



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 07:09 am BST

PDB ID : 3RGM
Title : Crystal structure of spin-labeled BtuB T156R1
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Deposited on : 2011-04-08
Resolution : 2.60 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

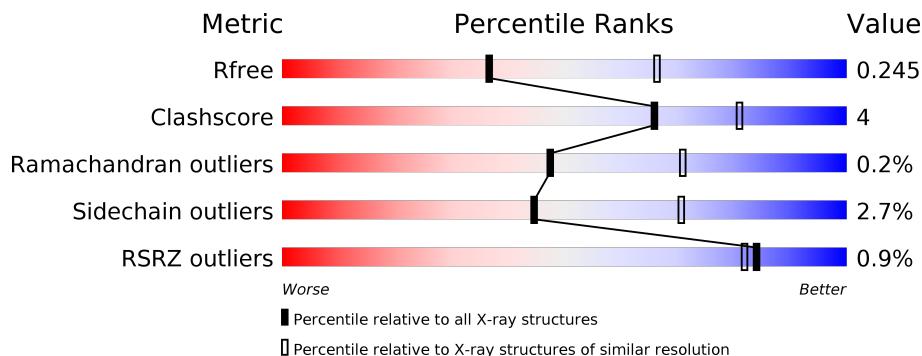
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 on 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	594	

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
2	C8E	A	805	-	-	-	X

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4531 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.

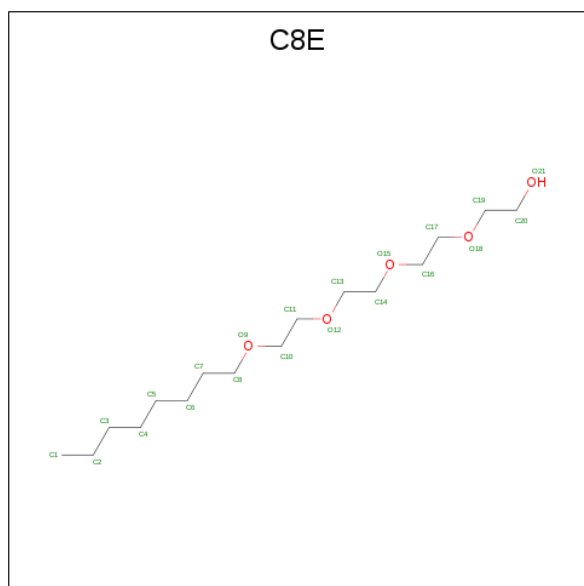
- Molecule 1 is a protein called Vitamin B12 transporter BtuB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	548	4300	2708	740	849	3	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	156	CYS	THR	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
2	A	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C	O	0	0
			21	16	5		

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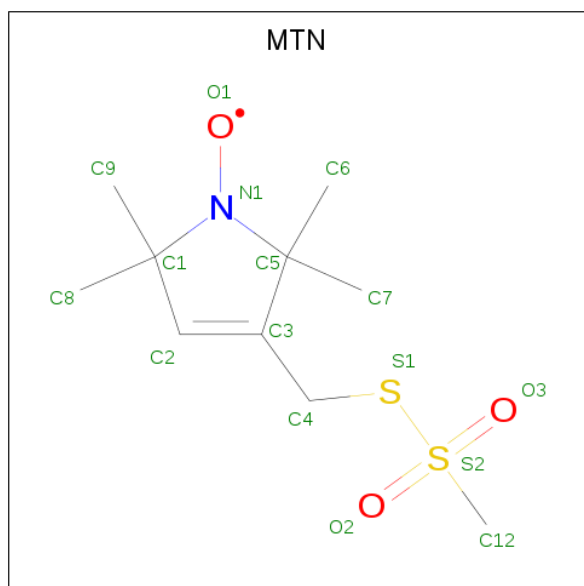
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C	O	0	0
			21	16	5		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	Mg	0	0
			9	9		

- Molecule 4 is S-[(1-oxyl-2,2,5,5-tetramethyl-2,5-dihydro-1H-pyrrol-3-yl)methyl] methanesulfonothioate (three-letter code: MTN) (formula: C₁₀H₁₈NO₃S₂).



