



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2024 – 11:56 AM EDT

PDB ID : 6PME
Title : TRK-A IN COMPLEX WITH LIGAND
Authors : Subramanian, G.; Brown, D.G.
Deposited on : 2019-07-01
Resolution : 3.00 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

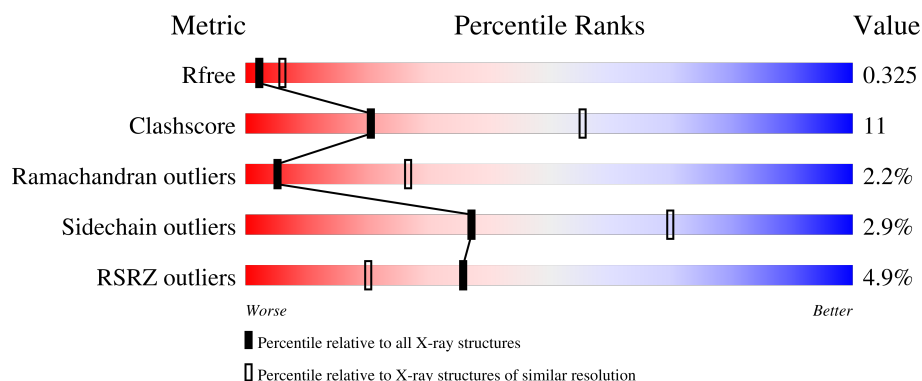
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	164625	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	311	
1	B	311	
1	C	311	

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
4	SRT	B	803	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6712 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.

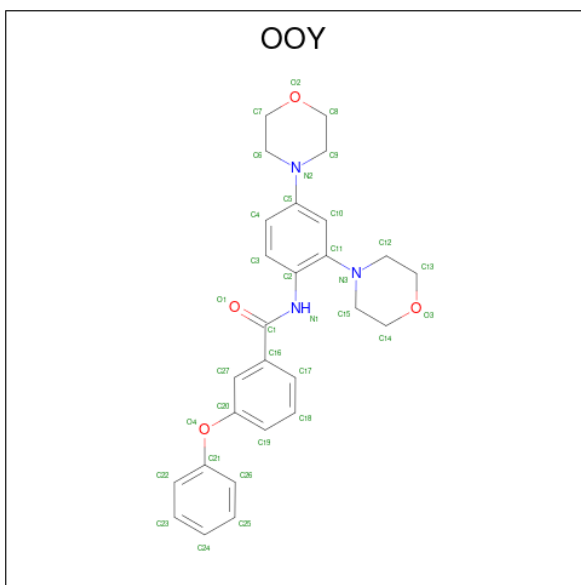
- Molecule 1 is a protein called High affinity nerve growth factor receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	268	Total	C	N	O	P	S	32	0	0
			2164	1380	391	376	1	16			
1	B	271	Total	C	N	O	P	S	21	1	0
			2202	1404	397	384	1	16			
1	C	274	Total	C	N	O	P	S	21	1	0
			2220	1416	404	383	1	16			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

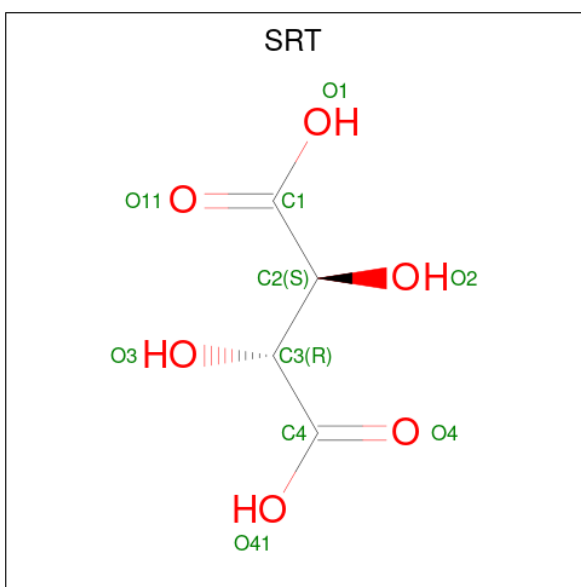
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is N-[2,4-bis(morpholin-4-yl)phenyl]-3-phenoxybenzamide (three-letter code: OOO) (formula: C₂₇H₂₉N₃O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			34	27	3	4		
3	B	1	Total	C	N	O	0	0
			34	27	3	4		
3	C	1	Total	C	N	O	0	0
			34	27	3	4		

- Molecule 4 is S,R MESO-TARTARIC ACID (three-letter code: SRT) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	4	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			10	4	6		

