N	211	-	17,18,18	2.73	4 (23%)	15,23,23	1.58	2 (13%)
2	09S	D	211	-	17,18,18	2.82	4 (23%)	15,23,23	1.86	5 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	09S	L	211	-	-	1/7/16/16	0/2/2/2
2	09S	C	211	-	-	0/7/16/16	0/2/2/2
2	09S	A	211	-	-	0/7/16/16	0/2/2/2
2	09S	I	211	-	-	0/7/16/16	0/2/2/2
2	09S	E	211	-	-	0/7/16/16	0/2/2/2
2	09S	T	211	-	-	1/7/16/16	0/2/2/2
2	09S	Q	211	-	-	0/7/16/16	0/2/2/2
2	09S	R	211	-	-	0/7/16/16	0/2/2/2
2	09S	H	211	-	-	0/7/16/16	0/2/2/2
2	09S	O	211	-	-	0/7/16/16	0/2/2/2
2	09S	F	211	-	-	1/7/16/16	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	09S	P	211	-	-	0/7/16/16	0/2/2/2
2	09S	M	211	-	-	0/7/16/16	0/2/2/2
4	NAG	G	301	1	-	0/6/23/26	0/1/1/1
4	NAG	C	300	1	-	2/6/23/26	0/1/1/1
2	09S	G	211	-	-	0/7/16/16	0/2/2/2
2	09S	K	211	-	-	1/7/16/16	0/2/2/2
4	NAG	T	212	1	-	0/6/23/26	0/1/1/1
2	09S	J	211	-	-	1/7/16/16	1/2/2/2
2	09S	S	211	-	-	0/7/16/16	0/2/2/2
2	09S	B	211	-	-	1/7/16/16	0/2/2/2
2	09S	N	211	-	-	0/7/16/16	0/2/2/2
2	09S	D	211	-	-	1/7/16/16	0/2/2/2

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	211	09S	BR1-C6	-10.97	1.73	1.90
2	B	211	09S	BR1-C6	-10.92	1.73	1.90
2	F	211	09S	BR1-C6	-10.86	1.73	1.90
2	A	211	09S	BR1-C6	-10.82	1.73	1.90
2	O	211	09S	BR1-C6	-10.76	1.73	1.90

The worst 5 of 78 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	211	09S	O1-C10-C6	5.10	122.92	116.60
2	H	211	09S	C9-C8-C7	-4.82	115.43	119.67
2	T	211	09S	C9-C8-C7	-4.82	115.43	119.67
2	Q	211	09S	C9-C8-C7	-4.67	115.57	119.67
2	D	211	09S	C9-C8-C7	-4.29	115.91	119.67

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	300	NAG	C4-C5-C6-O6
4	C	300	NAG	O5-C5-C6-O6
2	K	211	09S	C12-C11-O1-C10
2	L	211	09S	C12-C11-O1-C10
2	D	211	09S	C12-C11-O1-C10

All (1) ring outliers are listed below:

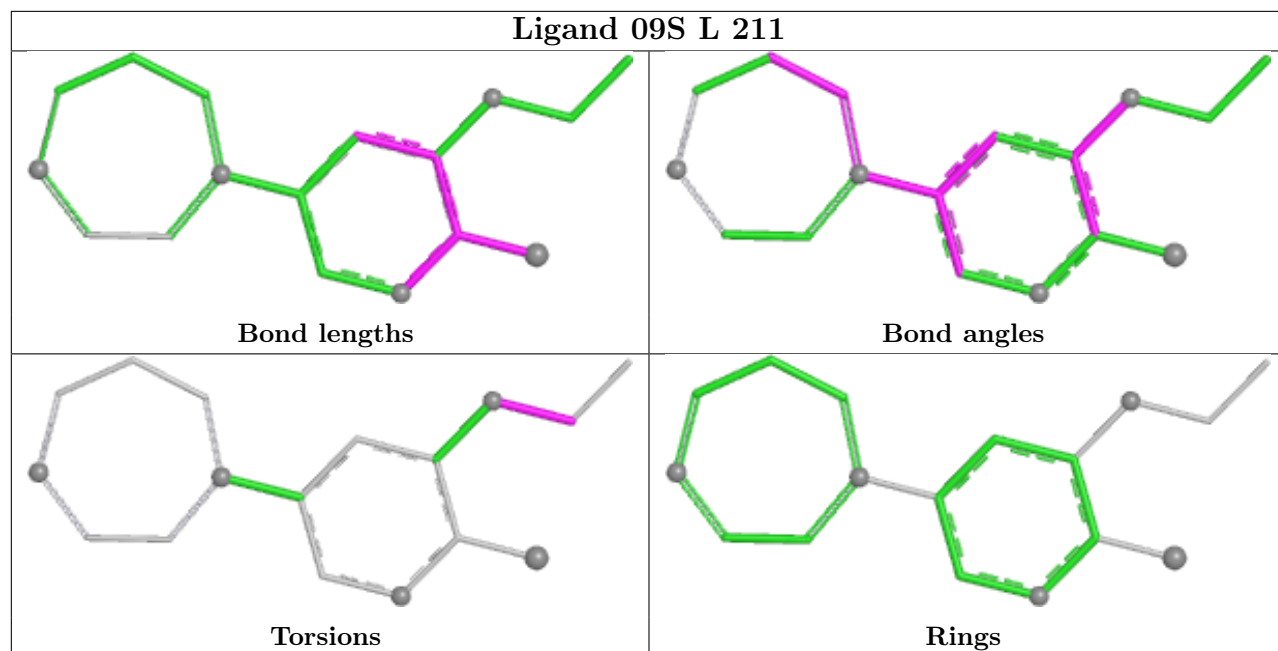
Mol	Chain	Res	Type	Atoms
2	J	211	09S	C1-C2-C3-C4-C5-N1-N2

18 monomers are involved in 42 short contacts:

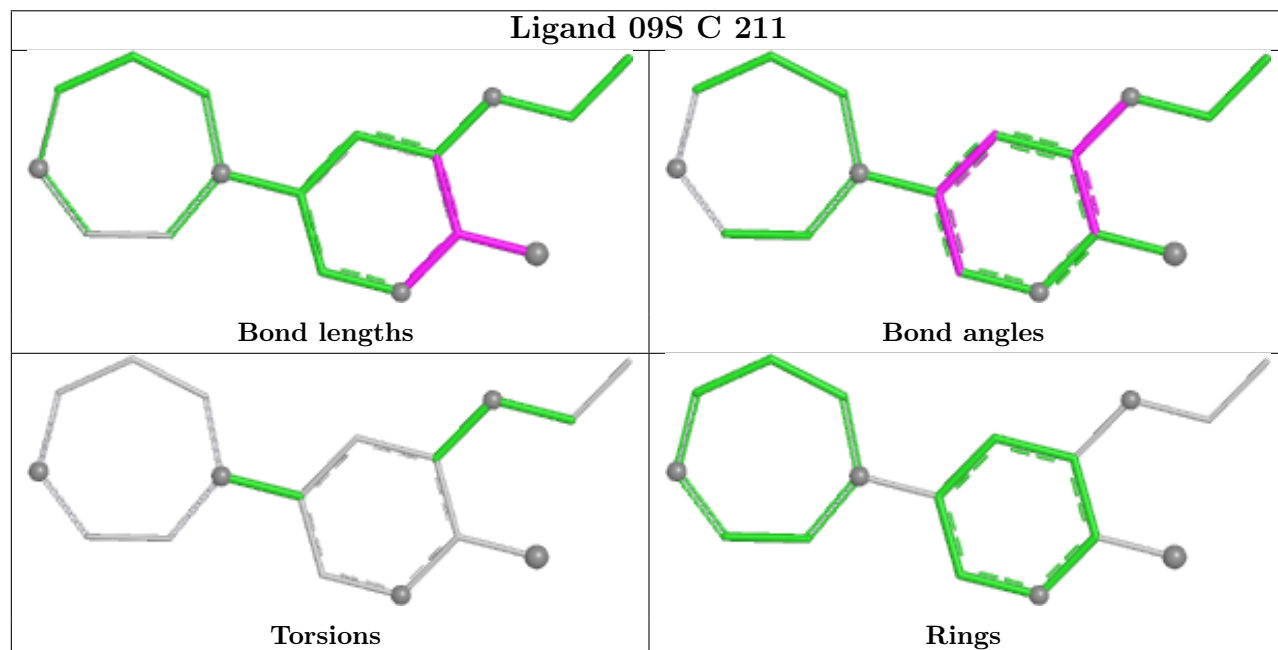
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	211	09S	1	0
2	C	211	09S	2	0
2	A	211	09S	1	0
2	E	211	09S	2	0
2	T	211	09S	5	0
2	Q	211	09S	1	0
2	R	211	09S	3	0
3	A	212	SO4	1	0
2	H	211	09S	2	0
2	F	211	09S	5	0
2	P	211	09S	4	0
2	M	211	09S	2	0
2	G	211	09S	1	0
2	K	211	09S	3	0
4	T	212	NAG	2	0
2	B	211	09S	2	0
2	N	211	09S	1	0
2	D	211	09S	4	0

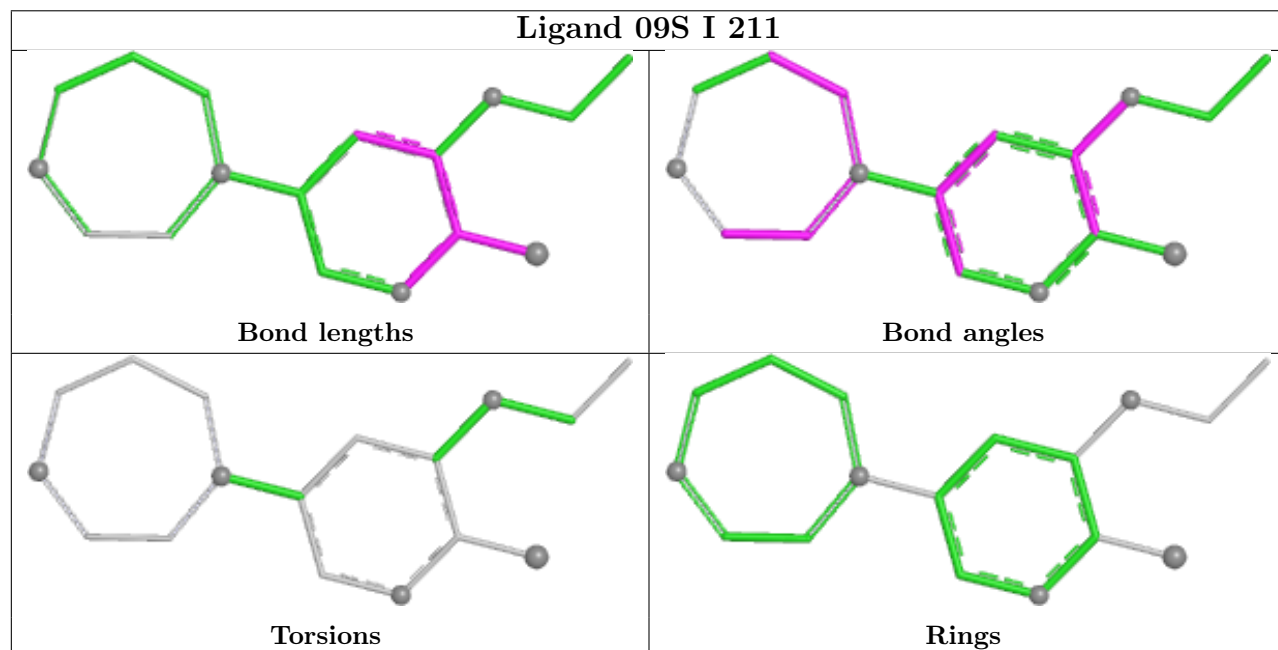
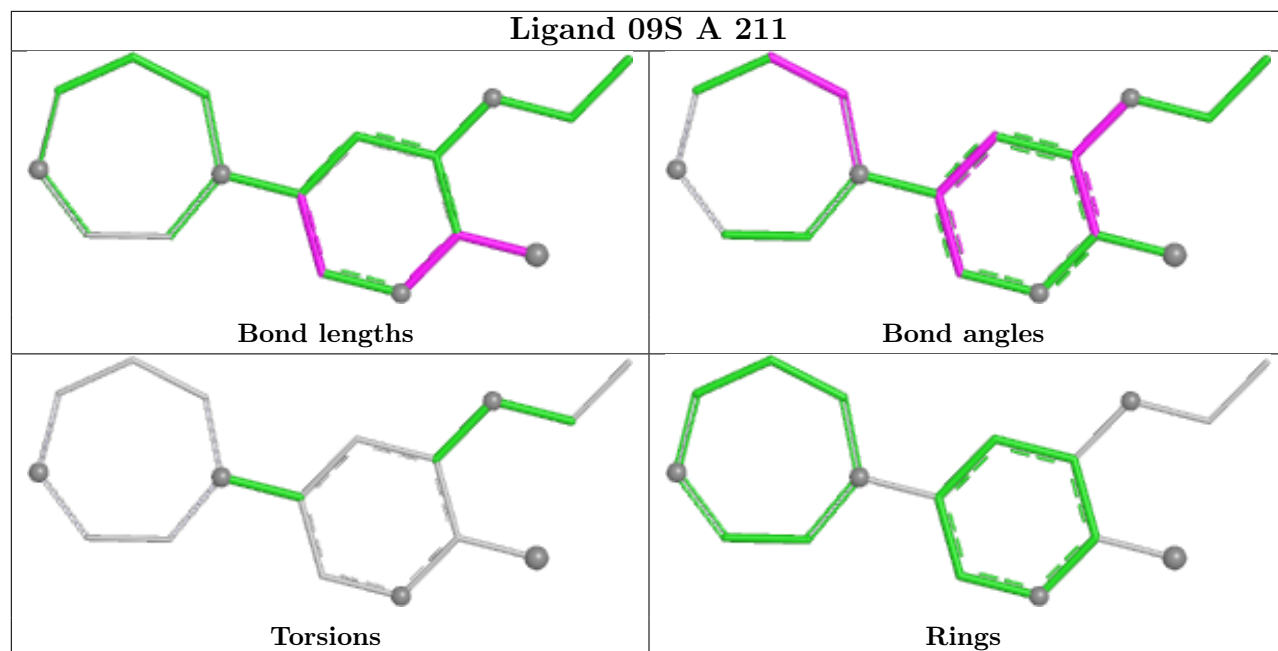
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

