Full wwPDB X-ray Structure Validation Report (i)

Jun 17, 2024 – 09:20 AM EDT

PDB ID	:	3RGN
Title	:	Crystal structure of spin-labeled BtuB W371R1
Authors	:	Freed, D.M.; Horanyi, P.S.; Wiener, M.C.; Cafiso, D.S.
Deposited on	:	2011-04-08
Resolution	:	2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 (i) 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 (i)) were used in the production of this report:

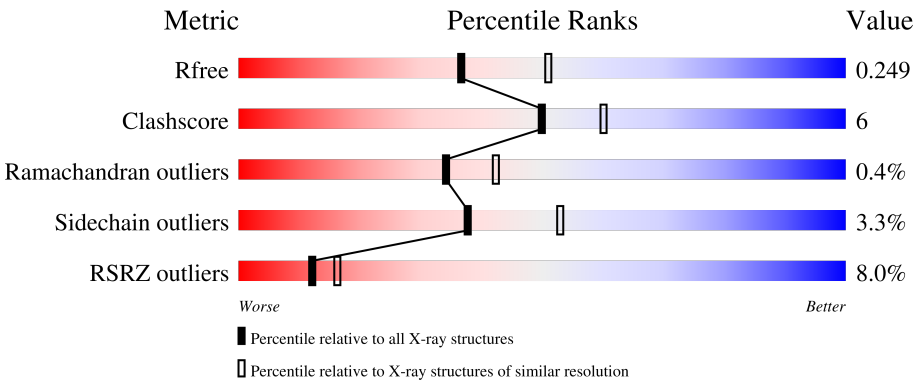
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	594	7% 80% 11% • 8%

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
2	C8E	A	803	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	C8E	A	806	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4612 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.

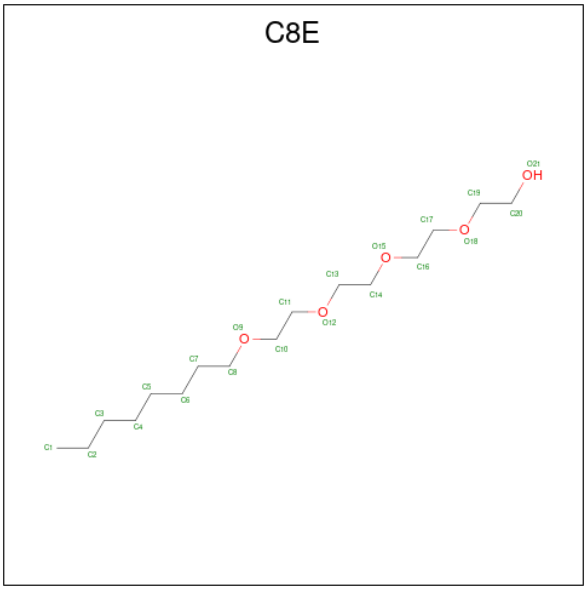
- Molecule 1 is a protein called Vitamin B12 transporter BtuB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	549	4320	2720	743	854	3	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	371	CYS	TRP	ENGINEERED MUTATION	UNP P06129

- Molecule 2 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: $C_{16}H_{34}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	21	16	5	0	0
			Total	C	O		
2	A	1	21	16	5	0	0

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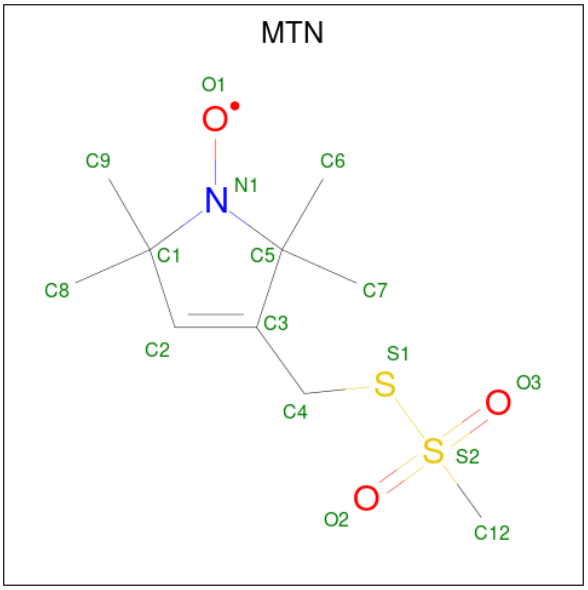
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
2	A	1	21	16	5		0	0
			Total	C	O			
2	A	1	21	16	5		0	0
			Total	C	O			
2	A	1	21	16	5		0	0
			Total	C	O			
2	A	1	21	16	5		0	0
			Total	C	O			
2	A	1	21	16	5		0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	3	3	3	0	0

- Molecule 4 is S-[(1-oxyl-2,2,5,5-tetramethyl-2,5-dihydro-1H-pyrrol-3-yl)methyl] methanesulf onothioate (three-letter code: MTN) (formula: $C_{10}H_{18}NO_3S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	12	9	1	1	1	0	0

- Molecule 5 is water.

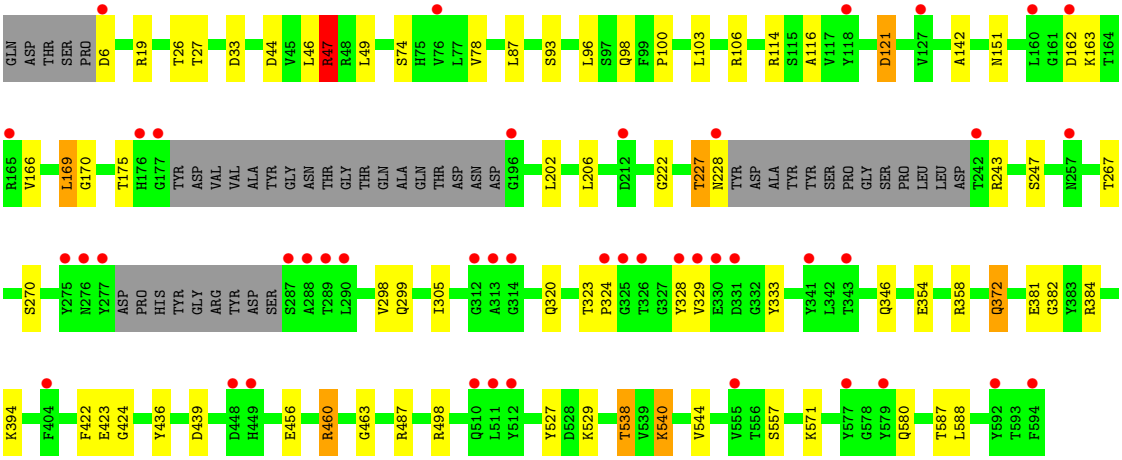
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	130	130	130	0	0

