



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 08:31 AM UTC

PDB ID : 5O87 / pdb_00005o87
Title : Crystal structure of wild type Aplysia californica AChBP in complex with nicotine
Authors : Dawson, A.; Hunter, W.N.; de Souza, J.O.; Trumper, P.
Deposited on : 2017-06-12
Resolution : 2.20 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 ⓘ](#)) 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

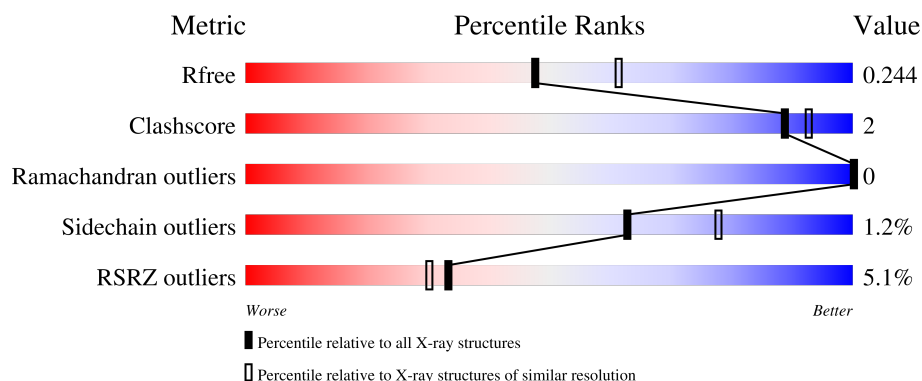
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	249	3% 78% • 17%
1	B	249	6% 80% •• 15%
1	C	249	4% 80% • 17%
1	D	249	4% 79% • 17%
1	E	249	3% 80% • 17%

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Mol	Chain	Length	Quality of chain
1	F	249	
1	G	249	
1	H	249	
1	I	249	
1	J	249	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	IPA	A	609	-	-	X	-
6	IPA	E	609	-	-	X	-
6	IPA	G	609	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18900 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 Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	B	212	Total	C	N	O	S	0	1	0
			1692	1072	277	333	10			
1	C	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	D	206	Total	C	N	O	S	0	3	0
			1658	1048	271	329	10			
1	E	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	F	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	G	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	H	205	Total	C	N	O	S	0	1	0
			1638	1037	266	325	10			
1	I	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			
1	J	206	Total	C	N	O	S	0	1	0
			1649	1043	270	326	10			

There are 150 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	VAL	ALA	conflict	UNP Q8WSF8
A	155	VAL	ALA	conflict	UNP Q8WSF8
A	237	GLU	-	expression tag	UNP Q8WSF8
A	238	ASN	-	expression tag	UNP Q8WSF8
A	239	LEU	-	expression tag	UNP Q8WSF8
A	240	TYR	-	expression tag	UNP Q8WSF8
A	241	PHE	-	expression tag	UNP Q8WSF8
A	242	GLN	-	expression tag	UNP Q8WSF8
A	243	GLY	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	244	HIS	-	expression tag	UNP Q8WSF8
A	245	HIS	-	expression tag	UNP Q8WSF8
A	246	HIS	-	expression tag	UNP Q8WSF8
A	247	HIS	-	expression tag	UNP Q8WSF8
A	248	HIS	-	expression tag	UNP Q8WSF8
A	249	HIS	-	expression tag	UNP Q8WSF8
B	60	VAL	ALA	conflict	UNP Q8WSF8
B	155	VAL	ALA	conflict	UNP Q8WSF8
B	237	GLU	-	expression tag	UNP Q8WSF8
B	238	ASN	-	expression tag	UNP Q8WSF8
B	239	LEU	-	expression tag	UNP Q8WSF8
B	240	TYR	-	expression tag	UNP Q8WSF8
B	241	PHE	-	expression tag	UNP Q8WSF8
B	242	GLN	-	expression tag	UNP Q8WSF8
B	243	GLY	-	expression tag	UNP Q8WSF8
B	244	HIS	-	expression tag	UNP Q8WSF8
B	245	HIS	-	expression tag	UNP Q8WSF8
B	246	HIS	-	expression tag	UNP Q8WSF8
B	247	HIS	-	expression tag	UNP Q8WSF8
B	248	HIS	-	expression tag	UNP Q8WSF8
B	249	HIS	-	expression tag	UNP Q8WSF8
C	60	VAL	ALA	conflict	UNP Q8WSF8
C	155	VAL	ALA	conflict	UNP Q8WSF8
C	237	GLU	-	expression tag	UNP Q8WSF8
C	238	ASN	-	expression tag	UNP Q8WSF8
C	239	LEU	-	expression tag	UNP Q8WSF8
C	240	TYR	-	expression tag	UNP Q8WSF8
C	241	PHE	-	expression tag	UNP Q8WSF8
C	242	GLN	-	expression tag	UNP Q8WSF8
C	243	GLY	-	expression tag	UNP Q8WSF8
C	244	HIS	-	expression tag	UNP Q8WSF8
C	245	HIS	-	expression tag	UNP Q8WSF8
C	246	HIS	-	expression tag	UNP Q8WSF8
C	247	HIS	-	expression tag	UNP Q8WSF8
C	248	HIS	-	expression tag	UNP Q8WSF8
C	249	HIS	-	expression tag	UNP Q8WSF8
D	60	VAL	ALA	conflict	UNP Q8WSF8
D	155	VAL	ALA	conflict	UNP Q8WSF8
D	237	GLU	-	expression tag	UNP Q8WSF8
D	238	ASN	-	expression tag	UNP Q8WSF8
D	239	LEU	-	expression tag	UNP Q8WSF8
D	240	TYR	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	241	PHE	-	expression tag	UNP Q8WSF8
D	242	GLN	-	expression tag	UNP Q8WSF8
D	243	GLY	-	expression tag	UNP Q8WSF8
D	244	HIS	-	expression tag	UNP Q8WSF8
D	245	HIS	-	expression tag	UNP Q8WSF8
D	246	HIS	-	expression tag	UNP Q8WSF8
D	247	HIS	-	expression tag	UNP Q8WSF8
D	248	HIS	-	expression tag	UNP Q8WSF8
D	249	HIS	-	expression tag	UNP Q8WSF8
E	60	VAL	ALA	conflict	UNP Q8WSF8
E	155	VAL	ALA	conflict	UNP Q8WSF8
E	237	GLU	-	expression tag	UNP Q8WSF8
E	238	ASN	-	expression tag	UNP Q8WSF8
E	239	LEU	-	expression tag	UNP Q8WSF8
E	240	TYR	-	expression tag	UNP Q8WSF8
E	241	PHE	-	expression tag	UNP Q8WSF8
E	242	GLN	-	expression tag	UNP Q8WSF8
E	243	GLY	-	expression tag	UNP Q8WSF8
E	244	HIS	-	expression tag	UNP Q8WSF8
E	245	HIS	-	expression tag	UNP Q8WSF8
E	246	HIS	-	expression tag	UNP Q8WSF8
E	247	HIS	-	expression tag	UNP Q8WSF8
E	248	HIS	-	expression tag	UNP Q8WSF8
E	249	HIS	-	expression tag	UNP Q8WSF8
F	60	VAL	ALA	conflict	UNP Q8WSF8
F	155	VAL	ALA	conflict	UNP Q8WSF8
F	237	GLU	-	expression tag	UNP Q8WSF8
F	238	ASN	-	expression tag	UNP Q8WSF8
F	239	LEU	-	expression tag	UNP Q8WSF8
F	240	TYR	-	expression tag	UNP Q8WSF8
F	241	PHE	-	expression tag	UNP Q8WSF8
F	242	GLN	-	expression tag	UNP Q8WSF8
F	243	GLY	-	expression tag	UNP Q8WSF8
F	244	HIS	-	expression tag	UNP Q8WSF8
F	245	HIS	-	expression tag	UNP Q8WSF8
F	246	HIS	-	expression tag	UNP Q8WSF8
F	247	HIS	-	expression tag	UNP Q8WSF8
F	248	HIS	-	expression tag	UNP Q8WSF8
F	249	HIS	-	expression tag	UNP Q8WSF8
G	60	VAL	ALA	conflict	UNP Q8WSF8
G	155	VAL	ALA	conflict	UNP Q8WSF8
G	237	GLU	-	expression tag	UNP Q8WSF8

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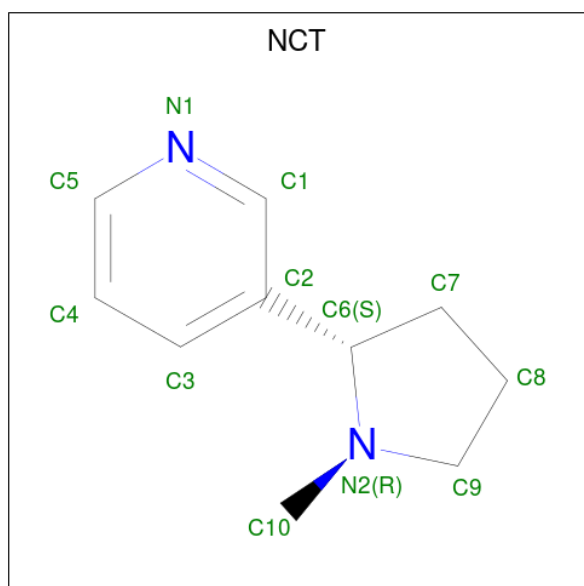
Chain	Residue	Modelled	Actual	Comment	Reference
G	238	ASN	-	expression tag	UNP Q8WSF8
G	239	LEU	-	expression tag	UNP Q8WSF8
G	240	TYR	-	expression tag	UNP Q8WSF8
G	241	PHE	-	expression tag	UNP Q8WSF8
G	242	GLN	-	expression tag	UNP Q8WSF8
G	243	GLY	-	expression tag	UNP Q8WSF8
G	244	HIS	-	expression tag	UNP Q8WSF8
G	245	HIS	-	expression tag	UNP Q8WSF8
G	246	HIS	-	expression tag	UNP Q8WSF8
G	247	HIS	-	expression tag	UNP Q8WSF8
G	248	HIS	-	expression tag	UNP Q8WSF8
G	249	HIS	-	expression tag	UNP Q8WSF8
H	60	VAL	ALA	conflict	UNP Q8WSF8
H	155	VAL	ALA	conflict	UNP Q8WSF8
H	237	GLU	-	expression tag	UNP Q8WSF8
H	238	ASN	-	expression tag	UNP Q8WSF8
H	239	LEU	-	expression tag	UNP Q8WSF8
H	240	TYR	-	expression tag	UNP Q8WSF8
H	241	PHE	-	expression tag	UNP Q8WSF8
H	242	GLN	-	expression tag	UNP Q8WSF8
H	243	GLY	-	expression tag	UNP Q8WSF8
H	244	HIS	-	expression tag	UNP Q8WSF8
H	245	HIS	-	expression tag	UNP Q8WSF8
H	246	HIS	-	expression tag	UNP Q8WSF8
H	247	HIS	-	expression tag	UNP Q8WSF8
H	248	HIS	-	expression tag	UNP Q8WSF8
H	249	HIS	-	expression tag	UNP Q8WSF8
I	60	VAL	ALA	conflict	UNP Q8WSF8
I	155	VAL	ALA	conflict	UNP Q8WSF8
I	237	GLU	-	expression tag	UNP Q8WSF8
I	238	ASN	-	expression tag	UNP Q8WSF8
I	239	LEU	-	expression tag	UNP Q8WSF8
I	240	TYR	-	expression tag	UNP Q8WSF8
I	241	PHE	-	expression tag	UNP Q8WSF8
I	242	GLN	-	expression tag	UNP Q8WSF8
I	243	GLY	-	expression tag	UNP Q8WSF8
I	244	HIS	-	expression tag	UNP Q8WSF8
I	245	HIS	-	expression tag	UNP Q8WSF8
I	246	HIS	-	expression tag	UNP Q8WSF8
I	247	HIS	-	expression tag	UNP Q8WSF8
I	248	HIS	-	expression tag	UNP Q8WSF8
I	249	HIS	-	expression tag	UNP Q8WSF8

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Chain	Residue	Modelled	Actual	Comment	Reference
J	60	VAL	ALA	conflict	UNP Q8WSF8
J	155	VAL	ALA	conflict	UNP Q8WSF8
J	237	GLU	-	expression tag	UNP Q8WSF8
J	238	ASN	-	expression tag	UNP Q8WSF8
J	239	LEU	-	expression tag	UNP Q8WSF8
J	240	TYR	-	expression tag	UNP Q8WSF8
J	241	PHE	-	expression tag	UNP Q8WSF8
J	242	GLN	-	expression tag	UNP Q8WSF8
J	243	GLY	-	expression tag	UNP Q8WSF8
J	244	HIS	-	expression tag	UNP Q8WSF8
J	245	HIS	-	expression tag	UNP Q8WSF8
J	246	HIS	-	expression tag	UNP Q8WSF8
J	247	HIS	-	expression tag	UNP Q8WSF8
J	248	HIS	-	expression tag	UNP Q8WSF8
J	249	HIS	-	expression tag	UNP Q8WSF8

- Molecule 2 is (S)-3-(1-METHYLPYRROLIDIN-2-YL)PYRIDINE (CCD ID: NCT) (formula: $C_{10}H_{14}N_2$) (labeled as "Ligand of Interest" by depositor).