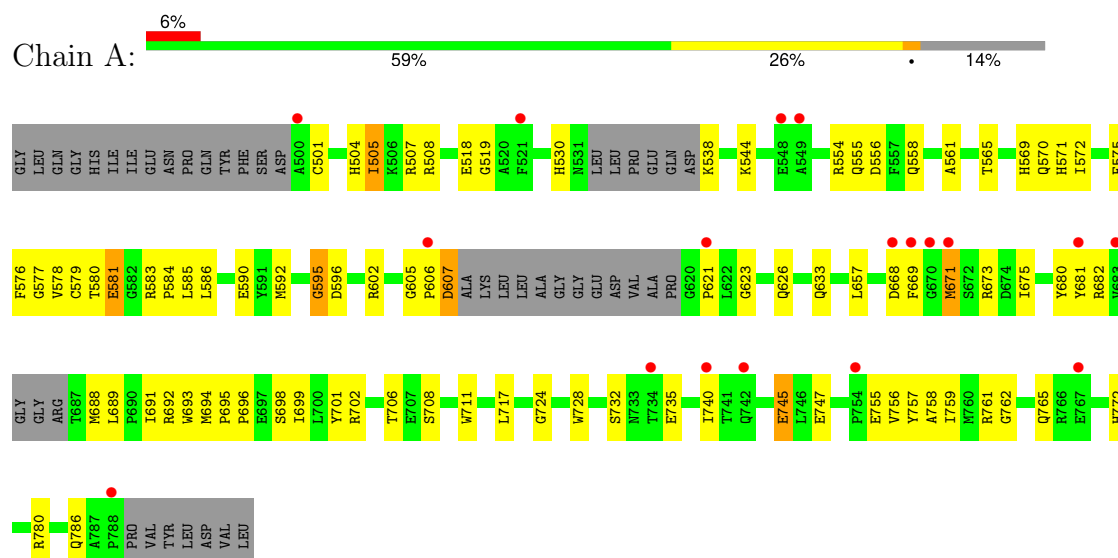
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	O	0	0
			1	1		

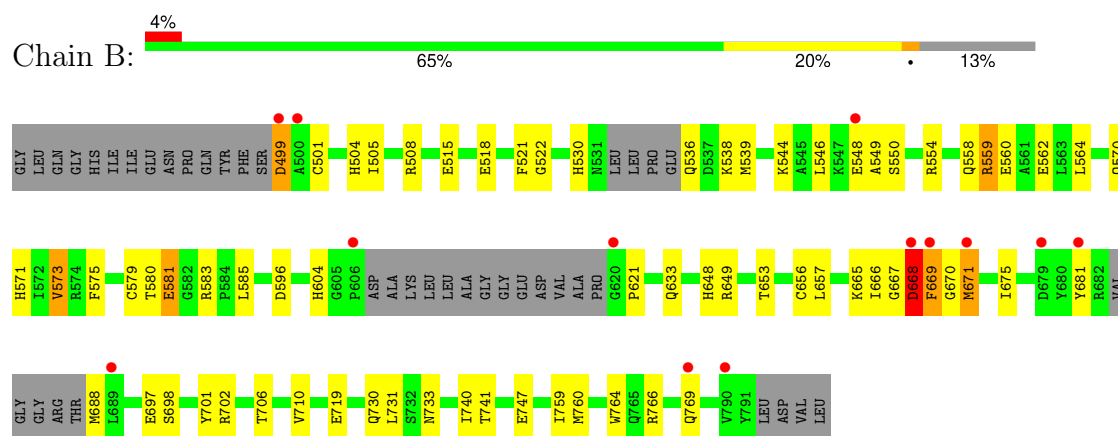
3 Residue-property plots

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: High affinity nerve growth factor receptor