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: Vitamin B12 transporter BtuB

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	81.68Å 81.68Å 227.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.38 – 2.30 33.38 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.2 (33.38-2.30) 95.1 (33.38-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.17 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.220 , 0.250 0.218 , 0.249	Depositor DCC
R_{free} test set	1911 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	57.6	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4612	wwPDB-VP
Average B, all atoms (Å^2)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, C8E, MTN

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	1.12	6/4422 (0.1%)	1.01	15/6015 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	372	GLN	CB-CG	-9.17	1.27	1.52
1	A	354	GLU	CD-OE2	7.57	1.33	1.25
1	A	354	GLU	CG-CD	5.95	1.60	1.51
1	A	320	GLN	CD-OE1	5.56	1.36	1.24
1	A	423	GLU	CB-CG	-5.35	1.42	1.52
1	A	381	GLU	CB-CG	5.16	1.61	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	384	ARG	NE-CZ-NH2	-9.90	115.35	120.30
1	A	121	ASP	CB-CG-OD2	-8.18	110.94	118.30
1	A	121	ASP	CB-CG-OD1	7.80	125.32	118.30
1	A	487	ARG	NE-CZ-NH2	-6.89	116.85	120.30
1	A	498	ARG	NE-CZ-NH1	6.89	123.74	120.30
1	A	384	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	A	460	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	47	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	498	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	456	GLU	C-N-CA	-5.99	109.73	122.30
1	A	439	ASP	CB-CG-OD2	5.56	123.30	118.30
1	A	33	ASP	CB-CG-OD2	-5.38	113.46	118.30
1	A	6	ASP	CB-CG-OD1	-5.22	113.60	118.30
1	A	106	ARG	NE-CZ-NH2	-5.04	117.78	120.30
1	A	47	ARG	NE-CZ-NH2	-5.02	117.79	120.30

There are no chirality outliers.

There are no planarity outliers.

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	4320	0	4073	41	0
2	A	147	0	238	11	0
3	A	3	0	0	0	0
4	A	12	0	15	1	0
5	A	130	0	0	1	0
All	All	4612	0	4326	51	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 6.

All (51) 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)
2:A:802:C8E:H13	2:A:802:C8E:H82	1.51	0.93
2:A:802:C8E:H13	2:A:802:C8E:H52	1.50	0.92
1:A:166:VAL:HG22	1:A:206:LEU:CD1	2.01	0.91
1:A:544:VAL:HG23	1:A:571:LYS:HE2	1.57	0.85
1:A:529:LYS:NZ	1:A:538:THR:HG22	1.91	0.84
1:A:166:VAL:HG22	1:A:206:LEU:HD12	1.58	0.84
2:A:802:C8E:H82	2:A:802:C8E:C1	2.17	0.73
1:A:529:LYS:HZ3	1:A:538:THR:HG22	1.58	0.67
1:A:544:VAL:CG2	1:A:571:LYS:HE2	2.26	0.66
2:A:802:C8E:H52	2:A:802:C8E:C1	2.26	0.58
2:A:806:C8E:H61	4:A:598:MTN:H71	1.85	0.58
1:A:422:PHE:CG	2:A:801:C8E:H11	2.39	0.57
1:A:527:TYR:CE1	1:A:540:LYS:HG3	2.39	0.57
1:A:169:LEU:C	1:A:169:LEU:HD23	2.25	0.56
1:A:299:GLN:O	1:A:299:GLN:HG3	2.05	0.56
1:A:329:VAL:CG1	1:A:333:TYR:HE2	2.19	0.55
1:A:305:ILE:HD13	1:A:305:ILE:N	2.22	0.53
2:A:802:C8E:H13	2:A:802:C8E:C8	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:587:THR:HG22	1:A:588:LEU:N	2.24	0.52
1:A:114:ARG:HA	1:A:372:GLN:OE1	2.12	0.50
1:A:267:THR:HG23	1:A:298:VAL:HG22	1.92	0.49
2:A:802:C8E:H13	2:A:802:C8E:C5	2.33	0.49
1:A:116:ALA:O	1:A:358:ARG:HB2	2.14	0.48
1:A:529:LYS:HZ1	1:A:538:THR:HG22	1.77	0.48
1:A:19:ARG:HE	1:A:26:THR:CG2	2.27	0.47
1:A:329:VAL:HG11	1:A:333:TYR:CE2	2.49	0.47
1:A:323:THR:HG23	1:A:324:PRO:HD2	1.95	0.47
1:A:162:ASP:O	1:A:163:LYS:HB2	2.15	0.47
2:A:802:C8E:H171	2:A:802:C8E:H11	1.98	0.46
1:A:222:GLY:HA2	1:A:247:SER:O	2.16	0.46
1:A:98:GLN:HE22	1:A:227:THR:HG21	1.80	0.46
1:A:100:PRO:HG2	1:A:103:LEU:HD12	1.98	0.46
1:A:166:VAL:HG22	1:A:206:LEU:HD11	1.95	0.45
1:A:142:ALA:HA	1:A:151:ASN:O	2.17	0.45
1:A:329:VAL:HG11	1:A:333:TYR:HE2	1.82	0.45
1:A:529:LYS:CE	1:A:538:THR:HG22	2.47	0.44
2:A:802:C8E:C1	2:A:802:C8E:H171	2.47	0.44
1:A:78:VAL:HG11	1:A:96:LEU:HD21	2.00	0.44
1:A:227:THR:HG23	1:A:243:ARG:HB3	2.00	0.44
1:A:44:ASP:HA	1:A:47:ARG:HG2	1.99	0.44
2:A:803:C8E:H22	2:A:805:C8E:H132	1.99	0.44
1:A:529:LYS:NZ	1:A:538:THR:CG2	2.72	0.44
1:A:382:GLY:O	1:A:424:GLY:HA2	2.19	0.43
1:A:27:THR:HG21	1:A:49:LEU:HD22	2.00	0.43
1:A:19:ARG:HE	1:A:26:THR:HG23	1.84	0.42
1:A:169:LEU:HD23	1:A:170:GLY:N	2.34	0.42
1:A:436:TYR:CZ	1:A:463:GLY:HA3	2.54	0.42
1:A:74:SER:HB2	1:A:394:LYS:HE2	2.02	0.41
1:A:460:ARG:HG3	5:A:725:HOH:O	2.22	0.40
1:A:19:ARG:NH2	1:A:26:THR:O	2.53	0.40
1:A:587:THR:CG2	1:A:588:LEU:N	2.83	0.40