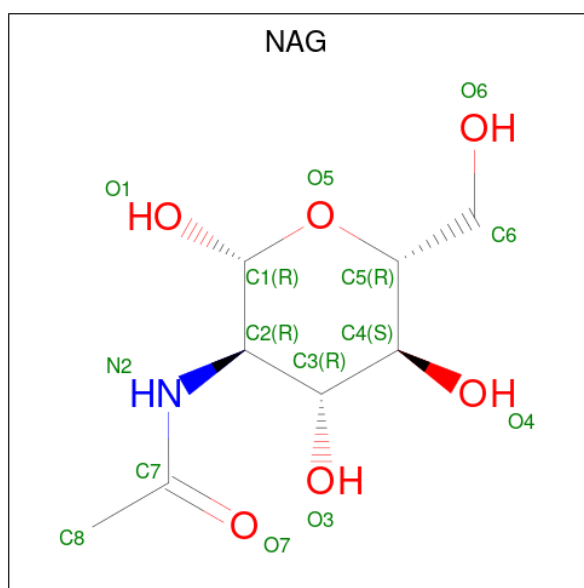
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			12	10	2		
2	B	1	Total	C	N	0	0
			12	10	2		
2	C	1	Total	C	N	0	0
			12	10	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	N	0	0
			12	10	2		
2	E	1	Total	C	N	0	0
			12	10	2		
2	F	1	Total	C	N	0	0
			12	10	2		
2	G	1	Total	C	N	0	0
			12	10	2		
2	H	1	Total	C	N	0	0
			12	10	2		
2	I	1	Total	C	N	0	0
			12	10	2		
2	J	1	Total	C	N	0	0
			12	10	2		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



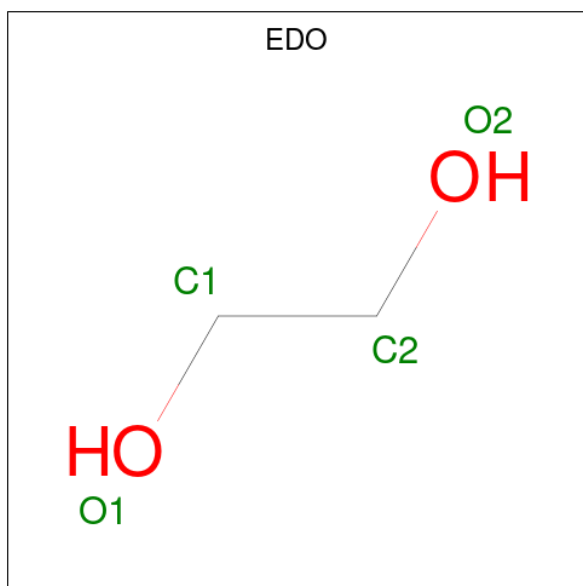
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	H	1	Total	C	N	O	0	0
			14	8	1	5		
3	I	1	Total	C	N	O	0	0
			14	8	1	5		
3	J	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

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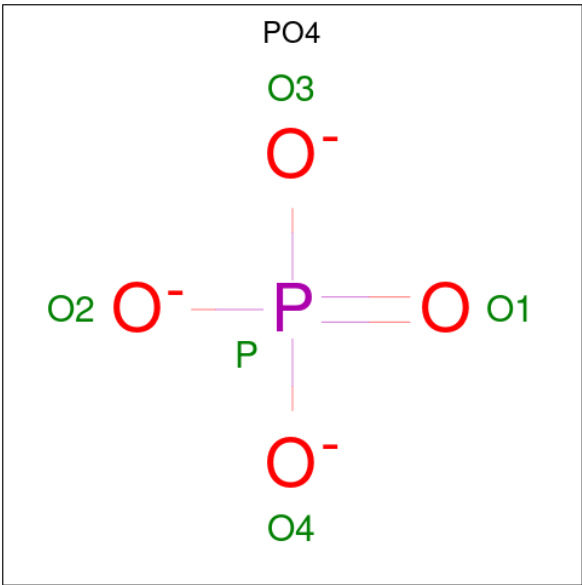
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	B	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	C	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	D	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0
4	E	1	Total 4	C 2	O 2	0	0
4	F	1	Total 4	C 2	O 2	0	0
4	F	1	Total 4	C 2	O 2	0	0
4	F	1	Total 4	C 2	O 2	0	0
4	F	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	F	1	Total	C	O	0	0
			4	2	2		
4	G	1	Total	C	O	0	0
			4	2	2		
4	G	1	Total	C	O	0	0
			4	2	2		
4	G	1	Total	C	O	0	0
			4	2	2		
4	G	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	H	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	I	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		
4	J	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



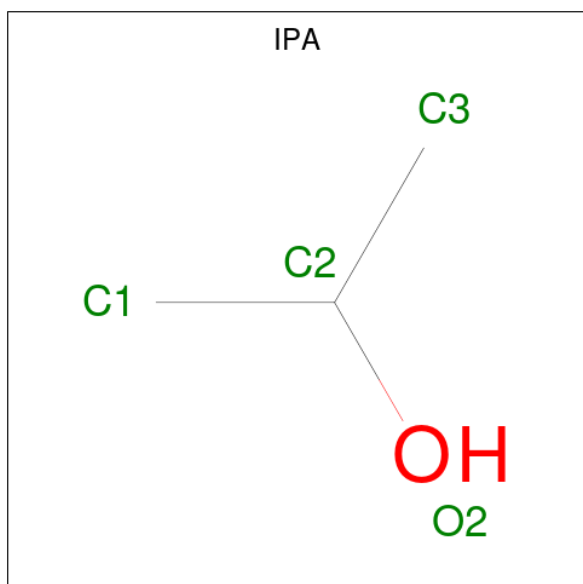
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	E	1	Total	O	P	0	0
			5	4	1		
5	E	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		
5	G	1	Total	O	P	0	0
			5	4	1		
5	G	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	H	1	Total	O	P	0	0
			5	4	1		
5	H	1	Total	O	P	0	0
			5	4	1		
5	I	1	Total	O	P	0	0
			5	4	1		
5	I	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		
5	J	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is ISOPROPYL ALCOHOL (CCD ID: IPA) (formula: C_3H_8O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	3	1		
6	B	1	Total	C	O	0	0
			4	3	1		
6	C	1	Total	C	O	0	0
			4	3	1		
6	D	1	Total	C	O	0	0
			4	3	1		
6	E	1	Total	C	O	0	0
			4	3	1		

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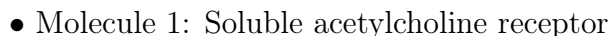
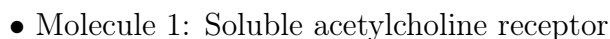
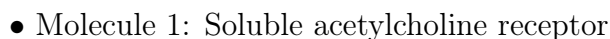
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	F	1	Total	C	O	0	0
			4	3	1		
6	G	1	Total	C	O	0	0
			4	3	1		
6	H	1	Total	C	O	0	0
			4	3	1		
6	I	1	Total	C	O	0	0
			4	3	1		
6	J	1	Total	C	O	0	0
			4	3	1		

- Molecule 7 is water.

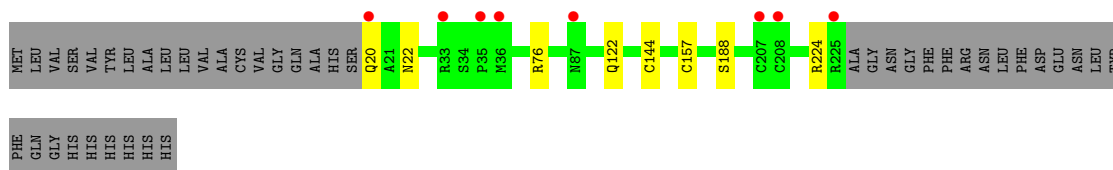
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	196	Total	O	0	0
			196	196		
7	B	206	Total	O	0	0
			206	206		
7	C	196	Total	O	0	0
			196	196		
7	D	165	Total	O	0	0
			165	165		
7	E	189	Total	O	0	0
			189	189		
7	F	165	Total	O	0	0
			165	165		
7	G	181	Total	O	0	0
			181	181		
7	H	168	Total	O	0	0
			168	168		
7	I	158	Total	O	0	0
			158	158		
7	J	177	Total	O	0	0
			177	177		

- Molecule 1: Soluble acetylcholine receptor



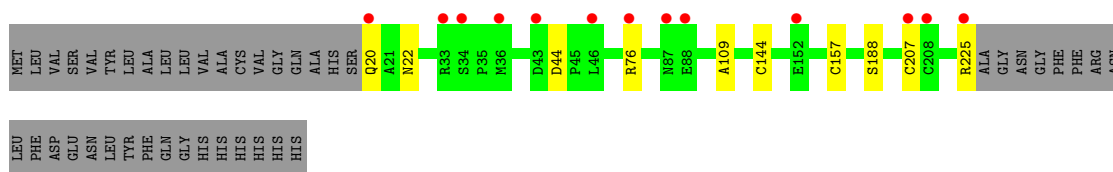
● Molecule 1: Soluble acetylcholine receptor

Chain E: 



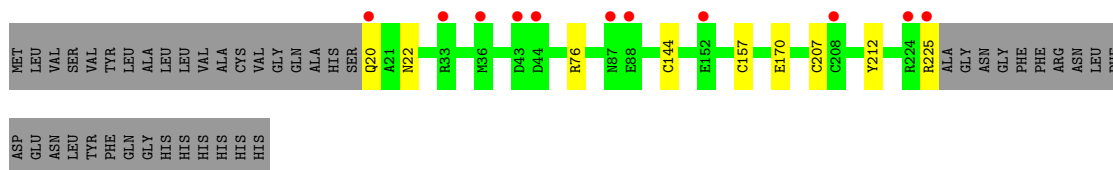
● Molecule 1: Soluble acetylcholine receptor

Chain F: 



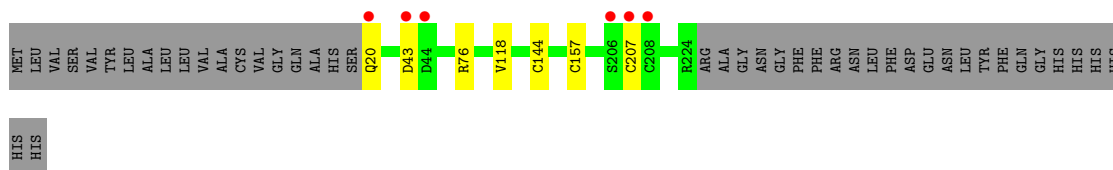
● Molecule 1: Soluble acetylcholine receptor

Chain G: 



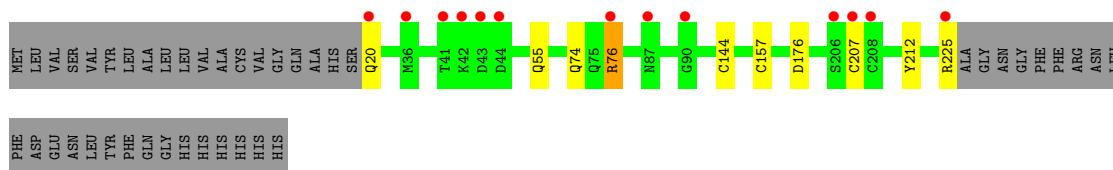
● Molecule 1: Soluble acetylcholine receptor

Chain H: 

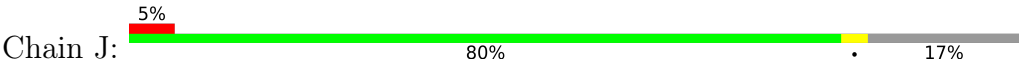


● Molecule 1: Soluble acetylcholine receptor

Chain I: 



● Molecule 1: Soluble acetylcholine receptor



MET	ASP
LEU	GLU
VAL	ASN
SER	LEU
VAL	TYR
TYR	PHE
LEU	GLN
ALA	GLY
LEU	HIS
LEU	HIS
VAL	HIS
ALA	HIS
CYS	HIS
VAL	HIS
GLY	HIS
GLN	
ALA	
HIS	
SER	
Q20	
A21	
N22	
R33	
R36	
K42	
D43	
K76	
R87	
C144	
E152	
E153	
C157	
Y186	
C207	
C208	
Y212	
R224	
R225	
ALA	
GLY	
ASN	
GLY	
PHE	
PHE	
ARG	
ASN	
LEU	
PHE	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	210.78Å 132.00Å 130.66Å 90.00° 103.15° 90.00°	Depositor
Resolution (Å)	25.20 – 2.20 25.20 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (25.20-2.20) 99.7 (25.20-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.203 , 0.235 0.213 , 0.244	Depositor DCC
R_{free} test set	8664 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.412	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.57$, $\langle L^2 \rangle = 0.41$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18900	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IPA, NAG, PO4, EDO, NCT

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	0.70	1/1693 (0.1%)	0.79	0/2309
1	B	0.69	0/1738	0.81	1/2369 (0.0%)
1	C	0.60	0/1693	0.73	0/2309
1	D	0.63	0/1710	0.74	0/2332
1	E	0.60	0/1693	0.73	0/2309
1	F	0.57	0/1693	0.73	0/2309
1	G	0.61	0/1693	0.74	0/2309
1	H	0.63	0/1682	0.75	0/2295
1	I	0.59	0/1693	0.73	0/2309
1	J	0.60	0/1693	0.74	0/2309
All	All	0.62	1/16981 (0.0%)	0.75	1/23159 (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	A	0	1
1	B	0	1
1	C	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	204	HIS	C-O	-5.44	1.16	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	224	ARG	O-C-N	-5.12	116.51	122.96

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	207	CYS	Peptide
1	B	207	CYS	Peptide
1	C	207	CYS	Peptide
1	F	207	CYS	Peptide
1	G	207	CYS	Peptide