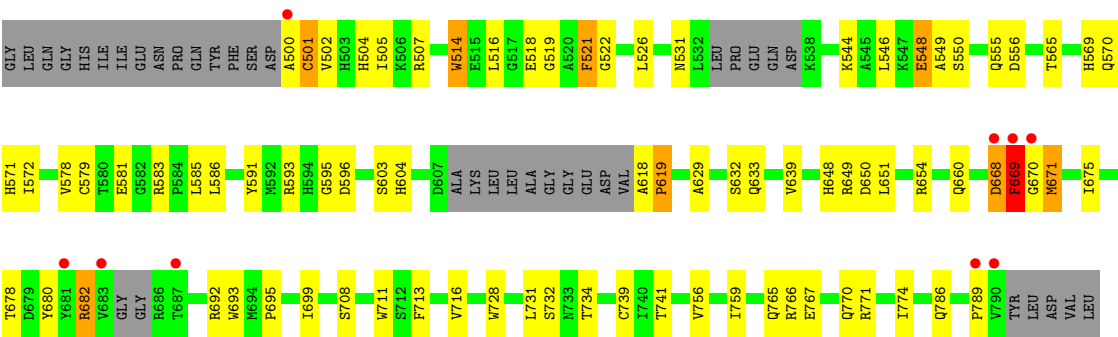


- Molecule 1: High affinity nerve growth factor receptor



- Molecule 1: High affinity nerve growth factor receptor





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	131.44Å 152.09Å 156.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.51 – 3.00 48.51 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.8 (48.51-3.00) 94.8 (48.51-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.258 , 0.315 0.263 , 0.325	Depositor DCC
R_{free} test set	572 reflections (1.90%)	wwPDB-VP
Wilson B-factor (Å ²)	68.1	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 27.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.002 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6712	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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: ZN, SEP, OOO, SRT

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	1.02	9/2205 (0.4%)	1.16	9/2976 (0.3%)
1	B	1.01	5/2245 (0.2%)	1.24	11/3031 (0.4%)
1	C	1.12	5/2263 (0.2%)	1.41	14/3056 (0.5%)
All	All	1.05	19/6713 (0.3%)	1.28	34/9063 (0.4%)

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	B	0	4
1	C	0	2
All	All	0	6

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	668	ASP	C-N	-25.45	0.75	1.34
1	C	669	PHE	CB-CG	20.87	1.86	1.51
1	C	682	ARG	NE-CZ	19.68	1.58	1.33
1	C	521	PHE	CB-CG	19.52	1.84	1.51
1	B	669	PHE	CB-CG	-9.83	1.34	1.51

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	669	PHE	CB-CG-CD2	-29.68	100.02	120.80
1	C	669	PHE	CB-CG-CD1	29.20	141.24	120.80
1	B	668	ASP	O-C-N	-20.97	89.15	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	521	PHE	CB-CG-CD2	-20.33	106.57	120.80
1	B	669	PHE	CB-CG-CD2	-19.45	107.19	120.80

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	499	ASP	Peptide
1	B	522	GLY	Peptide
1	B	668	ASP	Mainchain
1	B	669	PHE	Sidechain
1	C	522	GLY	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	2164	0	2145	49	0
1	B	2202	0	2170	53	0
1	C	2220	0	2208	47	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	34	0	0	1	0
3	B	34	0	0	0	0
3	C	34	0	0	2	0
4	A	10	0	4	0	0
4	B	10	0	4	0	0
5	C	1	0	0	0	0
All	All	6712	0	6531	144	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 11.

The worst 5 of 144 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:A:691:ILE:HA	1:A:694:MET:HE3	1.51	0.92
1:A:755:GLU:O	1:A:758:ALA:HB3	1.77	0.84
1:B:573:VAL:HG21	1:B:667:GLY:HA2	1.58	0.84
1:A:584:PRO:O	1:A:586:LEU:CD1	2.27	0.83
1:B:521:PHE:O	1:B:546:LEU:HD12	1.79	0.83

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	259/311 (83%)	234 (90%)	21 (8%)	4 (2%)	8	36
1	B	263/311 (85%)	241 (92%)	17 (6%)	5 (2%)	6	31
1	C	266/311 (86%)	240 (90%)	18 (7%)	8 (3%)	3	20
All	All	788/933 (84%)	715 (91%)	56 (7%)	17 (2%)	5	27

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	621	PRO
1	A	668	ASP
1	B	573	VAL
1	B	668	ASP
1	C	548	GLU

5.3.2 Protein sidechains [i](#)

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	226/260 (87%)	219 (97%)	7 (3%)	35	68
1	B	230/260 (88%)	223 (97%)	7 (3%)	36	69
1	C	232/260 (89%)	226 (97%)	6 (3%)	41	72
All	All	688/780 (88%)	668 (97%)	20 (3%)	37	70

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	596	ASP
1	C	678	THR
1	C	734	THR
1	C	732	SER
1	A	786	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	742	GLN
1	B	769	GLN
1	C	770	GLN
1	C	742	GLN
1	C	769	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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
1	SEP	A	677	1	8,9,10	0.62	0	7,12,14	0.89	0
1	SEP	C	677	1	8,9,10	0.59	0	7,12,14	0.92	0
1	SEP	B	677	1	8,9,10	0.67	0	7,12,14	1.08	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
1	SEP	A	677	1	-	1/6/8/10	-
1	SEP	C	677	1	-	2/6/8/10	-
1	SEP	B	677	1	-	1/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	677	SEP	N-CA-CB-OG
1	C	677	SEP	C-CA-CB-OG
1	A	677	SEP	N-CA-CB-OG
1	B	677	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 for Mogul analysis.