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	541/594 (91%)	522 (96%)	17 (3%)	2 (0%)	34 42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	ASP
1	A	87	LEU

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	453/495 (92%)	438 (97%)	15 (3%)	38 53

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	47	ARG
1	A	93	SER
1	A	169	LEU
1	A	175	THR
1	A	202	LEU
1	A	227	THR
1	A	228	ASN
1	A	270	SER

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Mol	Chain	Res	Type
1	A	328	TYR
1	A	346	GLN
1	A	538	THR
1	A	540	LYS
1	A	557	SER
1	A	580	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 3 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
2	C8E	A	802	-	20,20,20	0.60	0	19,19,19	1.00	1 (5%)
2	C8E	A	806	-	20,20,20	0.54	0	19,19,19	0.54	0
2	C8E	A	805	-	20,20,20	0.63	0	19,19,19	0.81	1 (5%)
2	C8E	A	804	-	20,20,20	0.43	0	19,19,19	0.69	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	C8E	A	801	-	20,20,20	0.49	0	19,19,19	0.83	0
2	C8E	A	803	-	20,20,20	0.46	0	19,19,19	0.51	0
2	C8E	A	800	-	20,20,20	0.34	0	19,19,19	0.66	0
4	MTN	A	598	1	9,12,16	2.01	4 (44%)	11,20,27	1.95	4 (36%)

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	C8E	A	802	-	-	7/18/18/18	-
2	C8E	A	806	-	-	13/18/18/18	-
2	C8E	A	805	-	-	10/18/18/18	-
2	C8E	A	804	-	-	6/18/18/18	-
2	C8E	A	801	-	-	9/18/18/18	-
2	C8E	A	803	-	-	13/18/18/18	-
2	C8E	A	800	-	-	7/18/18/18	-
4	MTN	A	598	1	-	0/0/25/29	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	598	MTN	C1-C2	3.45	1.54	1.50
4	A	598	MTN	C5-N1	-3.27	1.46	1.50
4	A	598	MTN	C2-C3	2.33	1.35	1.32
4	A	598	MTN	C4-S1	2.21	1.86	1.82

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	598	MTN	C2-C1-N1	3.69	101.97	99.43
4	A	598	MTN	C7-C5-C3	-3.14	106.97	112.17
4	A	598	MTN	C3-C4-S1	2.81	117.76	111.01
2	A	802	C8E	C10-O9-C8	-2.18	103.70	113.26
4	A	598	MTN	C8-C1-C2	-2.11	110.76	112.77
2	A	805	C8E	O15-C16-C17	2.10	119.93	110.35

There are no chirality outliers.

All (65) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	806	C8E	O12-C13-C14-O15
2	A	803	C8E	O15-C16-C17-O18
2	A	801	C8E	O12-C13-C14-O15
2	A	803	C8E	O9-C10-C11-O12
2	A	801	C8E	O15-C16-C17-O18
2	A	802	C8E	O12-C13-C14-O15
2	A	804	C8E	O15-C16-C17-O18
2	A	800	C8E	O9-C10-C11-O12
2	A	802	C8E	C6-C7-C8-O9
2	A	805	C8E	C6-C7-C8-O9
2	A	803	C8E	O18-C19-C20-O21
2	A	806	C8E	C5-C6-C7-C8
2	A	806	C8E	O9-C10-C11-O12
2	A	803	C8E	C4-C5-C6-C7
2	A	803	C8E	C6-C7-C8-O9
2	A	801	C8E	C16-C17-O18-C19
2	A	806	C8E	C4-C5-C6-C7
2	A	804	C8E	O18-C19-C20-O21
2	A	805	C8E	O18-C19-C20-O21
2	A	802	C8E	O9-C10-C11-O12
2	A	801	C8E	C5-C6-C7-C8
2	A	805	C8E	C5-C6-C7-C8
2	A	806	C8E	C11-C10-O9-C8
2	A	806	C8E	C2-C3-C4-C5
2	A	803	C8E	C5-C6-C7-C8
2	A	804	C8E	C2-C3-C4-C5
2	A	803	C8E	O12-C13-C14-O15
2	A	804	C8E	O12-C13-C14-O15
2	A	805	C8E	C1-C2-C3-C4
2	A	801	C8E	C1-C2-C3-C4
2	A	805	C8E	O15-C16-C17-O18
2	A	801	C8E	O9-C10-C11-O12
2	A	806	C8E	C3-C4-C5-C6
2	A	806	C8E	O15-C16-C17-O18
2	A	800	C8E	C14-C13-O12-C11
2	A	805	C8E	C17-C16-O15-C14
2	A	805	C8E	C10-C11-O12-C13
2	A	800	C8E	C20-C19-O18-C17
2	A	800	C8E	C17-C16-O15-C14
2	A	802	C8E	C14-C13-O12-C11
2	A	806	C8E	C14-C13-O12-C11
2	A	801	C8E	O18-C19-C20-O21
2	A	806	C8E	C17-C16-O15-C14

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Mol	Chain	Res	Type	Atoms
2	A	802	C8E	C2-C3-C4-C5
2	A	804	C8E	C10-C11-O12-C13
2	A	803	C8E	C13-C14-O15-C16
2	A	802	C8E	C20-C19-O18-C17
2	A	801	C8E	C4-C5-C6-C7
2	A	806	C8E	O18-C19-C20-O21
2	A	800	C8E	C11-C10-O9-C8
2	A	800	C8E	C13-C14-O15-C16
2	A	806	C8E	C16-C17-O18-C19
2	A	803	C8E	C3-C4-C5-C6
2	A	803	C8E	C10-C11-O12-C13
2	A	805	C8E	O12-C13-C14-O15
2	A	803	C8E	C1-C2-C3-C4
2	A	806	C8E	C13-C14-O15-C16
2	A	804	C8E	C7-C8-O9-C10
2	A	805	C8E	C4-C5-C6-C7
2	A	802	C8E	C17-C16-O15-C14
2	A	803	C8E	C14-C13-O12-C11
2	A	800	C8E	C2-C3-C4-C5
2	A	805	C8E	C20-C19-O18-C17
2	A	801	C8E	C10-C11-O12-C13
2	A	803	C8E	C17-C16-O15-C14

There are no ring outliers.