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

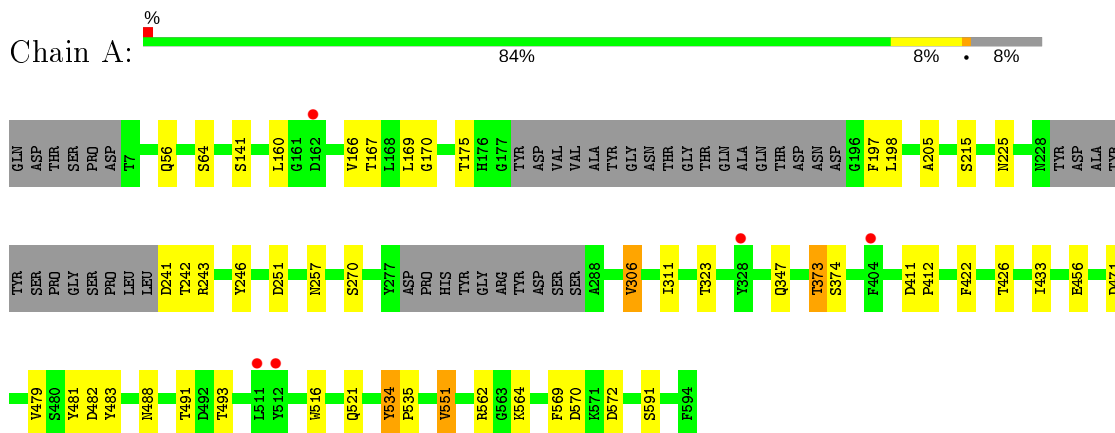
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	84	Total	O	0	0
			84	84		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	81.63Å 81.63Å 227.73Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.34 – 2.60 44.34 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.3 (44.34-2.60) 98.3 (44.34-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.211 , 0.254 0.210 , 0.245	Depositor DCC
R_{free} test set	1370 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	50.2	Xtrriage
Anisotropy	0.099	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.036 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4531	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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: MG, MTN, C8E

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	0.95	2/4402 (0.0%)	0.91	8/5989 (0.1%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	426	THR	CB-CG2	-5.45	1.34	1.52
1	A	246	TYR	CG-CD2	5.09	1.45	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	534	TYR	C-N-CD	-8.61	101.66	120.60
1	A	482	ASP	CB-CG-OD1	5.78	123.50	118.30
1	A	306	VAL	CB-CA-C	-5.68	100.61	111.40
1	A	373	THR	CB-CA-C	-5.39	97.05	111.60
1	A	471	ASP	CB-CG-OD1	5.25	123.03	118.30
1	A	572	ASP	CB-CG-OD1	5.19	122.97	118.30
1	A	562	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	A	471	ASP	CB-CG-OD2	-5.13	113.68	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	534	TYR	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	4300	0	4035	30	0
2	A	126	0	204	7	0
3	A	9	0	0	0	0
4	A	12	0	15	0	0
5	A	84	0	0	3	0
All	All	4531	0	4254	35	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 4.

All (35) 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:801:C8E:H192	5:A:687:HOH:O	1.86	0.76
2:A:802:C8E:H13	2:A:802:C8E:H52	1.67	0.75
1:A:257:ASN:HB2	5:A:610:HOH:O	1.95	0.67
1:A:516:TRP:CE3	1:A:551:VAL:HG13	2.32	0.65
1:A:160:LEU:HD22	1:A:166:VAL:CG2	2.28	0.64
1:A:491:THR:HG23	1:A:493:THR:HG23	1.80	0.64
1:A:160:LEU:HD22	1:A:166:VAL:HG21	1.83	0.61
1:A:169:LEU:C	1:A:169:LEU:HD23	2.27	0.55
2:A:802:C8E:H172	2:A:802:C8E:H11	1.89	0.55
1:A:169:LEU:HD23	1:A:170:GLY:N	2.23	0.53
1:A:516:TRP:CZ3	1:A:551:VAL:HG13	2.44	0.52
1:A:422:PHE:CG	2:A:801:C8E:H11	2.46	0.51
1:A:160:LEU:CD2	1:A:166:VAL:HG21	2.41	0.50
1:A:175:THR:HG23	1:A:175:THR:O	2.11	0.50
1:A:433:ILE:HD12	2:A:802:C8E:C1	2.44	0.48
1:A:198:LEU:O	1:A:225:ASN:HA	2.14	0.48
2:A:803:C8E:C10	2:A:803:C8E:H172	2.46	0.46
1:A:175:THR:CG2	1:A:175:THR:O	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:GLN:HB3	5:A:624:HOH:O	2.15	0.45
1:A:516:TRP:CE3	1:A:551:VAL:CG1	2.99	0.45
1:A:411:ASP:HB3	1:A:412:PRO:CD	2.47	0.45
1:A:488:ASN:CG	1:A:491:THR:HG22	2.37	0.44
1:A:411:ASP:HB3	1:A:412:PRO:HD2	1.99	0.44
1:A:488:ASN:HB3	1:A:491:THR:HG22	1.98	0.44
1:A:569:PHE:O	1:A:570:ASP:C	2.56	0.43
1:A:175:THR:HG22	1:A:197:PHE:HB3	2.01	0.43
1:A:311:ILE:HD13	1:A:311:ILE:HG21	1.82	0.43
1:A:56:GLN:HG3	1:A:64:SER:HB3	2.00	0.43
1:A:373:THR:HG22	1:A:374:SER:N	2.35	0.42
2:A:800:C8E:H131	2:A:805:C8E:H81	2.00	0.42
1:A:481:TYR:OH	1:A:483:TYR:HB2	2.19	0.41
1:A:516:TRP:CZ3	1:A:551:VAL:CG1	3.03	0.41
1:A:167:THR:HB	1:A:205:ALA:HB3	2.02	0.41
1:A:242:THR:HG22	1:A:243:ARG:N	2.36	0.41
1:A:479:VAL:HG13	1:A:479:VAL:O	2.22	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	540/594 (91%)	523 (97%)	16 (3%)	1 (0%)	47 71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	535	PRO