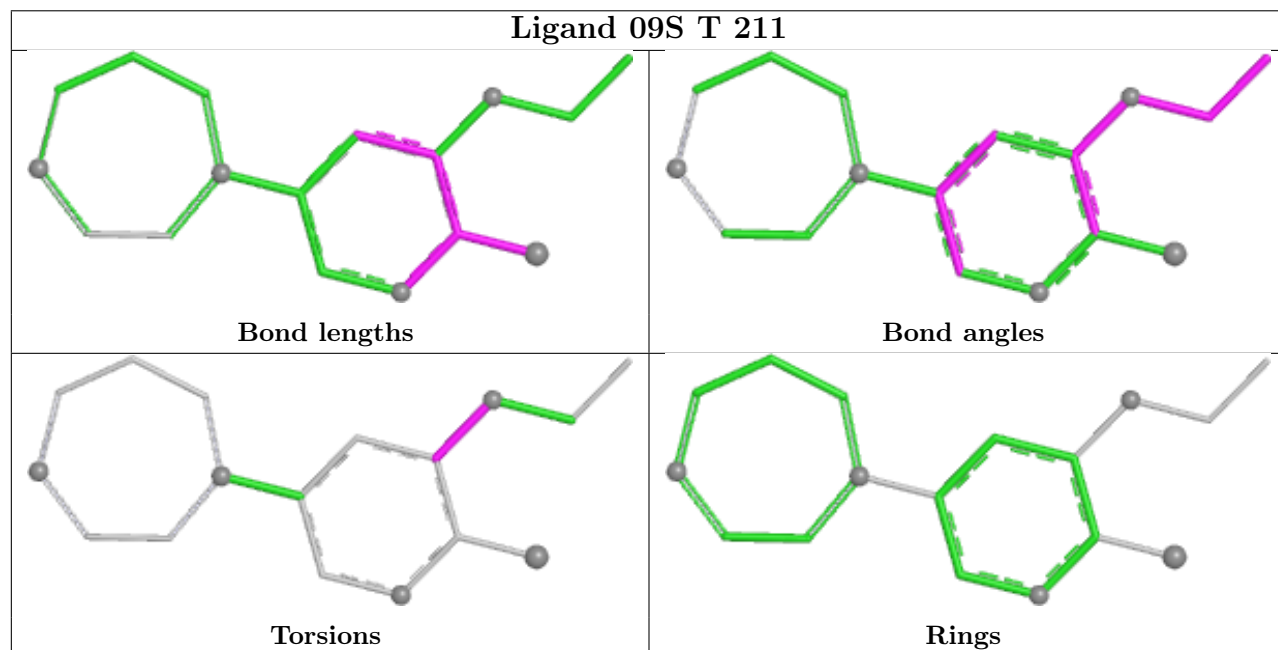
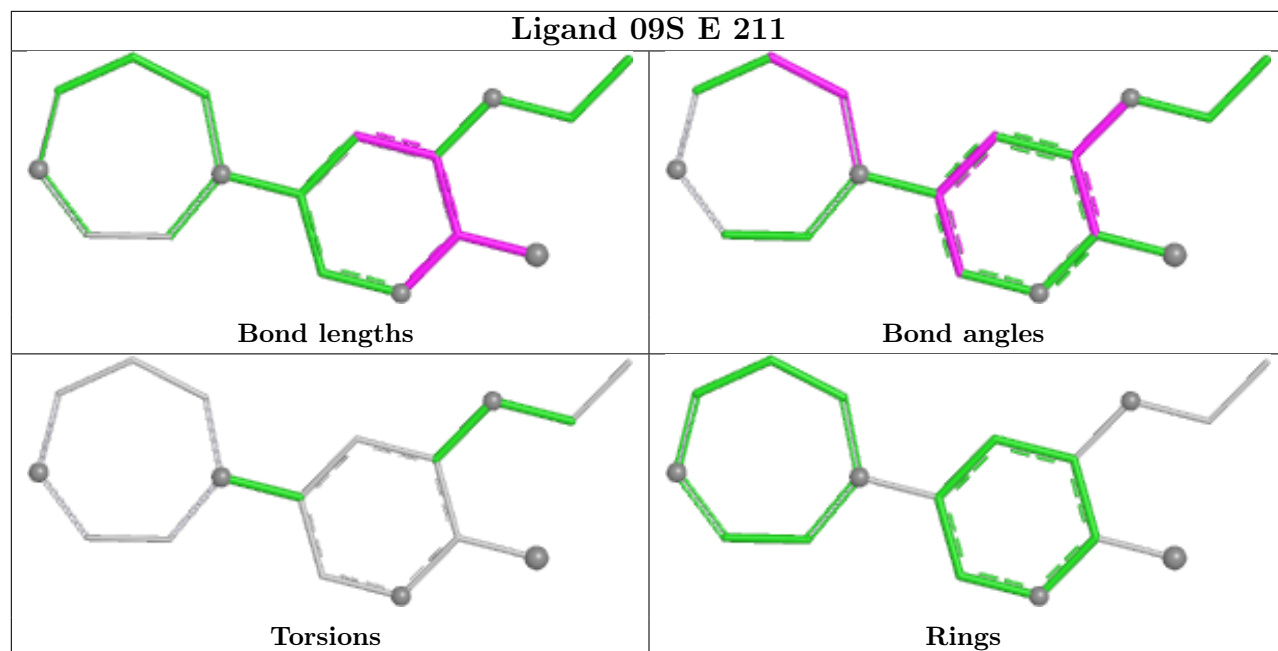
Ligand 09S L 211