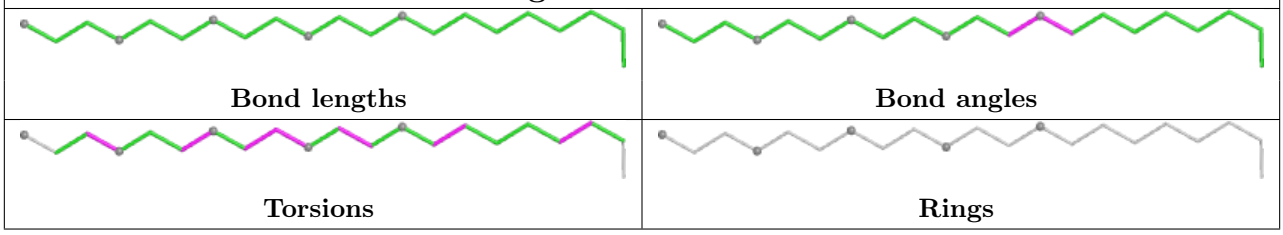
6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	802	C8E	8	0
2	A	806	C8E	1	0
2	A	805	C8E	1	0
2	A	801	C8E	1	0
2	A	803	C8E	1	0
4	A	598	MTN	1	0

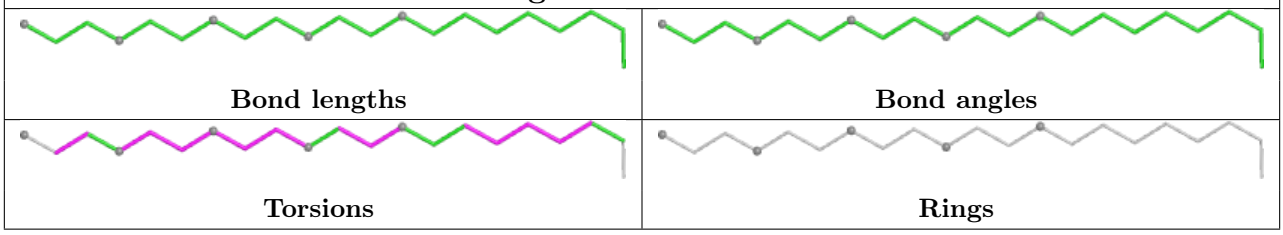
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

