wwPDB X-ray Structure Validation Summary Report (i)

Sep 25, 2023 – 07:00 AM EDT

PDB ID	:	5VOO
Title	:	Methionine synthase folate-binding domain with methyltetrahydrofolate from Thermus thermophilus HB8
Authors	:	Koutmos, M.; Yamada, K.
Deposited on	:	2017-05-03
Resolution	:	2.40 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 (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:

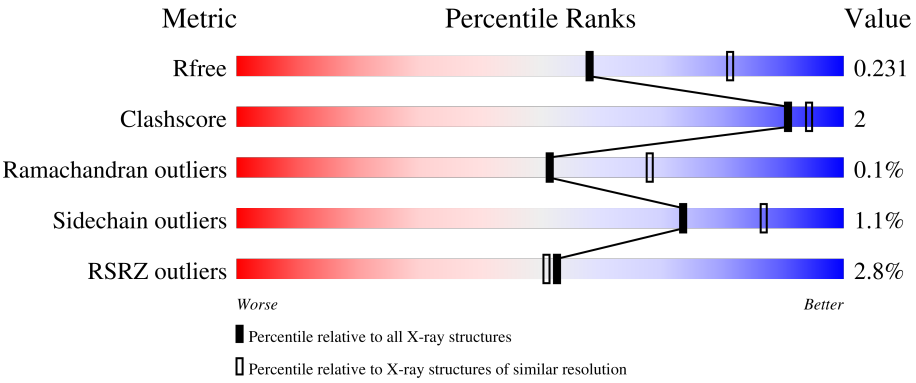
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	296	90% 5% 5%
1	B	296	90% 5% 5%
1	C	296	91% • • 5%
1	D	296	3% 91% • 5%
1	E	296	6% 91% • 5%

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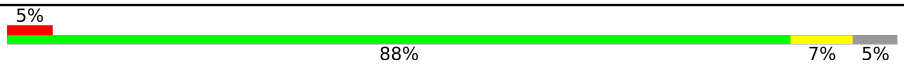
Mol	Chain	Length	Quality of chain
1	F	296	

2 Entry composition (i)

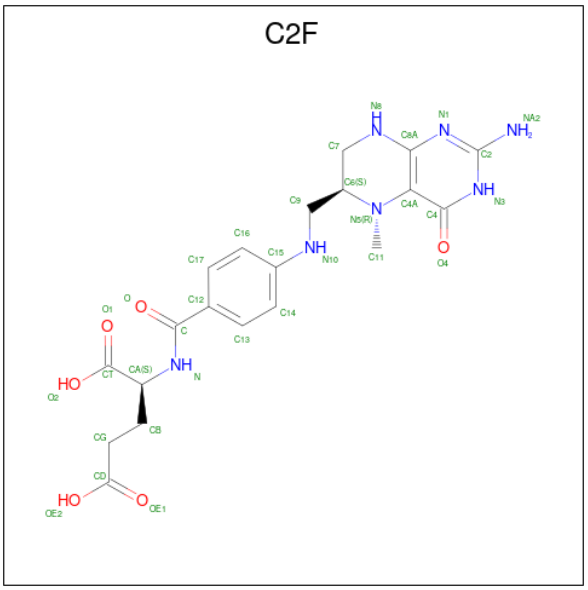
There are 7 unique types of molecules in this entry. The entry contains 27574 atoms, of which 13747 are hydrogens and 0 are deuteriums.

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 5-methyltetrahydrofolate homocysteine S-methyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	282	Total	C	H	N	O	S	0	1	0
			4500	1417	2275	393	408	7			
1	B	282	Total	C	H	N	O	S	0	0	0
			4480	1412	2263	390	408	7			
1	C	282	Total	C	H	N	O	S	0	1	0
			4495	1414	2275	391	408	7			
1	D	280	Total	C	H	N	O	S	0	0	0
			4453	1403	2251	386	406	7			
1	E	281	Total	C	H	N	O	S	0	0	0
			4464	1406	2257	387	407	7			
1	F	280	Total	C	H	N	O	S	0	0	0
			4454	1403	2252	386	406	7			

- Molecule 2 is 5-METHYL-5,6,7,8-TETRAHYDROFOLIC ACID (three-letter code: C2F) (formula: $C_{20}H_{25}N_7O_6$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	0	0
			56	20	23	7	6		
2	B	1	Total	C	H	N	O	0	0
			56	20	23	7	6		
2	C	1	Total	C	H	N	O	0	0
			56	20	23	7	6		
2	D	1	Total	C	H	N	O	0	0
			56	20	23	7	6		
2	E	1	Total	C	H	N	O	0	0
			56	20	23	7	6		
2	F	1	Total	C	H	N	O	0	0
			56	20	23	7	6		

