



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2024 – 12:20 PM JST

PDB ID : 5ZKU
Title : Crystal structure of DFA-IIIase from *Arthrobacter chlorophenicus* A6 in complex with DFA-III
Authors : Yu, S.H.; Shen, H.; Li, X.; Mu, W.M.
Deposited on : 2018-03-26
Resolution : 2.32 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 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

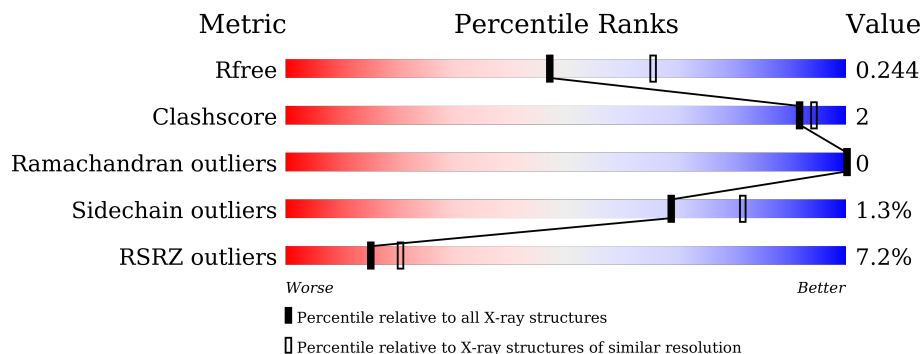
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.32 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	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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 $\leq 5\%$. 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	445	7% (poor fit), 95% (0-1 outliers), 5% (2 outliers), 5% (3+ outliers), 5% (not modelled)
1	B	445	6% (poor fit), 94% (0-1 outliers), 5% (2 outliers), 5% (3+ outliers), 5% (not modelled)
1	C	445	5% (poor fit), 94% (0-1 outliers), 5% (2 outliers), 5% (3+ outliers), 5% (not modelled)
1	D	445	8% (poor fit), 95% (0-1 outliers), 5% (2 outliers), 5% (3+ outliers), 5% (not modelled)
1	E	445	8% (poor fit), 94% (0-1 outliers), 5% (2 outliers), 5% (3+ outliers), 5% (not modelled)
1	F	445	9% (poor fit), 93% (0-1 outliers), 6% (2 outliers), 5% (3+ outliers), 5% (not modelled)

2 Entry composition [i](#)

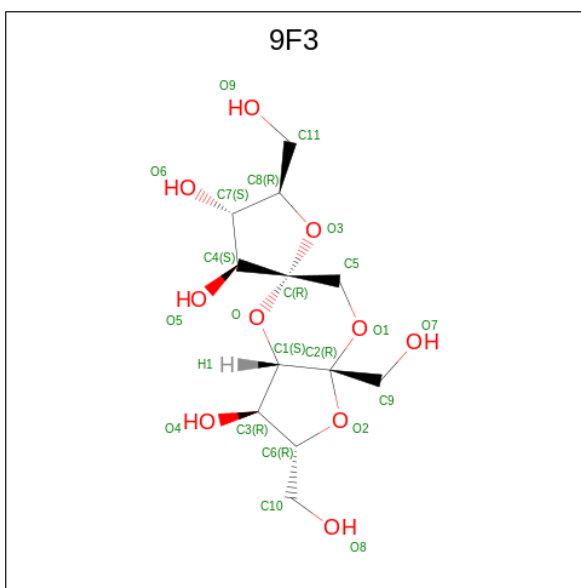
There are 3 unique types of molecules in this entry. The entry contains 20245 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DFA-IIIase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	442	Total 3303	C 2053	N 589	O 654	S 7	0	0	0
1	B	442	Total 3300	C 2050	N 589	O 654	S 7	0	0	0
1	C	442	Total 3300	C 2050	N 589	O 654	S 7	0	0	0
1	D	442	Total 3300	C 2050	N 589	O 654	S 7	0	0	0
1	E	442	Total 3300	C 2050	N 589	O 654	S 7	0	0	0
1	F	443	Total 3307	C 2055	N 590	O 655	S 7	0	0	0

- Molecule 2 is (2R,3'S,4'S,4aR,5'R,6R,7R,7aS)-4a,5',6-tris(hydroxymethyl)spiro[3,6,7,7a-tetrahydrofuro[2,3-b][1,4]dioxine-2,2'-oxolane]-3',4',7-triol (three-letter code: 9F3) (formula: C₁₂H₂₀O₁₀).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			22	12	10		
2	B	1	Total	C	O	0	0
			22	12	10		
2	C	1	Total	C	O	0	0
			22	12	10		
2	D	1	Total	C	O	0	0
			22	12	10		
2	E	1	Total	C	O	0	0
			22	12	10		
2	F	1	Total	C	O	0	0
			22	12	10		

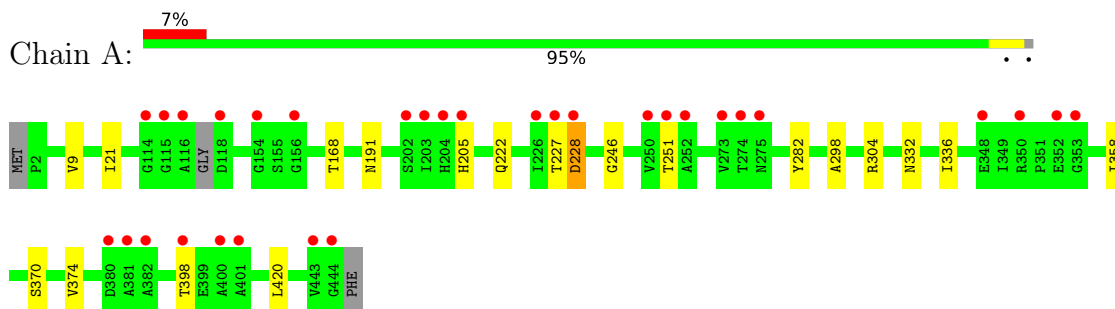
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	54	Total	O	0	0
			54	54		
3	B	48	Total	O	0	0
			48	48		
3	C	62	Total	O	0	0
			62	62		
3	D	30	Total	O	0	0
			30	30		
3	E	50	Total	O	0	0
			50	50		
3	F	59	Total	O	0	0
			59	59		

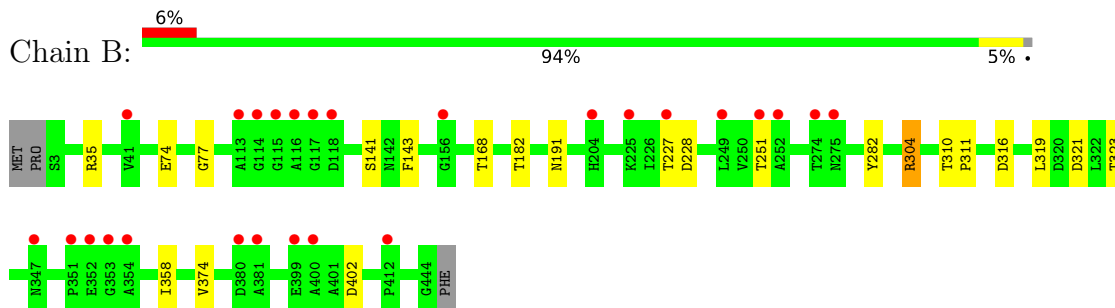
3 Residue-property plots [i](#)

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.