5.2 Too-close contacts [i](#)

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	1649	0	1582	8	0
1	B	1692	0	1617	6	0
1	C	1649	0	1582	3	0
1	D	1658	0	1586	6	0
1	E	1649	0	1582	8	0
1	F	1649	0	1582	7	0
1	G	1649	0	1582	7	0
1	H	1638	0	1569	3	0
1	I	1649	0	1582	5	0
1	J	1649	0	1582	5	0
2	A	12	0	14	1	0
2	B	12	0	14	1	0
2	C	12	0	14	0	0
2	D	12	0	14	1	0
2	E	12	0	14	0	0
2	F	12	0	14	0	0
2	G	12	0	14	1	0
2	H	12	0	14	0	0
2	I	12	0	14	1	0
2	J	12	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
3	D	14	0	13	1	0
3	E	14	0	13	0	0
3	F	14	0	13	0	0
3	G	14	0	13	2	0
3	H	14	0	13	0	0
3	I	14	0	13	0	0
3	J	14	0	13	0	0
4	A	16	0	24	1	0
4	B	20	0	30	0	0
4	C	16	0	24	1	0
4	D	20	0	30	0	0
4	E	16	0	24	1	0
4	F	20	0	30	2	0
4	G	16	0	24	0	0
4	H	12	0	18	0	0
4	I	20	0	30	1	0
4	J	12	0	18	1	0
5	A	10	0	0	1	0
5	B	10	0	0	0	0
5	C	10	0	0	0	0
5	D	10	0	0	0	0
5	E	10	0	0	0	0
5	F	10	0	0	0	0
5	G	10	0	0	1	0
5	H	10	0	0	0	0
5	I	10	0	0	0	0
5	J	10	0	0	0	0
6	A	4	0	8	6	0
6	B	4	0	8	1	0
6	C	4	0	8	2	0
6	D	4	0	8	2	0
6	E	4	0	8	4	0
6	F	4	0	8	3	0
6	G	4	0	8	4	0
6	H	4	0	8	0	0
6	I	4	0	8	1	0
6	J	4	0	8	2	0
7	A	196	0	0	2	0
7	B	206	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	196	0	0	1	0
7	D	165	0	0	0	0
7	E	189	0	0	2	0
7	F	165	0	0	0	0
7	G	181	0	0	1	0
7	H	168	0	0	1	0
7	I	158	0	0	0	0
7	J	177	0	0	1	0
All	All	18900	0	16448	64	0

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 2.

The worst 5 of 64 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:22:ASN:HB2	6:E:609:IPA:H32	1.68	0.76
1:E:122:GLN:OE1	7:E:701:HOH:O	2.06	0.72
1:A:22:ASN:HD22	6:A:609:IPA:H32	1.55	0.71
1:D:178[A]:ASP:HB2	1:D:198:GLN:O	1.93	0.68
6:J:608:IPA:H11	7:J:865:HOH:O	1.96	0.66

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	205/249 (82%)	203 (99%)	2 (1%)	0	100	100
1	B	211/249 (85%)	208 (99%)	3 (1%)	0	100	100
1	C	205/249 (82%)	203 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	207/249 (83%)	206 (100%)	1 (0%)	0	100	100
1	E	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
1	F	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
1	G	205/249 (82%)	203 (99%)	2 (1%)	0	100	100
1	H	204/249 (82%)	203 (100%)	1 (0%)	0	100	100
1	I	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
1	J	205/249 (82%)	204 (100%)	1 (0%)	0	100	100
All	All	2057/2490 (83%)	2042 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	190/224 (85%)	188 (99%)	2 (1%)	65	79
1	B	193/224 (86%)	189 (98%)	4 (2%)	47	63
1	C	190/224 (85%)	189 (100%)	1 (0%)	81	90
1	D	192/224 (86%)	189 (98%)	3 (2%)	55	71
1	E	190/224 (85%)	189 (100%)	1 (0%)	81	90
1	F	190/224 (85%)	188 (99%)	2 (1%)	65	79
1	G	190/224 (85%)	188 (99%)	2 (1%)	65	79
1	H	189/224 (84%)	187 (99%)	2 (1%)	65	79
1	I	190/224 (85%)	187 (98%)	3 (2%)	55	71
1	J	190/224 (85%)	187 (98%)	3 (2%)	55	71
All	All	1904/2240 (85%)	1881 (99%)	23 (1%)	63	78

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	225	ARG
1	I	20	GLN
1	H	76	ARG
1	I	76	ARG
1	C	20	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	75	GLN
1	I	138	GLN
1	H	80	ASN
1	I	74	GLN
1	J	75	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](#)

92 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
4	EDO	F	607	-	3,3,3	0.40	0	2,2,2	0.36	0
6	IPA	A	609	-	3,3,3	0.54	0	3,3,3	0.33	0
4	EDO	F	608	-	3,3,3	0.38	0	2,2,2	0.40	0
5	PO4	D	605	-	4,4,4	1.04	0	6,6,6	0.71	0
4	EDO	E	608	-	3,3,3	0.39	0	2,2,2	0.29	0
4	EDO	B	604	-	3,3,3	0.47	0	2,2,2	0.13	0
4	EDO	D	604	-	3,3,3	0.44	0	2,2,2	0.57	0
4	EDO	B	608	-	3,3,3	0.47	0	2,2,2	0.10	0
4	EDO	C	603	-	3,3,3	0.44	0	2,2,2	0.34	0
3	NAG	H	602	1	14,14,15	0.54	0	17,19,21	2.15	3 (17%)
5	PO4	I	606	-	4,4,4	0.91	0	6,6,6	0.43	0
2	NCT	B	601	-	13,13,13	0.81	0	17,17,17	0.96	1 (5%)
6	IPA	G	609	-	3,3,3	0.64	0	3,3,3	0.85	0
4	EDO	I	609	-	3,3,3	0.53	0	2,2,2	0.20	0
4	EDO	C	608	-	3,3,3	0.44	0	2,2,2	0.16	0
4	EDO	A	604	-	3,3,3	0.36	0	2,2,2	0.76	0
3	NAG	B	602	1	14,14,15	0.50	0	17,19,21	2.38	7 (41%)
2	NCT	D	601	-	13,13,13	0.77	1 (7%)	17,17,17	1.13	1 (5%)
4	EDO	I	607	-	3,3,3	0.43	0	2,2,2	0.30	0
5	PO4	B	605	-	4,4,4	1.02	0	6,6,6	0.65	0
4	EDO	A	607	-	3,3,3	0.37	0	2,2,2	0.19	0
2	NCT	F	601	-	13,13,13	0.80	0	17,17,17	1.17	1 (5%)
4	EDO	E	607	-	3,3,3	0.46	0	2,2,2	0.05	0
5	PO4	A	606	-	4,4,4	0.81	0	6,6,6	0.74	0
5	PO4	D	606	-	4,4,4	0.83	0	6,6,6	0.70	0
4	EDO	B	603	-	3,3,3	0.44	0	2,2,2	0.64	0
5	PO4	H	604	-	4,4,4	1.19	0	6,6,6	0.61	0
3	NAG	I	602	1	14,14,15	0.57	0	17,19,21	1.30	2 (11%)
4	EDO	B	607	-	3,3,3	0.40	0	2,2,2	0.21	0
4	EDO	J	603	-	3,3,3	0.48	0	2,2,2	0.60	0
6	IPA	D	610	-	3,3,3	0.68	0	3,3,3	0.30	0
3	NAG	A	602	1	14,14,15	0.81	0	17,19,21	1.44	2 (11%)
3	NAG	D	602	1	14,14,15	0.69	0	17,19,21	1.56	3 (17%)
4	EDO	F	609	-	3,3,3	0.43	0	2,2,2	0.18	0
3	NAG	F	602	1	14,14,15	0.54	0	17,19,21	1.74	5 (29%)
4	EDO	G	607	-	3,3,3	0.46	0	2,2,2	0.21	0
4	EDO	D	609	-	3,3,3	0.43	0	2,2,2	0.28	0
4	EDO	C	604	-	3,3,3	0.20	0	2,2,2	1.09	0
5	PO4	J	605	-	4,4,4	1.01	0	6,6,6	0.83	0
4	EDO	C	607	-	3,3,3	0.39	0	2,2,2	0.19	0
4	EDO	F	604	-	3,3,3	0.44	0	2,2,2	0.21	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	E	604	-	3,3,3	0.44	0	2,2,2	0.25	0
5	PO4	F	606	-	4,4,4	0.81	0	6,6,6	0.72	0
2	NCT	E	601	-	13,13,13	0.87	0	17,17,17	1.19	2 (11%)
4	EDO	J	604	-	3,3,3	0.38	0	2,2,2	0.47	0
5	PO4	I	605	-	4,4,4	0.92	0	6,6,6	0.95	0
3	NAG	C	602	1	14,14,15	0.43	0	17,19,21	1.05	0
6	IPA	I	610	-	3,3,3	0.61	0	3,3,3	0.99	0
4	EDO	H	606	-	3,3,3	0.37	0	2,2,2	0.17	0
5	PO4	E	606	-	4,4,4	0.97	0	6,6,6	0.56	0
3	NAG	E	602	1	14,14,15	0.54	0	17,19,21	1.07	1 (5%)
5	PO4	B	606	-	4,4,4	0.87	0	6,6,6	0.66	0
6	IPA	J	608	-	3,3,3	0.48	0	3,3,3	0.41	0
4	EDO	D	603	-	3,3,3	0.30	0	2,2,2	0.57	0
2	NCT	A	601	-	13,13,13	0.87	1 (7%)	17,17,17	1.17	1 (5%)
3	NAG	J	602	1	14,14,15	0.48	0	17,19,21	1.70	4 (23%)
4	EDO	B	609	-	3,3,3	0.46	0	2,2,2	0.18	0
6	IPA	B	610	-	3,3,3	0.35	0	3,3,3	0.40	0
2	NCT	J	601	-	13,13,13	0.75	0	17,17,17	1.20	1 (5%)
4	EDO	D	607	-	3,3,3	0.42	0	2,2,2	0.12	0
4	EDO	E	603	-	3,3,3	0.41	0	2,2,2	0.45	0
5	PO4	C	606	-	4,4,4	0.83	0	6,6,6	0.79	0
5	PO4	A	605	-	4,4,4	1.10	0	6,6,6	0.70	0
6	IPA	C	609	-	3,3,3	0.82	0	3,3,3	0.50	0
2	NCT	C	601	-	13,13,13	0.83	0	17,17,17	1.11	1 (5%)
4	EDO	H	603	-	3,3,3	0.41	0	2,2,2	0.56	0
4	EDO	J	607	-	3,3,3	0.42	0	2,2,2	0.15	0
5	PO4	E	605	-	4,4,4	1.05	0	6,6,6	1.03	0
4	EDO	H	607	-	3,3,3	0.47	0	2,2,2	0.28	0
5	PO4	C	605	-	4,4,4	1.02	0	6,6,6	0.83	0
4	EDO	A	603	-	3,3,3	0.43	0	2,2,2	0.49	0
4	EDO	G	604	-	3,3,3	0.47	0	2,2,2	0.16	0
5	PO4	G	605	-	4,4,4	1.12	0	6,6,6	0.97	0
6	IPA	E	609	-	3,3,3	0.42	0	3,3,3	0.32	0
4	EDO	F	603	-	3,3,3	0.53	0	2,2,2	0.35	0
4	EDO	A	608	-	3,3,3	0.45	0	2,2,2	0.21	0
2	NCT	G	601	-	13,13,13	0.70	0	17,17,17	1.19	1 (5%)
5	PO4	H	605	-	4,4,4	0.94	0	6,6,6	0.60	0
4	EDO	I	604	-	3,3,3	0.27	0	2,2,2	0.67	0
4	EDO	G	603	-	3,3,3	0.45	0	2,2,2	0.60	0
4	EDO	I	603	-	3,3,3	0.40	0	2,2,2	0.72	0
5	PO4	G	606	-	4,4,4	0.88	0	6,6,6	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	G	602	1	14,14,15	0.98	1 (7%)	17,19,21	1.50	3 (17%)
5	PO4	F	605	-	4,4,4	1.05	0	6,6,6	0.59	0
2	NCT	I	601	-	13,13,13	0.74	0	17,17,17	1.08	1 (5%)
2	NCT	H	601	-	13,13,13	0.93	0	17,17,17	1.18	2 (11%)
4	EDO	I	608	-	3,3,3	0.48	0	2,2,2	0.32	0
4	EDO	G	608	-	3,3,3	0.51	0	2,2,2	0.21	0
6	IPA	F	610	-	3,3,3	0.71	0	3,3,3	0.75	0
6	IPA	H	608	-	3,3,3	0.61	0	3,3,3	0.57	0
5	PO4	J	606	-	4,4,4	0.82	0	6,6,6	0.51	0
4	EDO	D	608	-	3,3,3	0.47	0	2,2,2	0.30	0