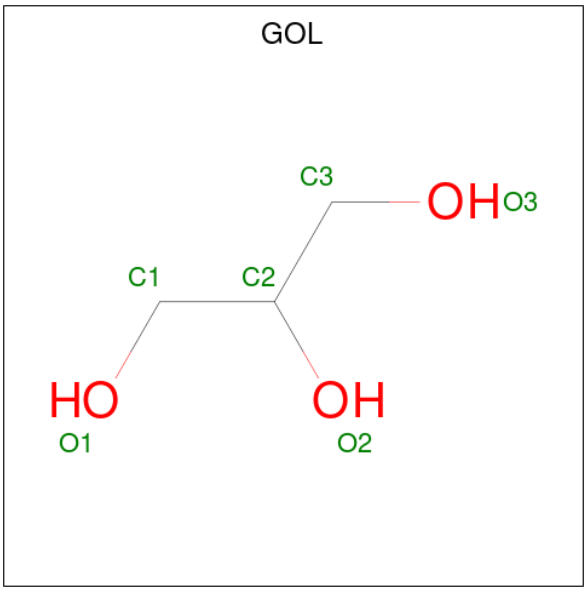
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Na	0	0
			3	3		
3	B	1	Total	Na	0	0
			1	1		
3	D	1	Total	Na	0	0
			1	1		
3	F	1	Total	Na	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

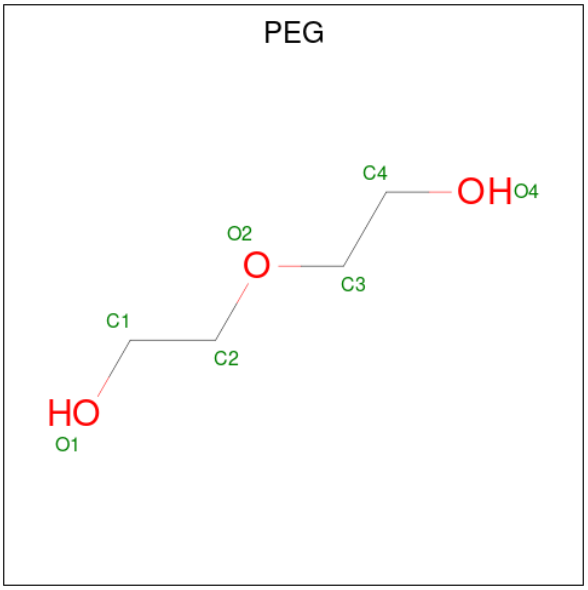
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	C	1	Total	Cl	0	0
			1	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	D	1	Total	C	H	O	0	0
			17	4	10	3		
6	E	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 7 is water.

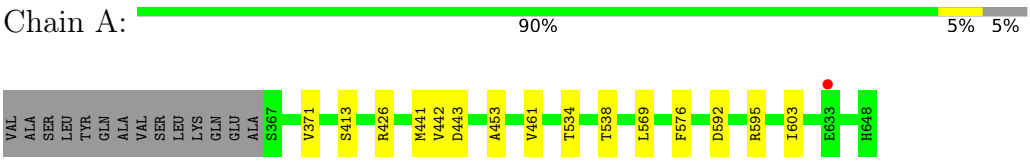
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	54	Total O 54 54	0	0
7	B	101	Total O 101 101	0	0
7	C	55	Total O 55 55	0	0
7	D	35	Total O 35 35	0	0
7	E	42	Total O 42 42	0	0
7	F	35	Total O 35 35	0	0

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.

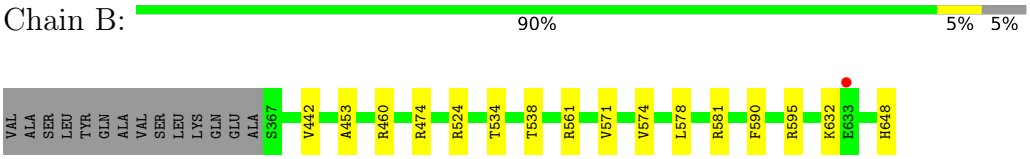
• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

Chain A:



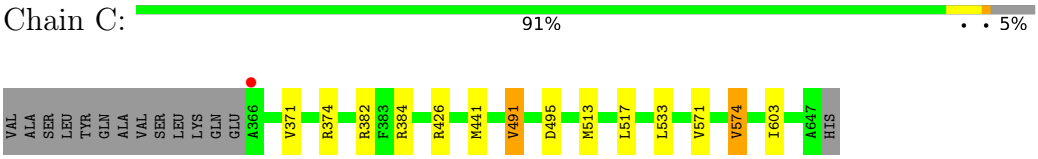
• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

Chain B:



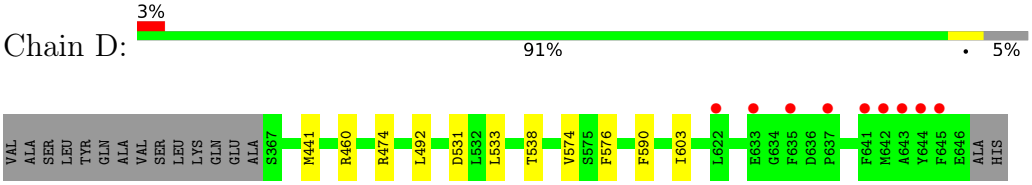
• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

Chain C:



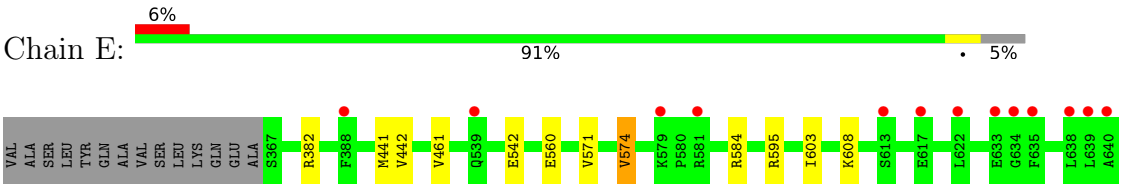
• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

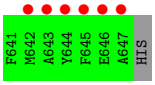
Chain D:



• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

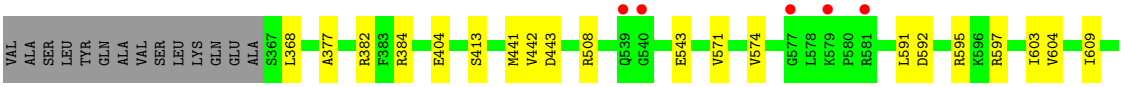
Chain E:

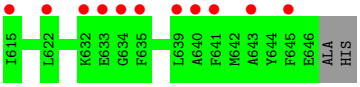




• Molecule 1: 5-methyltetrahydrofolate homocysteine S-methyltransferase

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α, β, γ	188.46Å 188.46Å 247.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	163.21 – 2.40 49.38 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.3 (163.21-2.40) 99.3 (49.38-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.02 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.190 , 0.230 0.197 , 0.231	Depositor DCC
R_{free} test set	5056 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	41.6	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 34.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	27574	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, C2F, NA, PEG, CL

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	0.48	0/2266	0.72	1/3062 (0.0%)
1	B	0.48	0/2255	0.78	5/3048 (0.2%)
1	C	0.46	0/2260	0.73	3/3054 (0.1%)
1	D	0.45	0/2239	0.72	0/3026
1	E	0.45	0/2244	0.70	1/3033 (0.0%)
1	F	0.45	0/2239	0.71	0/3026
All	All	0.46	0/13503	0.73	10/18249 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	561	ARG	NE-CZ-NH2	-6.22	117.19	120.30
1	B	460	ARG	NE-CZ-NH2	6.11	123.35	120.30
1	C	384	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	B	561	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	C	426	ARG	NE-CZ-NH1	5.35	122.97	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2225	2275	2275	9	0
1	B	2217	2263	2263	7	0
1	C	2220	2275	2275	8	0
1	D	2202	2251	2251	5	0
1	E	2207	2257	2257	6	0
1	F	2202	2252	2252	12	0
2	A	33	23	23	0	0
2	B	33	23	23	0	0
2	C	33	23	23	0	0
2	D	33	23	23	0	0
2	E	33	23	23	0	0
2	F	33	23	23	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	B	12	16	16	0	0
6	D	7	10	10	0	0
6	E	7	10	10	0	0
7	A	54	0	0	0	0
7	B	101	0	0	0	1
7	C	55	0	0	0	0
7	D	35	0	0	0	0
7	E	42	0	0	0	0
7	F	35	0	0	0	0
All	All	13827	13747	13747	45	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 45 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:538:THR:HG21	1:A:576:PHE:O	1.78	0.84
1:D:441:MET:HE1	1:D:603:ILE:HD11	1.72	0.70
1:B:442:VAL:HG21	1:B:453:ALA:CB	2.23	0.68
1:B:574:VAL:HG21	1:B:590:PHE:CD2	2.29	0.67
1:D:441:MET:CE	1:D:603:ILE:HD11	2.34	0.57

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:873:HOH:O	7:B:873:HOH:O[9_554]	1.99	0.21

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	281/296 (95%)	275 (98%)	6 (2%)	0	100	100
1	B	280/296 (95%)	275 (98%)	5 (2%)	0	100	100
1	C	281/296 (95%)	272 (97%)	8 (3%)	1 (0%)	34	48
1	D	278/296 (94%)	270 (97%)	7 (2%)	1 (0%)	34	48
1	E	279/296 (94%)	268 (96%)	11 (4%)	0	100	100
1	F	278/296 (94%)	267 (96%)	11 (4%)	0	100	100
All	All	1677/1776 (94%)	1627 (97%)	48 (3%)	2 (0%)	51	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	533	LEU
1	D	533	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	232/242 (96%)	232 (100%)	0	100	100
1	B	231/242 (96%)	229 (99%)	2 (1%)	78	90
1	C	231/242 (96%)	229 (99%)	2 (1%)	78	90
1	D	230/242 (95%)	228 (99%)	2 (1%)	78	90
1	E	230/242 (95%)	226 (98%)	4 (2%)	60	78
1	F	230/242 (95%)	225 (98%)	5 (2%)	52	71
All	All	1384/1452 (95%)	1369 (99%)	15 (1%)	73	87

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	542	GLU
1	F	543	GLU
1	E	560	GLU
1	F	597	ARG
1	F	404	GLU