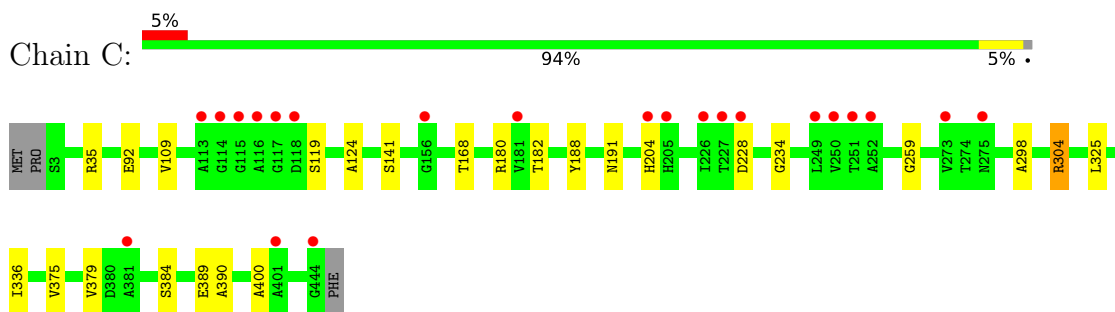
- Molecule 1: DFA-IIIase



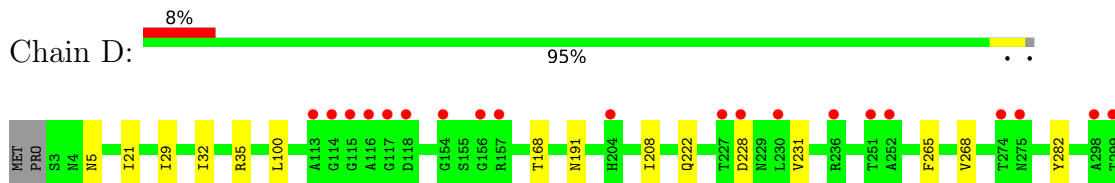
- Molecule 1: DFA-IIIase

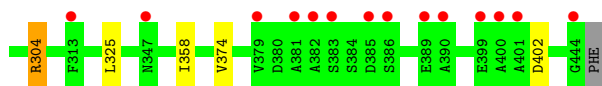


- Molecule 1: DFA-IIIase

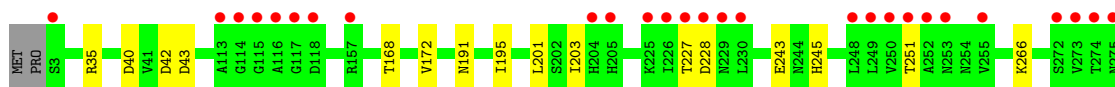
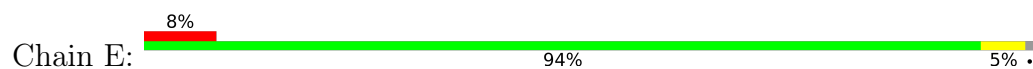


- Molecule 1: DFA-IIIase

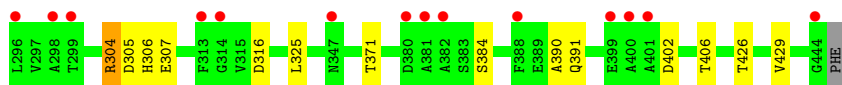
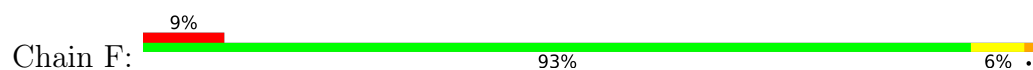




- Molecule 1: DFA-IIIase



- Molecule 1: DFA-IIIase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	116.47Å 77.17Å 139.72Å 90.00° 99.60° 90.00°	Depositor
Resolution (Å)	50.00 – 2.32 40.90 – 2.31	Depositor EDS
% Data completeness (in resolution range)	88.5 (50.00-2.32) 88.6 (40.90-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 2.31Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.188 , 0.240 0.196 , 0.244	Depositor DCC
R_{free} test set	4830 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtrriage
Anisotropy	0.260	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 28.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20245	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 3.56% 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: 9F3

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	0.49	0/3375	0.72	0/4601
1	B	0.49	0/3372	0.71	1/4598 (0.0%)
1	C	0.50	0/3372	0.72	2/4598 (0.0%)
1	D	0.49	0/3372	0.71	0/4598
1	E	0.49	0/3372	0.71	1/4598 (0.0%)
1	F	0.49	0/3380	0.71	1/4609 (0.0%)
All	All	0.49	0/20243	0.71	5/27602 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	35	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	C	180	ARG	NE-CZ-NH2	-5.45	117.57	120.30
1	B	35	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	C	35	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	F	35	ARG	NE-CZ-NH1	5.04	122.82	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	3303	0	3151	10	0
1	B	3300	0	3147	11	0
1	C	3300	0	3147	13	0
1	D	3300	0	3147	11	0
1	E	3300	0	3147	10	0
1	F	3307	0	3155	13	0
2	A	22	0	0	0	0
2	B	22	0	0	0	0
2	C	22	0	0	0	0
2	D	22	0	0	0	0
2	E	22	0	0	1	0
2	F	22	0	0	0	0
3	A	54	0	0	0	0
3	B	48	0	0	1	0
3	C	62	0	0	1	0
3	D	30	0	0	0	0
3	E	50	0	0	0	0
3	F	59	0	0	0	0
All	All	20245	0	18894	62	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.

All (62) 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:398:THR:HG21	3:B:632:HOH:O	1.79	0.81
1:D:222:GLN:HE22	1:F:391:GLN:HB3	1.55	0.70
1:D:304:ARG:HG2	1:D:325:LEU:HD11	1.77	0.66
1:F:5:ASN:OD1	1:F:35:ARG:NH2	2.28	0.66
1:C:384:SER:HB3	1:C:390:ALA:HB2	1.88	0.56
1:E:358:ILE:HD13	1:E:374:VAL:HG13	1.88	0.56
1:C:379:VAL:HG12	1:C:400:ALA:HB2	1.88	0.56
1:F:168:THR:HA	1:F:191:ASN:O	2.07	0.55
1:E:201:LEU:HD21	1:E:203:ILE:HD11	1.91	0.52
1:F:304:ARG:HG2	1:F:325:LEU:HD11	1.91	0.51
1:D:168:THR:HA	1:D:191:ASN:O	2.11	0.51
1:B:168:THR:HA	1:B:191:ASN:O	2.12	0.50
1:C:304:ARG:HG2	1:C:325:LEU:HD11	1.93	0.50
1:A:168:THR:HA	1:A:191:ASN:O	2.12	0.49
1:F:406:THR:HG23	1:F:429:VAL:HG23	1.95	0.49
1:F:282:TYR:CE1	1:F:316:ASP:HA	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:306:HIS:HD2	1:F:307:GLU:O	1.96	0.48
1:E:168:THR:HA	1:E:191:ASN:O	2.13	0.48
1:F:153:ASP:HB2	1:F:162:THR:HG21	1.95	0.48
1:A:358:ILE:HD13	1:A:374:VAL:CG1	2.44	0.47
1:B:304:ARG:NH2	1:B:321:ASP:OD1	2.43	0.47
1:E:227:THR:HG22	1:E:251:THR:HG22	1.96	0.47
1:E:42:ASP:O	1:E:43:ASP:HB2	2.15	0.47
1:C:168:THR:HA	1:C:191:ASN:O	2.15	0.47
1:C:119:SER:HB3	3:C:660:HOH:O	2.14	0.47
1:C:92:GLU:OE1	1:F:243:GLU:OE2	2.34	0.46
1:C:234:GLY:O	1:C:259:GLY:HA2	2.16	0.46
1:C:389:GLU:OE2	1:E:398:THR:HG23	2.15	0.45
1:D:100:LEU:HD12	1:E:40:ASP:HB2	1.98	0.45
1:A:9:VAL:HG11	1:A:21:ILE:HD11	1.98	0.44
1:E:379:VAL:HG12	1:E:400:ALA:HB2	1.97	0.44
1:B:358:ILE:HD13	1:B:374:VAL:HG13	2.00	0.44
1:D:208:ILE:O	1:D:231:VAL:HA	2.16	0.44
1:A:227:THR:HA	1:A:251:THR:O	2.18	0.44
1:B:227:THR:HG22	1:B:251:THR:HG22	1.99	0.44
1:D:358:ILE:HD13	1:D:374:VAL:HG13	1.99	0.43
1:D:358:ILE:HD13	1:D:374:VAL:CG1	2.48	0.43
1:B:310:THR:HB	1:B:311:PRO:HD3	1.99	0.43
1:D:222:GLN:NE2	1:F:391:GLN:HB3	2.29	0.43
1:A:370:SER:HA	1:A:420:LEU:O	2.19	0.43
1:C:109:VAL:HG22	1:C:124:ALA:HB2	2.01	0.43
1:D:265:PHE:HB3	1:D:268:VAL:HB	2.01	0.43
2:E:501:9F3:O9	1:F:199:ASP:OD1	2.37	0.43
1:B:77:GLY:O	1:B:143:PHE:HA	2.19	0.42
1:A:332:ASN:HB3	1:C:375:VAL:HG21	2.01	0.42
1:B:282:TYR:CE1	1:B:316:ASP:HA	2.55	0.42
1:A:222:GLN:HA	1:A:246:GLY:O	2.20	0.41
1:C:182:THR:HA	1:C:204:HIS:O	2.20	0.41
1:B:319:LEU:HD13	1:B:323:THR:HG21	2.02	0.41
1:B:141:SER:HA	1:B:182:THR:O	2.19	0.41
1:A:298:ALA:HA	1:A:336:ILE:O	2.21	0.41
1:B:74:GLU:HA	1:B:141:SER:O	2.21	0.41
1:C:141:SER:HA	1:C:182:THR:O	2.21	0.41
1:D:5:ASN:OD1	1:D:35:ARG:NH2	2.47	0.41
1:E:243:GLU:HA	1:E:266:LYS:O	2.21	0.41
1:F:281:PHE:HA	1:F:305:ASP:O	2.20	0.41
1:F:384:SER:HB3	1:F:390:ALA:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:298:ALA:HA	1:C:336:ILE:O	2.21	0.40
1:A:205:HIS:HA	1:A:228:ASP:O	2.22	0.40
1:D:29:ILE:HA	1:D:32:ILE:HD12	2.02	0.40
1:B:227:THR:HA	1:B:251:THR:O	2.22	0.40
1:E:172:VAL:HB	1:E:195:ILE:HG23	2.03	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	438/445 (98%)	417 (95%)	21 (5%)	0	100	100
1	B	440/445 (99%)	417 (95%)	23 (5%)	0	100	100
1	C	440/445 (99%)	416 (94%)	24 (6%)	0	100	100
1	D	440/445 (99%)	421 (96%)	19 (4%)	0	100	100
1	E	440/445 (99%)	416 (94%)	24 (6%)	0	100	100
1	F	441/445 (99%)	418 (95%)	23 (5%)	0	100	100
All	All	2639/2670 (99%)	2505 (95%)	134 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	351/353 (99%)	348 (99%)	3 (1%)	78	89
1	B	350/353 (99%)	347 (99%)	3 (1%)	78	89
1	C	350/353 (99%)	347 (99%)	3 (1%)	78	89
1	D	350/353 (99%)	345 (99%)	5 (1%)	67	80
1	E	350/353 (99%)	345 (99%)	5 (1%)	67	80
1	F	351/353 (99%)	342 (97%)	9 (3%)	46	62
All	All	2102/2118 (99%)	2074 (99%)	28 (1%)	69	81