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	SRT	B	803	-	9,9,9	0.97	0	12,12,12	1.51	2 (16%)
3	OOY	C	802	-	38,38,38	0.63	1 (2%)	50,51,51	1.10	3 (6%)
3	OOY	A	802	-	38,38,38	0.72	2 (5%)	50,51,51	0.93	3 (6%)
4	SRT	A	803	-	9,9,9	1.15	1 (11%)	12,12,12	0.87	0
3	OOY	B	802	-	38,38,38	0.71	1 (2%)	50,51,51	0.99	4 (8%)

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	SRT	B	803	-	-	12/12/12/12	-
3	OOY	C	802	-	-	2/20/36/36	0/5/5/5
3	OOY	A	802	-	-	2/20/36/36	0/5/5/5
4	SRT	A	803	-	-	7/12/12/12	-
3	OOY	B	802	-	-	1/20/36/36	0/5/5/5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	OOY	C2-C11	2.18	1.43	1.40
3	B	802	OOY	C2-C11	2.15	1.42	1.40
4	A	803	SRT	O41-C4	-2.14	1.23	1.30
3	C	802	OOY	C4-C5	2.05	1.43	1.39
3	A	802	OOY	C4-C5	2.00	1.43	1.39

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	802	OOY	C10-C11-N3	-3.13	118.03	122.59
4	B	803	SRT	O11-C1-C2	-3.03	113.55	121.62
3	A	802	OOY	C15-N3-C11	2.72	122.65	116.19
3	A	802	OOY	C12-N3-C11	2.69	122.57	116.19
3	B	802	OOY	C15-N3-C12	2.59	117.39	111.57

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

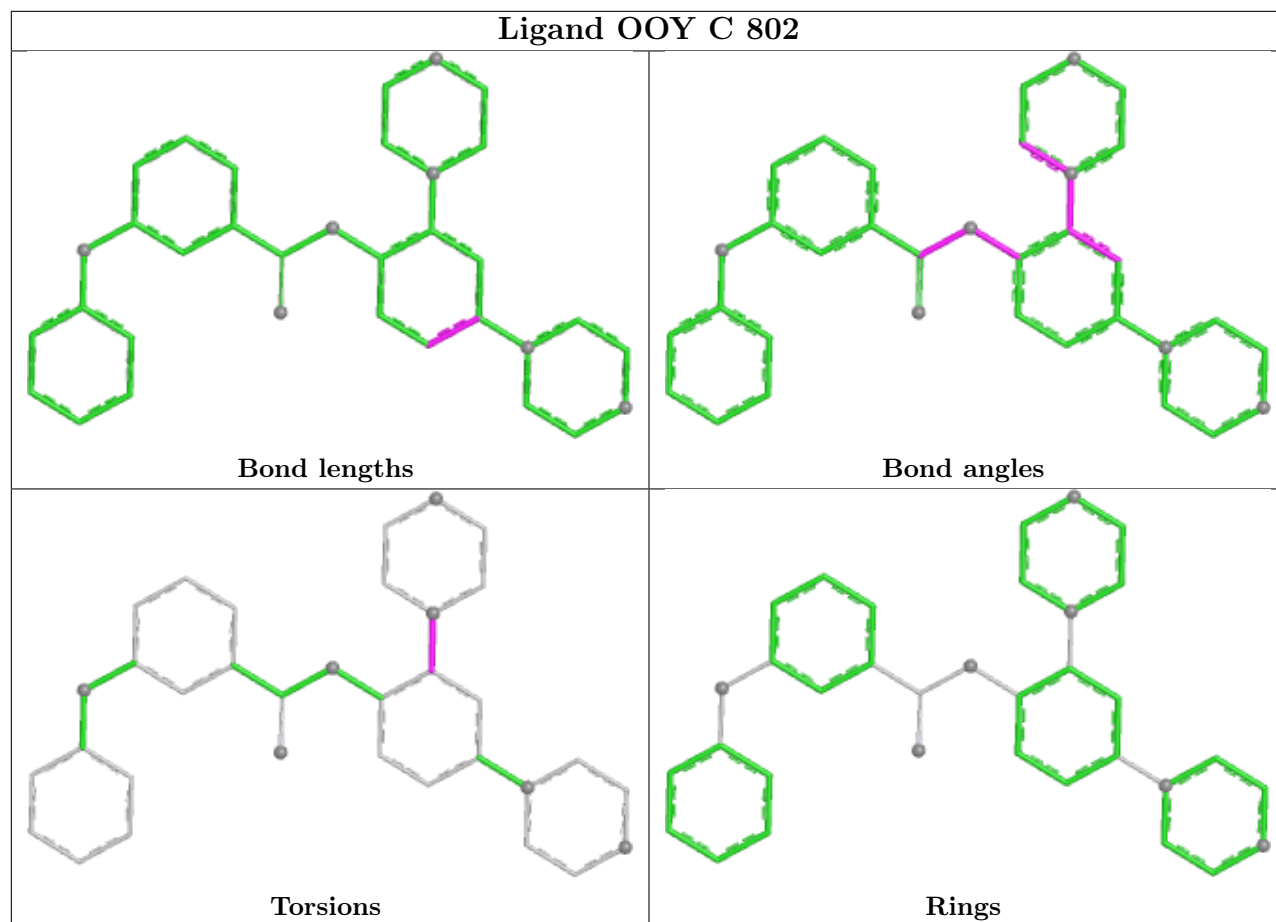
Mol	Chain	Res	Type	Atoms
4	B	803	SRT	O1-C1-C2-C3
4	B	803	SRT	O11-C1-C2-C3
4	B	803	SRT	O3-C3-C4-O4
4	B	803	SRT	O3-C3-C4-O41
4	B	803	SRT	O2-C2-C3-O3