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 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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	C2F	E	3001	-	33,35,35	1.38	3 (9%)	35,49,49	1.81	7 (20%)
5	GOL	B	701	-	5,5,5	0.36	0	5,5,5	0.46	0
6	PEG	D	3003	-	6,6,6	0.48	0	5,5,5	0.18	0
2	C2F	D	3001	-	33,35,35	1.25	3 (9%)	35,49,49	1.75	9 (25%)
5	GOL	B	704	-	5,5,5	0.49	0	5,5,5	0.59	0
2	C2F	B	702	-	33,35,35	1.26	2 (6%)	35,49,49	1.75	8 (22%)
2	C2F	F	3001	-	33,35,35	1.39	3 (9%)	35,49,49	1.80	8 (22%)
2	C2F	A	3001	-	33,35,35	1.38	3 (9%)	35,49,49	1.77	8 (22%)
2	C2F	C	702	-	33,35,35	1.42	3 (9%)	35,49,49	1.58	6 (17%)
6	PEG	E	3002	-	6,6,6	0.53	0	5,5,5	0.22	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
2	C2F	E	3001	-	-	2/22/35/35	0/3/3/3
5	GOL	B	701	-	-	1/4/4/4	-
6	PEG	D	3003	-	-	2/4/4/4	-
2	C2F	D	3001	-	-	2/22/35/35	0/3/3/3
5	GOL	B	704	-	-	4/4/4/4	-
2	C2F	B	702	-	-	4/22/35/35	0/3/3/3
2	C2F	F	3001	-	-	1/22/35/35	0/3/3/3
2	C2F	A	3001	-	-	4/22/35/35	0/3/3/3
2	C2F	C	702	-	-	4/22/35/35	0/3/3/3
6	PEG	E	3002	-	-	2/4/4/4	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	702	C2F	C4A-C4	5.70	1.49	1.41
2	A	3001	C2F	C4A-C4	5.51	1.49	1.41
2	E	3001	C2F	C4A-C4	5.43	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	3001	C2F	C4A-C4	5.23	1.48	1.41
2	B	702	C2F	C4A-C4	4.88	1.48	1.41

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	3001	C2F	C11-N5-C4A	4.88	119.94	113.30
2	F	3001	C2F	C2-N3-C4	4.64	123.31	115.93
2	E	3001	C2F	C11-N5-C4A	4.63	119.59	113.30
2	B	702	C2F	C2-N3-C4	4.42	122.95	115.93
2	E	3001	C2F	C8A-C4A-C4	4.33	117.82	114.44

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

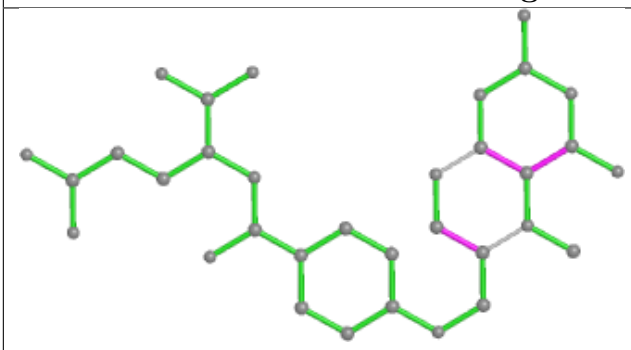
Mol	Chain	Res	Type	Atoms
2	A	3001	C2F	N-CA-CB-CG
2	B	702	C2F	N-CA-CB-CG
2	C	702	C2F	N-CA-CB-CG
2	E	3001	C2F	N-CA-CB-CG
2	A	3001	C2F	CT-CA-CB-CG

There are no ring outliers.

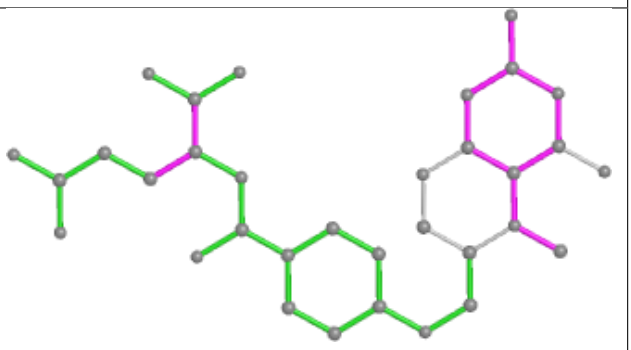
No monomer is involved in short contacts.

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.