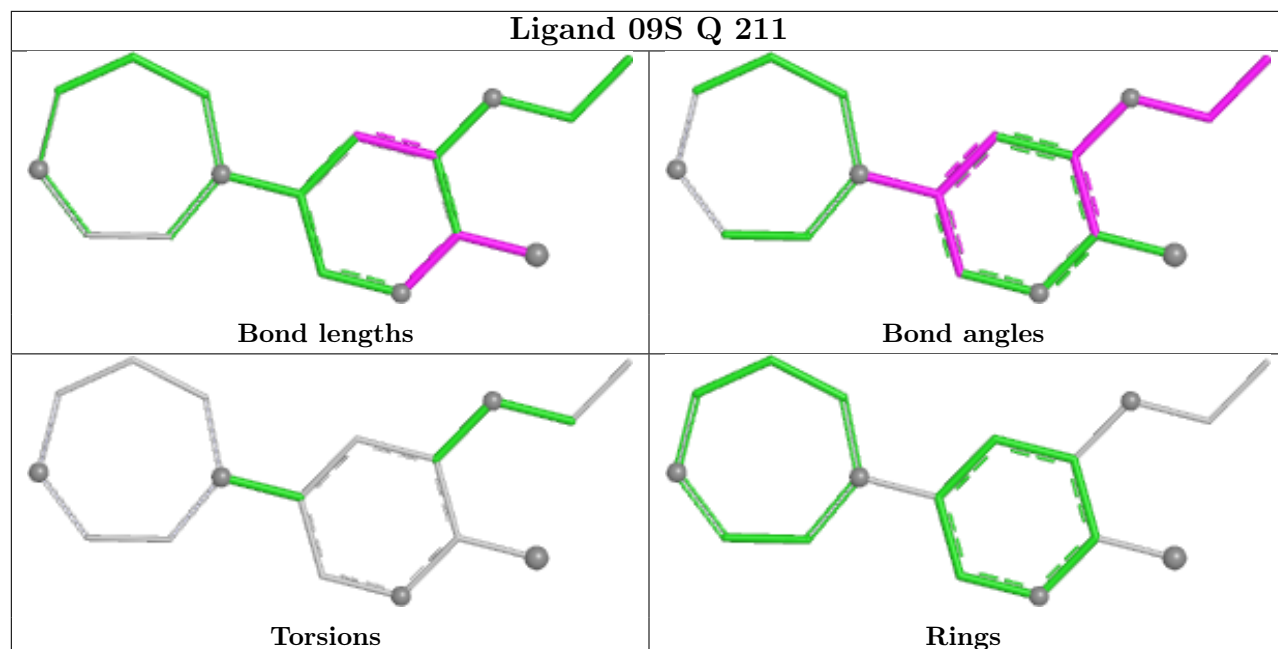
Ligand 09S C 211



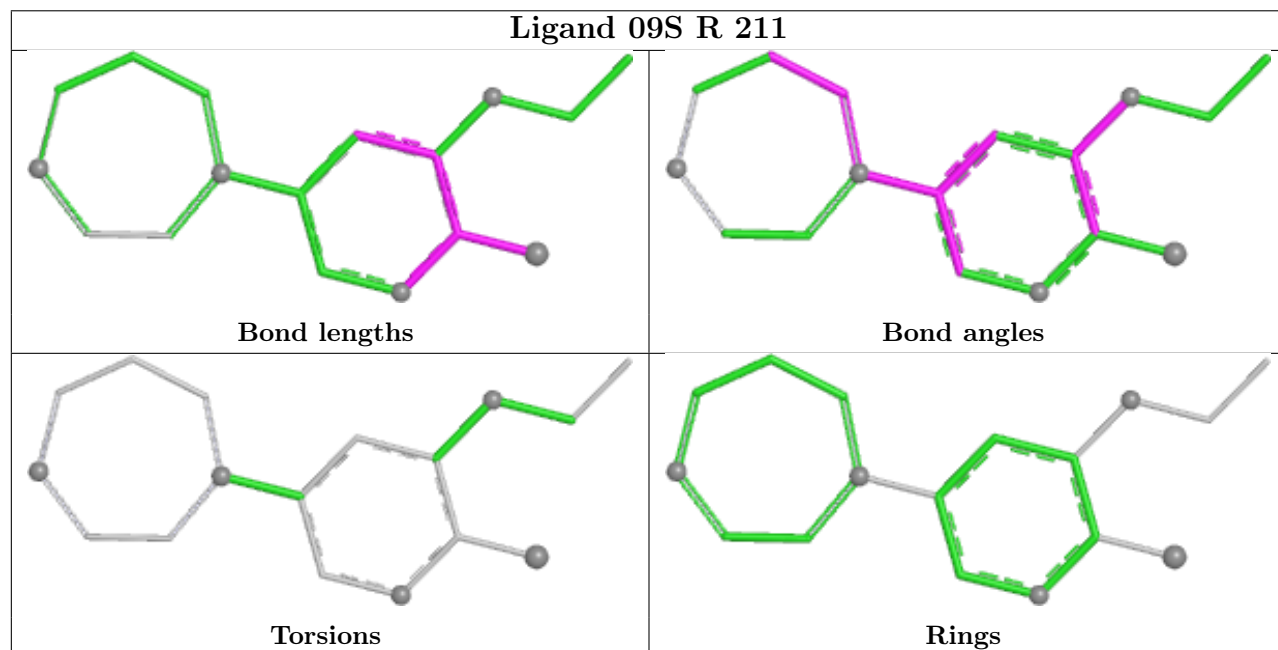


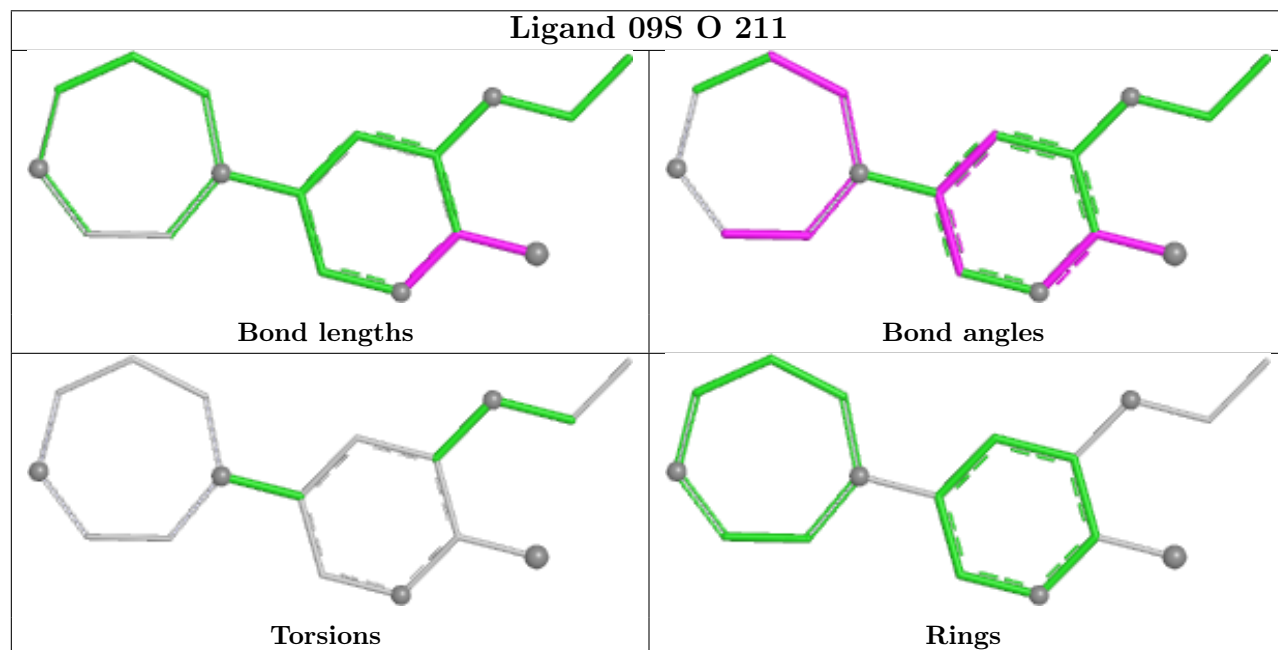
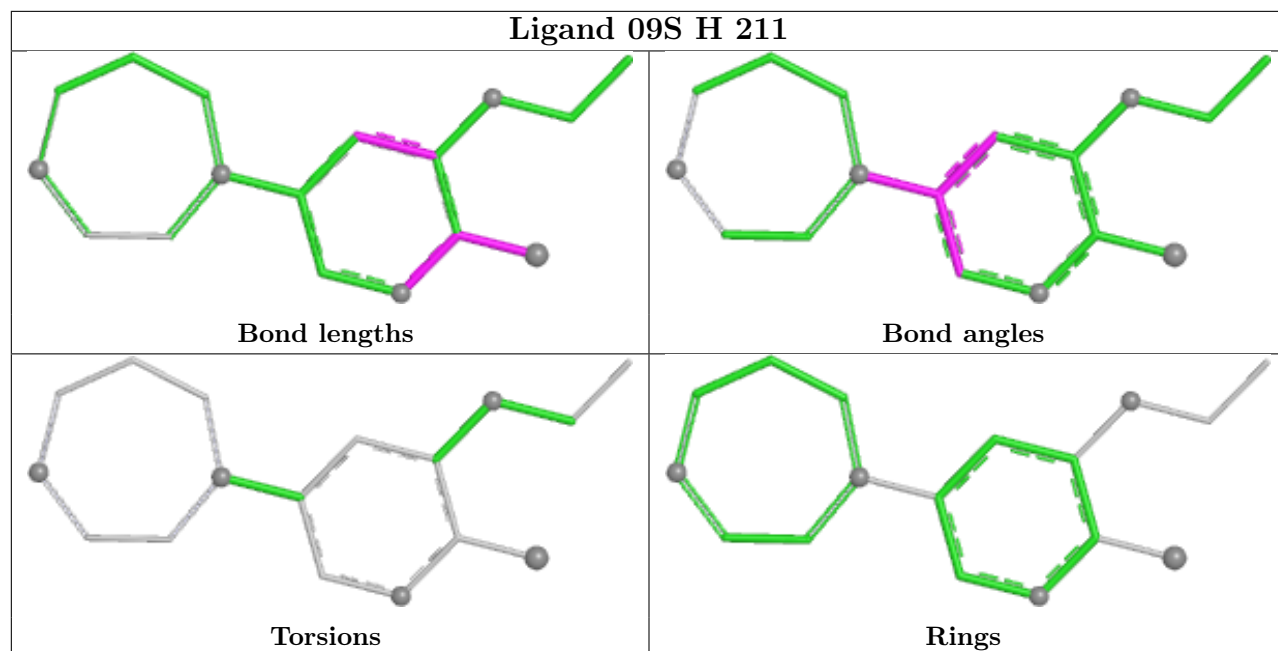


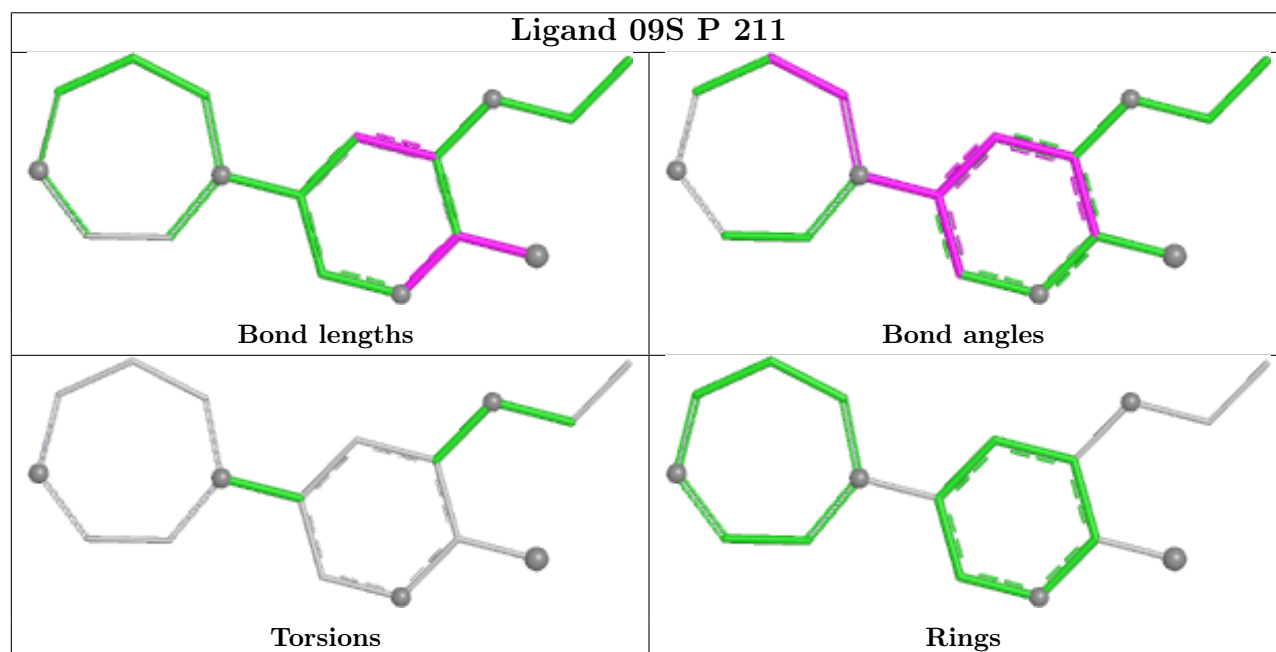
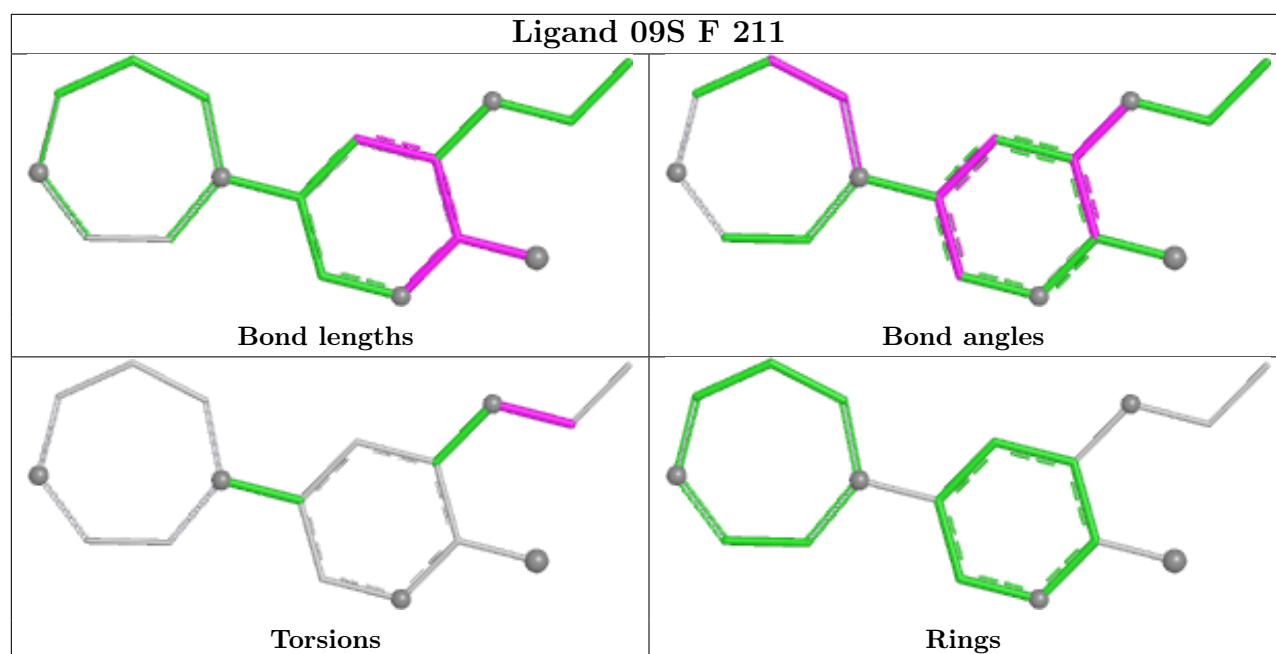
Ligand 09S Q 211