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	228	ASP
1	A	282	TYR
1	A	304	ARG
1	B	228	ASP
1	B	304	ARG
1	B	402	ASP
1	C	188	TYR
1	C	228	ASP
1	C	304	ARG
1	D	21	ILE
1	D	228	ASP
1	D	282	TYR
1	D	304	ARG
1	D	402	ASP
1	E	228	ASP
1	E	245	HIS
1	E	352	GLU
1	E	402	ASP
1	E	412	PRO
1	F	19	LYS
1	F	70	PHE
1	F	228	ASP
1	F	245	HIS
1	F	282	TYR
1	F	304	ARG
1	F	371	THR
1	F	402	ASP
1	F	426	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	306	HIS
1	C	306	HIS
1	D	222	GLN
1	D	306	HIS
1	E	291	ASN
1	F	291	ASN
1	F	306	HIS

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](#)

6 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
2	9F3	D	501	-	24,24,24	1.03	1 (4%)	33,38,38	1.30	4 (12%)
2	9F3	E	501	-	24,24,24	1.27	4 (16%)	33,38,38	1.23	3 (9%)
2	9F3	A	501	-	24,24,24	0.96	1 (4%)	33,38,38	1.86	7 (21%)
2	9F3	F	501	-	24,24,24	1.22	2 (8%)	33,38,38	1.45	6 (18%)
2	9F3	B	501	-	24,24,24	1.06	2 (8%)	33,38,38	1.74	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	9F3	C	501	-	24,24,24	1.06	1 (4%)	33,38,38	1.36	4 (12%)

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	9F3	D	501	-	-	2/7/57/57	0/3/3/3
2	9F3	E	501	-	-	2/7/57/57	0/3/3/3
2	9F3	A	501	-	-	2/7/57/57	0/3/3/3
2	9F3	F	501	-	-	2/7/57/57	0/3/3/3
2	9F3	B	501	-	-	5/7/57/57	0/3/3/3
2	9F3	C	501	-	-	0/7/57/57	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	501	9F3	O-C	3.61	1.50	1.42
2	F	501	9F3	O-C1	3.59	1.50	1.43
2	B	501	9F3	O1-C2	3.11	1.47	1.42
2	E	501	9F3	O1-C2	2.92	1.46	1.42
2	A	501	9F3	O-C1	2.48	1.48	1.43
2	E	501	9F3	O2-C6	2.47	1.49	1.43
2	F	501	9F3	O-C	2.44	1.47	1.42
2	E	501	9F3	O-C1	2.40	1.48	1.43
2	D	501	9F3	C5-C	2.35	1.56	1.52
2	E	501	9F3	C2-C1	2.35	1.57	1.54
2	B	501	9F3	C5-C	2.14	1.56	1.52

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	9F3	C5-O1-C2	6.97	125.59	113.63
2	B	501	9F3	C5-O1-C2	5.55	123.16	113.63
2	F	501	9F3	O3-C8-C11	-3.80	98.29	108.85
2	C	501	9F3	O1-C5-C	-3.78	105.71	111.70
2	B	501	9F3	C9-C2-C1	-3.54	108.53	116.36
2	A	501	9F3	O1-C2-O2	3.29	116.43	109.48
2	D	501	9F3	O3-C8-C11	-3.20	99.93	108.85
2	B	501	9F3	O1-C2-C9	2.93	110.99	103.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	9F3	O3-C8-C11	-2.92	100.71	108.85
2	C	501	9F3	O1-C2-C9	2.84	110.76	103.65
2	A	501	9F3	O-C-C5	2.75	113.16	110.09
2	A	501	9F3	O1-C5-C	2.65	115.89	111.70
2	C	501	9F3	O-C1-C2	2.59	114.88	110.53
2	D	501	9F3	O1-C2-C9	2.57	110.09	103.65
2	A	501	9F3	O9-C11-C8	-2.56	102.52	111.29
2	B	501	9F3	O2-C2-C1	2.51	109.30	104.92
2	E	501	9F3	O-C1-C2	2.47	114.68	110.53
2	F	501	9F3	C5-O1-C2	2.40	117.75	113.63
2	F	501	9F3	C9-C2-C1	-2.37	111.12	116.36
2	D	501	9F3	O1-C2-O2	-2.36	104.49	109.48
2	F	501	9F3	O5-C4-C7	-2.29	105.41	113.32
2	A	501	9F3	O3-C-C4	-2.27	100.81	105.49
2	A	501	9F3	C10-C6-C3	-2.25	109.65	115.09
2	B	501	9F3	C11-C8-C7	-2.25	109.67	115.09
2	F	501	9F3	O9-C11-C8	-2.23	103.65	111.29
2	D	501	9F3	C9-C2-C1	-2.20	111.50	116.36
2	F	501	9F3	O1-C2-C9	2.16	109.07	103.65
2	E	501	9F3	C11-C8-C7	2.15	120.26	115.09
2	B	501	9F3	O-C-C5	2.06	112.39	110.09
2	C	501	9F3	C10-C6-C3	-2.05	110.15	115.09

There are no chirality outliers.

All (13) torsion outliers are listed below:

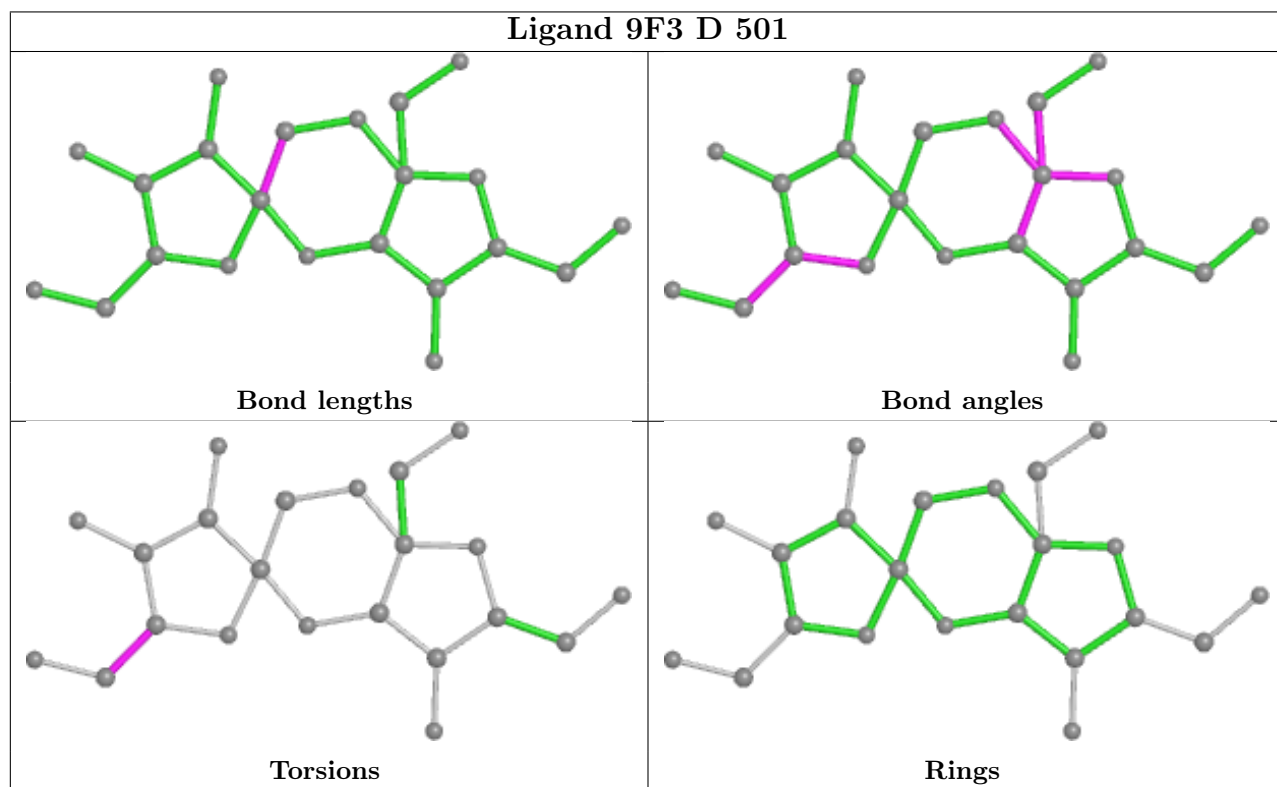
Mol	Chain	Res	Type	Atoms
2	D	501	9F3	O9-C11-C8-O3
2	F	501	9F3	O9-C11-C8-O3
2	A	501	9F3	O9-C11-C8-O3
2	A	501	9F3	O9-C11-C8-C7
2	F	501	9F3	O9-C11-C8-C7
2	D	501	9F3	O9-C11-C8-C7
2	E	501	9F3	O9-C11-C8-C7
2	B	501	9F3	O9-C11-C8-C7
2	B	501	9F3	O9-C11-C8-O3
2	E	501	9F3	O9-C11-C8-O3
2	B	501	9F3	O2-C2-C9-O7
2	B	501	9F3	O1-C2-C9-O7
2	B	501	9F3	C1-C2-C9-O7

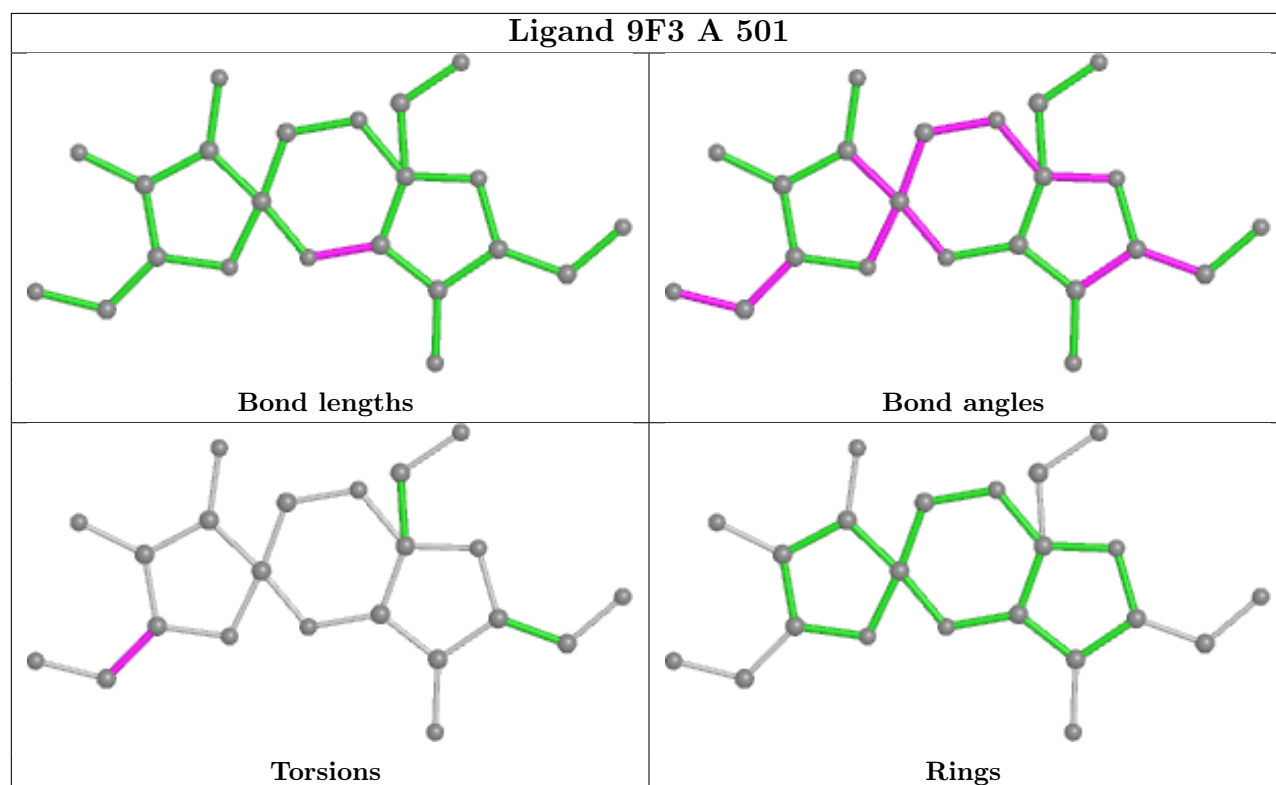
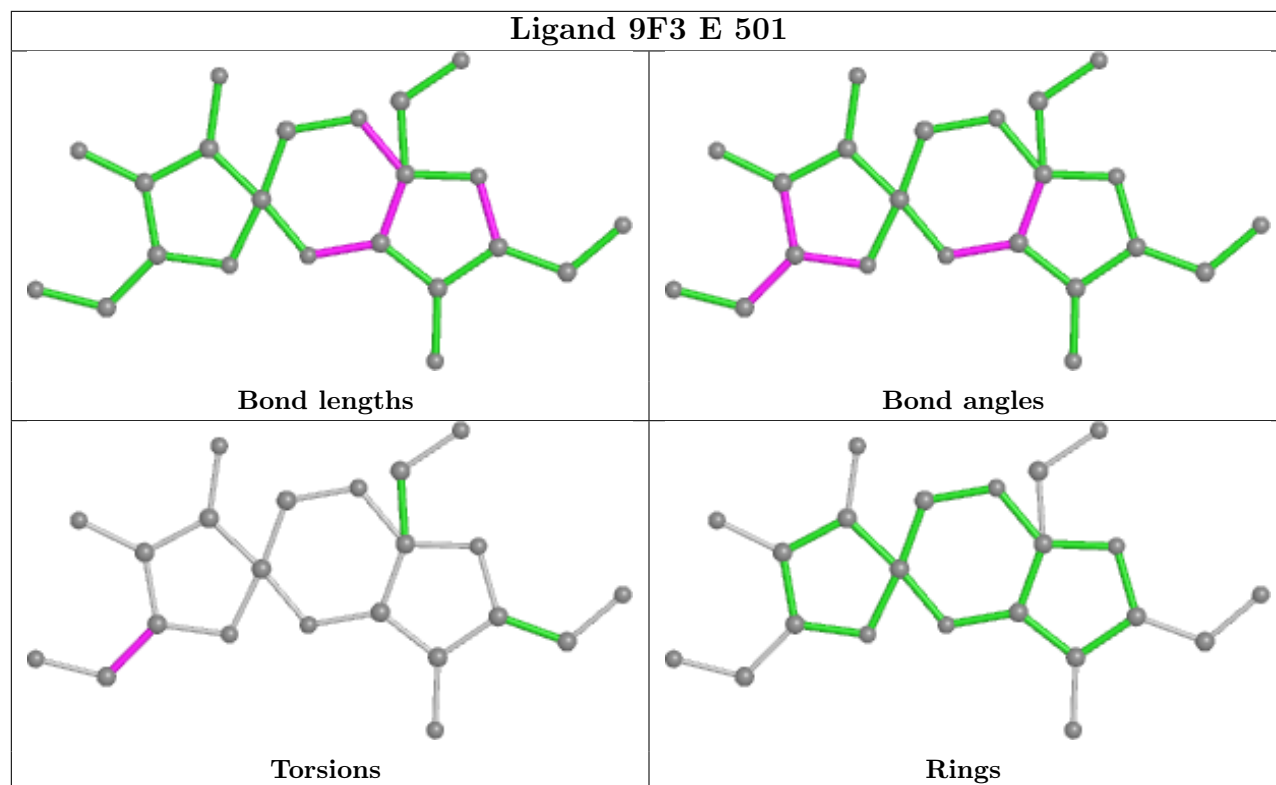
There are no ring outliers.