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	447/495 (90%)	435 (97%)	12 (3%)	44 71

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	141	SER
1	A	215	SER
1	A	241	ASP
1	A	251	ASP
1	A	270	SER
1	A	306	VAL
1	A	323	THR
1	A	456	GLU
1	A	521	GLN
1	A	551	VAL
1	A	564	LYS
1	A	591	SER

Some 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 carbohydrates in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 9 are monoatomic - leaving 7 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	800	-	20,20,20	0.47	0	19,19,19	0.86	1 (5%)
2	C8E	A	804	-	20,20,20	0.41	0	19,19,19	0.62	0
2	C8E	A	803	-	20,20,20	0.50	0	19,19,19	0.97	0
2	C8E	A	801	-	20,20,20	0.46	0	19,19,19	0.71	0
2	C8E	A	805	-	20,20,20	0.48	0	19,19,19	0.74	0
2	C8E	A	802	-	20,20,20	0.43	0	19,19,19	1.02	2 (10%)
4	MTN	A	604	1	9,12,16	2.24	1 (11%)	9,20,27	4.23	4 (44%)

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	800	-	-	5/18/18/18	-
2	C8E	A	804	-	-	10/18/18/18	-
2	C8E	A	803	-	-	10/18/18/18	-
2	C8E	A	801	-	-	11/18/18/18	-
2	C8E	A	805	-	-	11/18/18/18	-
2	C8E	A	802	-	-	10/18/18/18	-
4	MTN	A	604	1	-	0/0/25/29	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	604	MTN	C5-N1	-6.42	1.42	1.50

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	604	MTN	C2-C1-N1	6.87	104.66	99.37
4	A	604	MTN	C3-C5-N1	6.79	104.72	99.27
4	A	604	MTN	C8-C1-C2	-5.64	107.04	112.79
4	A	604	MTN	C1-C2-C3	-5.52	109.32	113.64
2	A	800	C8E	O9-C10-C11	-2.11	100.87	110.39
2	A	802	C8E	O12-C11-C10	-2.04	101.22	110.39
2	A	802	C8E	C13-O12-C11	2.03	122.07	113.29

There are no chirality outliers.

All (57) torsion outliers are listed below:

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

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

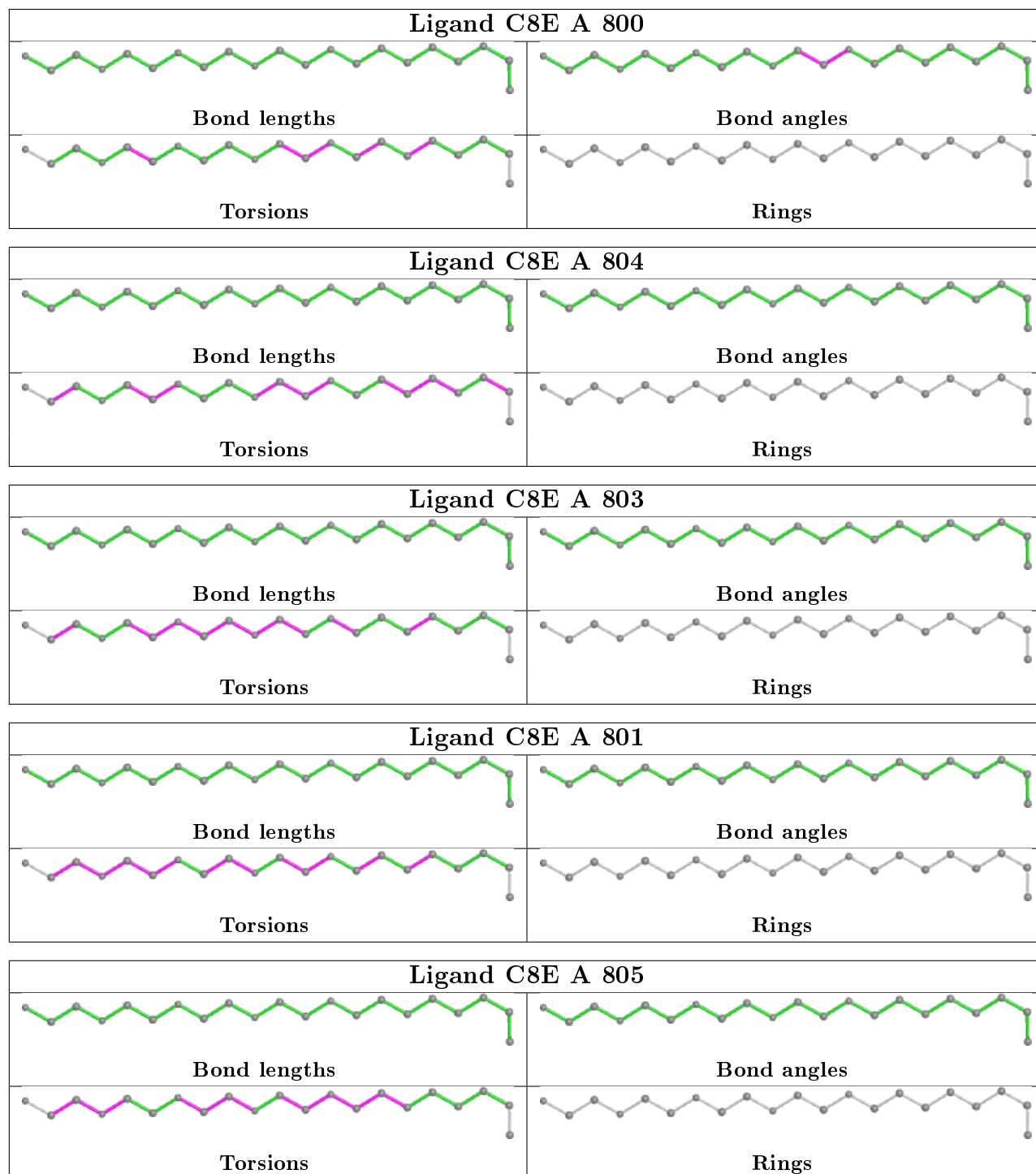
There are no ring outliers.