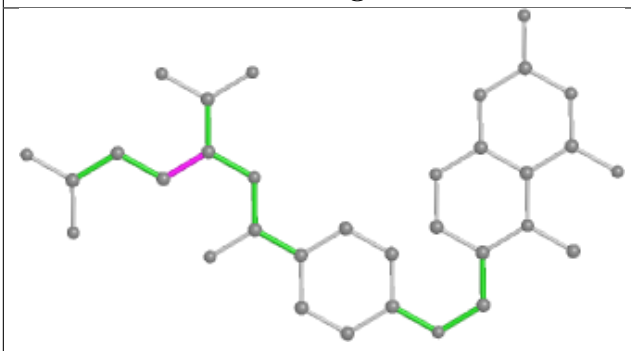
Ligand C2F E 3001



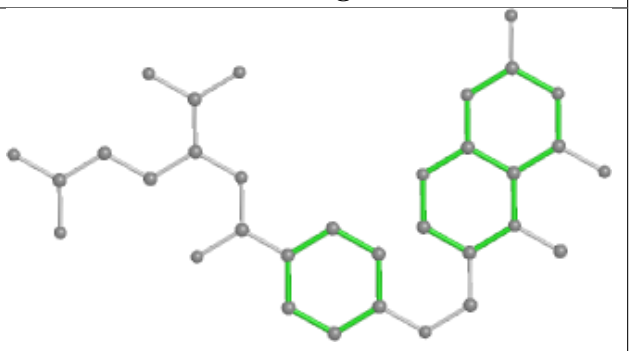
Bond lengths



Bond angles

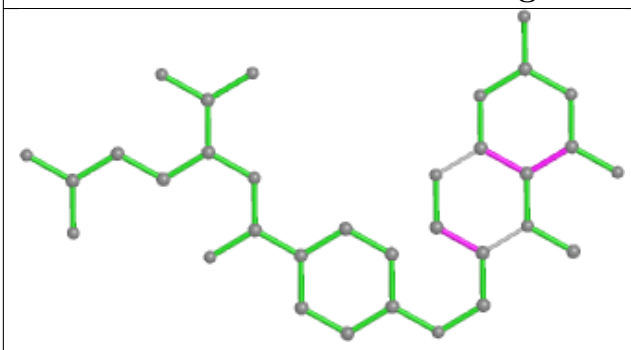


Torsions

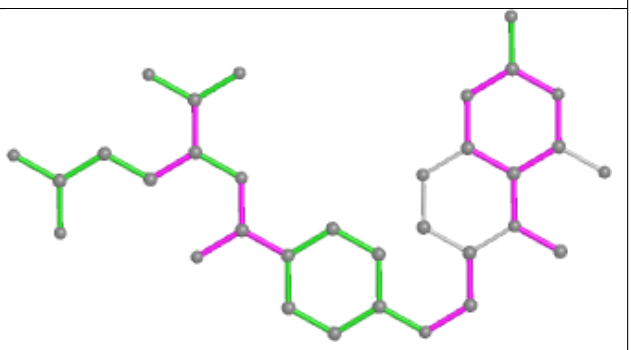


Rings

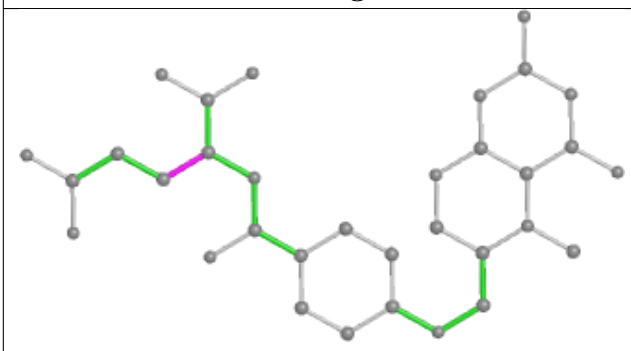
Ligand C2F D 3001



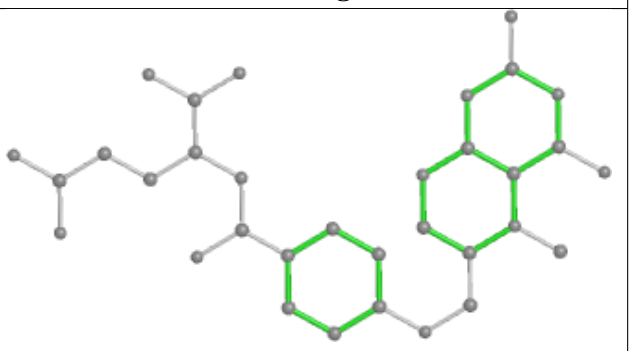
Bond lengths



Bond angles

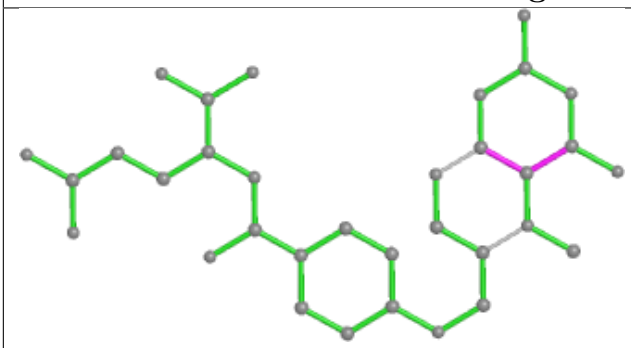


Torsions

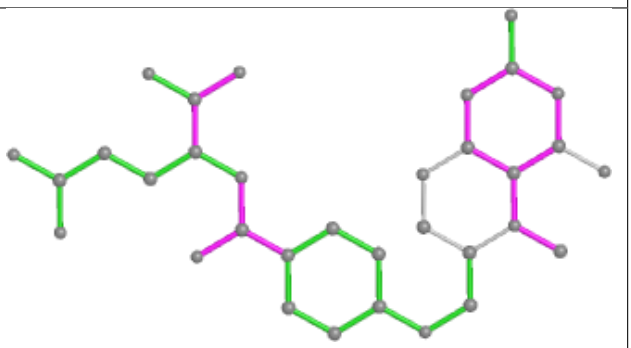


Rings

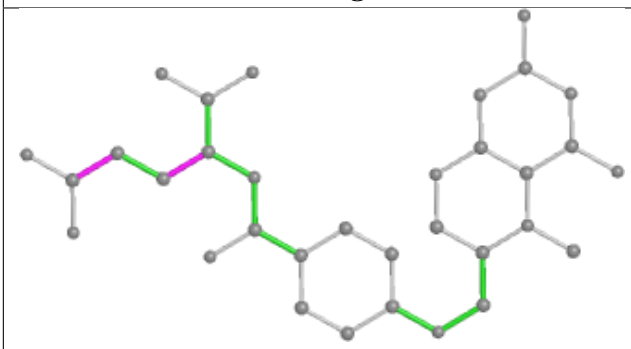
Ligand C2F B 702



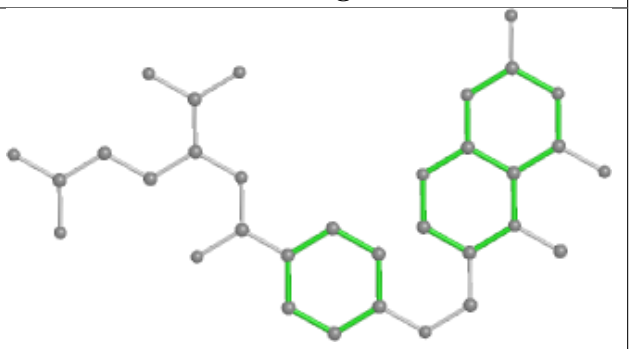
Bond lengths



Bond angles

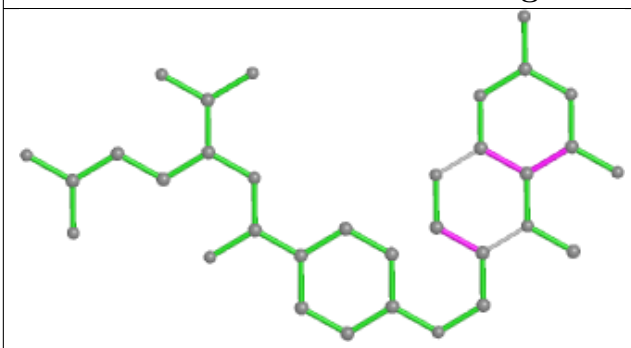


Torsions

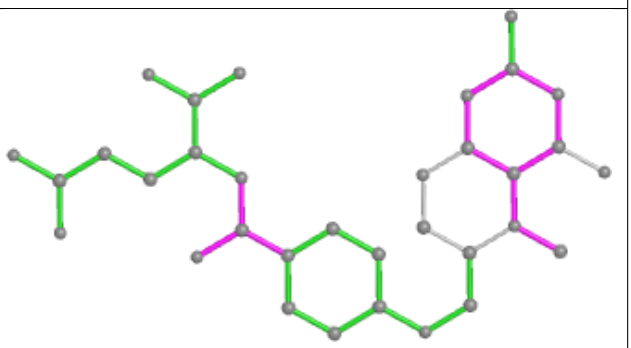


Rings

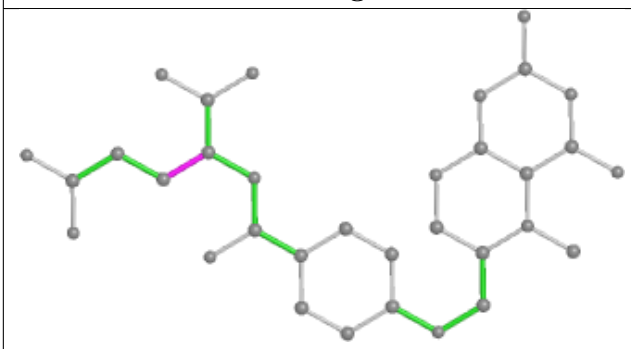