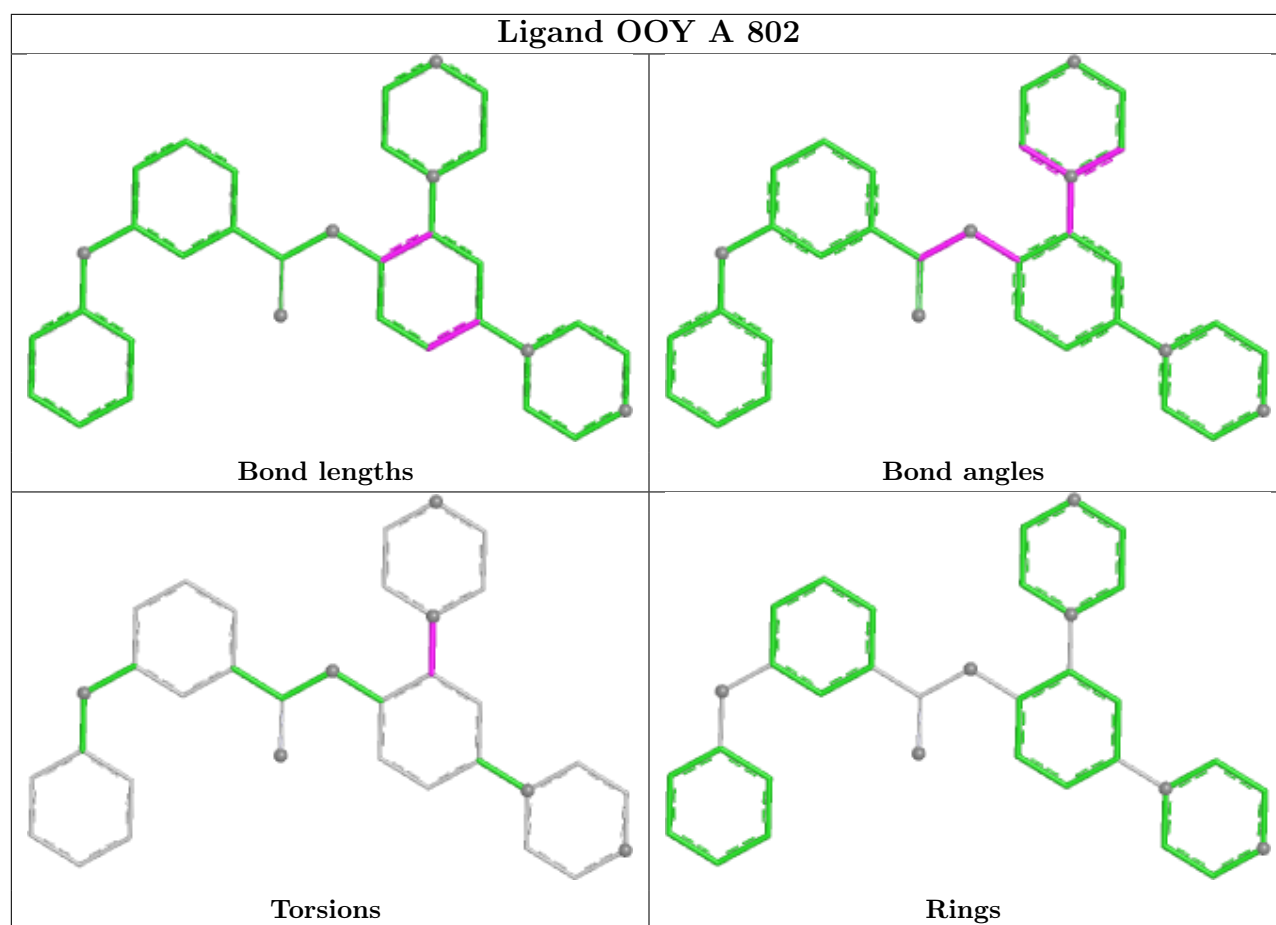
There are no ring outliers.