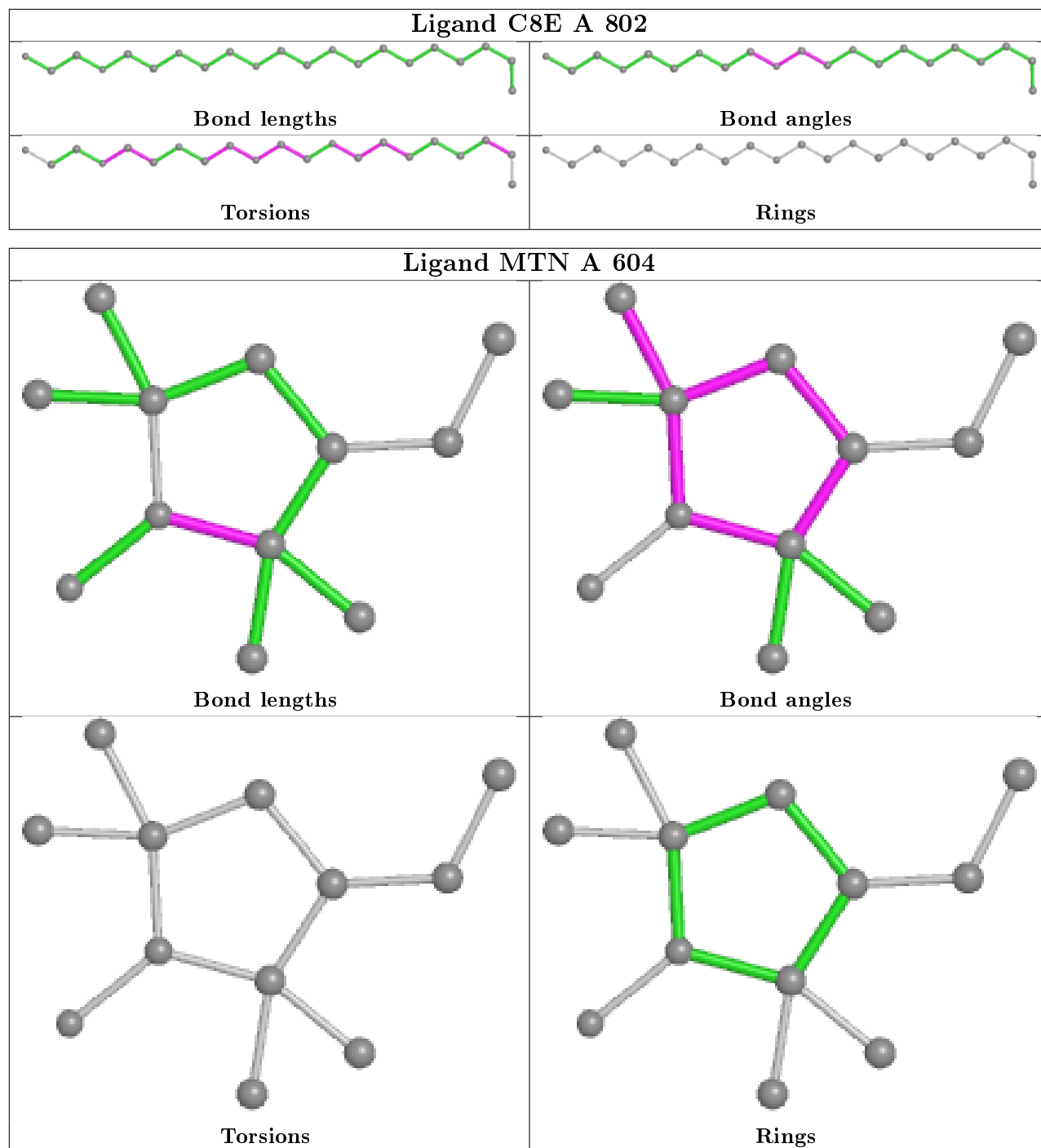
5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	800	C8E	1	0
2	A	803	C8E	1	0
2	A	801	C8E	2	0
2	A	805	C8E	1	0
2	A	802	C8E	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.