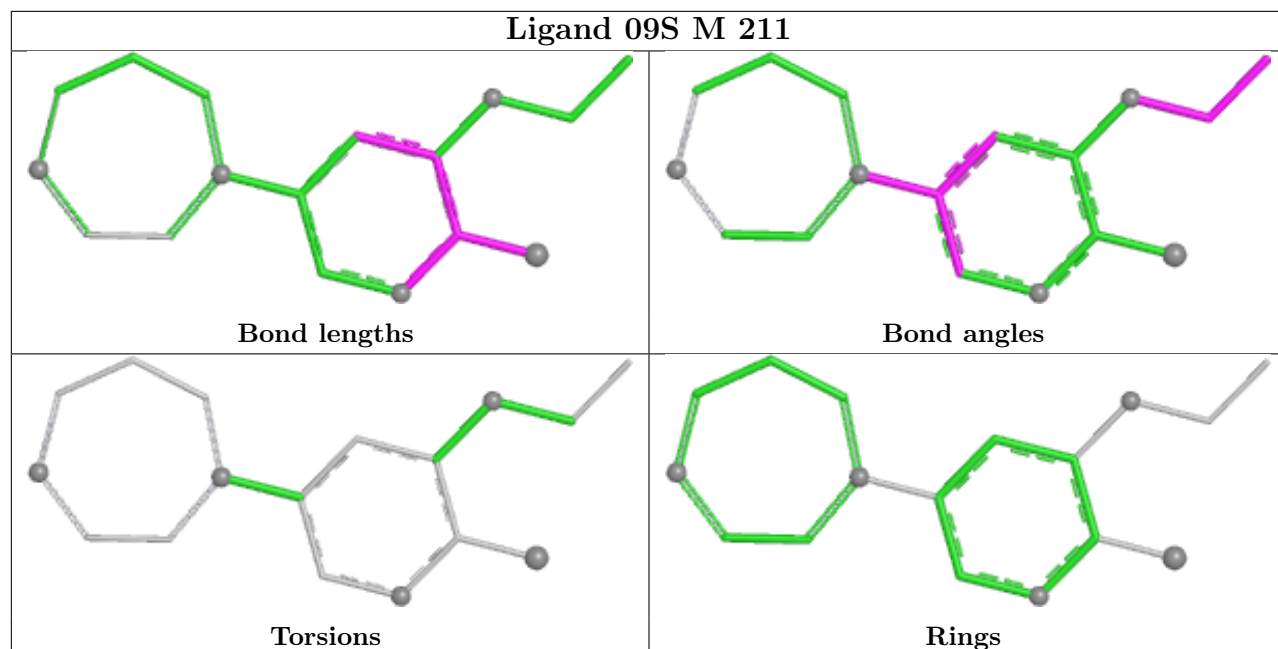
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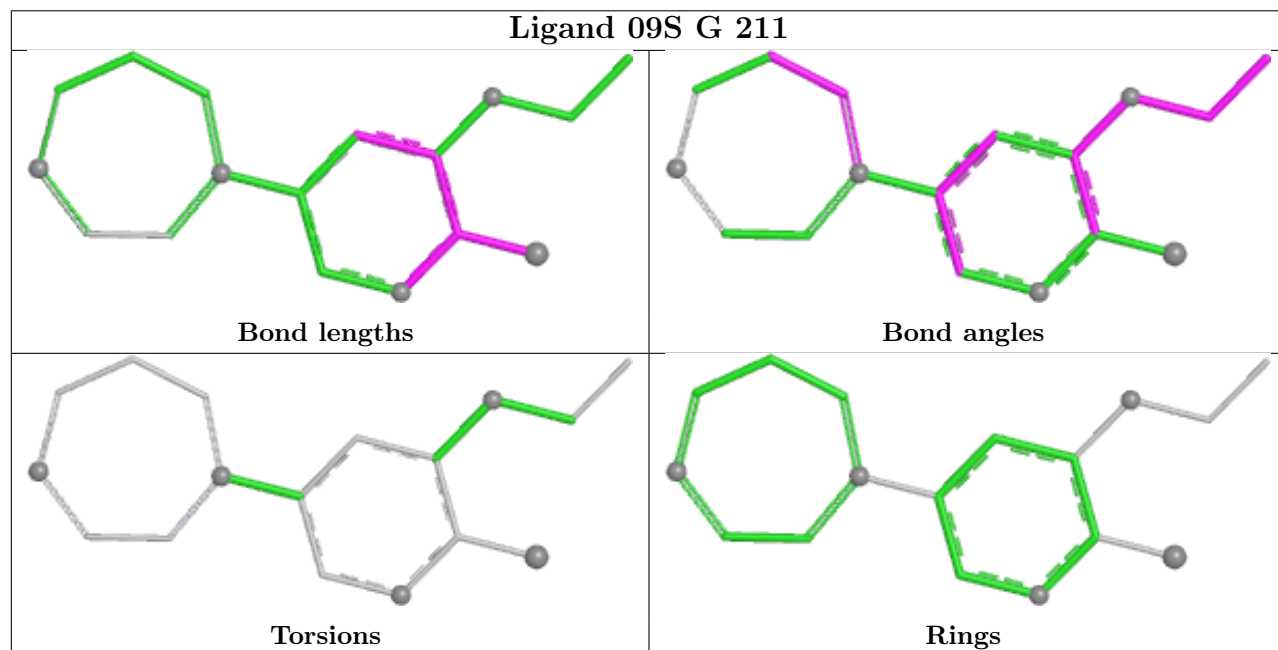




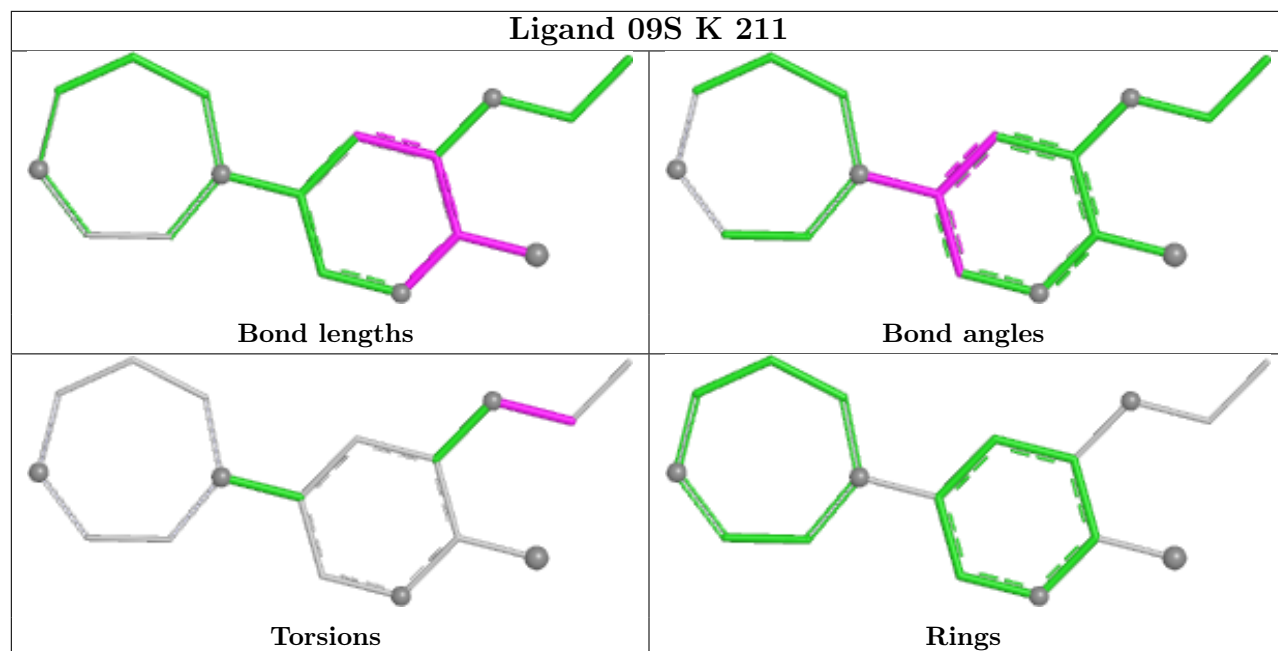
Ligand 09S M 211



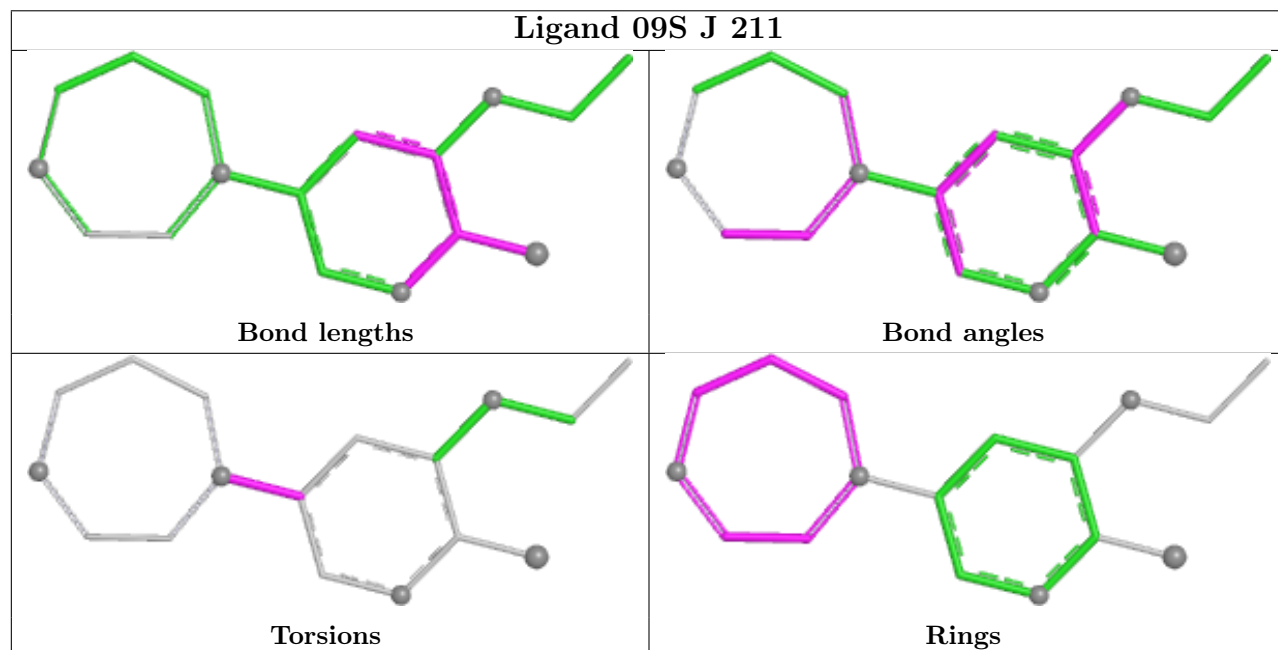
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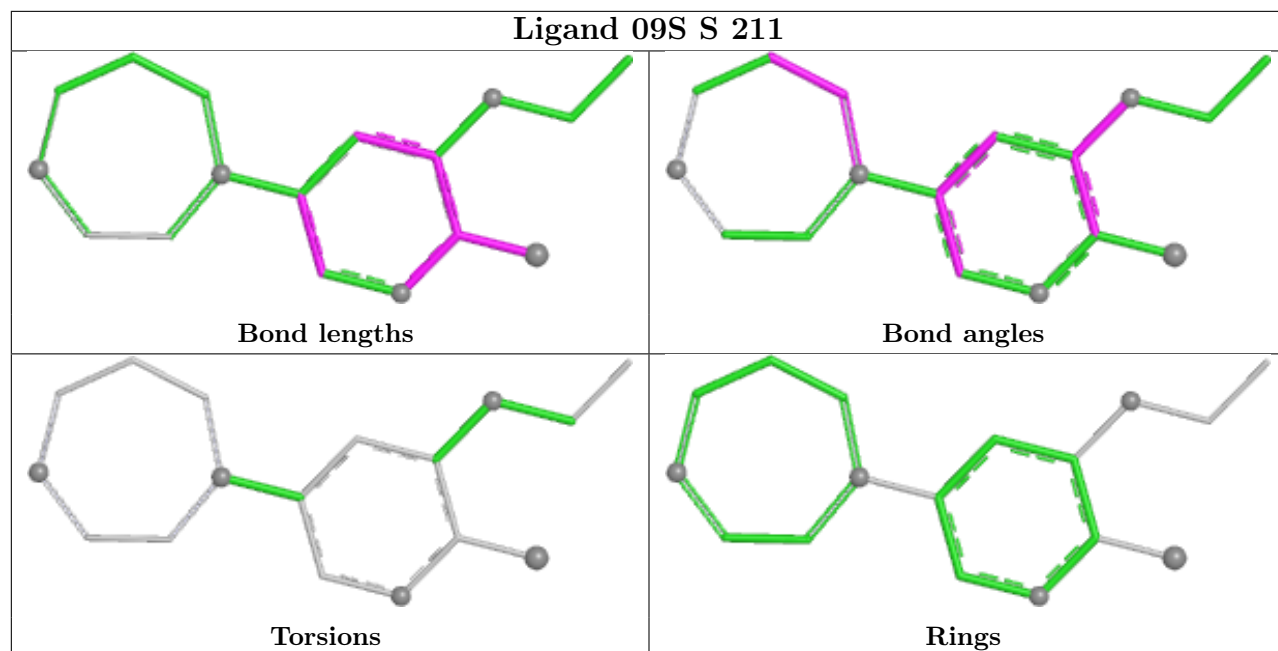
Ligand 09S K 211