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
4	EDO	A	607	-	-	0/1/1/1	-
4	EDO	J	604	-	-	1/1/1/1	-
4	EDO	F	607	-	-	0/1/1/1	-
2	NCT	F	601	-	-	3/4/14/14	0/2/2/2
4	EDO	G	604	-	-	1/1/1/1	-
3	NAG	C	602	1	-	0/6/23/26	0/1/1/1
4	EDO	E	607	-	-	0/1/1/1	-
4	EDO	F	603	-	-	0/1/1/1	-
4	EDO	A	608	-	-	0/1/1/1	-
4	EDO	F	608	-	-	0/1/1/1	-
4	EDO	B	603	-	-	0/1/1/1	-
4	EDO	H	606	-	-	0/1/1/1	-
3	NAG	I	602	1	-	1/6/23/26	0/1/1/1
4	EDO	A	603	-	-	0/1/1/1	-
4	EDO	E	608	-	-	1/1/1/1	-
4	EDO	B	607	-	-	0/1/1/1	-
4	EDO	J	603	-	-	0/1/1/1	-
4	EDO	B	604	-	-	1/1/1/1	-
4	EDO	D	604	-	-	0/1/1/1	-
3	NAG	A	602	1	-	2/6/23/26	0/1/1/1
3	NAG	D	602	1	-	1/6/23/26	0/1/1/1
3	NAG	E	602	1	-	0/6/23/26	0/1/1/1
4	EDO	F	609	-	-	1/1/1/1	-
4	EDO	B	608	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	C	603	-	-	0/1/1/1	-
3	NAG	F	602	1	-	4/6/23/26	0/1/1/1
4	EDO	G	607	-	-	1/1/1/1	-
4	EDO	D	603	-	-	0/1/1/1	-
2	NCT	G	601	-	-	2/4/14/14	0/2/2/2
3	NAG	H	602	1	-	1/6/23/26	0/1/1/1
4	EDO	D	609	-	-	0/1/1/1	-
2	NCT	A	601	-	-	3/4/14/14	0/2/2/2
4	EDO	G	603	-	-	0/1/1/1	-
4	EDO	I	604	-	-	0/1/1/1	-
3	NAG	J	602	1	-	1/6/23/26	0/1/1/1
4	EDO	B	609	-	-	1/1/1/1	-
4	EDO	C	604	-	-	0/1/1/1	-
4	EDO	I	603	-	-	0/1/1/1	-
2	NCT	B	601	-	-	0/4/14/14	0/2/2/2
3	NAG	G	602	1	-	6/6/23/26	0/1/1/1
2	NCT	J	601	-	-	2/4/14/14	0/2/2/2
4	EDO	D	607	-	-	0/1/1/1	-
4	EDO	E	603	-	-	1/1/1/1	-
4	EDO	I	609	-	-	1/1/1/1	-
4	EDO	C	608	-	-	1/1/1/1	-
4	EDO	A	604	-	-	0/1/1/1	-
4	EDO	C	607	-	-	0/1/1/1	-
4	EDO	F	604	-	-	1/1/1/1	-
2	NCT	C	601	-	-	2/4/14/14	0/2/2/2
3	NAG	B	602	1	-	3/6/23/26	0/1/1/1
2	NCT	I	601	-	-	0/4/14/14	0/2/2/2
4	EDO	E	604	-	-	1/1/1/1	-
4	EDO	H	603	-	-	0/1/1/1	-
4	EDO	J	607	-	-	1/1/1/1	-
4	EDO	H	607	-	-	1/1/1/1	-
2	NCT	H	601	-	-	2/4/14/14	0/2/2/2
4	EDO	I	608	-	-	0/1/1/1	-
2	NCT	D	601	-	-	2/4/14/14	0/2/2/2
4	EDO	G	608	-	-	1/1/1/1	-
4	EDO	I	607	-	-	1/1/1/1	-
2	NCT	E	601	-	-	2/4/14/14	0/2/2/2
4	EDO	D	608	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	602	NAG	C1-C2	2.40	1.55	1.52
2	A	601	NCT	C1-C2	2.09	1.41	1.39
2	D	601	NCT	C1-C2	2.08	1.41	1.39

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	602	NAG	C2-N2-C7	6.13	131.12	122.90
3	H	602	NAG	C1-O5-C5	4.74	118.54	112.19
3	H	602	NAG	C2-N2-C7	4.65	129.12	122.90
3	H	602	NAG	C1-C2-N2	4.30	117.21	110.43
3	B	602	NAG	C8-C7-N2	4.13	122.96	116.12

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	NCT	C1-C2-C6-N2
3	B	602	NAG	C1-C2-N2-C7
3	H	602	NAG	C1-C2-N2-C7
3	J	602	NAG	C1-C2-N2-C7
3	G	602	NAG	C4-C5-C6-O6

There are no ring outliers.

26 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	609	IPA	6	0
2	B	601	NCT	1	0
6	G	609	IPA	4	0
4	A	604	EDO	1	0
2	D	601	NCT	1	0
4	I	607	EDO	1	0
5	A	606	PO4	1	0
6	D	610	IPA	2	0
3	D	602	NAG	1	0
4	C	604	EDO	1	0
4	F	604	EDO	1	0
4	E	604	EDO	1	0
4	J	604	EDO	1	0
6	I	610	IPA	1	0
6	J	608	IPA	2	0

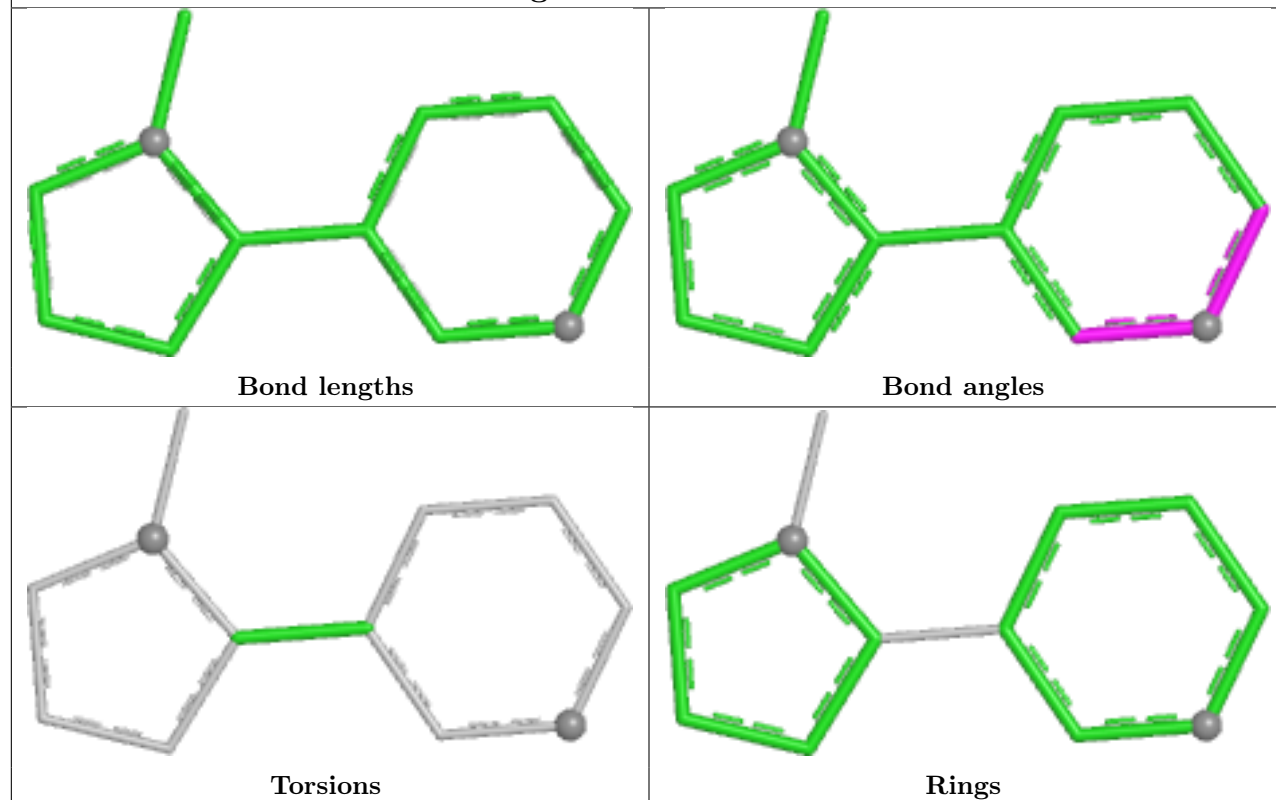
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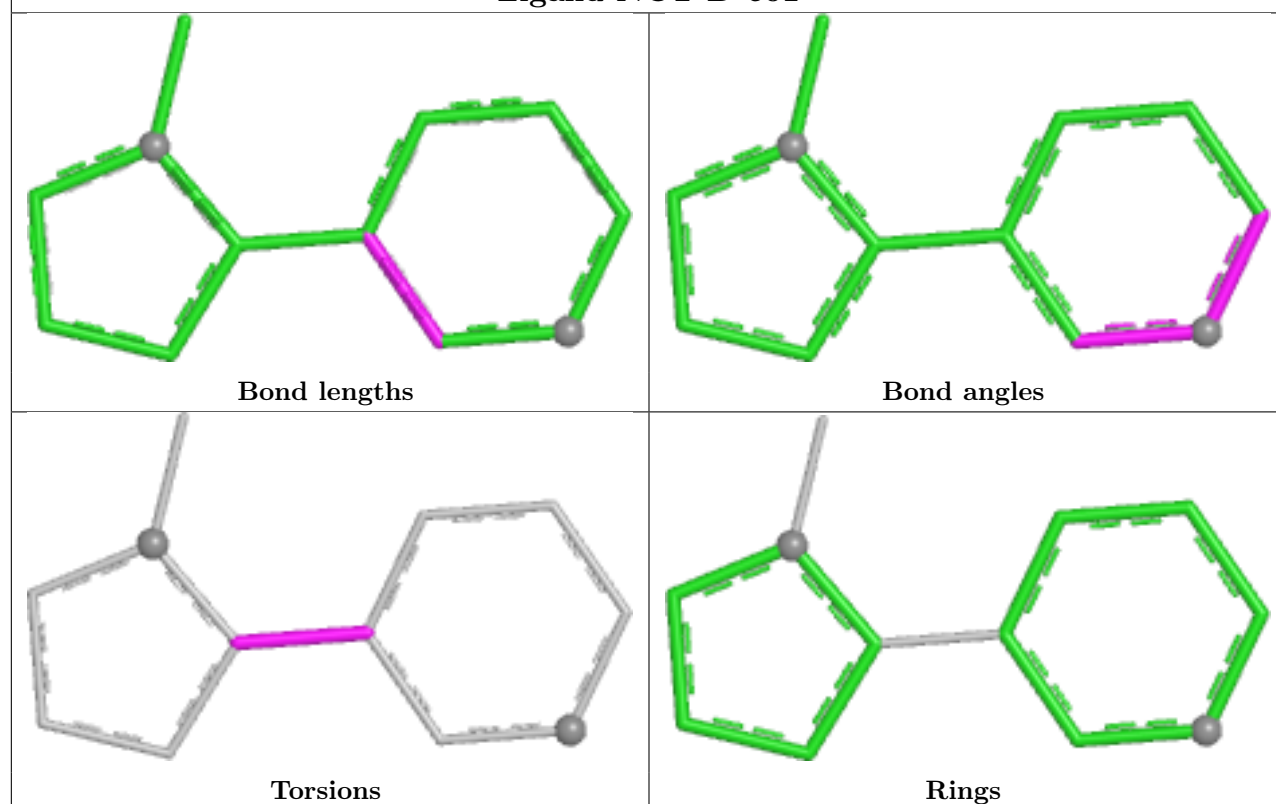
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	NCT	1	0
6	B	610	IPA	1	0
2	J	601	NCT	1	0
6	C	609	IPA	2	0
5	G	605	PO4	1	0
6	E	609	IPA	4	0
4	F	603	EDO	1	0
2	G	601	NCT	1	0
3	G	602	NAG	2	0
2	I	601	NCT	1	0
6	F	610	IPA	3	0

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.