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	548/594 (92%)	-0.30	5 (0%) 84 82	21, 43, 72, 91	1 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	404	PHE	3.1
1	A	328	TYR	2.9
1	A	511	LEU	2.4
1	A	162	ASP	2.1
1	A	512	TYR	2.1

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 [i](#)

There are no carbohydrates 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.

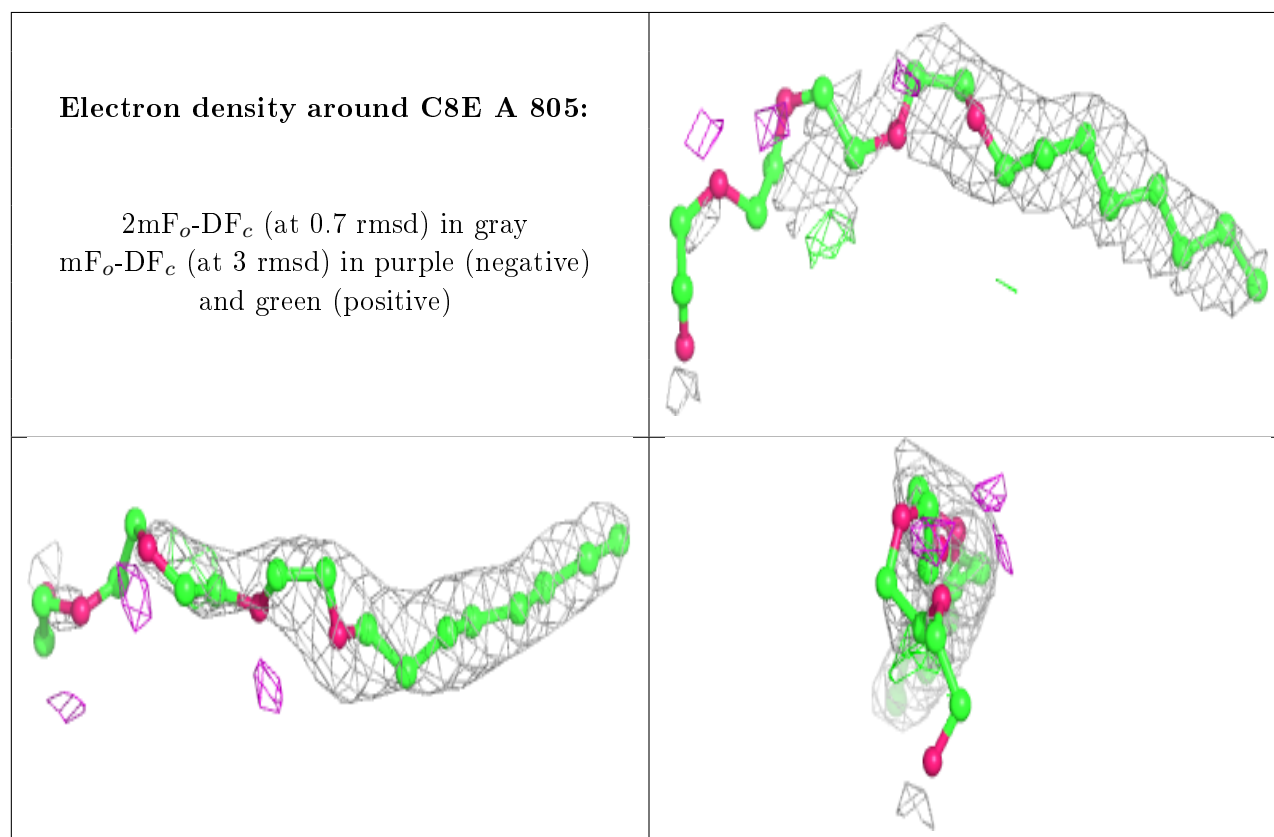
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	A	601	1/1	0.25	0.15	88,88,88,88	0
3	MG	A	602	1/1	0.39	0.17	93,93,93,93	0