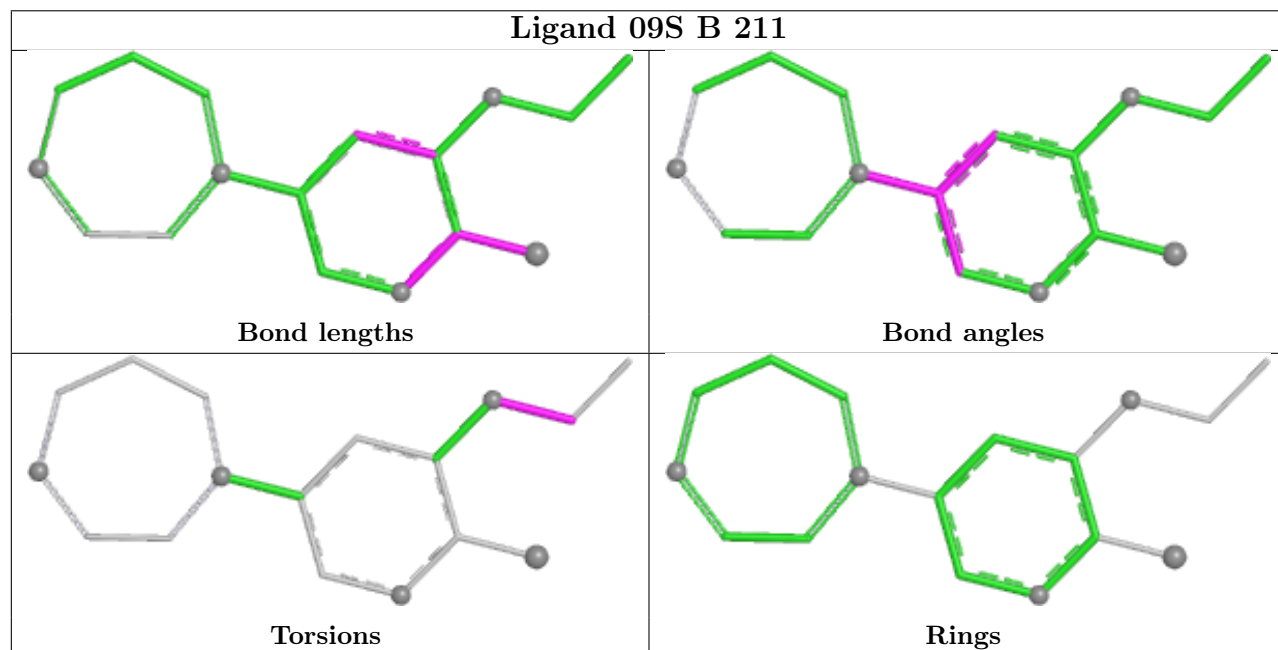
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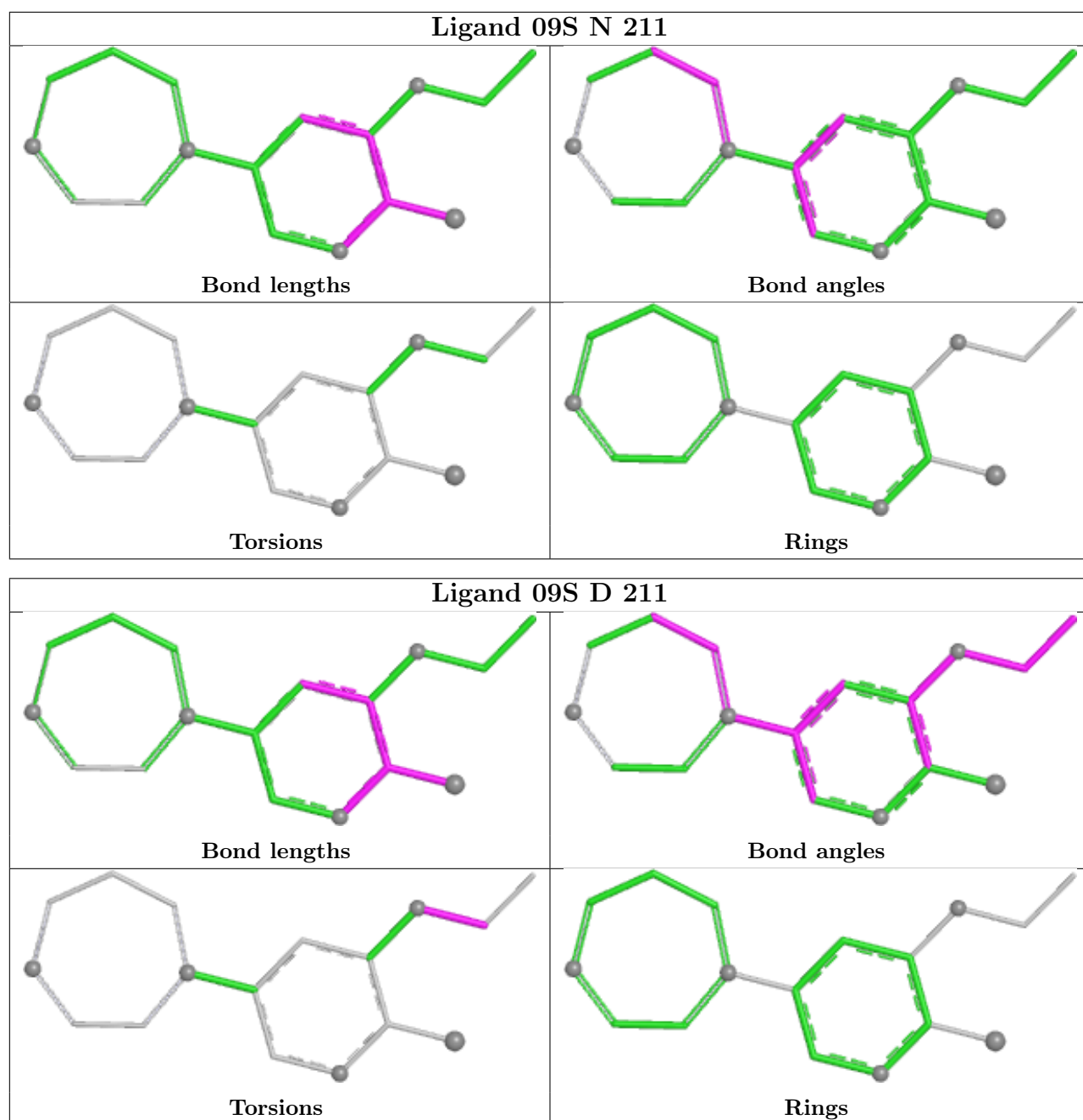


Ligand 09S S 211



Ligand 09S B 211





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	201/210 (95%)	-0.20	7 (3%)	47	53	11, 21, 54, 92	1 (0%)
1	B	203/210 (96%)	-0.16	11 (5%)	31	37	11, 20, 55, 106	2 (0%)
1	C	204/210 (97%)	-0.21	5 (2%)	58	64	11, 20, 56, 94	1 (0%)
1	D	205/210 (97%)	-0.16	5 (2%)	59	66	10, 20, 53, 72	2 (0%)
1	E	201/210 (95%)	-0.23	7 (3%)	47	53	7, 20, 54, 95	4 (1%)
1	F	204/210 (97%)	-0.16	5 (2%)	58	64	11, 23, 56, 212	2 (0%)
1	G	201/210 (95%)	-0.19	5 (2%)	58	64	14, 22, 57, 98	1 (0%)
1	H	201/210 (95%)	-0.22	5 (2%)	58	64	12, 21, 56, 92	1 (0%)
1	I	203/210 (96%)	-0.19	5 (2%)	58	64	12, 23, 58, 97	3 (1%)
1	J	201/210 (95%)	-0.19	5 (2%)	58	64	14, 23, 56, 95	1 (0%)
1	K	204/210 (97%)	-0.16	6 (2%)	53	60	12, 22, 56, 82	1 (0%)
1	L	200/210 (95%)	-0.13	6 (3%)	52	59	12, 23, 60, 105	2 (1%)
1	M	202/210 (96%)	-0.21	4 (1%)	65	70	10, 21, 54, 89	2 (0%)
1	N	198/210 (94%)	-0.20	8 (4%)	42	48	11, 21, 56, 99	2 (1%)
1	O	201/210 (95%)	-0.20	5 (2%)	58	64	13, 21, 55, 83	1 (0%)
1	P	203/210 (96%)	-0.15	4 (1%)	65	70	13, 23, 54, 71	1 (0%)
1	Q	203/210 (96%)	-0.17	6 (2%)	52	59	12, 23, 58, 100	1 (0%)
1	R	200/210 (95%)	-0.18	4 (2%)	65	70	13, 23, 60, 96	1 (0%)
1	S	203/210 (96%)	-0.05	8 (3%)	43	49	14, 25, 59, 101	2 (0%)
1	T	201/210 (95%)	-0.06	6 (2%)	52	59	12, 24, 57, 97	3 (1%)
All	All	4039/4200 (96%)	-0.17	117 (2%)	53	60	7, 22, 58, 212	34 (0%)

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	155	THR	6.2
1	F	155	THR	5.2
1	I	155	THR	4.8
1	R	155	THR	4.7
1	S	155	THR	4.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	G	301	14/15	0.68	0.16	65,84,88,88	0
4	NAG	C	300	14/15	0.74	0.16	63,71,79,80	0
3	SO4	P	212	5/5	0.80	0.19	93,96,100,107	0
4	NAG	T	212	14/15	0.83	0.12	64,73,81,91	0
3	SO4	S	212	5/5	0.86	0.15	66,82,89,93	0
2	09S	F	211	17/17	0.91	0.09	16,28,40,72	0
2	09S	I	211	17/17	0.93	0.11	15,36,64,72	0
3	SO4	P	213	5/5	0.93	0.10	55,66,76,79	0
2	09S	T	211	17/17	0.93	0.11	15,37,60,75	0
2	09S	J	211	17/17	0.94	0.10	13,32,44,68	0
2	09S	L	211	17/17	0.94	0.10	18,29,55,59	0
2	09S	S	211	17/17	0.94	0.10	27,37,64,71	0
2	09S	B	211	17/17	0.94	0.09	9,19,41,68	0
3	SO4	A	212	5/5	0.94	0.13	56,56,60,71	0
3	SO4	N	212	5/5	0.94	0.12	56,58,71,72	0
2	09S	N	211	17/17	0.95	0.08	8,27,42,57	0
2	09S	O	211	17/17	0.95	0.09	13,28,46,59	0
2	09S	Q	211	17/17	0.95	0.09	18,28,43,64	0
2	09S	H	211	17/17	0.95	0.09	16,30,56,68	0

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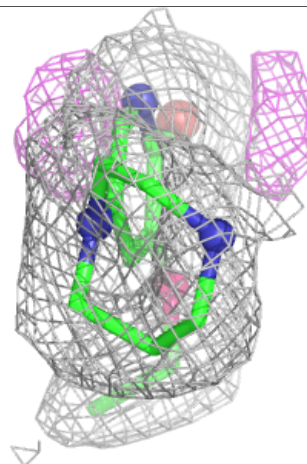
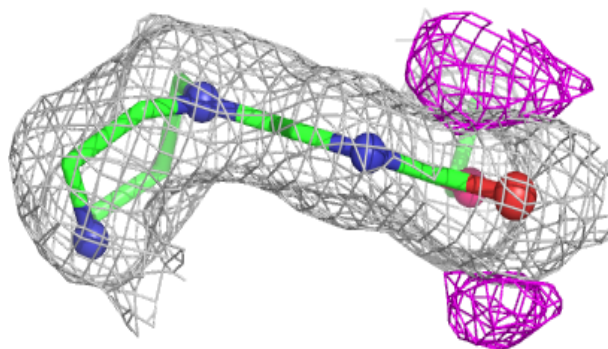
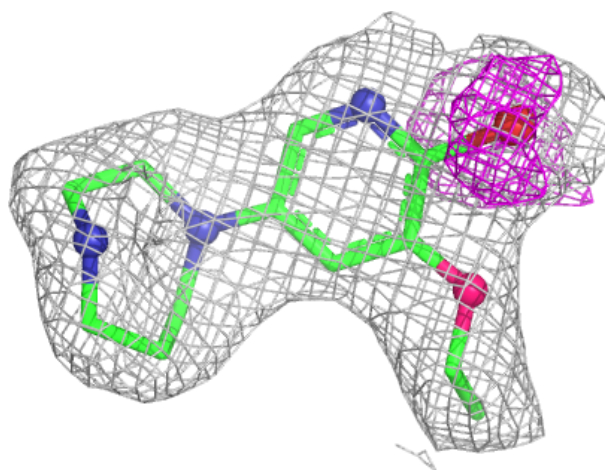
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	09S	K	211	17/17	0.95	0.08	20,28,39,61	0
2	09S	A	211	17/17	0.95	0.07	5,18,36,58	0
3	SO4	H	212	5/5	0.95	0.09	59,62,64,65	0
2	09S	P	211	17/17	0.96	0.07	14,27,41,64	0
2	09S	G	211	17/17	0.96	0.09	18,31,55,73	0
2	09S	R	211	17/17	0.96	0.09	11,33,61,62	0
2	09S	D	211	17/17	0.96	0.08	10,25,44,52	0
2	09S	M	211	17/17	0.96	0.07	11,24,37,57	0
2	09S	E	211	17/17	0.96	0.08	4,24,40,56	0
2	09S	C	211	17/17	0.96	0.08	11,23,56,56	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