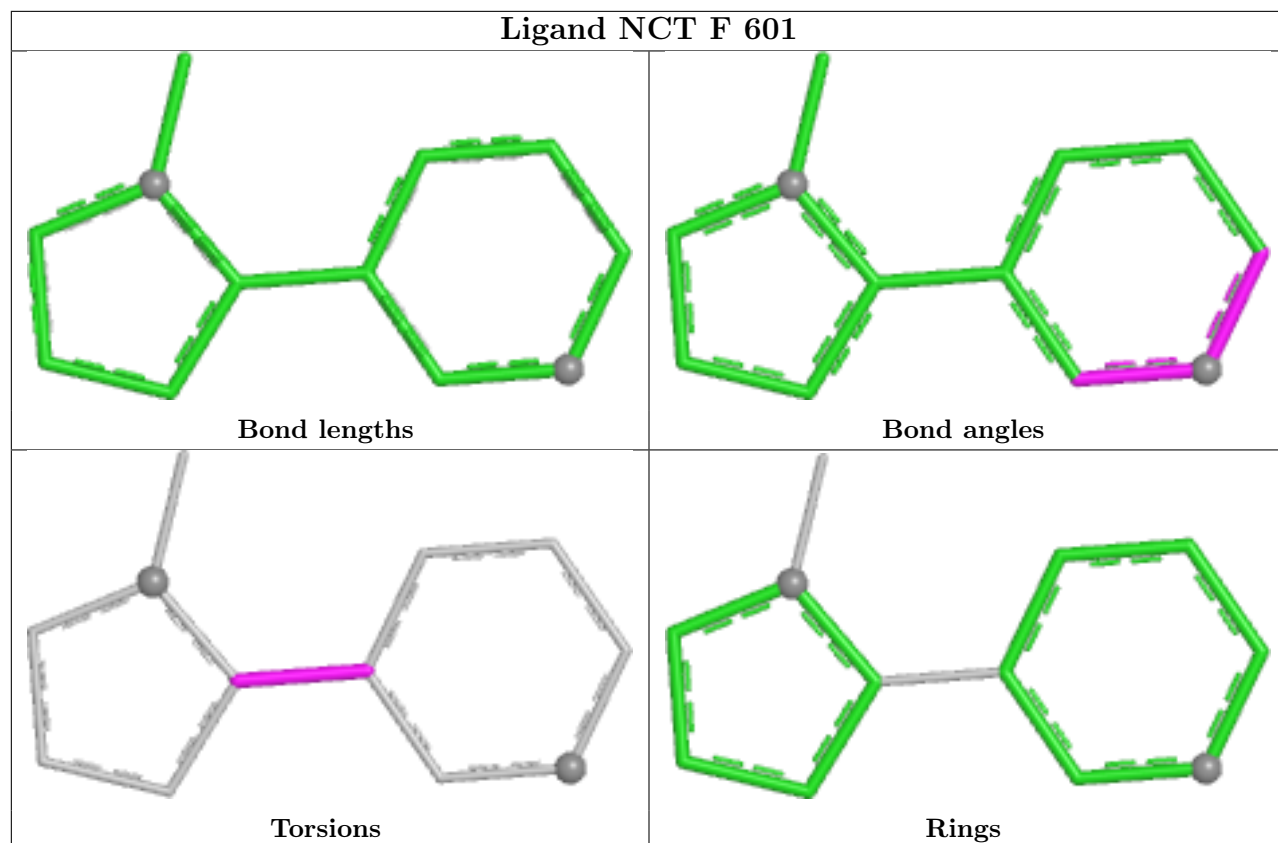
Ligand NCT B 601



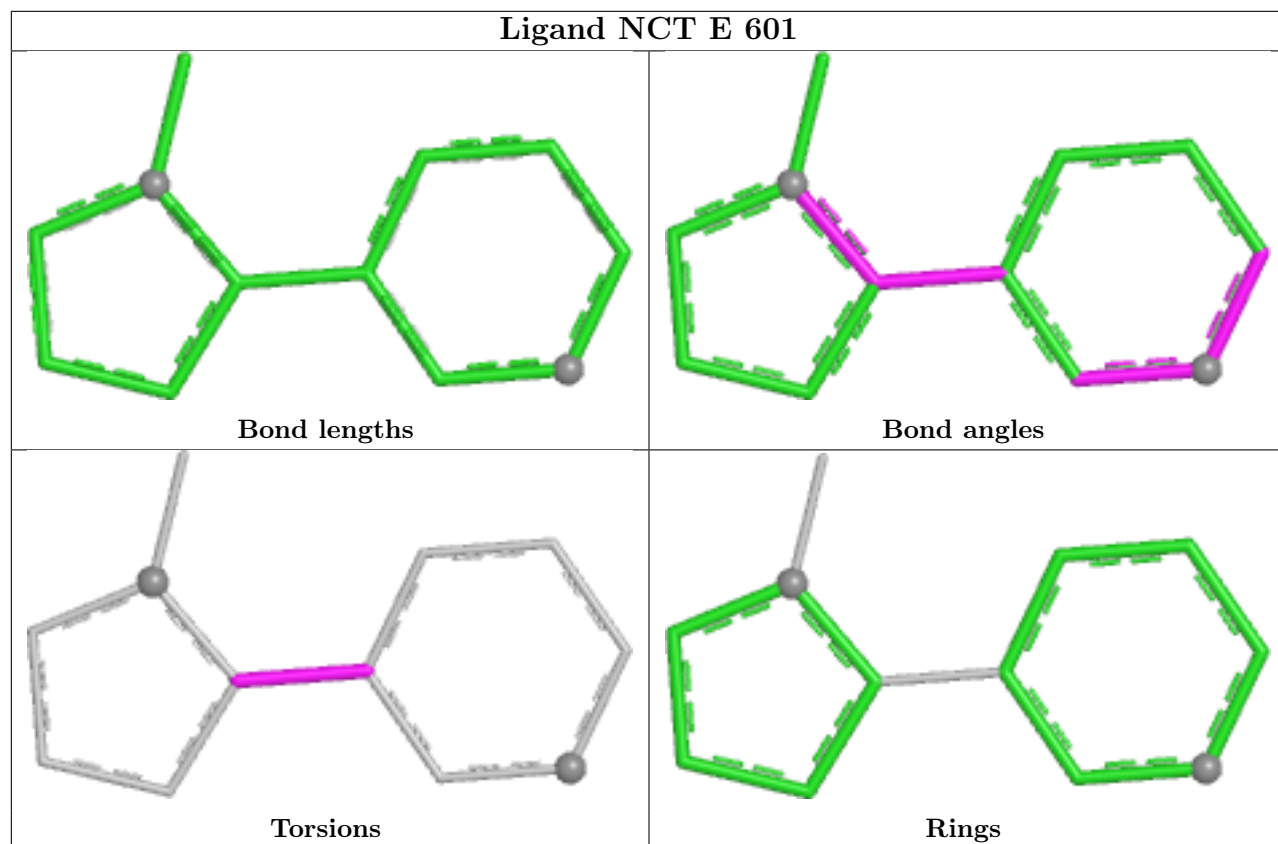
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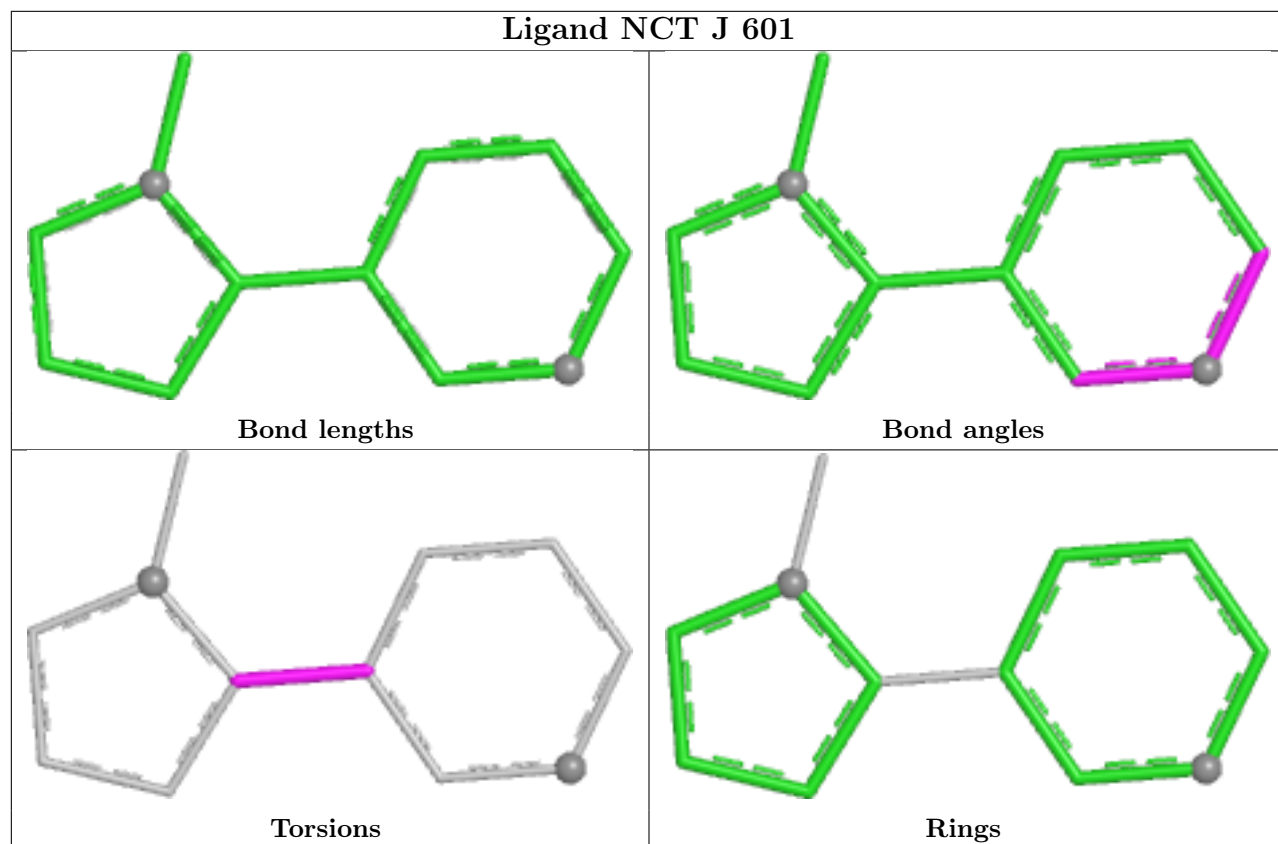
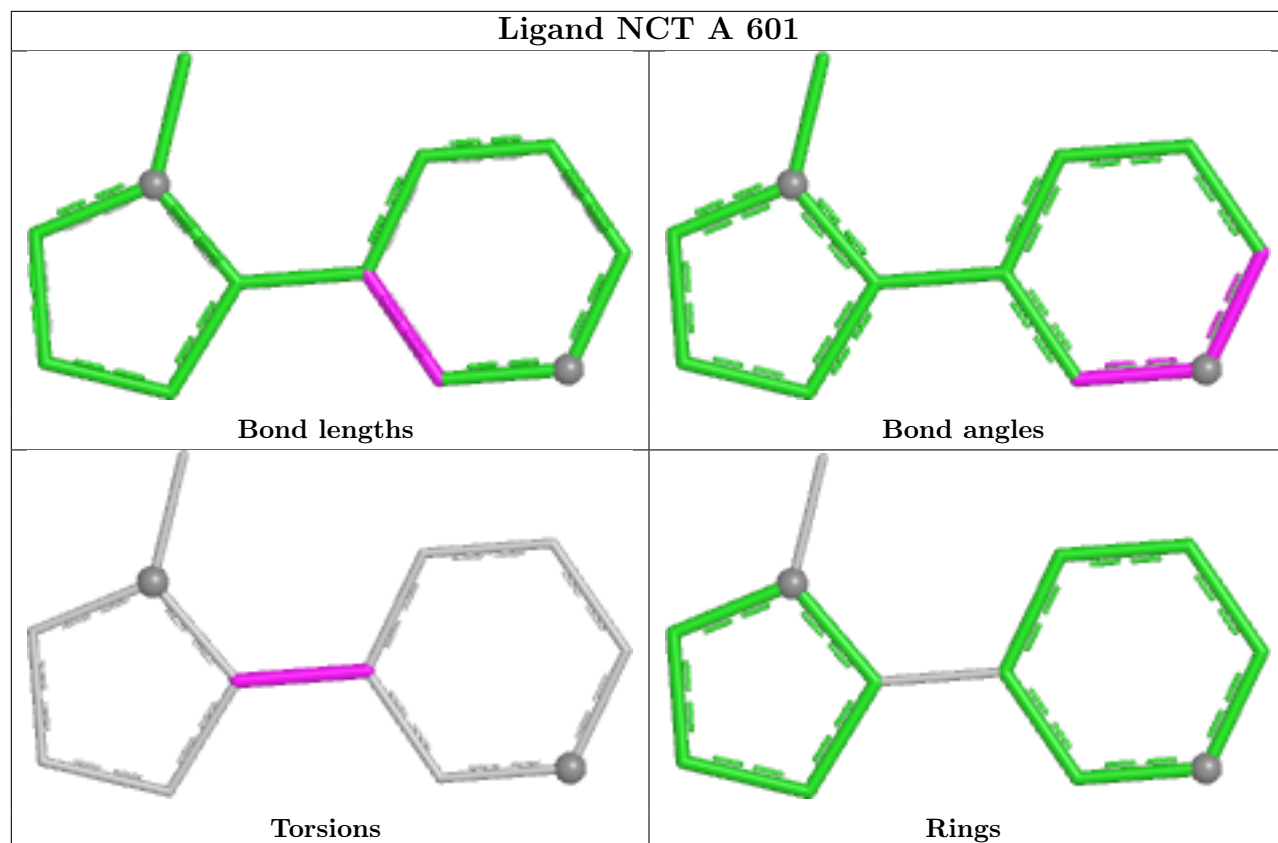