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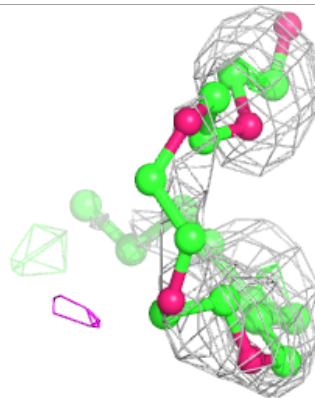
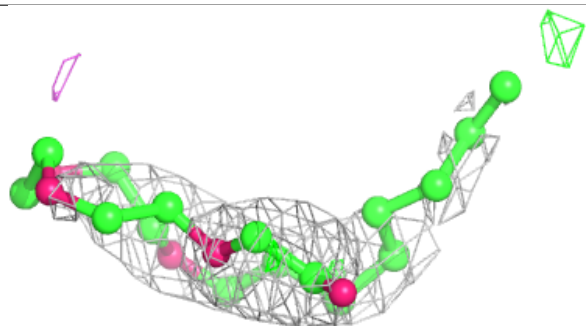
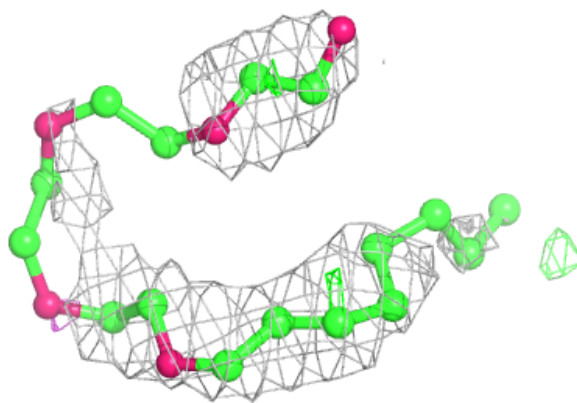
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	C8E	A	805	21/21	0.57	0.42	52,73,98,98	0
2	C8E	A	803	21/21	0.75	0.44	74,78,90,90	0
3	MG	A	600	1/1	0.79	0.16	54,54,54,54	0
2	C8E	A	801	21/21	0.82	0.24	58,71,78,78	0
3	MG	A	599	1/1	0.82	0.08	62,62,62,62	0
3	MG	A	595	1/1	0.87	0.25	55,55,55,55	0
4	MTN	A	604	12/16	0.89	0.43	35,37,37,37	12
2	C8E	A	804	21/21	0.90	0.18	43,46,53,57	0
2	C8E	A	800	21/21	0.91	0.20	31,46,53,54	0
2	C8E	A	802	21/21	0.92	0.26	40,44,59,66	0
3	MG	A	597	1/1	0.92	0.08	67,67,67,67	0
3	MG	A	603	1/1	0.93	0.16	53,53,53,53	0
3	MG	A	596	1/1	0.93	0.16	47,47,47,47	0
3	MG	A	598	1/1	0.96	0.20	55,55,55,55	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.

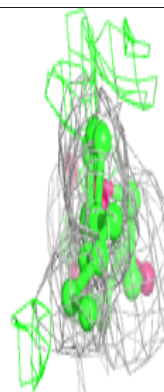
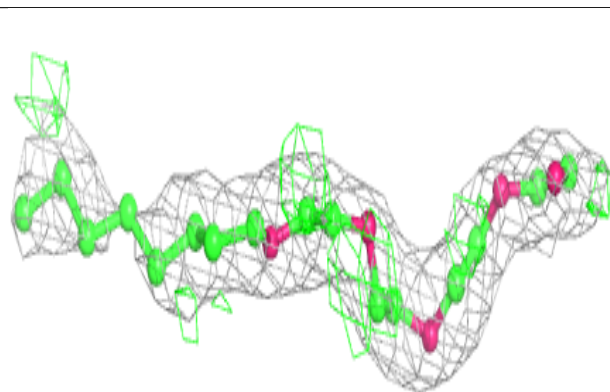
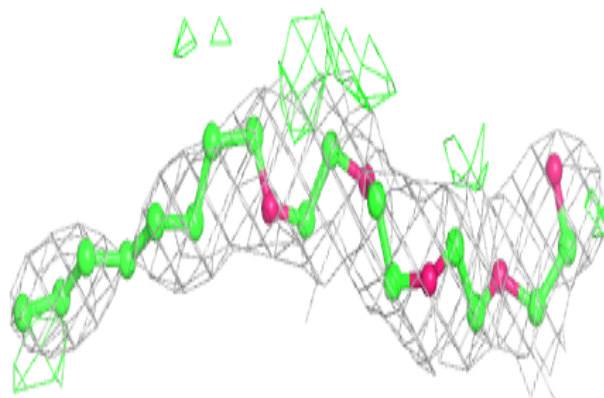