Ligand C2F F 3001



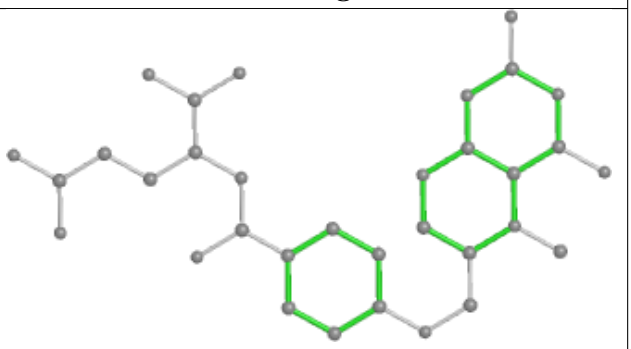
Bond lengths



Bond angles

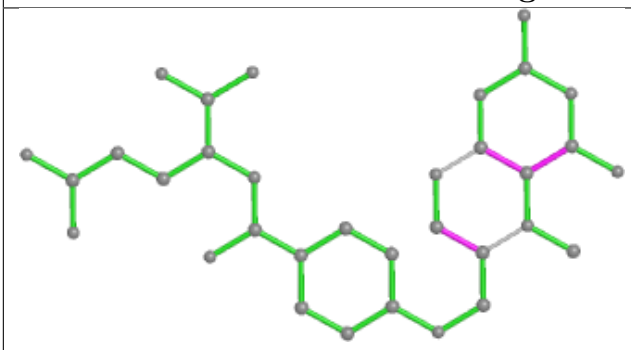


Torsions

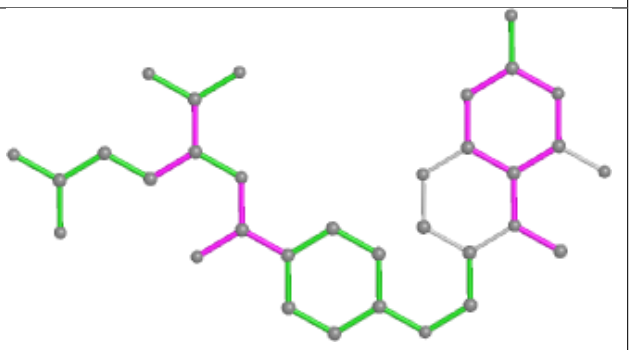


Rings

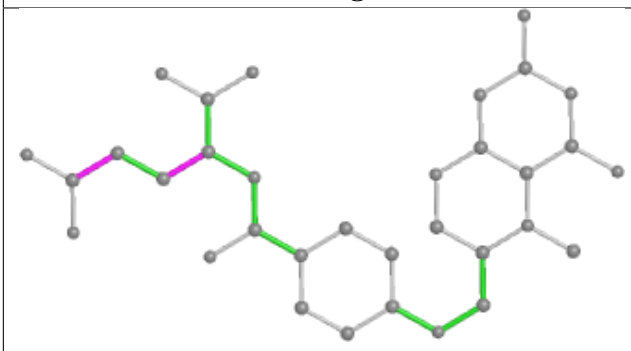
Ligand C2F A 3001



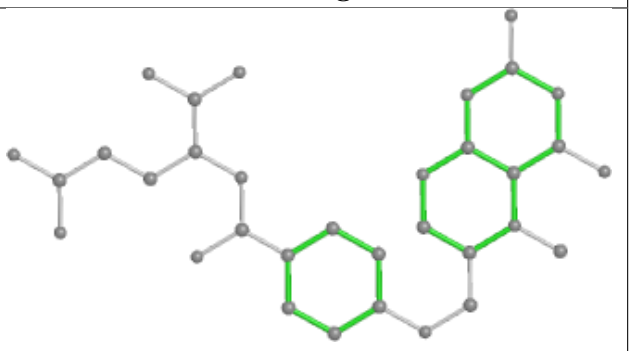
Bond lengths



Bond angles

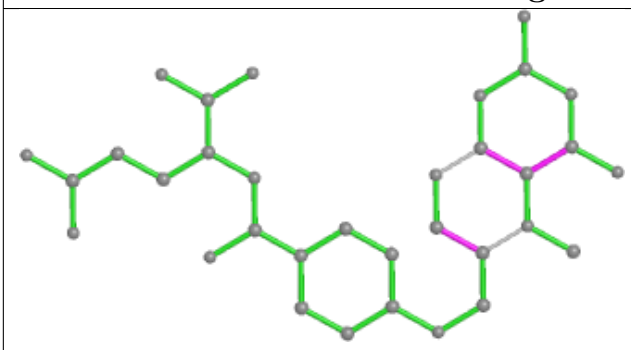


Torsions

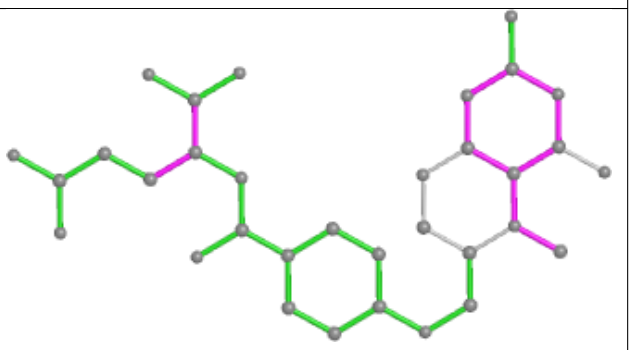


Rings

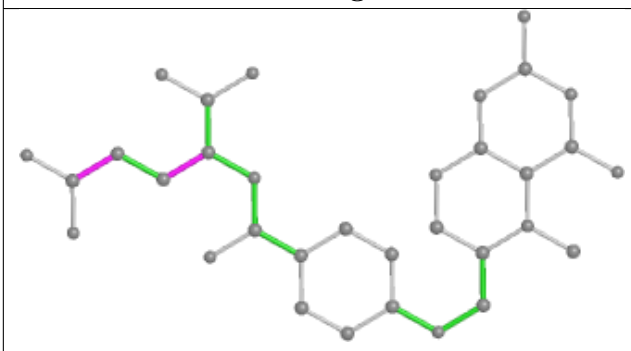
Ligand C2F C 702



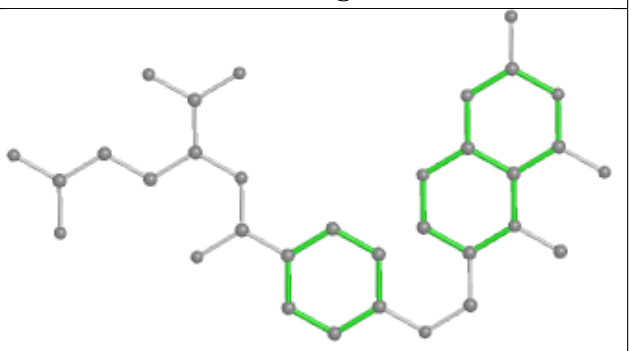
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	282/296 (95%)	-0.20	1 (0%)	92	91	31, 41, 59, 86	0
1	B	282/296 (95%)	-0.16	1 (0%)	92	91	30, 40, 60, 96	0
1	C	282/296 (95%)	-0.13	1 (0%)	92	91	34, 45, 68, 92	0