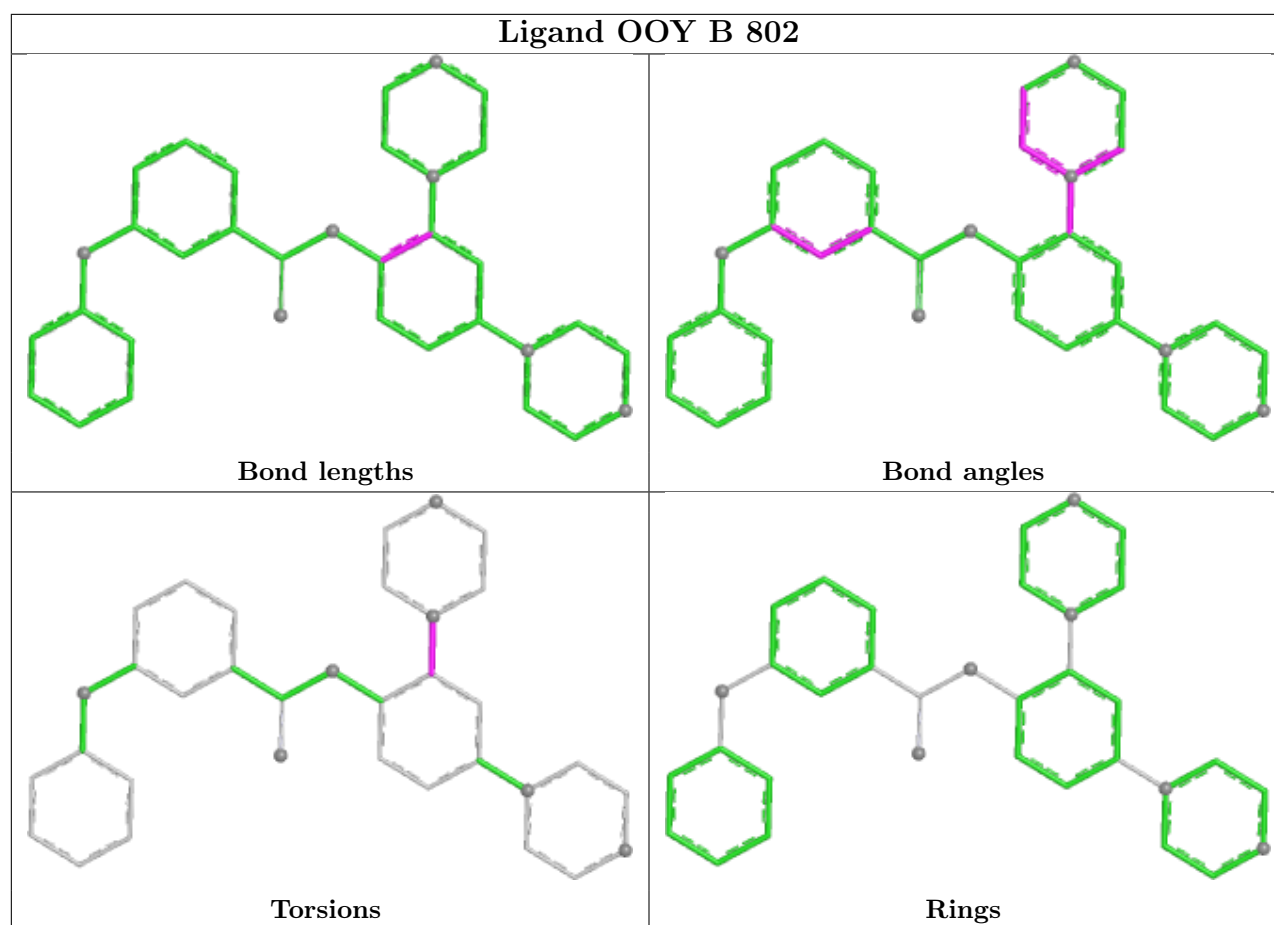
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	802	OOY	2	0
3	A	802	OOY	1	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.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	670:GLY	C	671:MET	N	1.19
1	B	668:ASP	C	669:PHE	N	0.75