Electron density around C8E A 803:

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

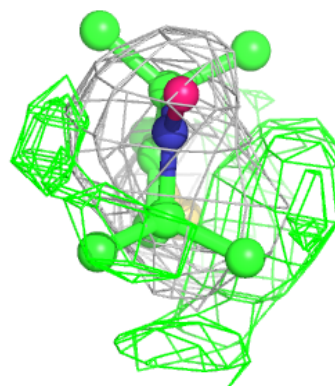
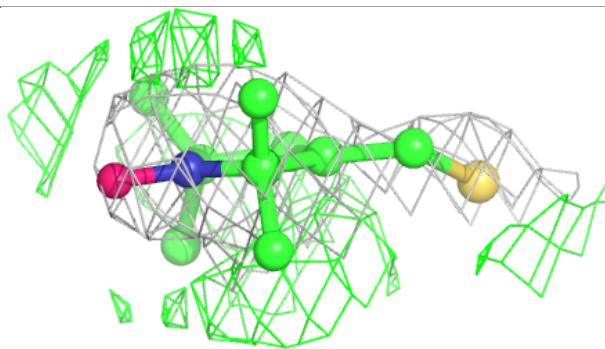
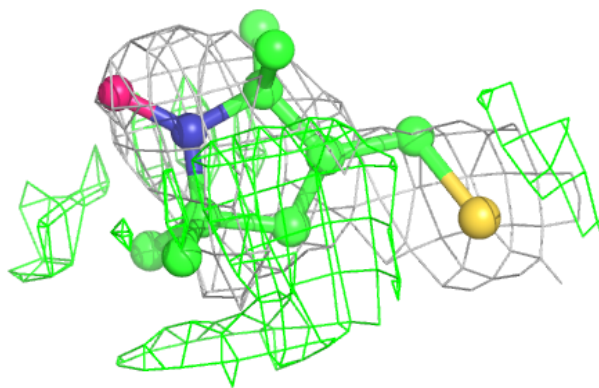
**Electron density around C8E A 801:**

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

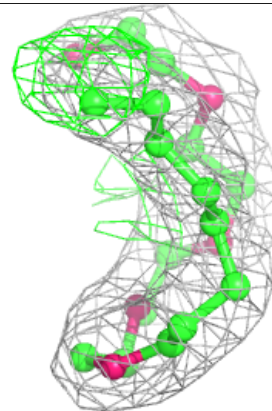
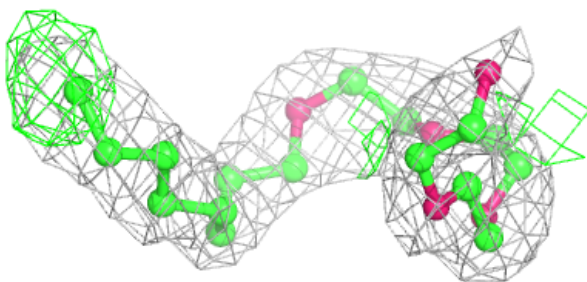
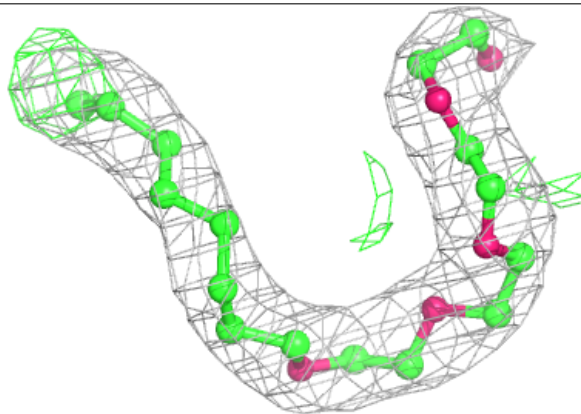


Electron density around MTN A 604:

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

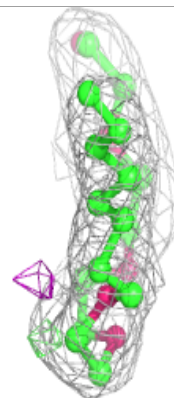
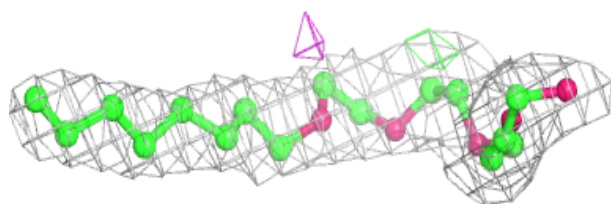
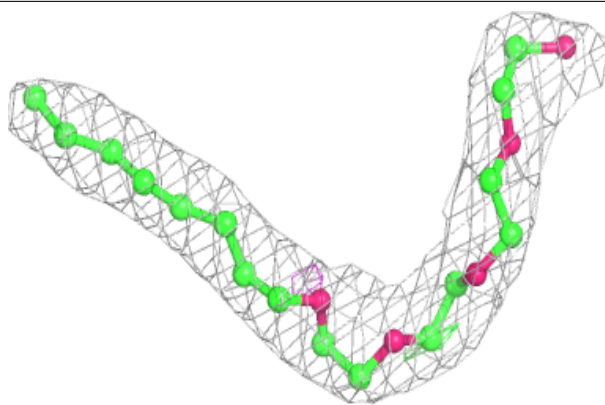
**Electron density around C8E A 804:**

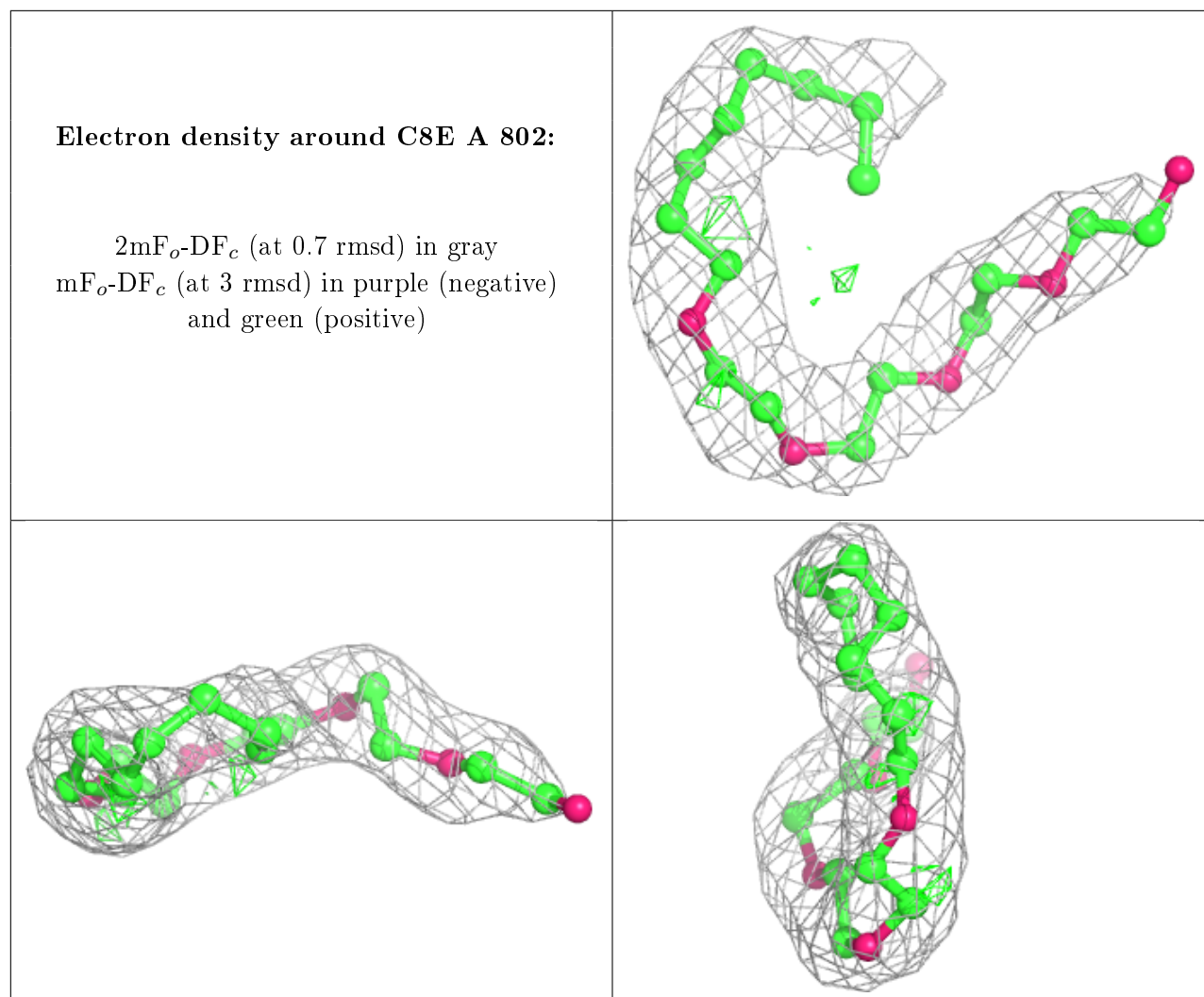
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around C8E A 800:

$2mF_o-DF_c$ (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.