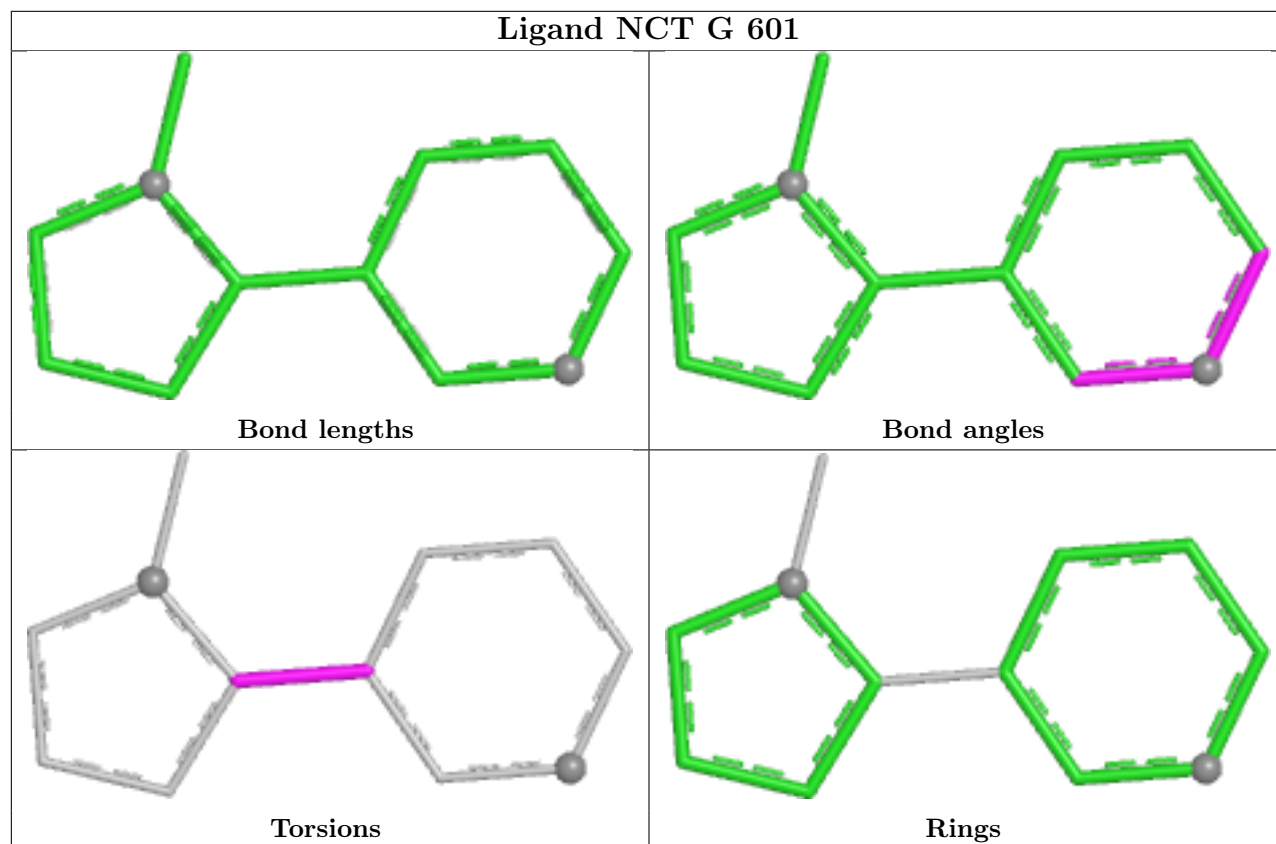
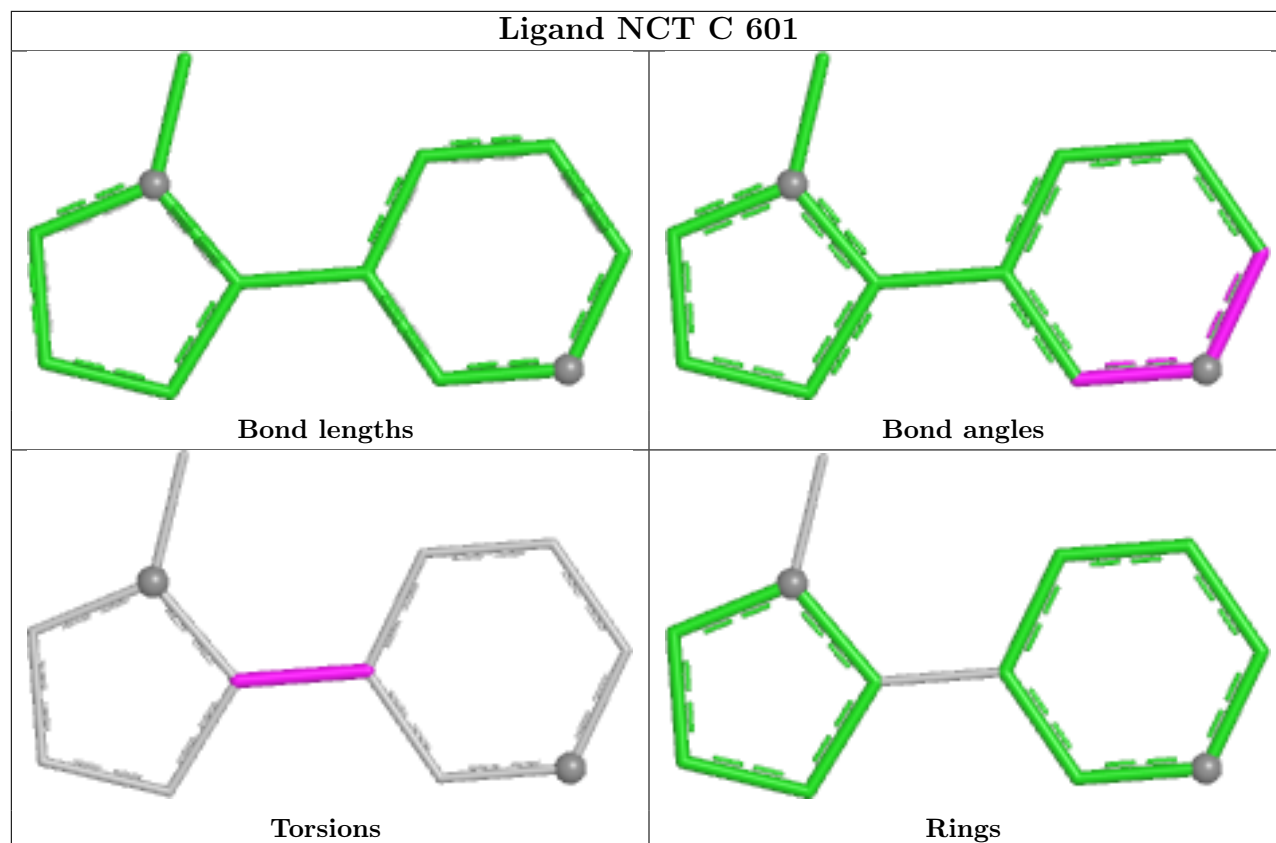
Ligand NCT F 601



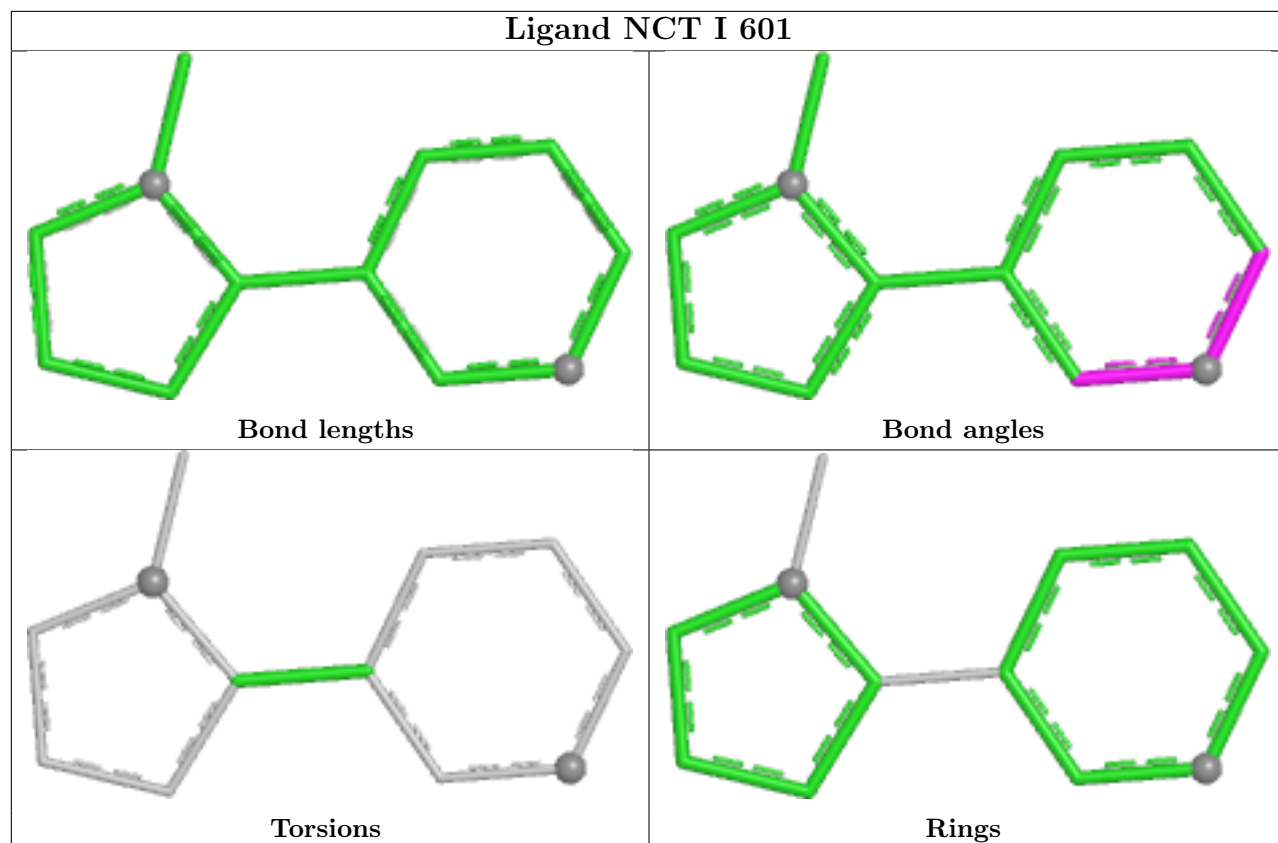
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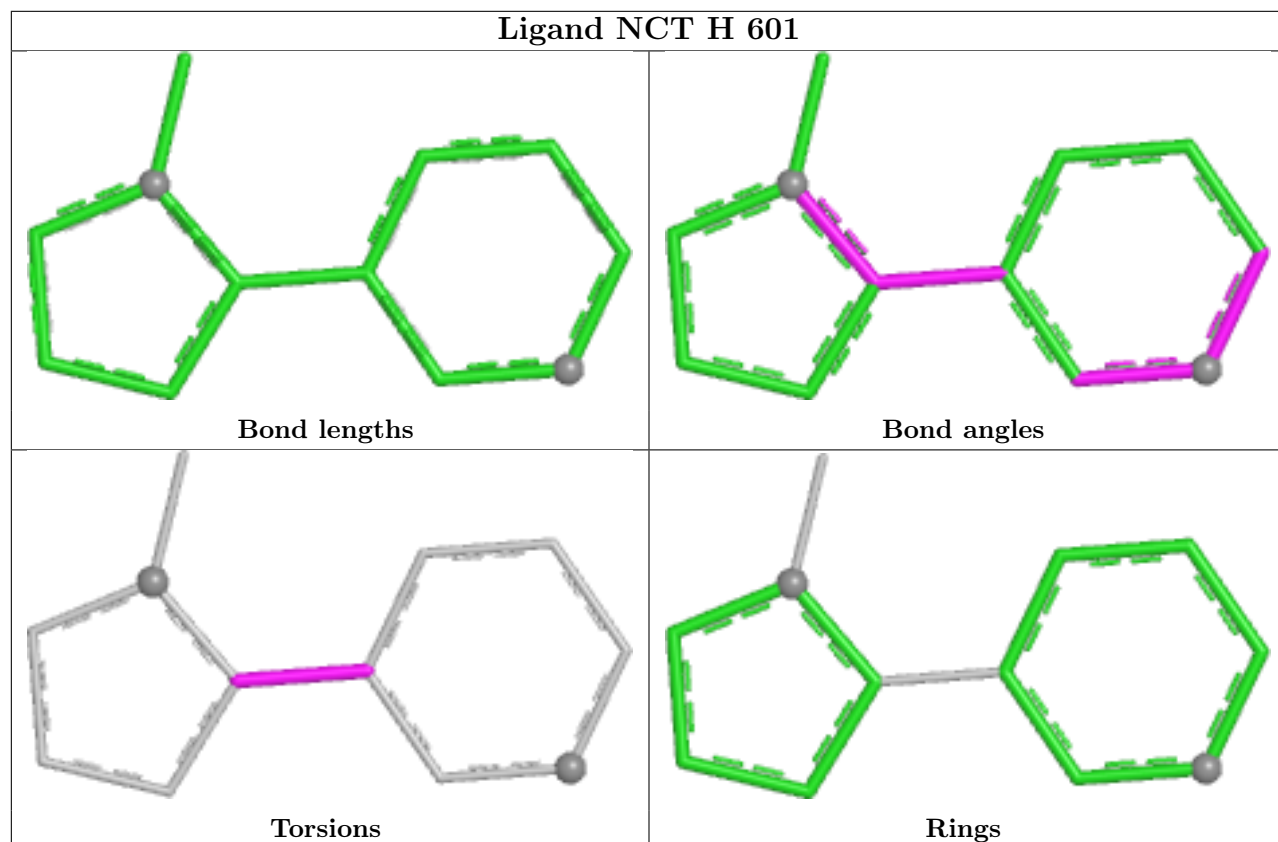




Ligand NCT I 601



Ligand NCT H 601



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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(Å ²)	Q<0.9
1	A	206/249 (82%)	0.13	7 (3%) 48 45	17, 27, 56, 101	1 (0%)
1	B	212/249 (85%)	0.32	15 (7%) 22 19	18, 28, 62, 133	1 (0%)
1	C	206/249 (82%)	0.25	9 (4%) 39 36	19, 30, 60, 102	1 (0%)
1	D	206/249 (82%)	0.28	11 (5%) 32 29	19, 29, 63, 112	3 (1%)
1	E	206/249 (82%)	0.21	8 (3%) 43 40	20, 30, 59, 95	1 (0%)
1	F	206/249 (82%)	0.36	13 (6%) 26 23	22, 33, 64, 94	1 (0%)
1	G	206/249 (82%)	0.30	11 (5%) 32 29	21, 31, 62, 91	1 (0%)
1	H	205/249 (82%)	0.28	6 (2%) 53 50	20, 30, 58, 70	1 (0%)
1	I	206/249 (82%)	0.31	13 (6%) 26 23	21, 32, 61, 100	1 (0%)
1	J	206/249 (82%)	0.40	12 (5%) 29 25	21, 33, 63, 95	1 (0%)
All	All	2065/2490 (82%)	0.29	105 (5%) 33 30	17, 31, 61, 133	12 (0%)

The worst 5 of 105 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	226	ALA	8.7
1	D	225	ARG	6.1
1	B	225	ARG	5.9
1	A	225	ARG	5.6
1	E	225	ARG	5.1