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	267/311 (85%)	0.44	18 (6%) 25 14	24, 41, 69, 104	9 (3%)
1	B	269/311 (86%)	0.37	13 (4%) 36 21	6, 44, 71, 96	5 (1%)
1	C	273/311 (87%)	0.28	9 (3%) 49 29	17, 44, 72, 101	6 (2%)
All	All	809/933 (86%)	0.36	40 (4%) 36 20	6, 43, 71, 104	20 (2%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	669	PHE	16.9
1	A	669	PHE	5.2
1	C	790	VAL	4.9
1	C	670	GLY	4.4
1	C	500	ALA	3.8

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	SEP	A	677	10/11	0.47	0.17	71,81,94,95	0
1	SEP	C	677	10/11	0.73	0.18	63,69,84,84	0
1	SEP	B	677	10/11	0.75	0.17	70,84,102,105	0

6.3 Carbohydrates [i](#)

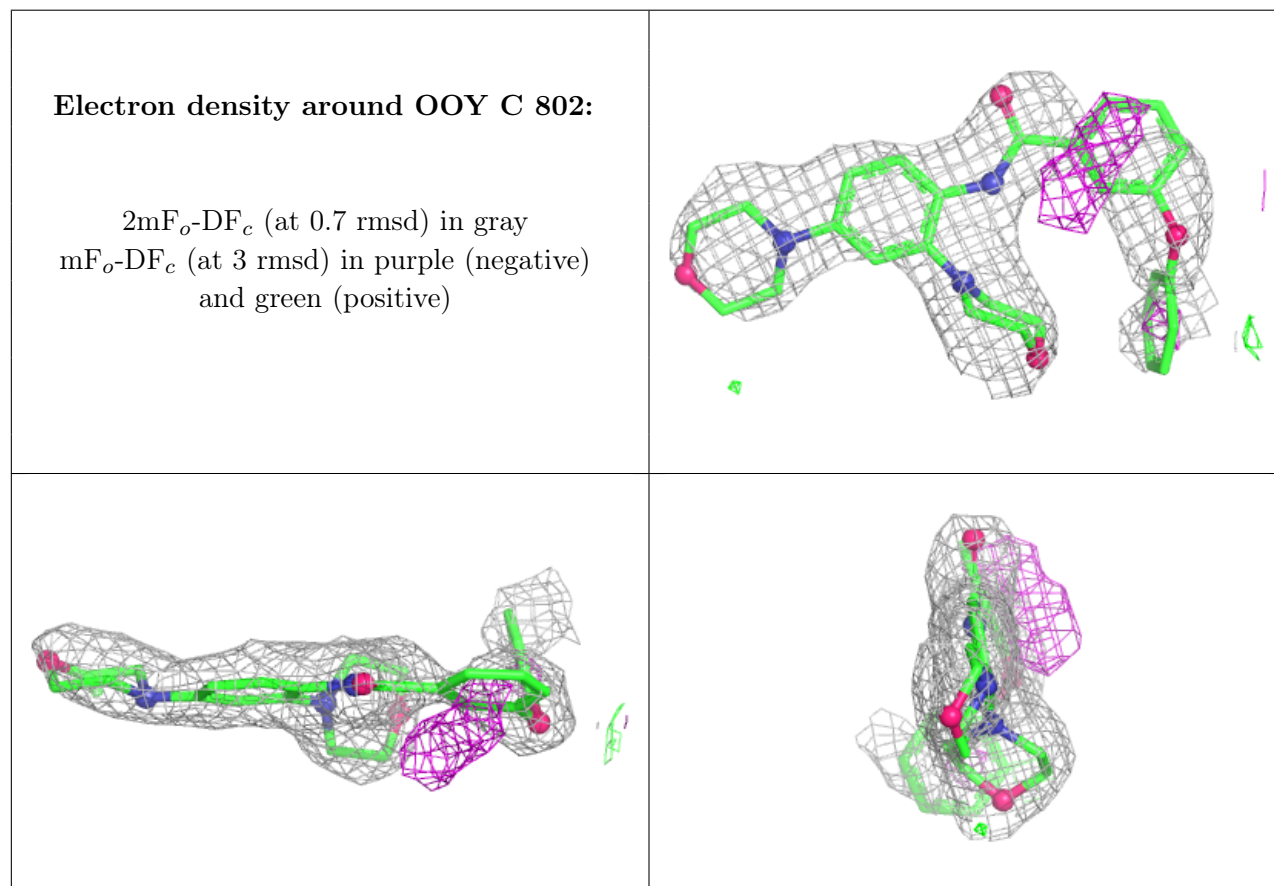
There are no monosaccharides in this entry.