1	D	280/296 (94%)	-0.02	9 (3%)	47	46	34, 48, 78, 108	0
1	E	281/296 (94%)	0.04	19 (6%)	17	15	37, 50, 84, 116	0
1	F	280/296 (94%)	0.13	16 (5%)	23	22	38, 54, 92, 126	0
All	All	1687/1776 (94%)	-0.06	47 (2%)	53	51	30, 46, 78, 126	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	540	GLY	8.0
1	E	634	GLY	5.8
1	F	635	PHE	5.5
1	F	634	GLY	5.2
1	F	643	ALA	5.2

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

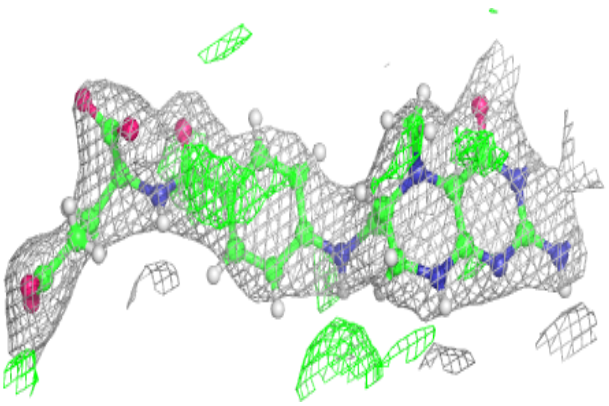
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

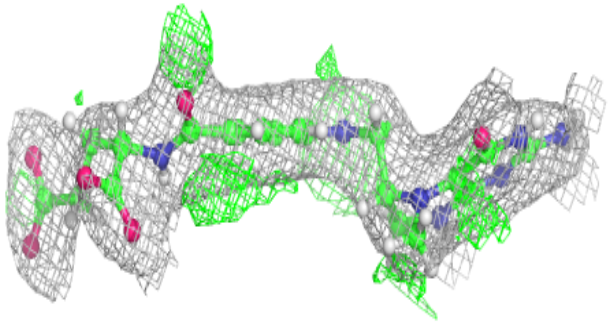
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NA	F	3002	1/1	0.79	0.12	64,64,64,64	0
6	PEG	D	3003	7/7	0.82	0.17	57,62,67,68	0
3	NA	D	3002	1/1	0.87	0.07	54,54,54,54	0
2	C2F	F	3001	33/33	0.90	0.18	35,44,58,61	56