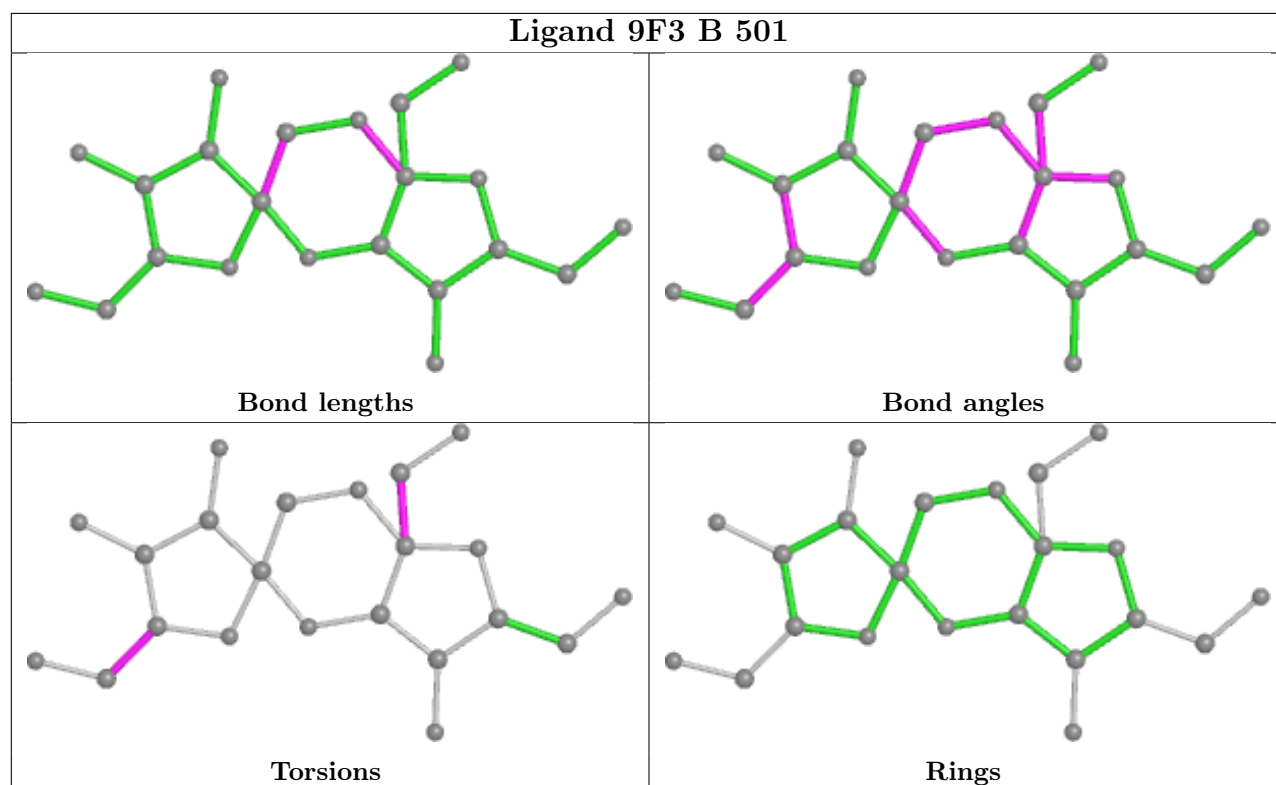
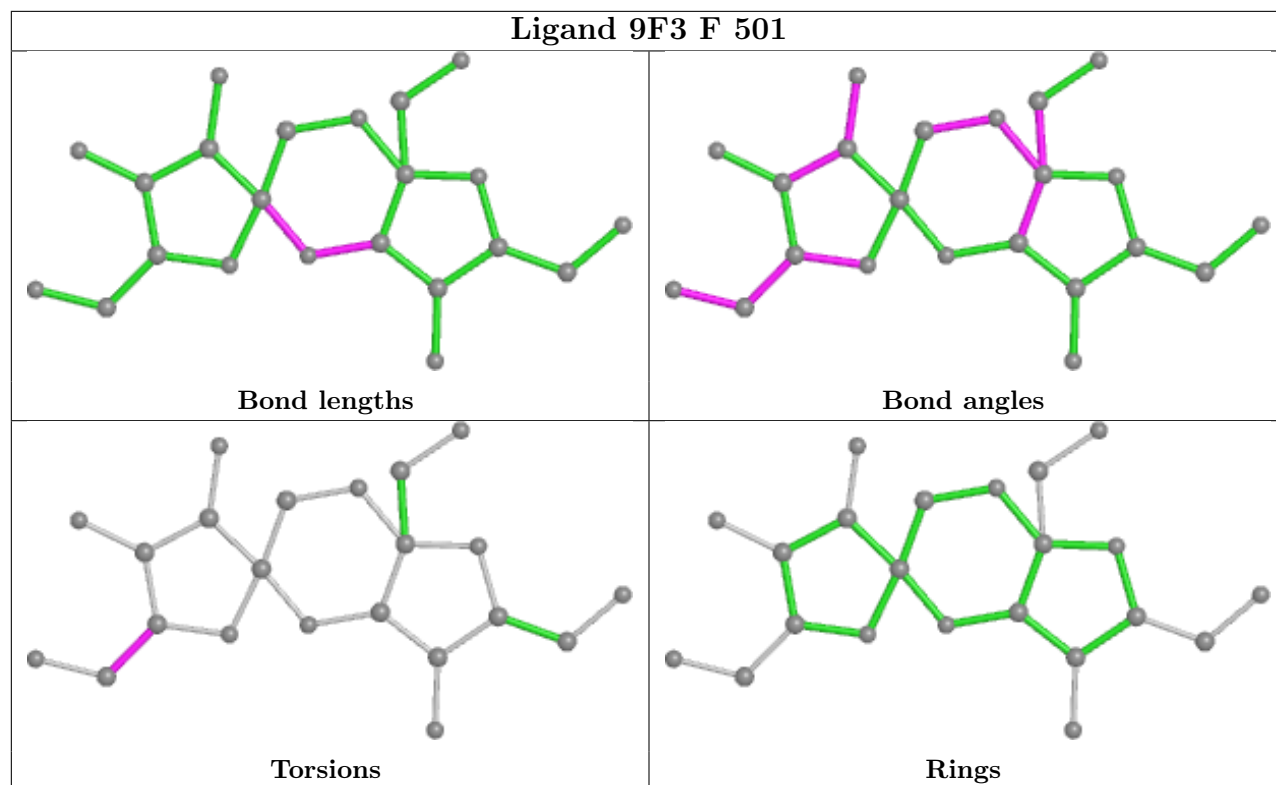
1 monomer is involved in 1 short contact:

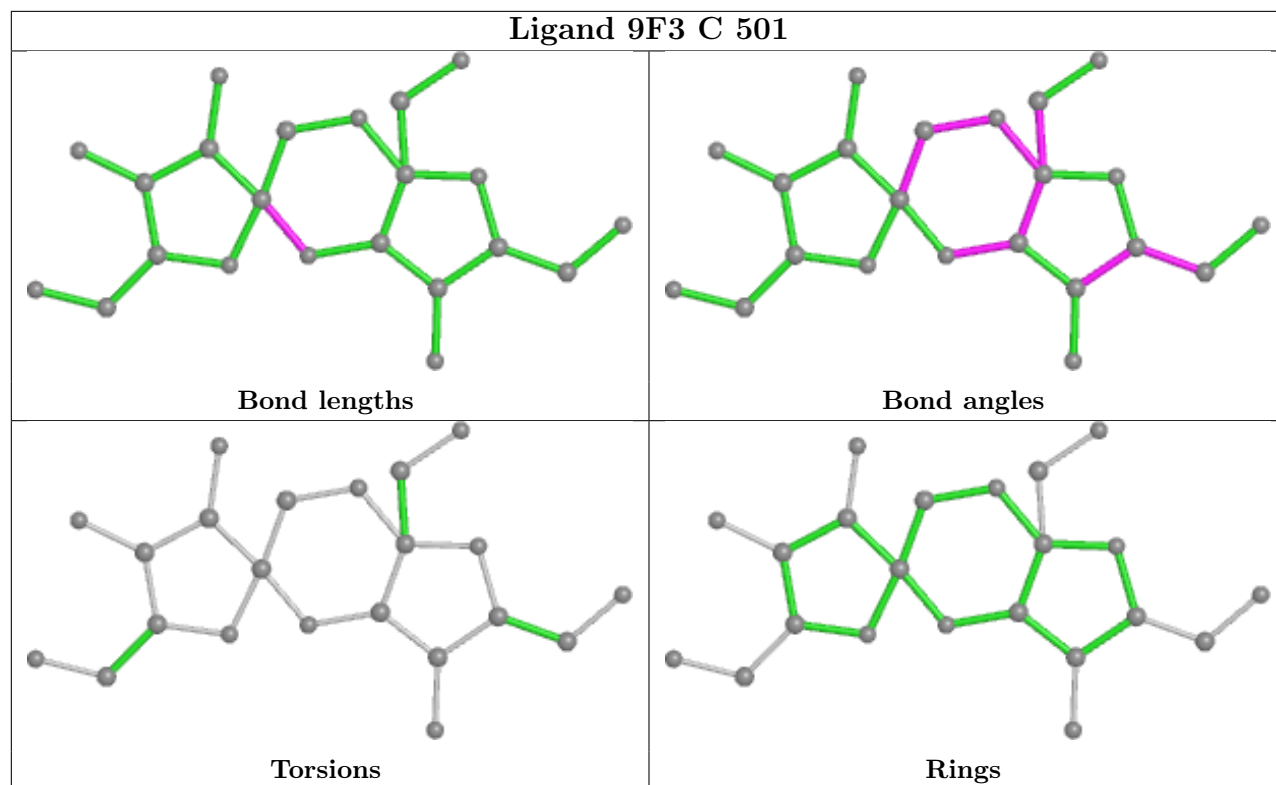
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	501	9F3	1	0