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.

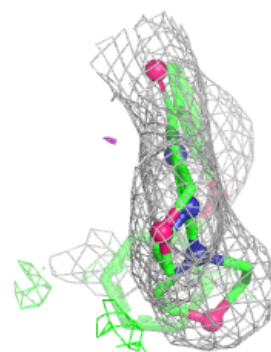
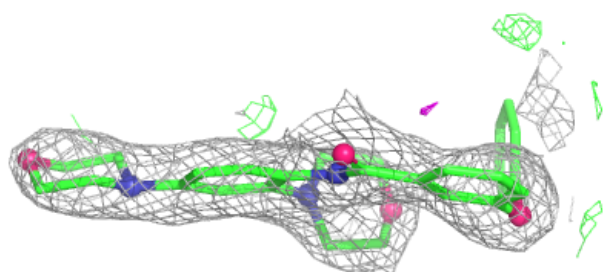
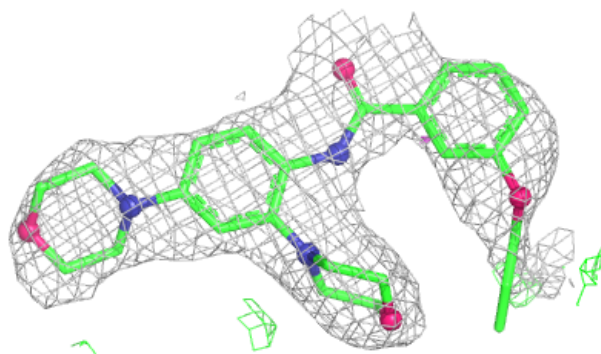
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SRT	A	803	10/10	0.76	0.17	80,95,103,105	0
3	OOY	C	802	34/34	0.85	0.20	44,60,80,83	0
3	OOY	A	802	34/34	0.88	0.15	46,49,80,83	0
3	OOY	B	802	34/34	0.88	0.16	47,57,80,87	0
4	SRT	B	803	10/10	0.90	0.19	42,64,78,98	0
2	ZN	A	801	1/1	0.98	0.05	46,46,46,46	0
2	ZN	C	801	1/1	0.99	0.04	48,48,48,48	0
2	ZN	B	801	1/1	1.00	0.05	49,49,49,49	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.

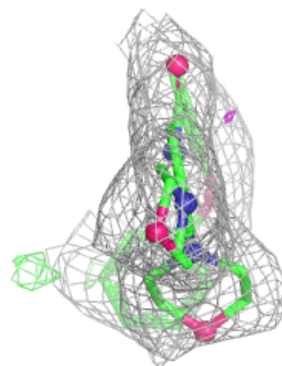
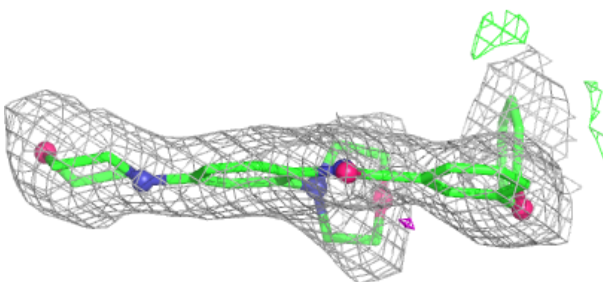
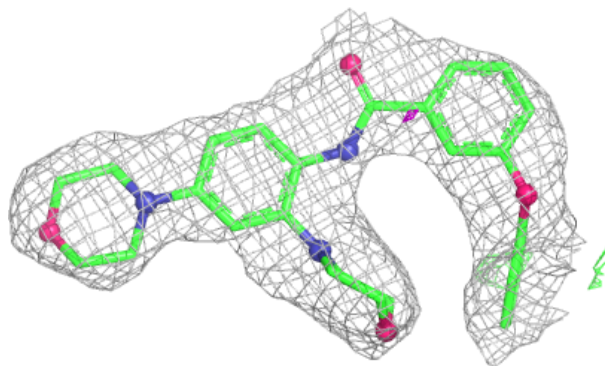


Electron density around OOO A 802:

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

**Electron density around OOO B 802:**

$2mF_o-DF_c$ (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.