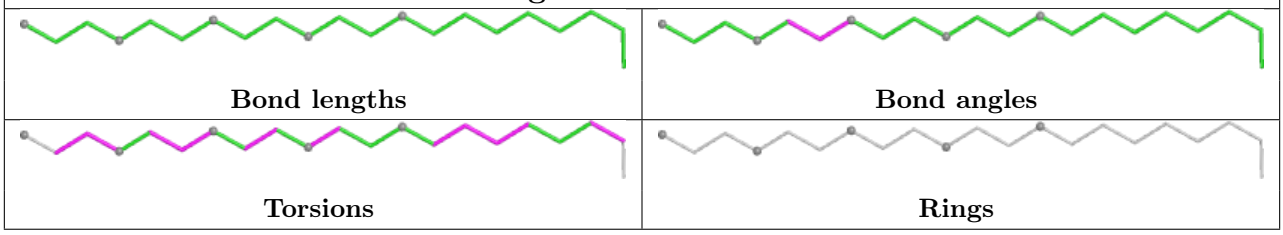
Ligand C8E A 802



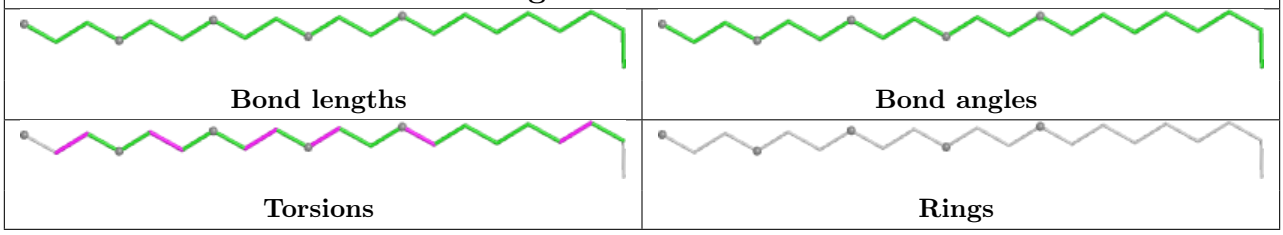
Ligand C8E A 806



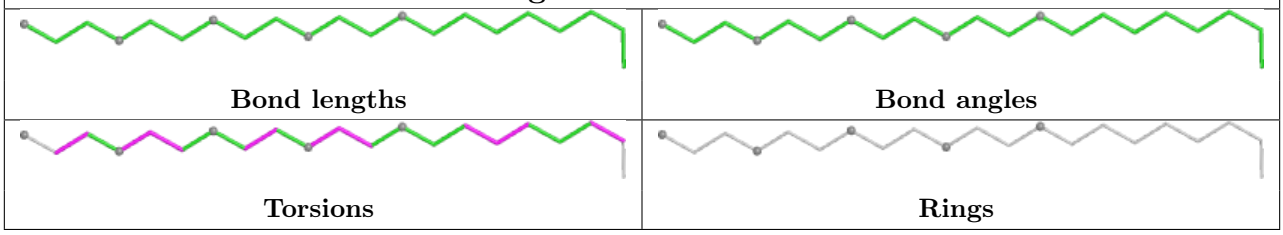
Ligand C8E A 805



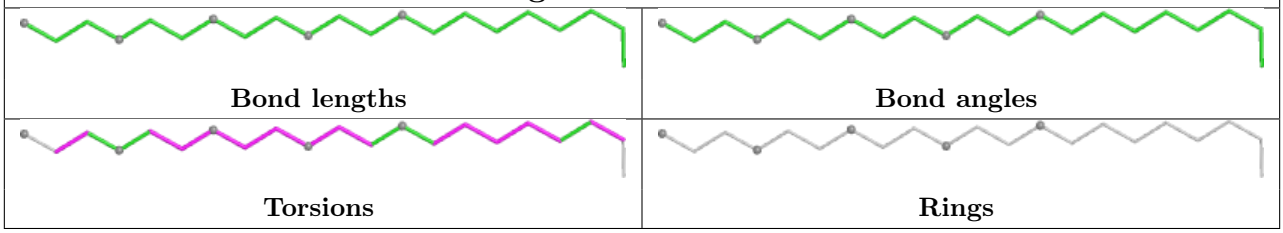
Ligand C8E A 804



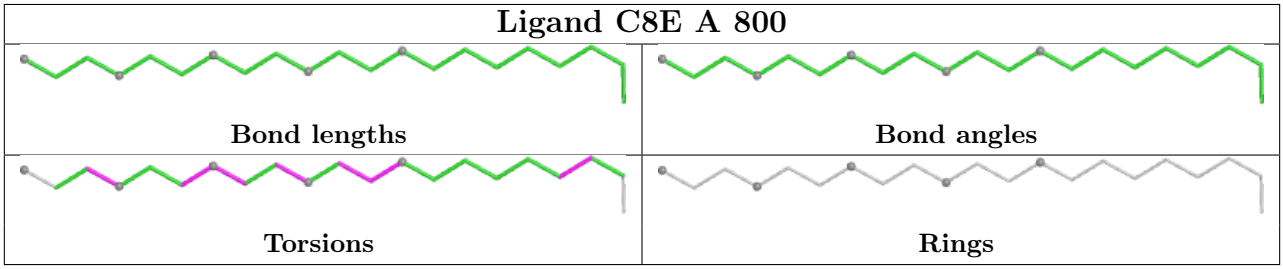
Ligand C8E A 801



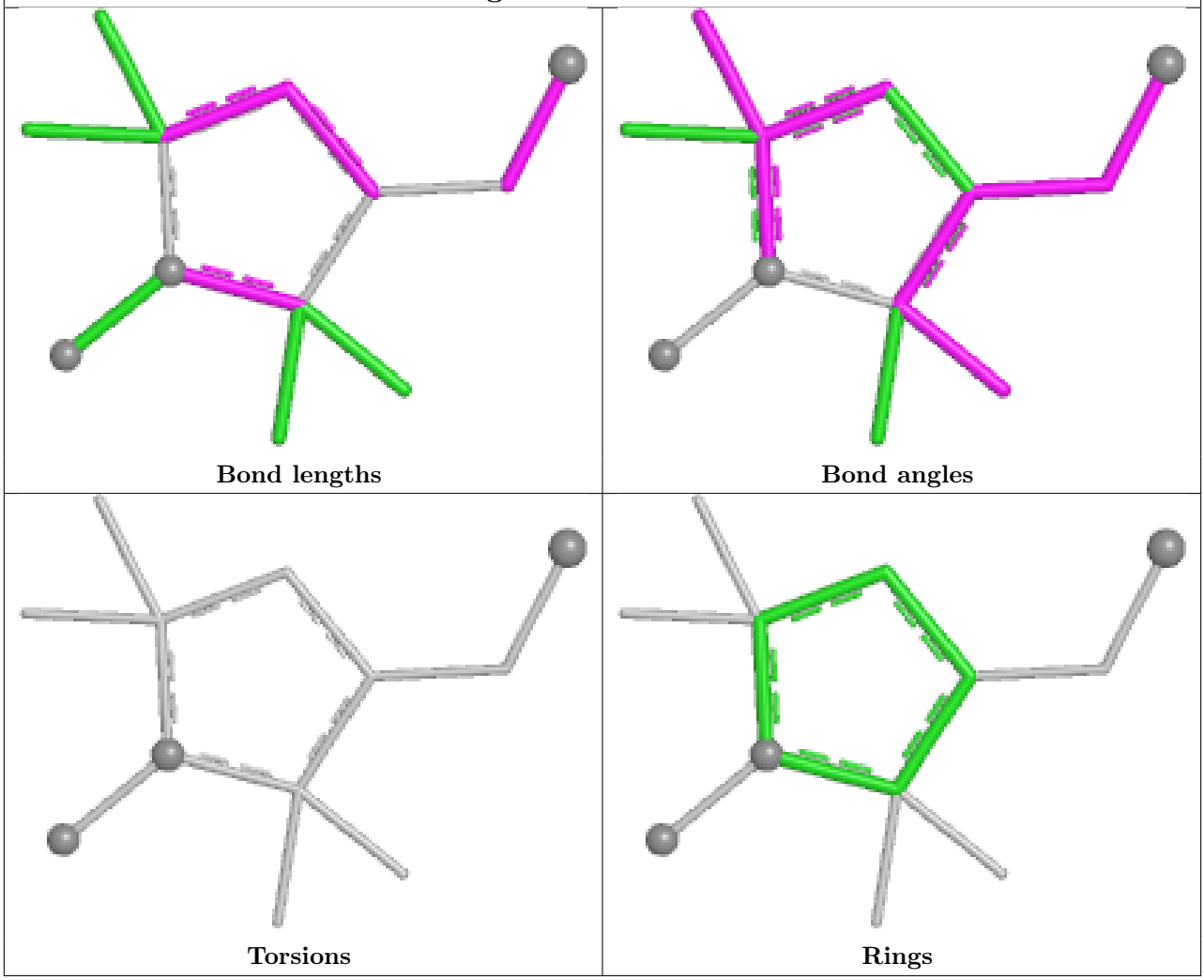
Ligand C8E A 803



Ligand C8E A 800



Ligand MTN A 598



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	549/594 (92%)	0.33	44 (8%) 12 16	34, 53, 82, 105	3 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	594	PHE	7.8
1	A	288	ALA	7.7
1	A	287	SER	6.0
1	A	277	TYR	5.6
1	A	177	GLY	5.0
1	A	404	PHE	4.9
1	A	325	GLY	4.9
1	A	328	TYR	4.6
1	A	324	PRO	4.3
1	A	329	VAL	4.1
1	A	579	TYR	4.0
1	A	511	LEU	4.0
1	A	162	ASP	3.6
1	A	512	TYR	3.6
1	A	242	THR	3.5
1	A	289	THR	3.4
1	A	276	ASN	3.4
1	A	330	GLU	3.4
1	A	448	ASP	3.3
1	A	212	ASP	3.1
1	A	290	LEU	3.0
1	A	449	HIS	2.9
1	A	341	TYR	2.9
1	A	160	LEU	2.8
1	A	326	THR	2.6
1	A	176	HIS	2.6
1	A	313	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	118	TYR	2.5
1	A	312	GLY	2.5
1	A	510	GLN	2.5
1	A	331	ASP	2.5
1	A	275	TYR	2.5
1	A	314	GLY	2.4
1	A	555	VAL	2.4
1	A	76	VAL	2.4
1	A	228	ASN	2.4
1	A	6	ASP	2.3
1	A	257	ASN	2.3
1	A	592	TYR	2.2
1	A	343	THR	2.1
1	A	577	TYR	2.1
1	A	196	GLY	2.1
1	A	127	VAL	2.0
1	A	165	ARG	2.0