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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	442/445 (99%)	0.13	31 (7%) 16 22	29, 38, 72, 110	0
1	B	442/445 (99%)	0.32	26 (5%) 22 29	28, 43, 71, 154	0
1	C	442/445 (99%)	0.09	22 (4%) 28 36	28, 39, 68, 129	0
1	D	442/445 (99%)	0.29	34 (7%) 13 18	33, 45, 79, 124	0
1	E	442/445 (99%)	0.33	37 (8%) 11 15	31, 42, 68, 137	0
1	F	443/445 (99%)	0.33	40 (9%) 9 13	30, 40, 75, 137	0
All	All	2653/2670 (99%)	0.25	190 (7%) 15 20	28, 41, 73, 154	0

All (190) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	117	GLY	17.4
1	B	116	ALA	14.8
1	E	116	ALA	12.2
1	E	117	GLY	11.2
1	F	116	ALA	10.1
1	D	117	GLY	9.3
1	C	116	ALA	8.6
1	B	117	GLY	8.4
1	A	116	ALA	8.0
1	C	115	GLY	7.9
1	B	115	GLY	7.9
1	E	115	GLY	7.5
1	D	116	ALA	7.0
1	A	444	GLY	6.9
1	C	117	GLY	6.6
1	B	118	ASP	6.2
1	F	115	GLY	6.0
1	F	382	ALA	5.8
1	E	118	ASP	5.5

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Mol	Chain	Res	Type	RSRZ
1	F	118	ASP	5.5
1	E	444	GLY	5.3
1	A	115	GLY	5.2
1	F	399	GLU	4.9
1	E	251	THR	4.8
1	C	444	GLY	4.7
1	A	443	VAL	4.6
1	E	250	VAL	4.5
1	A	381	ALA	4.4
1	E	249	LEU	4.4
1	E	114	GLY	4.4
1	A	401	ALA	4.3
1	E	113	ALA	4.3
1	D	382	ALA	4.3
1	F	156	GLY	4.3
1	D	400	ALA	4.2
1	D	156	GLY	4.2
1	D	115	GLY	4.1
1	F	114	GLY	4.1
1	E	227	THR	3.9
1	B	400	ALA	3.9
1	C	118	ASP	3.9
1	E	275	ASN	3.9
1	D	113	ALA	3.8
1	E	298	ALA	3.7
1	F	249	LEU	3.6
1	E	274	THR	3.6
1	F	252	ALA	3.6
1	C	252	ALA	3.6
1	E	252	ALA	3.6
1	C	113	ALA	3.5
1	E	299	THR	3.6
1	D	114	GLY	3.5
1	A	118	ASP	3.5
1	B	249	LEU	3.5
1	F	226	ILE	3.5
1	D	252	ALA	3.4
1	D	401	ALA	3.4
1	B	380	ASP	3.3
1	A	156	GLY	3.3
1	F	401	ALA	3.3
1	E	228	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	225	LYS	3.3
1	F	380	ASP	3.3
1	D	381	ALA	3.2
1	F	228	ASP	3.2
1	B	227	THR	3.2
1	F	275	ASN	3.2
1	F	250	VAL	3.2
1	F	251	THR	3.2
1	D	399	GLU	3.2
1	A	398	THR	3.1
1	C	114	GLY	3.1
1	D	299	THR	3.0
1	F	273	VAL	3.0
1	A	382	ALA	3.0
1	B	353	GLY	3.0
1	B	399	GLU	3.0
1	B	114	GLY	2.9
1	D	347	ASN	2.9
1	A	348	GLU	2.9
1	D	275	ASN	2.9
1	F	203	ILE	2.9
1	F	274	THR	2.9
1	E	226	ILE	2.9
1	C	251	THR	2.9
1	F	298	ALA	2.9
1	A	380	ASP	2.9
1	B	381	ALA	2.9
1	F	400	ALA	2.9
1	D	154	GLY	2.8
1	E	443	VAL	2.8
1	C	401	ALA	2.8
1	A	114	GLY	2.8
1	D	389	GLU	2.8
1	F	299	THR	2.7
1	D	444	GLY	2.7
1	B	274	THR	2.7
1	F	227	THR	2.7
1	F	14	ALA	2.7
1	E	157	ARG	2.7
1	A	400	ALA	2.7
1	D	298	ALA	2.7
1	B	251	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	153	ASP	2.7
1	F	113	ALA	2.7
1	A	275	ASN	2.7
1	B	347	ASN	2.7
1	F	388	PHE	2.7
1	B	252	ALA	2.6
1	E	205	HIS	2.6
1	C	249	LEU	2.6
1	C	250	VAL	2.6
1	E	272	SER	2.6
1	A	350	ARG	2.6
1	B	352	GLU	2.6
1	C	227	THR	2.6
1	F	296	LEU	2.6
1	F	248	LEU	2.6
1	A	352	GLU	2.6
1	E	225	LYS	2.6
1	E	273	VAL	2.5
1	D	274	THR	2.5
1	F	204	HIS	2.5
1	E	3	SER	2.5
1	C	381	ALA	2.5
1	A	251	THR	2.5
1	C	156	GLY	2.4
1	D	251	THR	2.4
1	B	113	ALA	2.4
1	D	118	ASP	2.4
1	D	390	ALA	2.4
1	E	255	VAL	2.4
1	D	385	ASP	2.4
1	D	204	HIS	2.4
1	A	227	THR	2.4
1	E	204	HIS	2.3
1	C	275	ASN	2.3
1	F	444	GLY	2.3
1	F	381	ALA	2.3
1	A	274	THR	2.3
1	A	228	ASP	2.3
1	D	228	ASP	2.3
1	E	230	LEU	2.3
1	A	226	ILE	2.3
1	D	383	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	203	ILE	2.3
1	A	252	ALA	2.3
1	D	386	SER	2.3
1	F	347	ASN	2.2
1	B	351	PRO	2.2
1	C	226	ILE	2.2
1	D	236	ARG	2.2
1	C	205	HIS	2.2
1	F	314	GLY	2.2
1	A	204	HIS	2.2
1	C	204	HIS	2.2
1	E	336	ILE	2.2
1	E	248	LEU	2.2
1	E	399	GLU	2.2
1	B	275	ASN	2.2
1	B	354	ALA	2.2
1	C	228	ASP	2.2
1	A	154	GLY	2.2
1	E	337	GLY	2.1
1	B	204	HIS	2.1
1	C	273	VAL	2.1
1	E	352	GLU	2.1
1	F	313	PHE	2.1
1	A	205	HIS	2.1
1	D	227	THR	2.1
1	A	250	VAL	2.1
1	E	229	ASN	2.1
1	E	253	ASN	2.1
1	F	276	ASN	2.1
1	A	202	SER	2.1
1	B	41	VAL	2.1
1	D	313	PHE	2.1
1	D	230	LEU	2.1
1	B	225	LYS	2.1
1	A	353	GLY	2.1
1	B	156	GLY	2.1
1	C	181	VAL	2.1
1	F	202	SER	2.1
1	B	412	PRO	2.1
1	E	348	GLU	2.0
1	D	379	VAL	2.0
1	D	157	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	E	296	LEU	2.0
1	F	154	GLY	2.0
1	A	273	VAL	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](#)