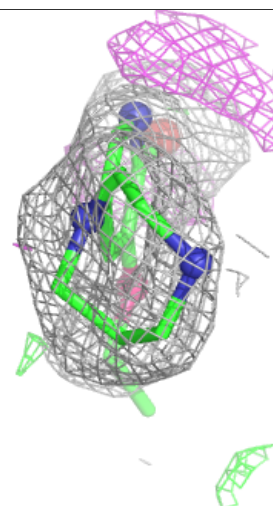
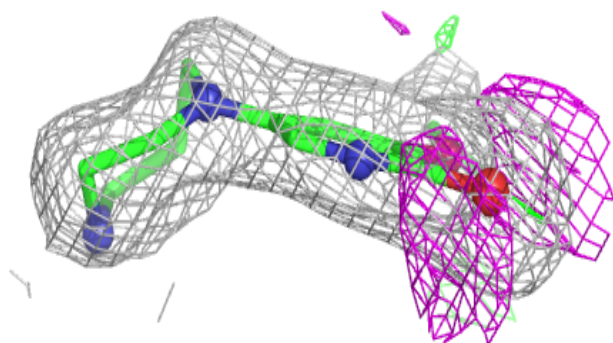
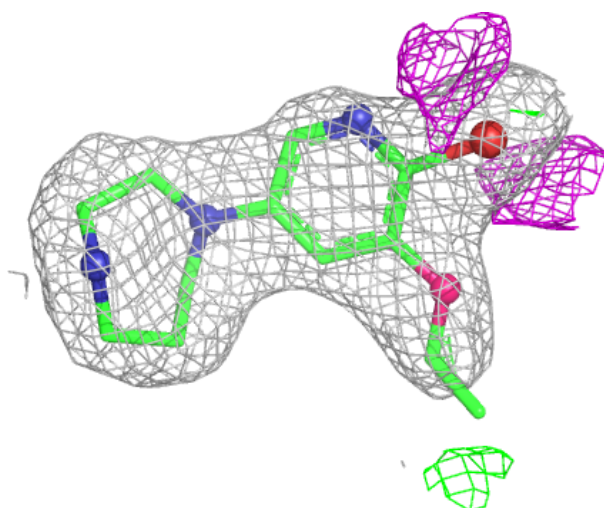
Electron density around 09S F 211:

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mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



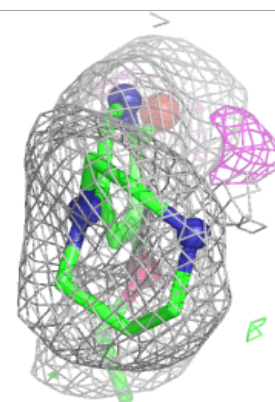
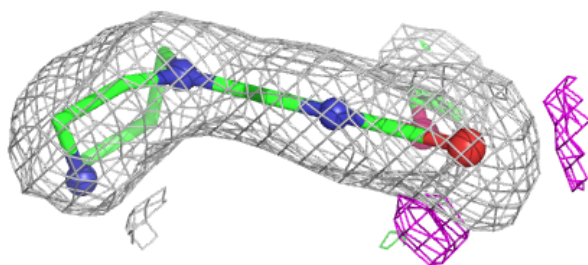
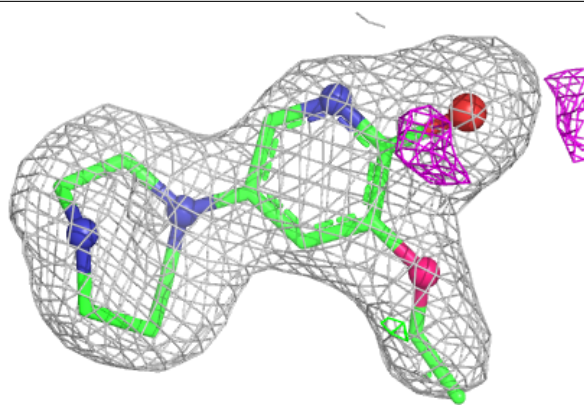
Electron density around 09S I 211:

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and green (positive)



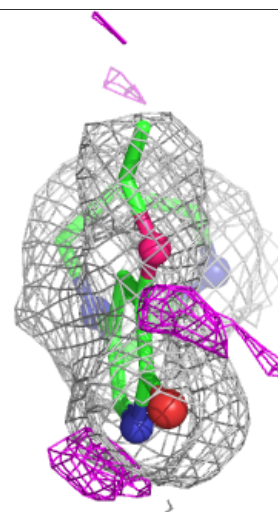
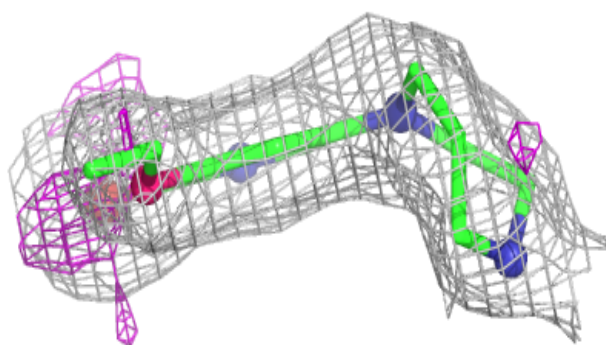
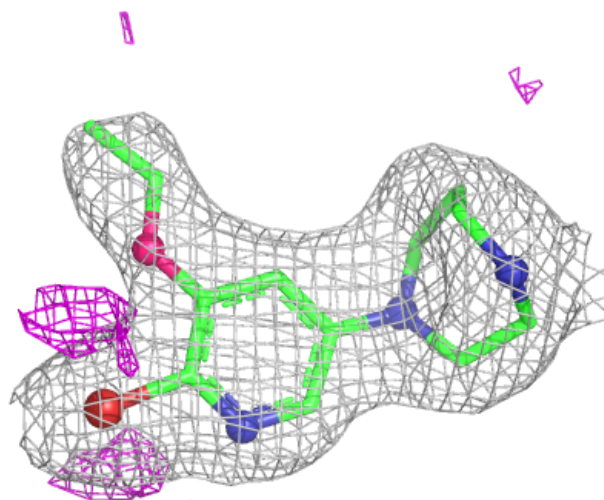
Electron density around 09S T 211:

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and green (positive)



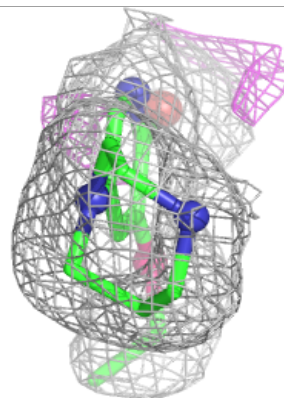
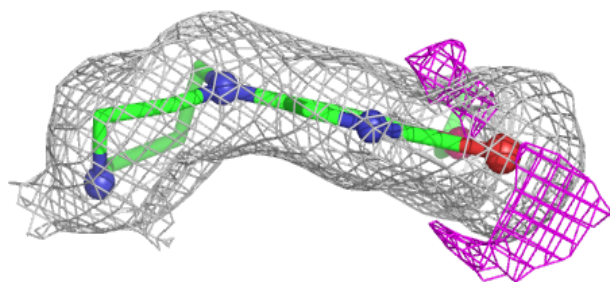
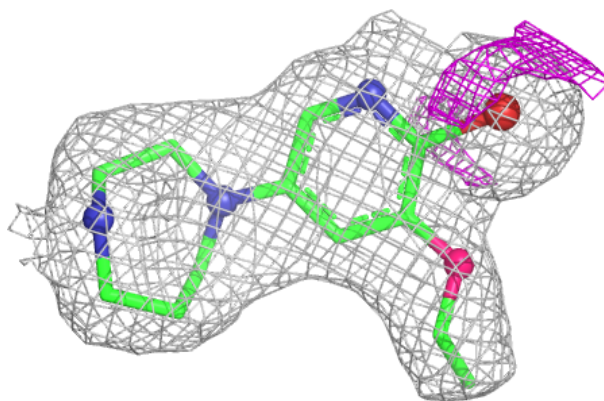
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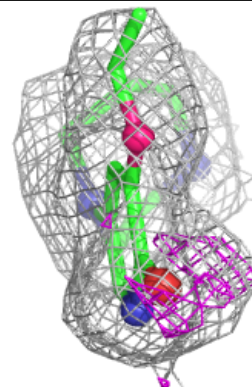
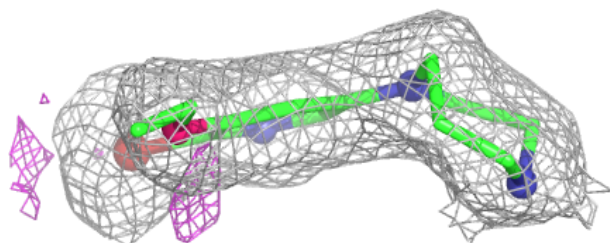
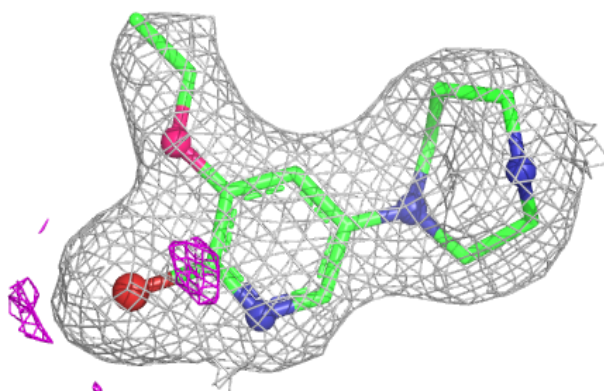


Electron density around 09S L 211:

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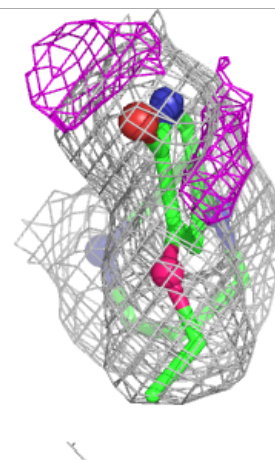
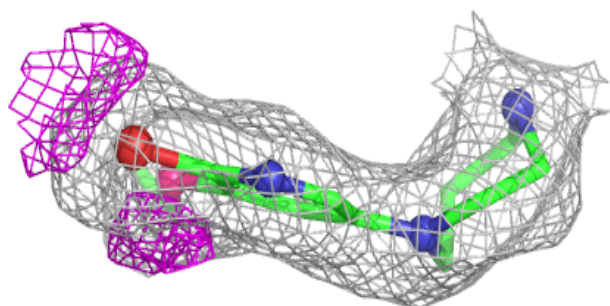
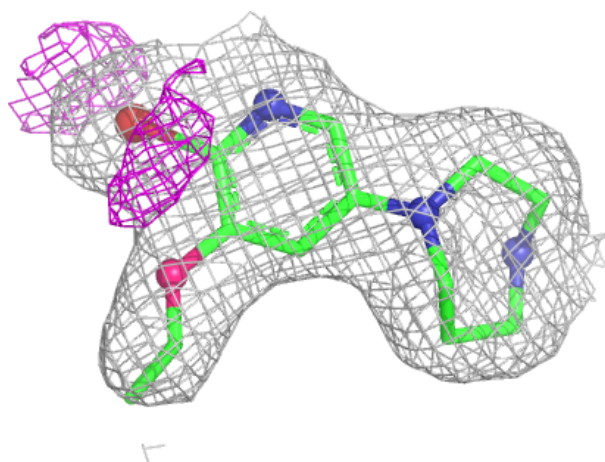
**Electron density around 09S S 211:**