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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(Å ²)	Q<0.9
3	NAG	J	602	14/15	0.12	0.28	65,120,135,156	0
3	NAG	H	602	14/15	0.27	0.22	64,136,174,202	0
3	NAG	A	602	14/15	0.28	0.25	67,111,131,141	0
3	NAG	B	602	14/15	0.28	0.25	66,126,153,165	0
3	NAG	D	602	14/15	0.36	0.23	66,101,146,163	0
3	NAG	I	602	14/15	0.37	0.25	83,115,138,140	0
3	NAG	F	602	14/15	0.37	0.23	67,121,137,149	0
3	NAG	E	602	14/15	0.40	0.22	65,99,132,139	0
3	NAG	C	602	14/15	0.43	0.20	64,113,138,139	0
6	IPA	H	608	4/4	0.48	0.39	46,65,71,71	0
6	IPA	G	609	4/4	0.53	0.35	48,54,66,67	0
6	IPA	D	610	4/4	0.54	0.31	46,50,59,66	0
3	NAG	G	602	14/15	0.55	0.21	74,104,122,132	0
6	IPA	C	609	4/4	0.58	0.33	35,49,52,63	0
6	IPA	A	609	4/4	0.59	0.26	39,51,59,59	0
6	IPA	F	610	4/4	0.66	0.32	41,55,67,72	0
6	IPA	I	610	4/4	0.66	0.31	40,60,64,71	0
4	EDO	J	604	4/4	0.68	0.26	42,60,61,63	0
6	IPA	J	608	4/4	0.69	0.27	39,42,50,65	0
5	PO4	D	606	5/5	0.70	0.20	65,74,84,99	0
4	EDO	D	604	4/4	0.75	0.19	52,53,63,66	0
5	PO4	I	606	5/5	0.76	0.24	71,87,107,124	0
6	IPA	E	609	4/4	0.77	0.22	39,49,60,63	0
4	EDO	C	604	4/4	0.77	0.17	35,35,41,44	0
4	EDO	B	609	4/4	0.78	0.21	49,51,59,67	0
4	EDO	B	604	4/4	0.79	0.17	40,42,51,53	0
4	EDO	I	609	4/4	0.80	0.21	48,53,59,72	0
6	IPA	B	610	4/4	0.80	0.20	25,33,54,55	0
4	EDO	D	609	4/4	0.80	0.19	54,60,63,70	0
4	EDO	F	604	4/4	0.80	0.19	38,40,51,53	0
4	EDO	G	604	4/4	0.80	0.20	43,52,66,67	0
4	EDO	F	609	4/4	0.81	0.18	54,56,58,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PO4	A	605	5/5	0.81	0.16	48,93,101,120	0
4	EDO	B	603	4/4	0.82	0.15	32,35,45,46	0
4	EDO	E	607	4/4	0.82	0.21	52,61,68,75	0
5	PO4	E	606	5/5	0.83	0.20	66,74,126,137	0
5	PO4	G	606	5/5	0.84	0.19	55,57,81,81	0
4	EDO	E	604	4/4	0.84	0.15	37,45,47,53	0
4	EDO	A	604	4/4	0.84	0.15	34,37,45,48	0
5	PO4	F	606	5/5	0.86	0.15	67,71,92,126	0
5	PO4	J	606	5/5	0.86	0.21	62,63,70,110	0
4	EDO	I	604	4/4	0.86	0.20	38,45,47,49	0
4	EDO	I	607	4/4	0.87	0.20	48,52,54,66	0
4	EDO	I	608	4/4	0.87	0.16	49,51,53,58	0
4	EDO	H	606	4/4	0.87	0.16	55,55,63,64	0
4	EDO	B	608	4/4	0.88	0.13	39,48,49,52	0
2	NCT	B	601	12/12	0.88	0.13	30,37,45,46	0
4	EDO	D	608	4/4	0.88	0.15	47,47,51,59	0
5	PO4	C	606	5/5	0.88	0.15	51,61,77,119	0
4	EDO	G	607	4/4	0.88	0.15	54,57,58,60	0
4	EDO	A	607	4/4	0.89	0.12	41,41,50,51	0
4	EDO	I	603	4/4	0.90	0.13	31,39,47,48	0
4	EDO	J	607	4/4	0.90	0.13	40,47,52,57	0
4	EDO	C	608	4/4	0.90	0.16	40,53,55,61	0
5	PO4	A	606	5/5	0.90	0.17	37,65,76,83	0
4	EDO	B	607	4/4	0.90	0.12	36,46,59,59	0
4	EDO	D	607	4/4	0.90	0.14	42,51,51,55	0
4	EDO	C	607	4/4	0.90	0.16	43,47,49,62	0
4	EDO	G	603	4/4	0.91	0.11	36,42,43,47	0
5	PO4	D	605	5/5	0.91	0.13	57,59,72,95	0
2	NCT	E	601	12/12	0.91	0.10	32,37,42,43	0
4	EDO	A	608	4/4	0.91	0.12	36,48,48,49	0
4	EDO	G	608	4/4	0.91	0.15	37,49,54,58	0
4	EDO	F	607	4/4	0.91	0.12	45,47,50,63	0
4	EDO	F	608	4/4	0.91	0.17	47,62,66,67	0
2	NCT	C	601	12/12	0.91	0.11	30,34,39,41	0
5	PO4	B	606	5/5	0.91	0.15	59,72,111,114	0
2	NCT	A	601	12/12	0.92	0.10	24,31,44,45	0
2	NCT	F	601	12/12	0.92	0.10	35,42,51,52	0
5	PO4	G	605	5/5	0.92	0.14	45,49,52,59	0
2	NCT	I	601	12/12	0.92	0.12	32,42,49,54	0
5	PO4	H	605	5/5	0.92	0.14	70,78,80,82	0
4	EDO	E	608	4/4	0.92	0.14	45,46,53,65	0
5	PO4	J	605	5/5	0.92	0.12	49,63,81,84	0

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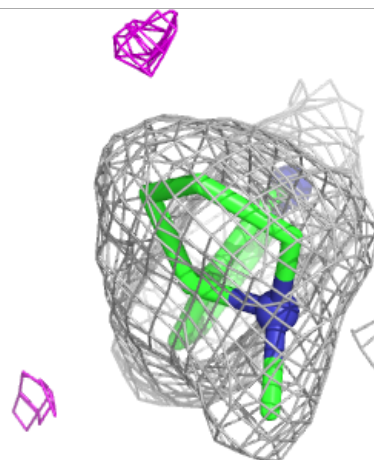
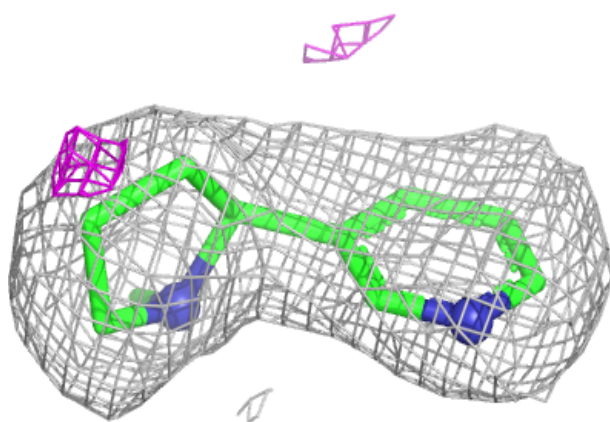
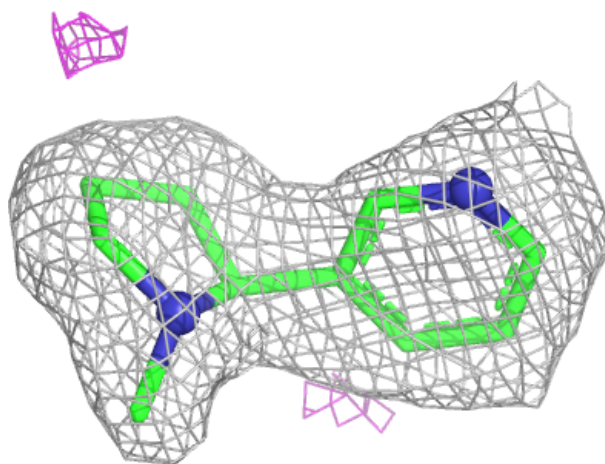
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	H	607	4/4	0.92	0.14	38,48,54,60	0
4	EDO	F	603	4/4	0.92	0.12	32,42,45,48	0
4	EDO	J	603	4/4	0.93	0.10	30,36,41,44	0
2	NCT	H	601	12/12	0.93	0.10	35,45,50,51	0
2	NCT	J	601	12/12	0.93	0.10	34,42,50,51	0
4	EDO	D	603	4/4	0.94	0.09	28,29,31,35	0
4	EDO	E	603	4/4	0.94	0.10	32,34,35,36	0
5	PO4	H	604	5/5	0.94	0.10	44,55,61,88	0
4	EDO	H	603	4/4	0.94	0.08	30,35,36,38	0
5	PO4	I	605	5/5	0.94	0.10	56,62,79,84	0
5	PO4	E	605	5/5	0.94	0.12	47,49,67,74	0
4	EDO	A	603	4/4	0.94	0.09	29,35,38,40	0
5	PO4	F	605	5/5	0.94	0.09	48,60,65,78	0
5	PO4	C	605	5/5	0.94	0.12	52,53,69,86	0
2	NCT	D	601	12/12	0.95	0.09	26,33,40,47	0
4	EDO	C	603	4/4	0.95	0.11	24,29,35,36	0
5	PO4	B	605	5/5	0.95	0.11	53,61,72,80	0
2	NCT	G	601	12/12	0.96	0.07	29,35,38,39	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.

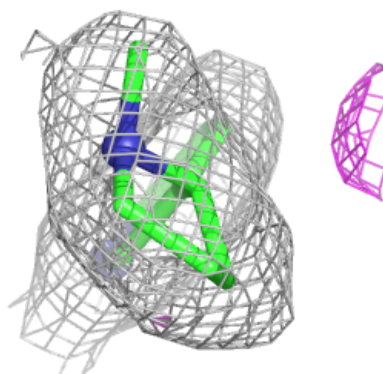
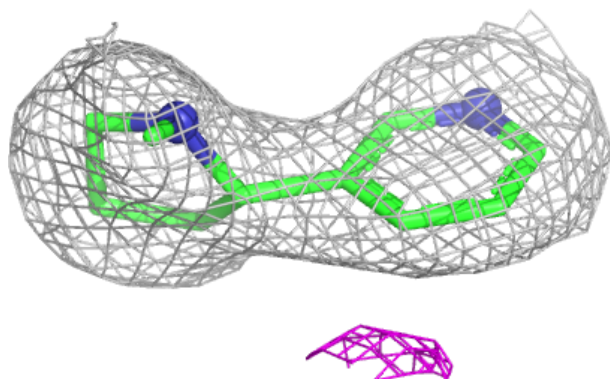
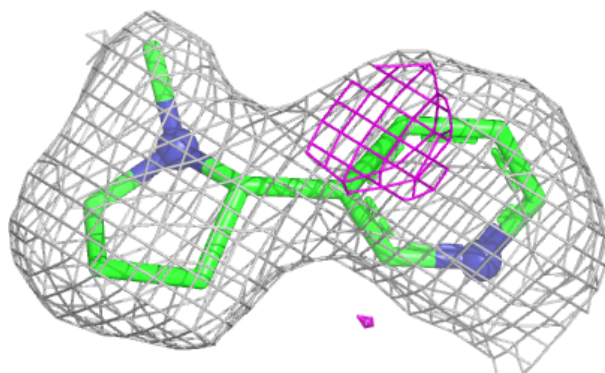
Electron density around NCT B 601:

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

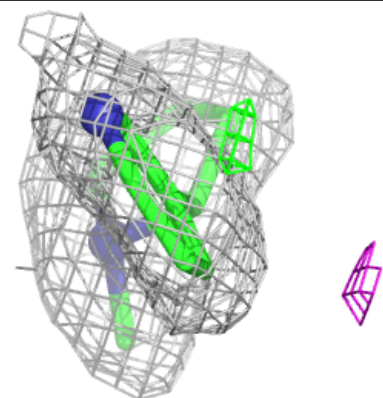
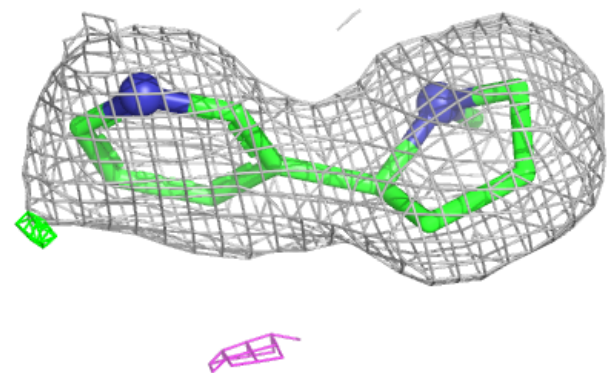
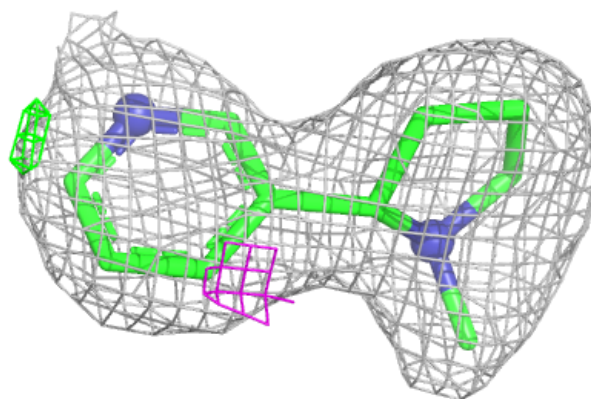


Electron density around NCT E 601:

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

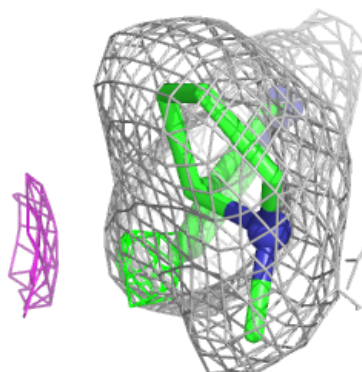
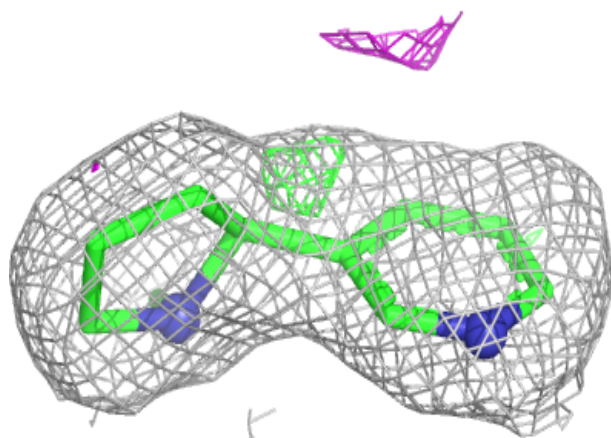
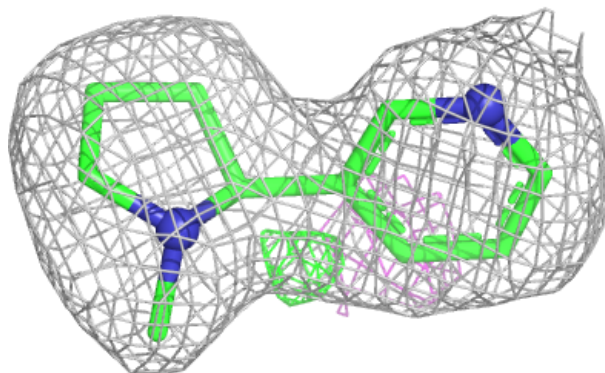
**Electron density around NCT C 601:**

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and green (positive)



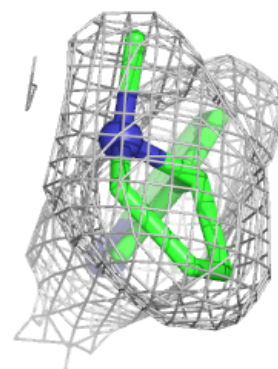
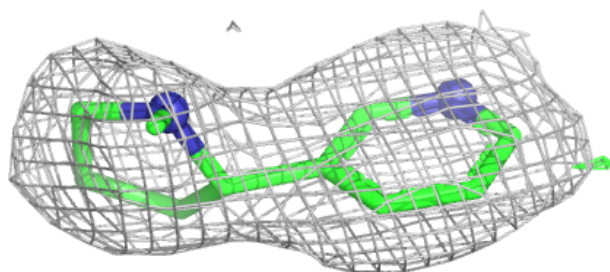
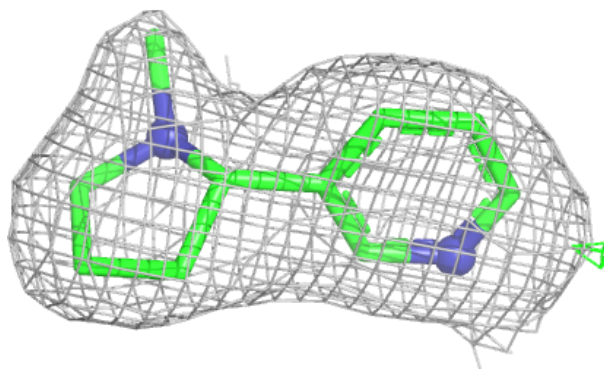
Electron density around NCT A 601:

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and green (positive)

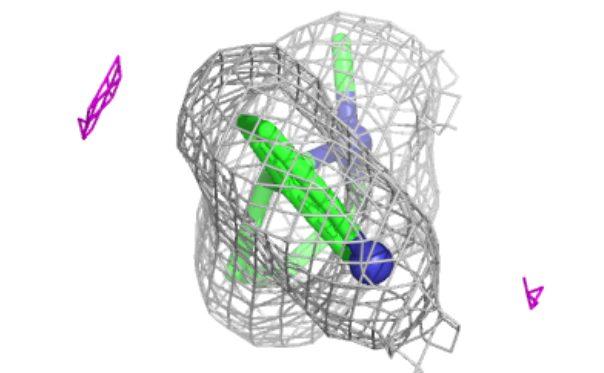
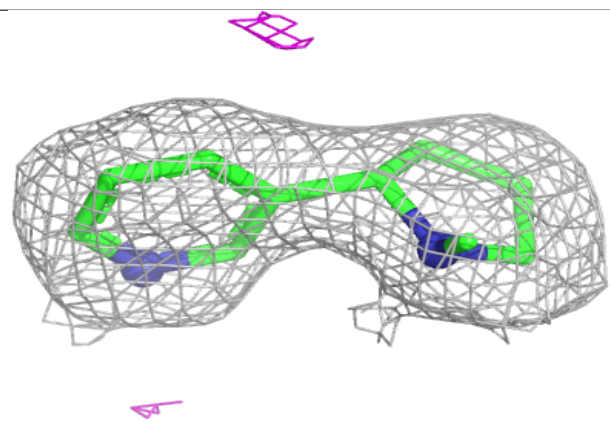
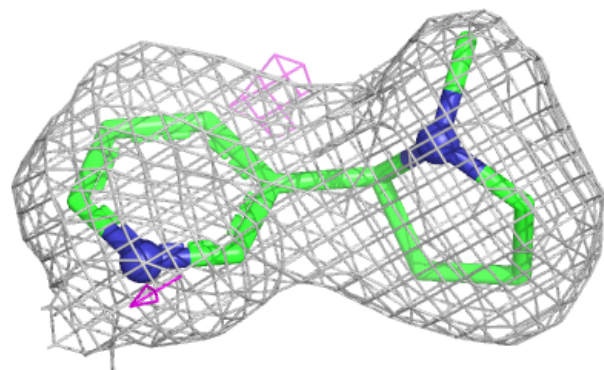


Electron density around NCT F 601:

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

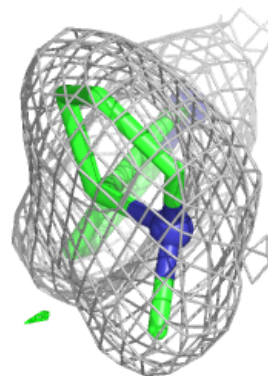
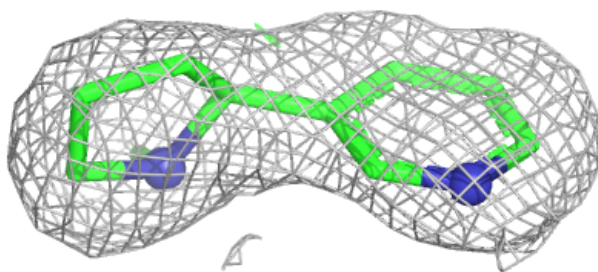
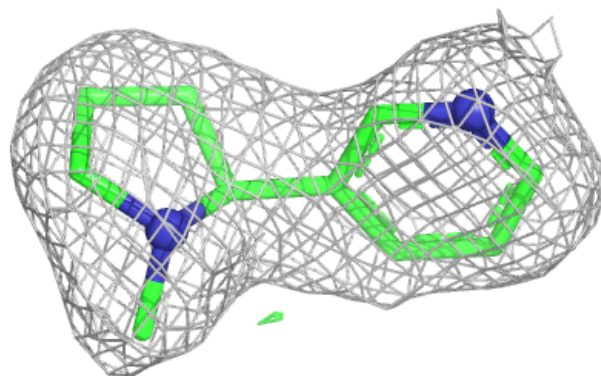
**Electron density around NCT I 601:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
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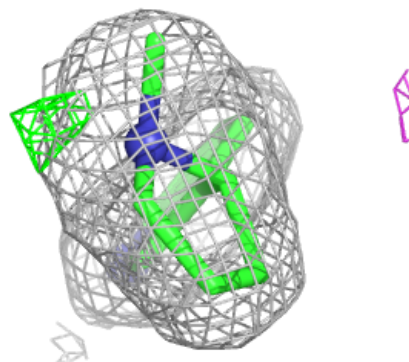
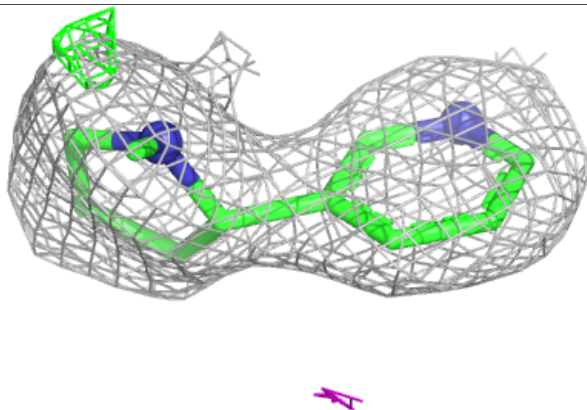
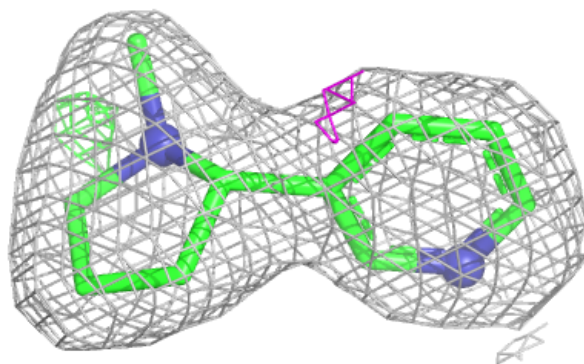


Electron density around NCT H 601:

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

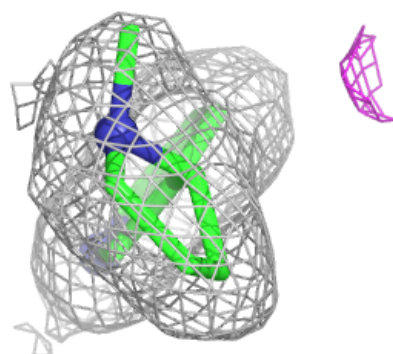
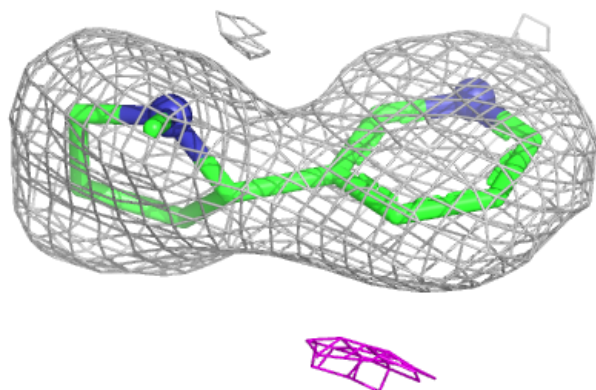
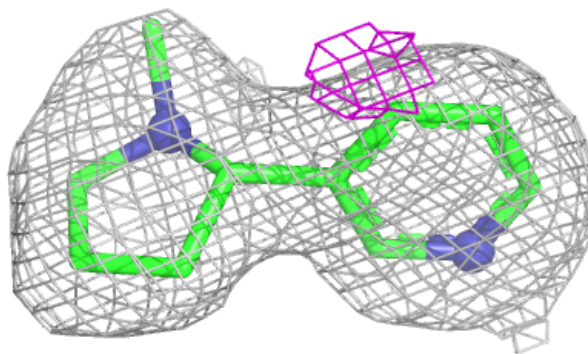
**Electron density around NCT J 601:**

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and green (positive)

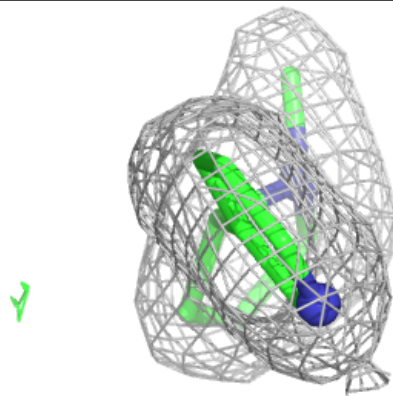
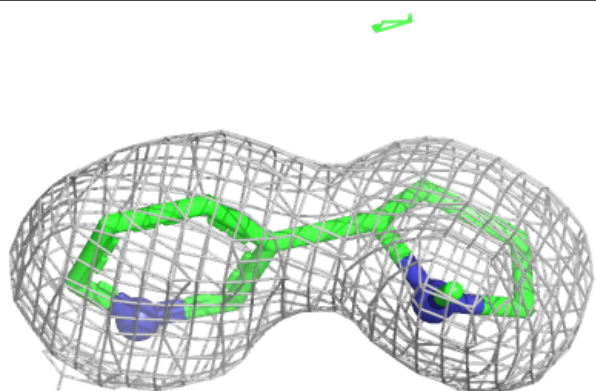
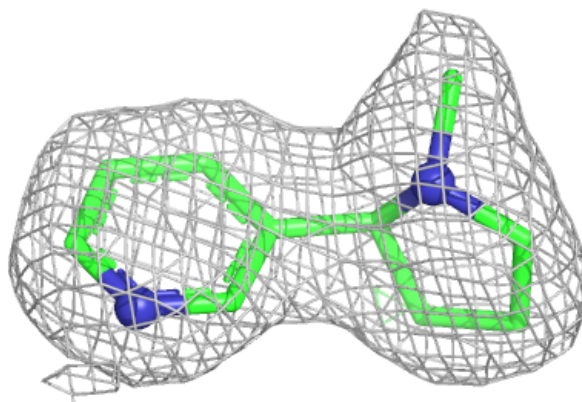


Electron density around NCT D 601:

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

**Electron density around NCT G 601:**

$2mF_o-DF_c$ (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.