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 monosaccharides 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(Å^2)	Q<0.9
2	C8E	A	806	21/21	0.42	0.42	58,94,121,122	0
2	C8E	A	803	21/21	0.56	0.48	85,97,107,107	0
2	C8E	A	805	21/21	0.65	0.39	76,97,100,101	0
4	MTN	A	598	12/16	0.75	0.32	51,57,60,61	12
2	C8E	A	801	21/21	0.76	0.28	68,76,91,92	0
2	C8E	A	800	21/21	0.77	0.24	44,56,77,81	0

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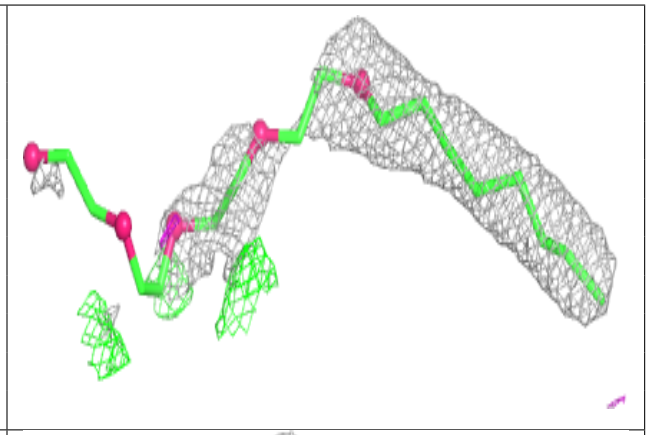
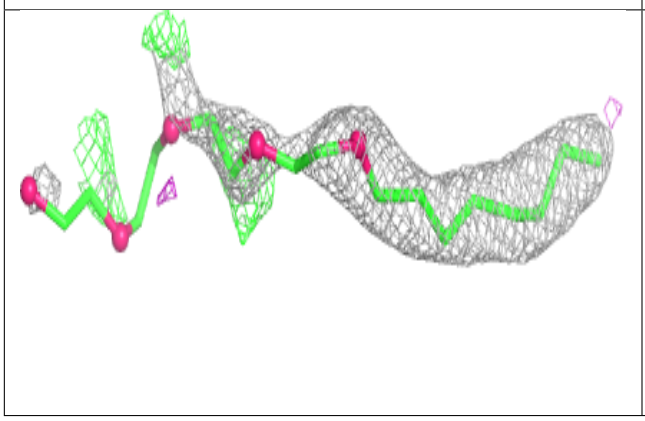
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	A	596	1/1	0.87	0.33	69,69,69,69	0
2	C8E	A	804	21/21	0.90	0.13	52,61,65,68	0
3	MG	A	597	1/1	0.92	0.20	72,72,72,72	0
2	C8E	A	802	21/21	0.93	0.33	45,56,70,74	0
3	MG	A	595	1/1	0.96	0.06	76,76,76,76	0

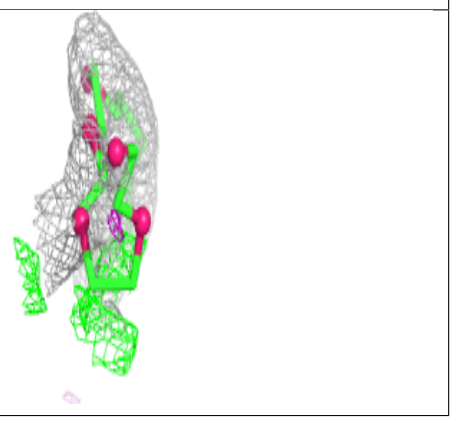
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around C8E A 806:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

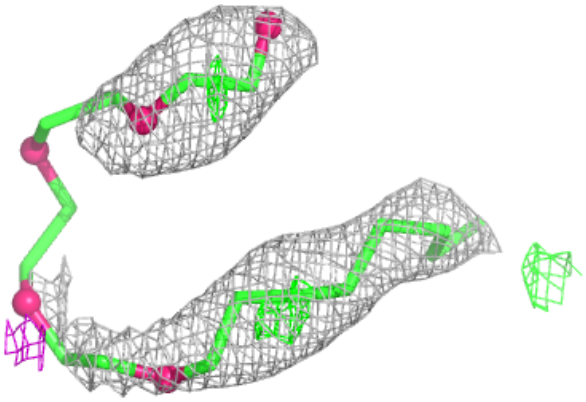


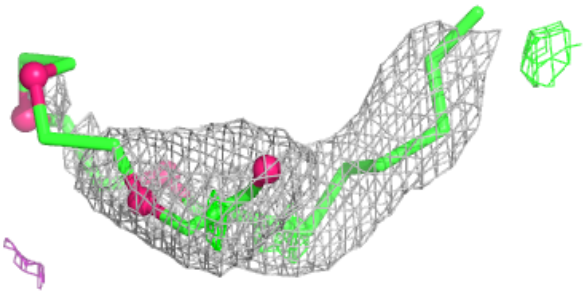


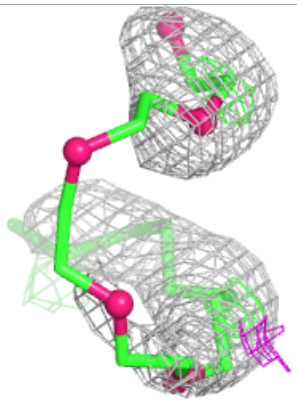


Electron density around C8E A 803:

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

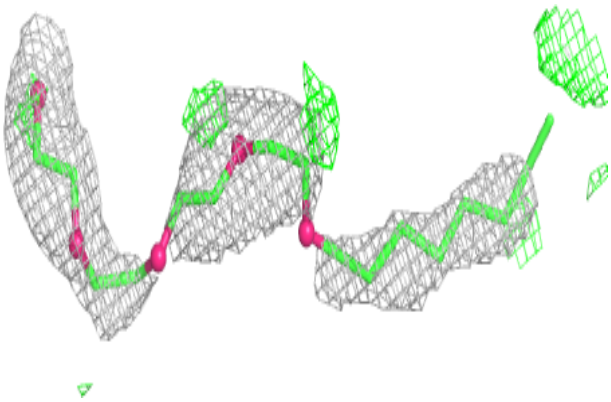


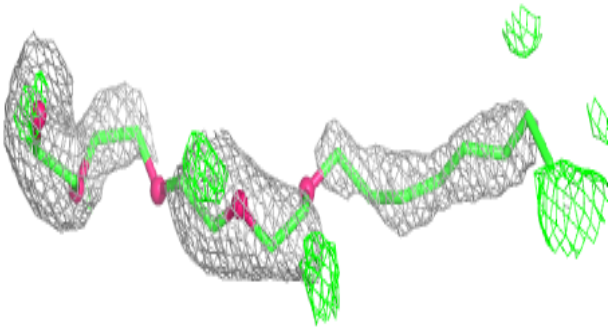


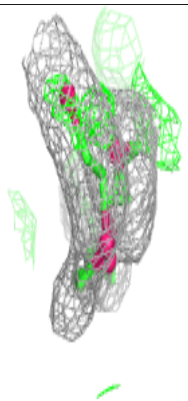


Electron density around C8E A 805:

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

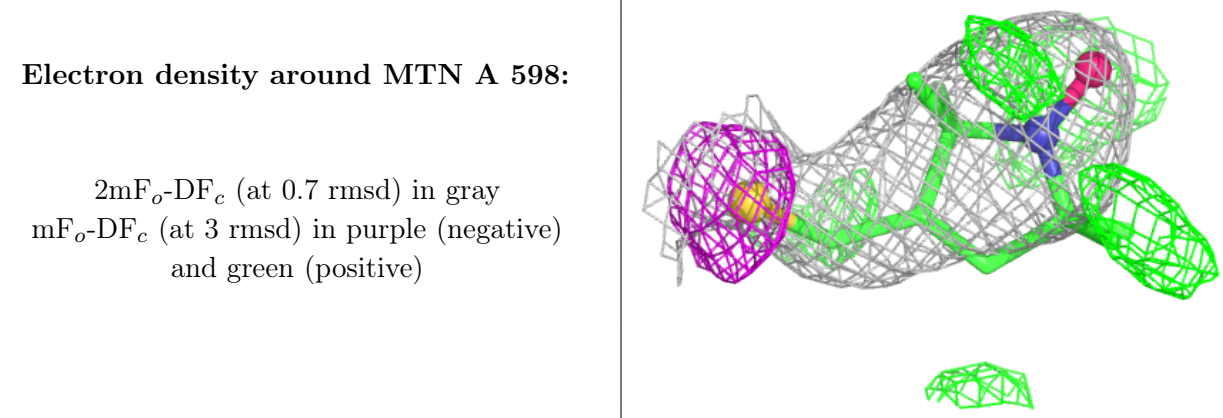


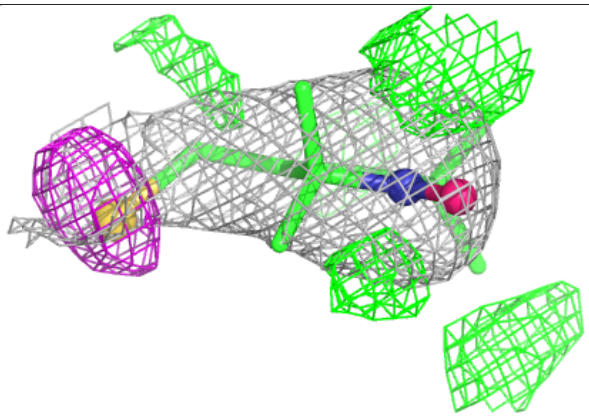


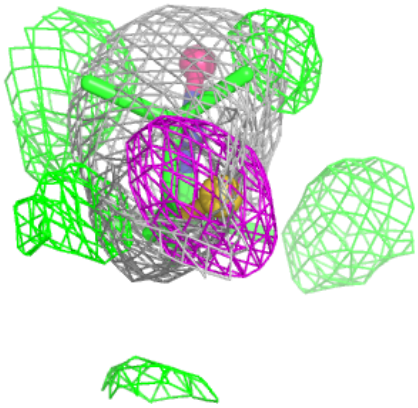


Electron density around MTN A 598:

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

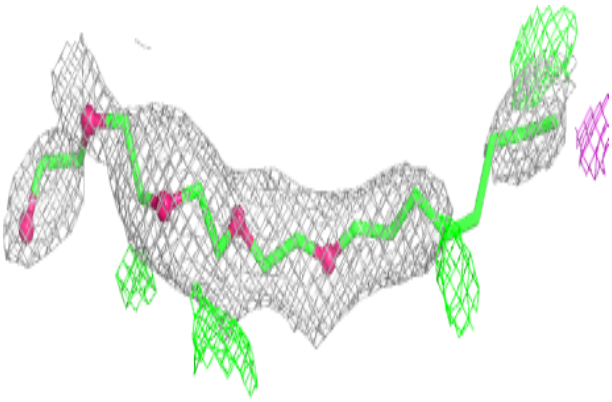


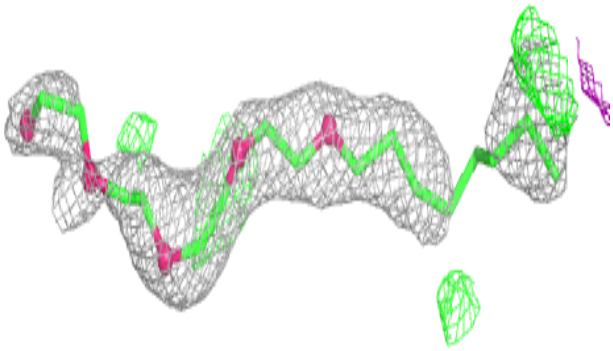


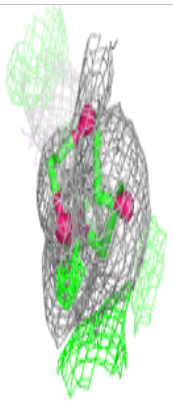


Electron density around C8E A 801:

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

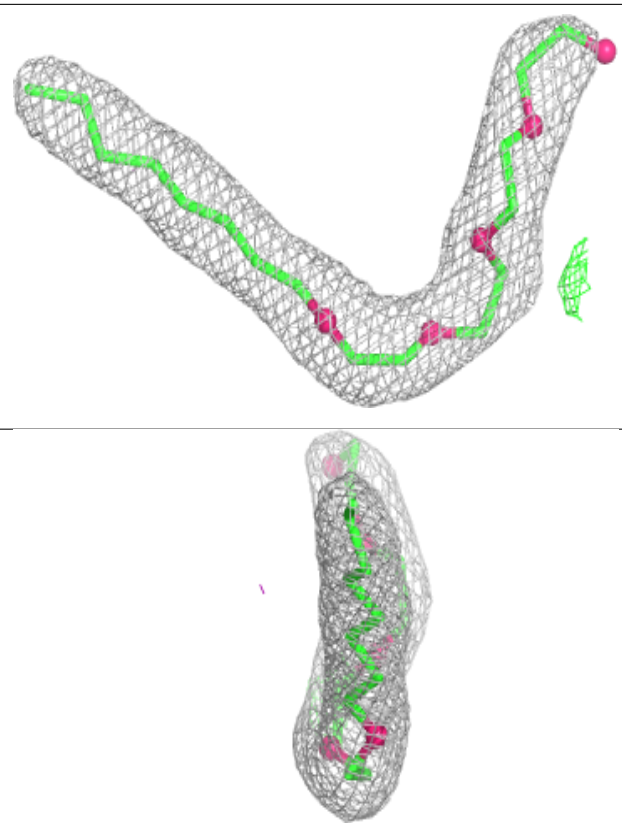


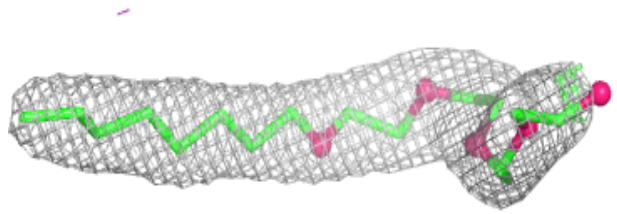




Electron density around C8E A 800:

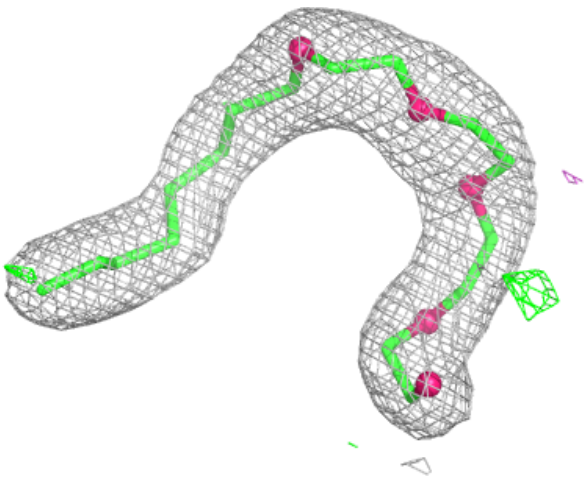
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

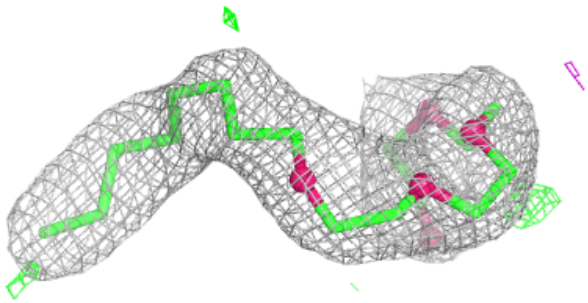


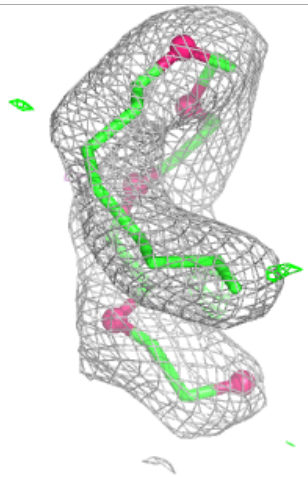


Electron density around C8E A 804:

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

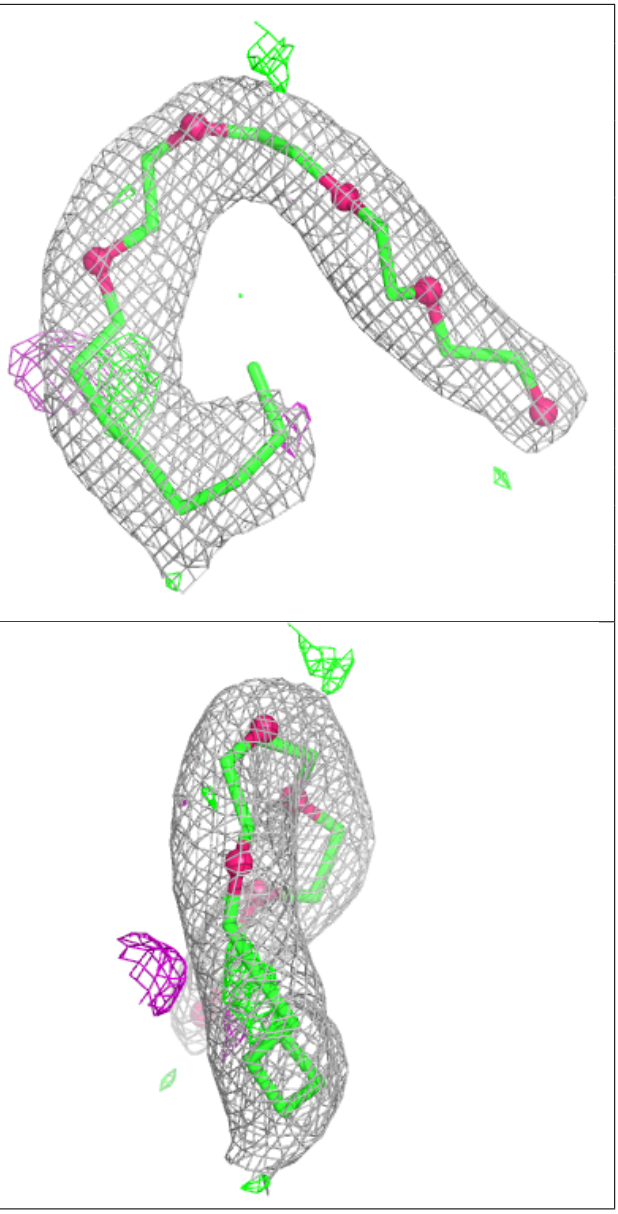






Electron density around C8E A 802:

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



6.5 Other polymers (i)

There are no such residues in this entry.