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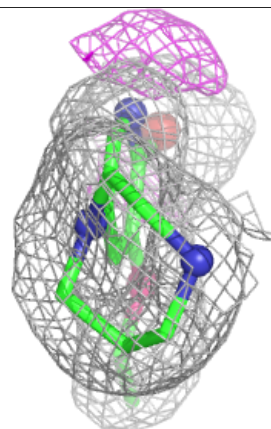
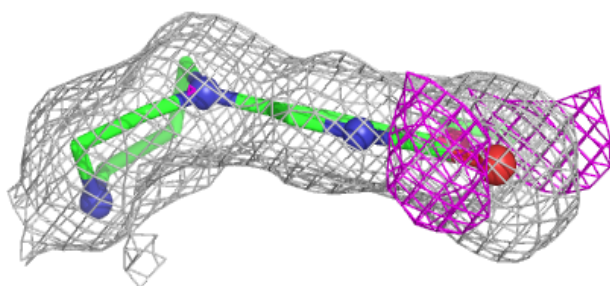
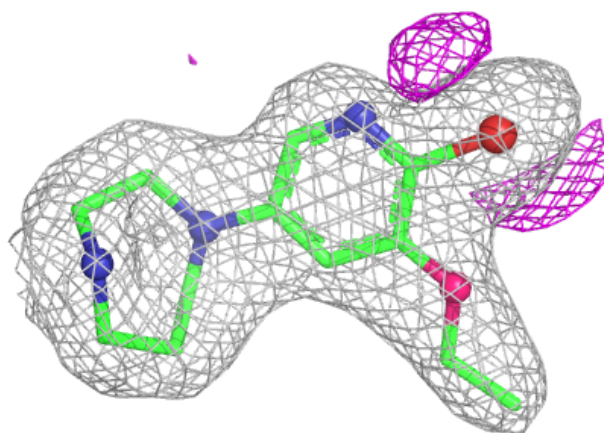
Electron density around 09S B 211:

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and green (positive)



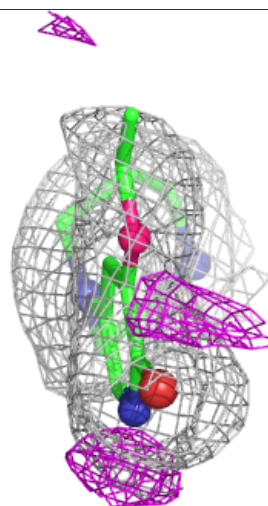
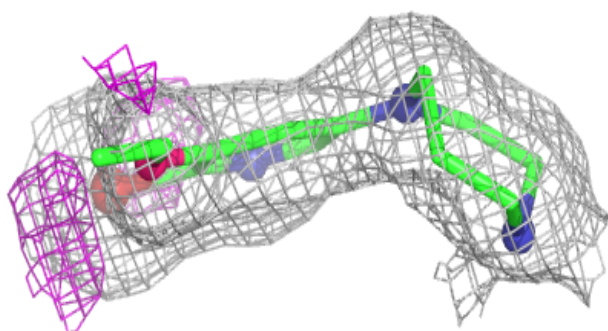
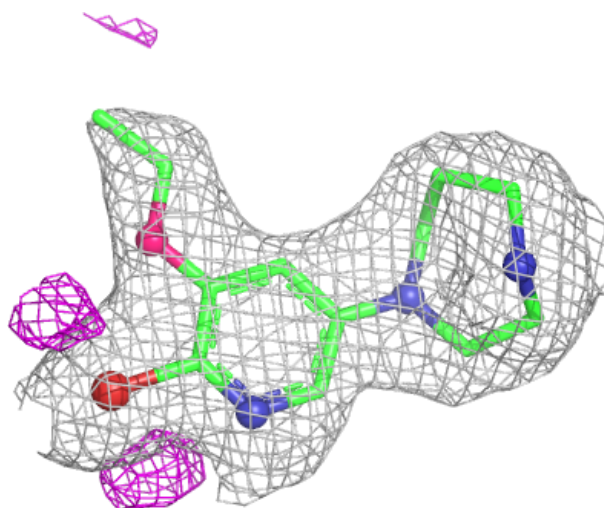
Electron density around 09S N 211:

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and green (positive)



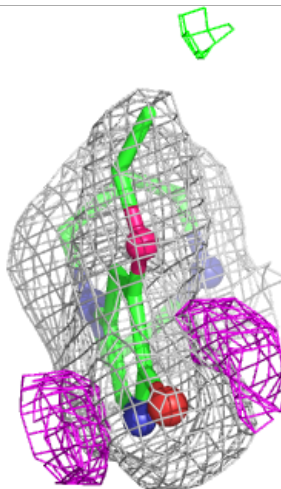
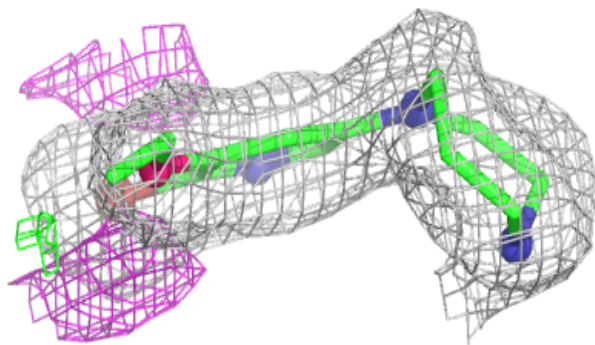
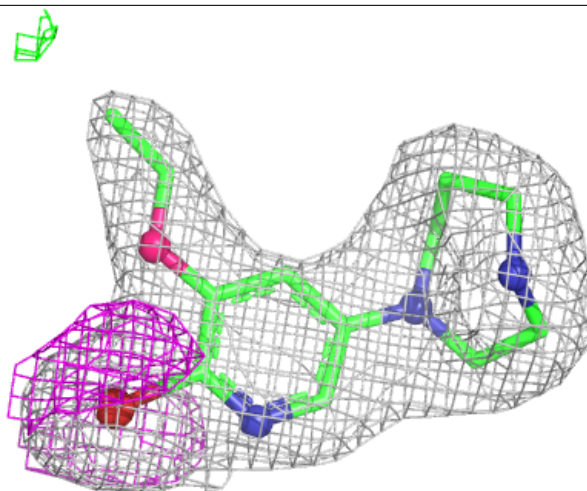
Electron density around 09S O 211:

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and green (positive)



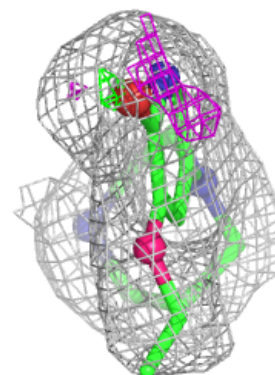
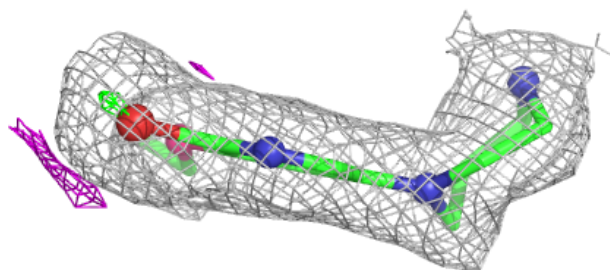
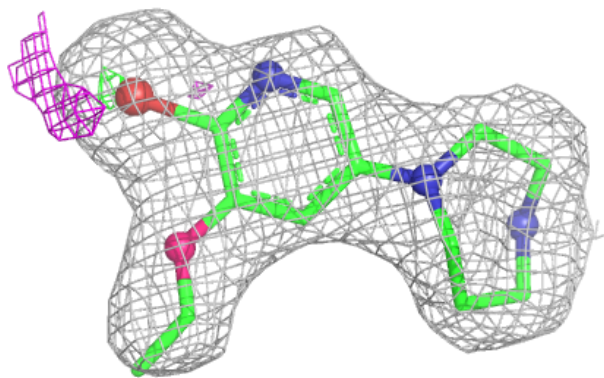
Electron density around 09S Q 211:

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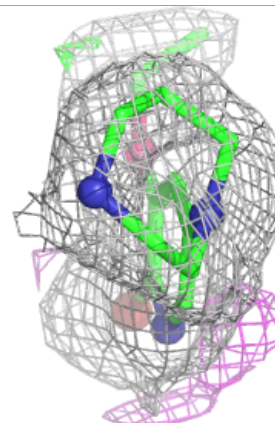
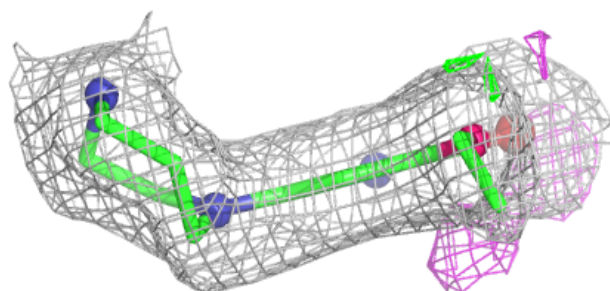
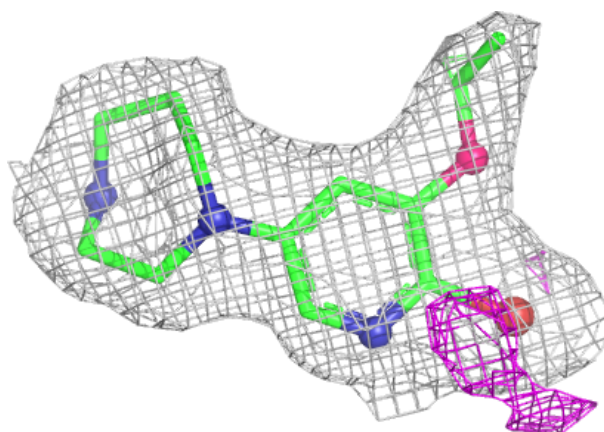


Electron density around 09S H 211:

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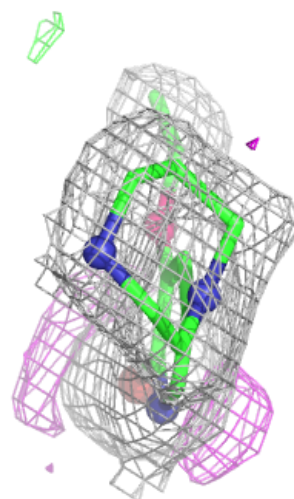
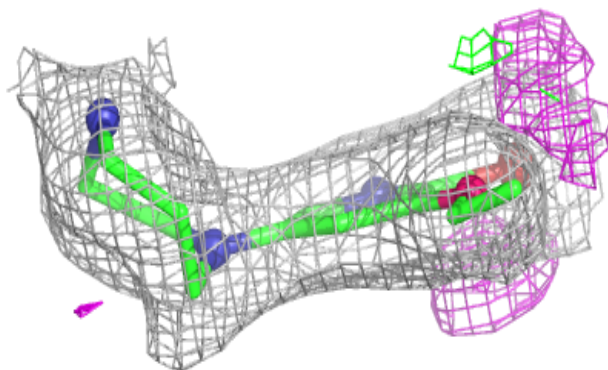
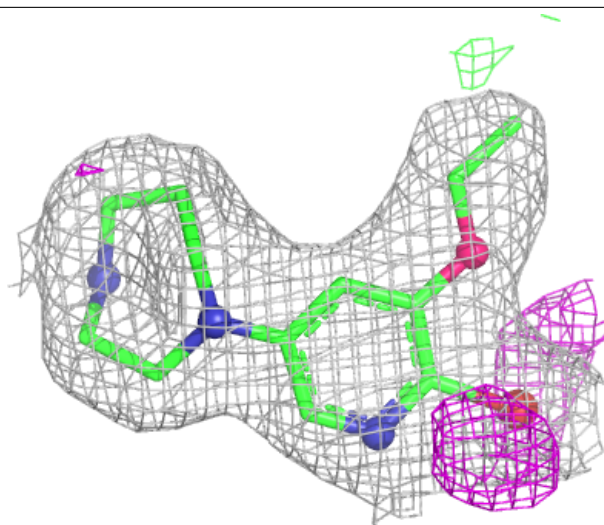
**Electron density around 09S K 211:**