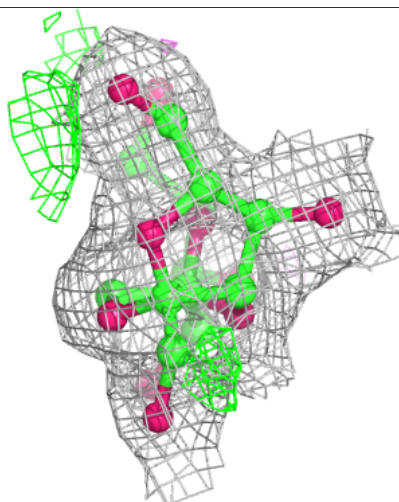
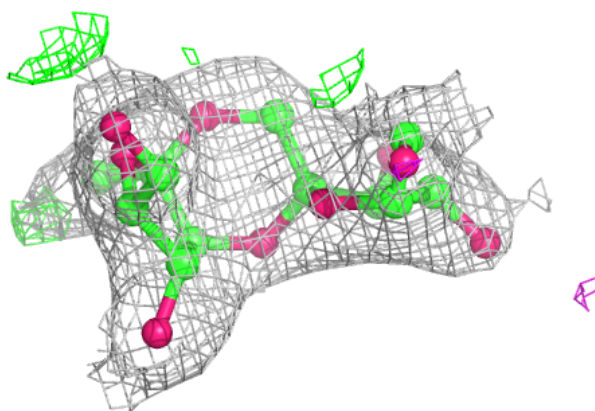
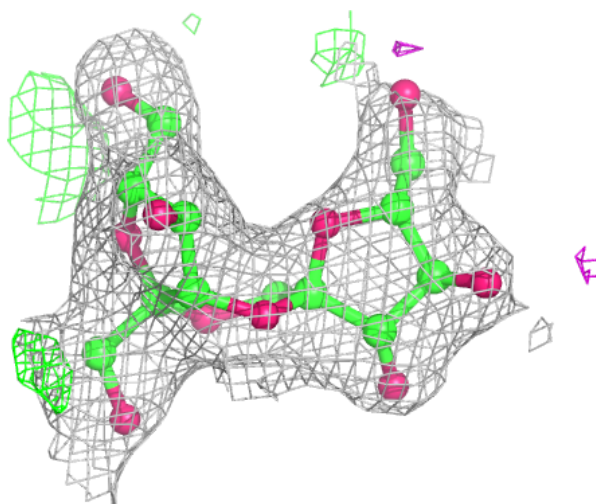
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	9F3	B	501	22/22	0.93	0.12	40,46,56,61	0
2	9F3	D	501	22/22	0.94	0.12	46,53,57,58	0
2	9F3	E	501	22/22	0.94	0.11	36,42,46,46	0
2	9F3	F	501	22/22	0.94	0.12	42,45,46,48	0
2	9F3	A	501	22/22	0.95	0.12	36,44,49,50	0
2	9F3	C	501	22/22	0.96	0.10	34,37,43,45	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.

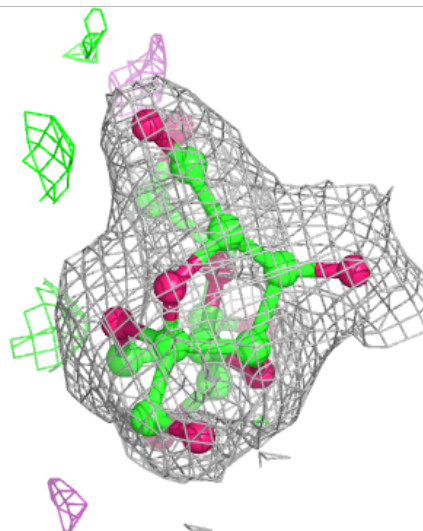
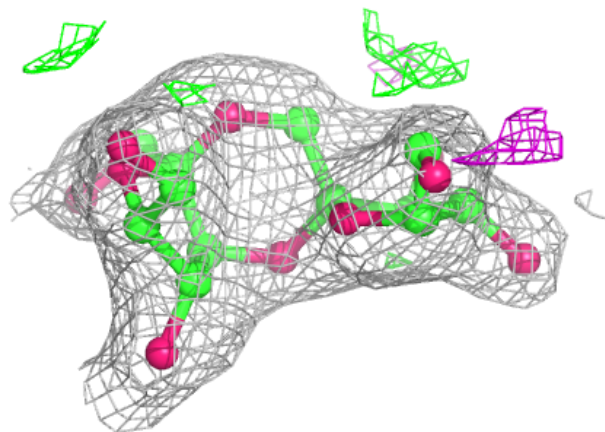
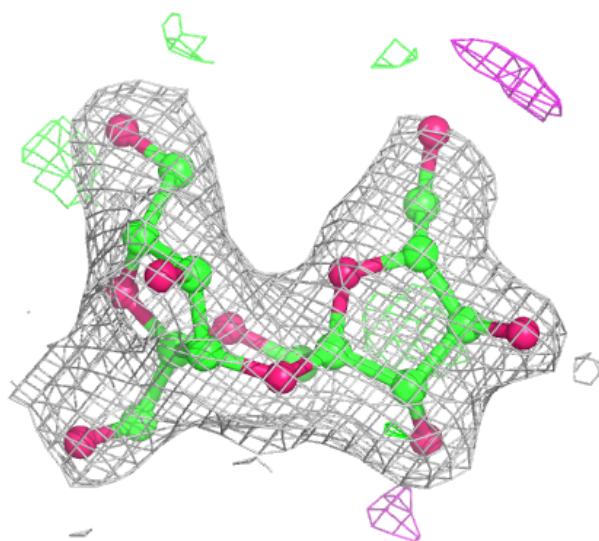
Electron density around 9F3 B 501:

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



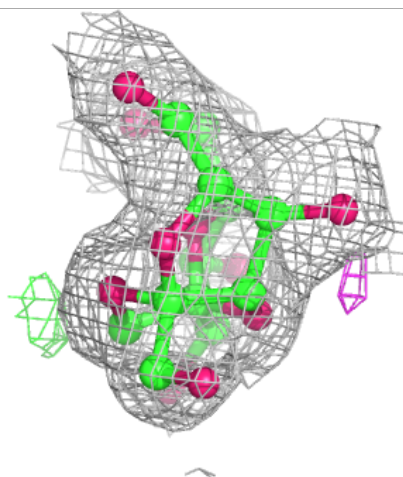
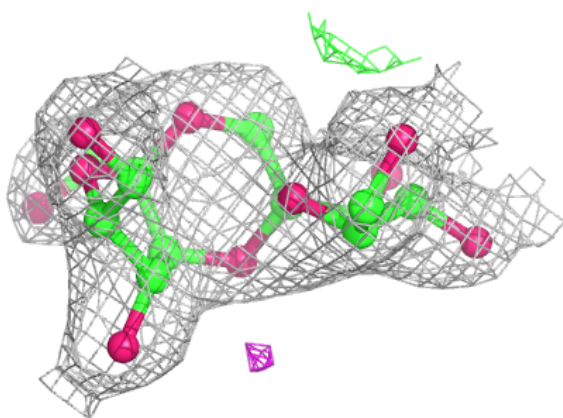
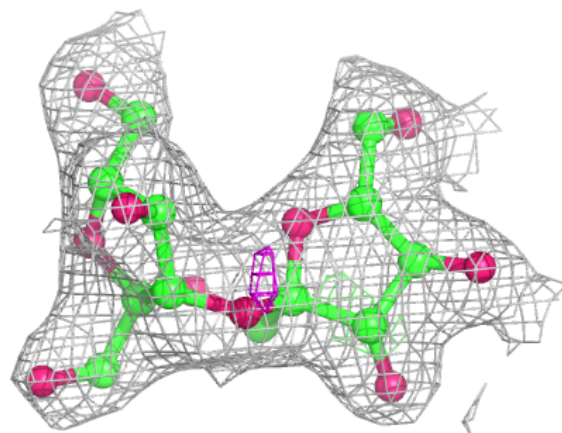
Electron density around 9F3 D 501:

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



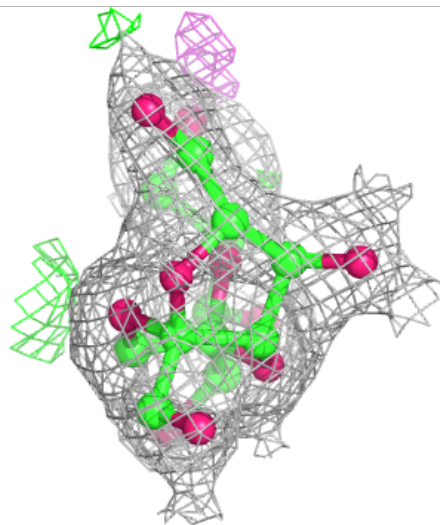
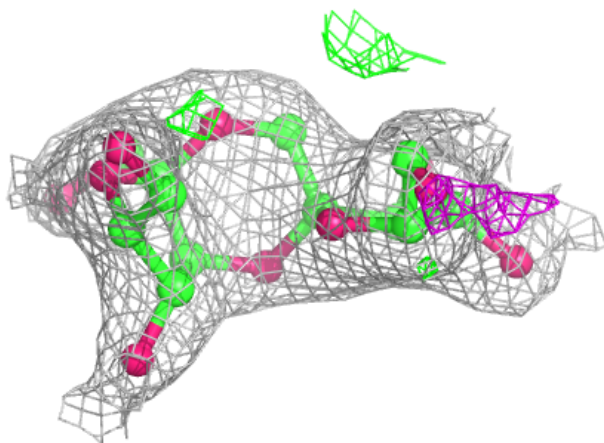
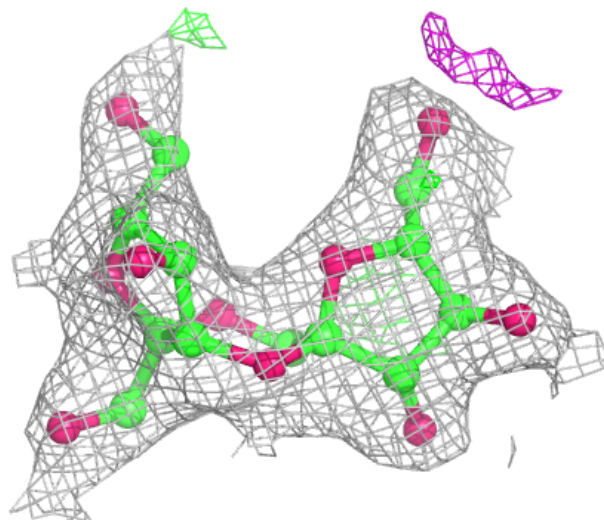
Electron density around 9F3 E 501:

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



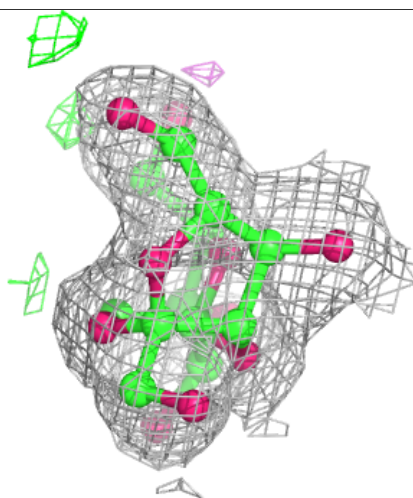
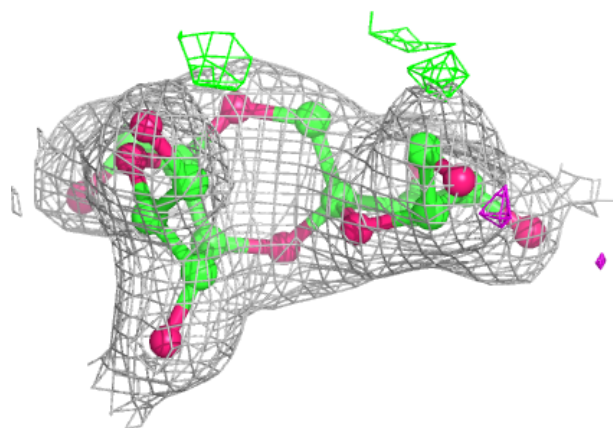
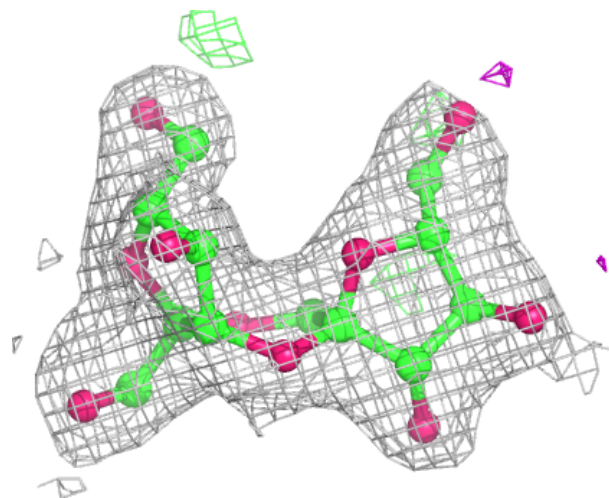
Electron density around 9F3 F 501:

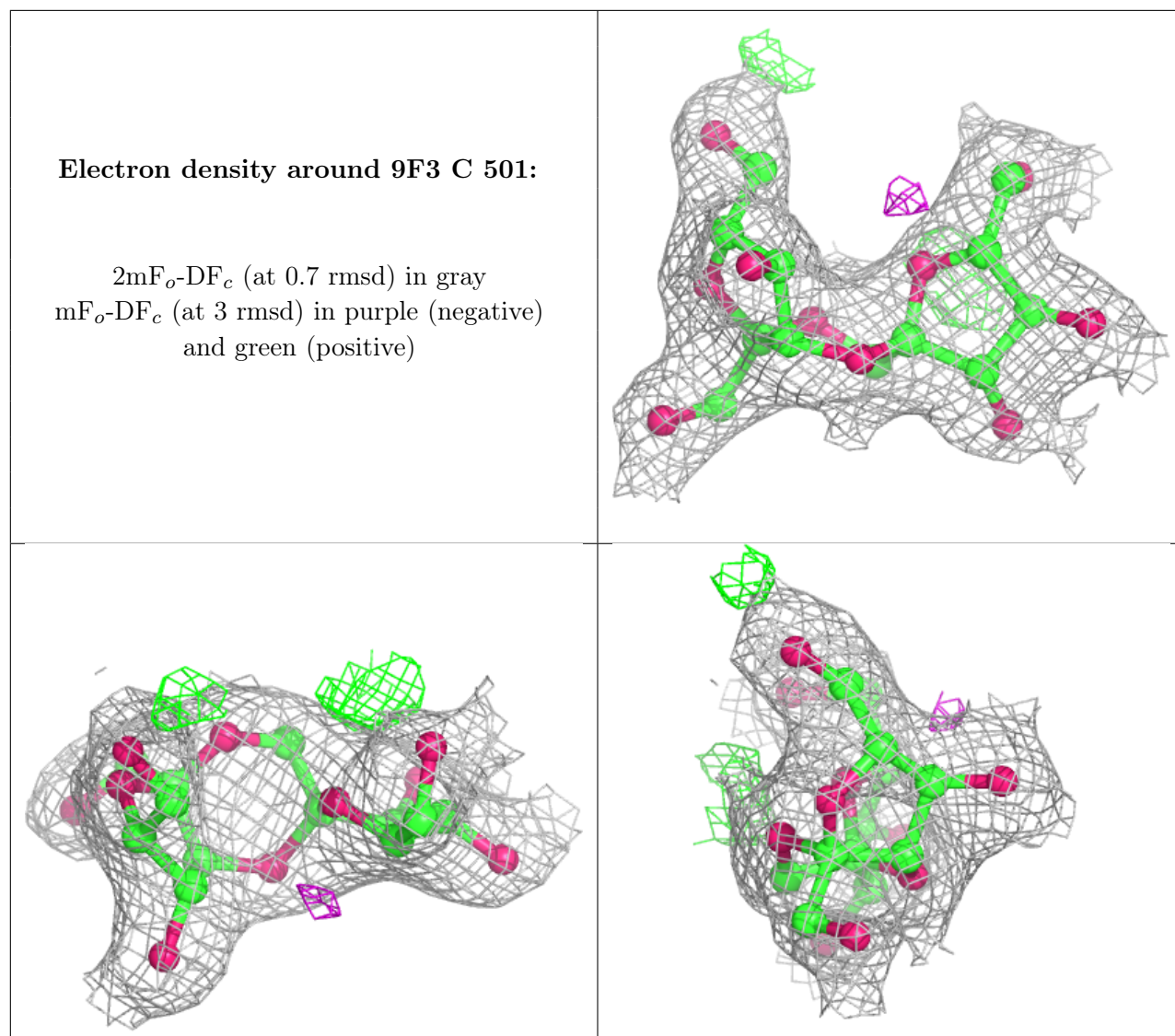
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 9F3 A 501:

$2mF_o-DF_c$ (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.