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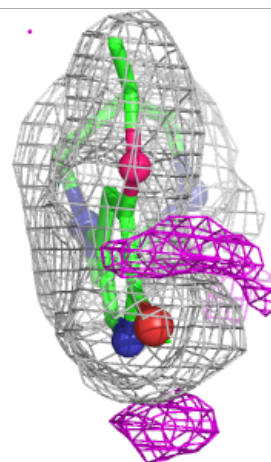
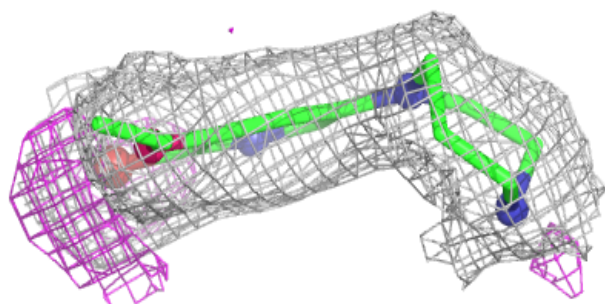
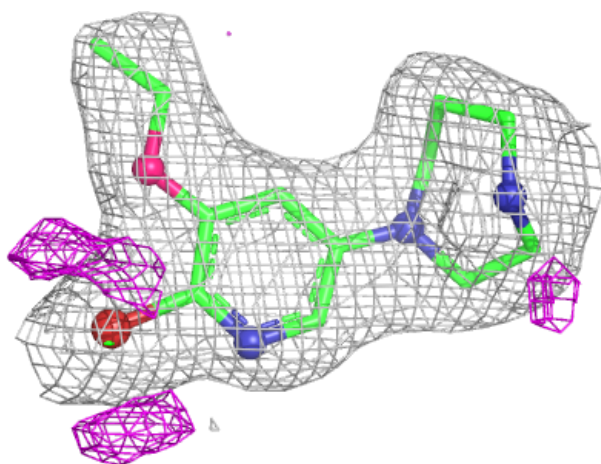
Electron density around 09S A 211:

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and green (positive)



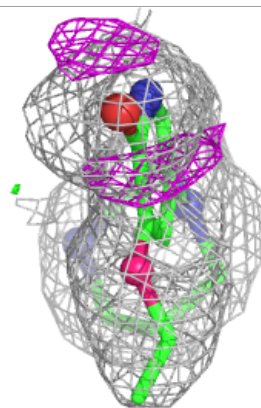
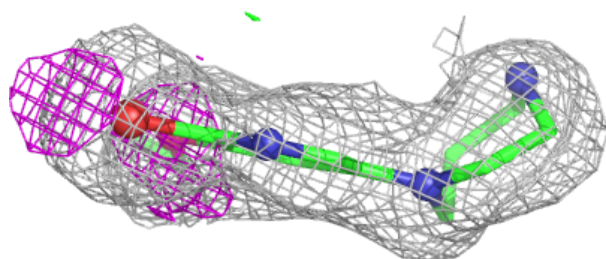
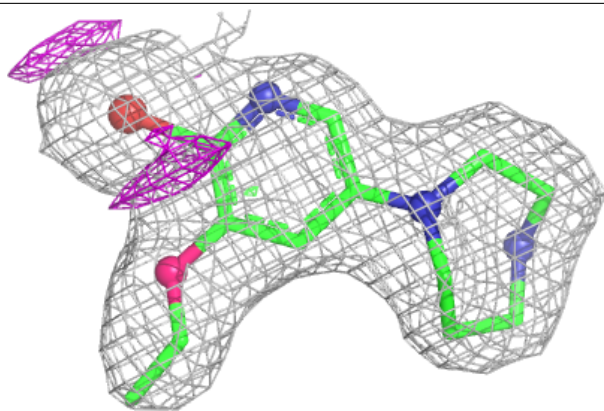
Electron density around 09S P 211:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

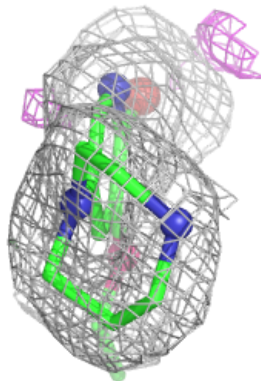
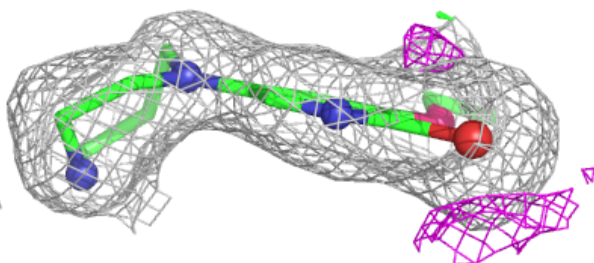
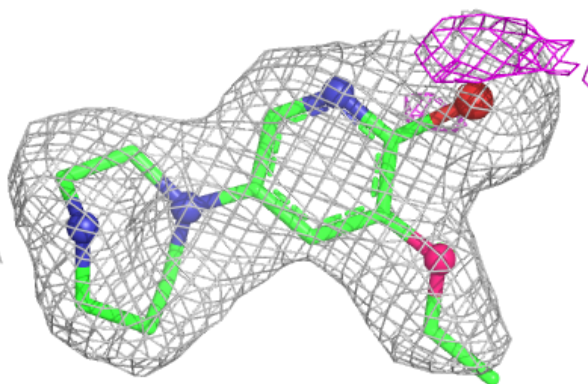


Electron density around 09S G 211:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

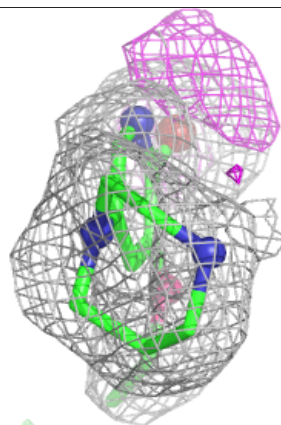
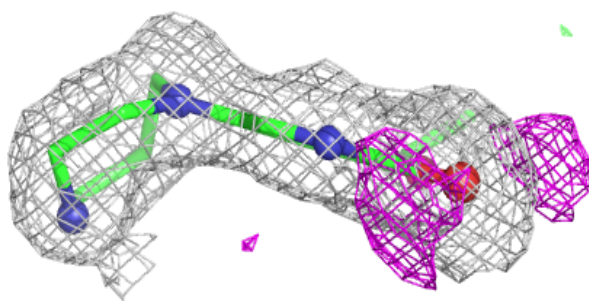
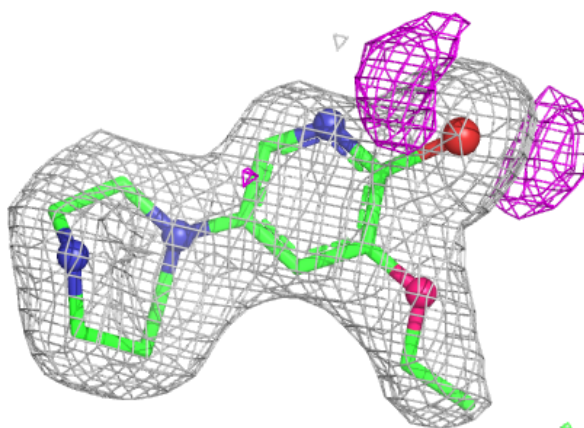
**Electron density around 09S R 211:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



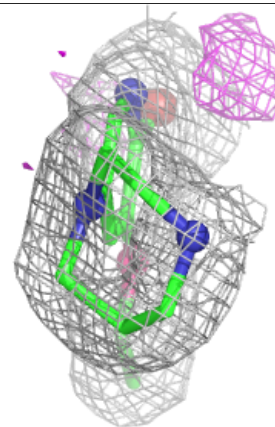
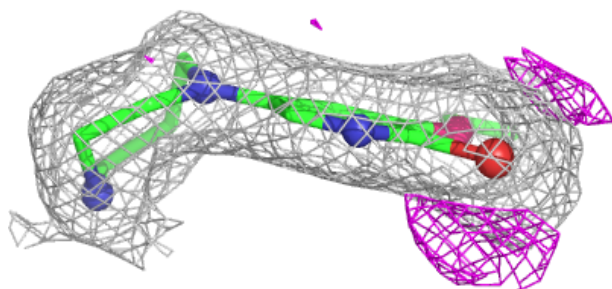
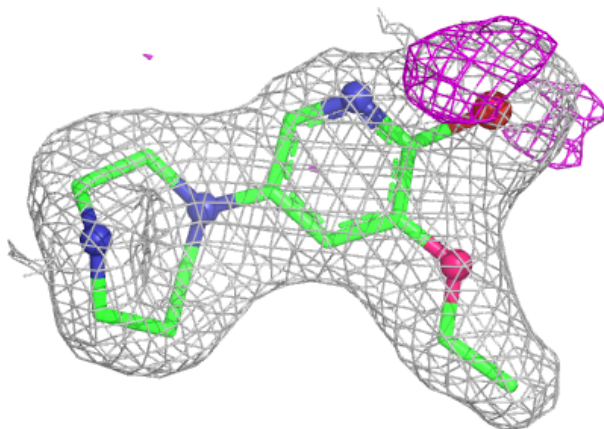
Electron density around 09S D 211:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



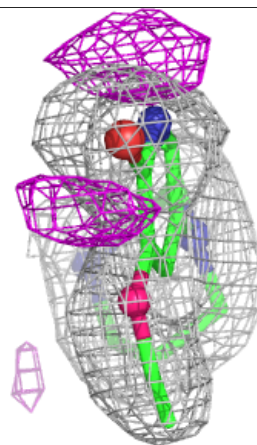
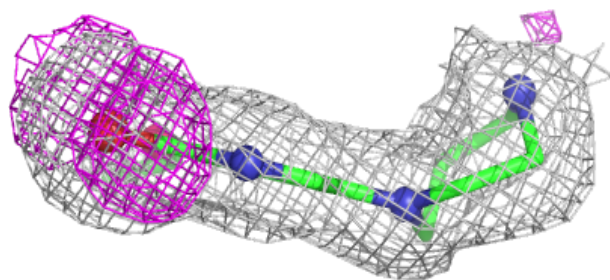
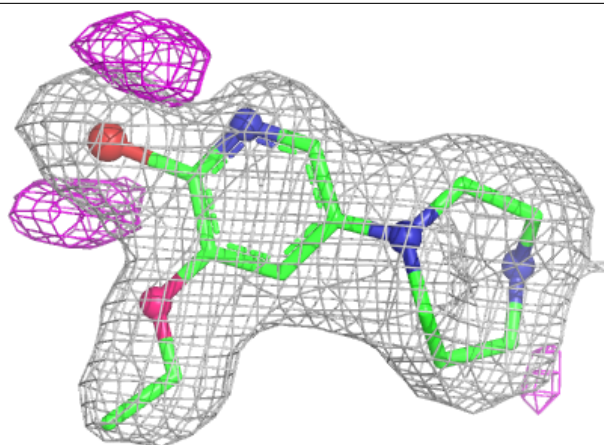
Electron density around 09S M 211:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



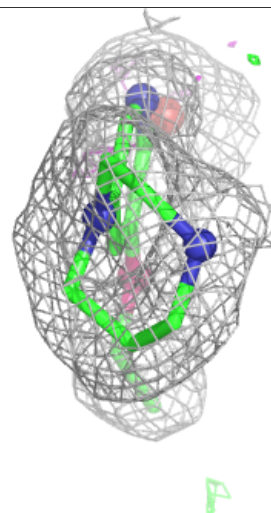
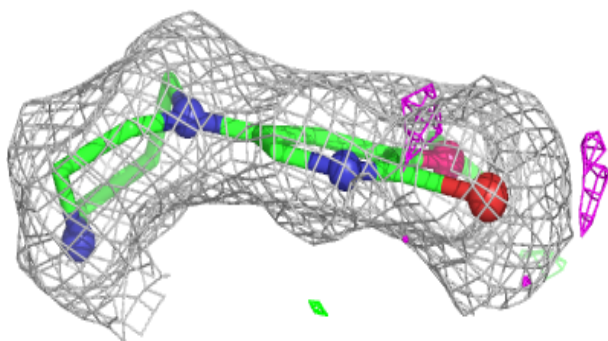
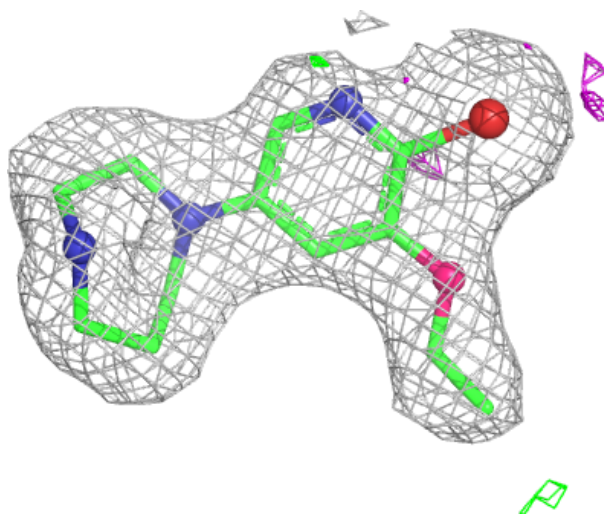
Electron density around 09S E 211:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 09S C 211:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.