2	C2F	E	3001	33/33	0.90	0.18	31,35,53,55	56
6	PEG	E	3002	7/7	0.90	0.16	60,64,65,68	0
3	NA	A	3003	1/1	0.91	0.24	58,58,58,58	0
4	CL	C	701	1/1	0.92	0.18	66,66,66,66	0
5	GOL	B	701	6/6	0.93	0.15	59,61,68,68	0
2	C2F	D	3001	33/33	0.94	0.17	28,34,50,56	56
5	GOL	B	704	6/6	0.95	0.20	35,36,37,37	14
2	C2F	A	3001	33/33	0.95	0.23	22,24,43,49	56
4	CL	A	3005	1/1	0.95	0.19	57,57,57,57	0
2	C2F	B	702	33/33	0.96	0.24	21,25,37,40	56
2	C2F	C	702	33/33	0.96	0.25	23,24,43,46	56
3	NA	B	703	1/1	0.98	0.18	40,40,40,40	0
3	NA	A	3002	1/1	0.98	0.19	38,38,38,38	0
3	NA	A	3004	1/1	0.98	0.24	50,50,50,50	0

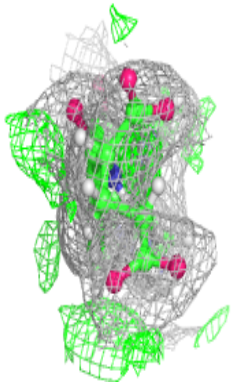
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around C2F F 3001:

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

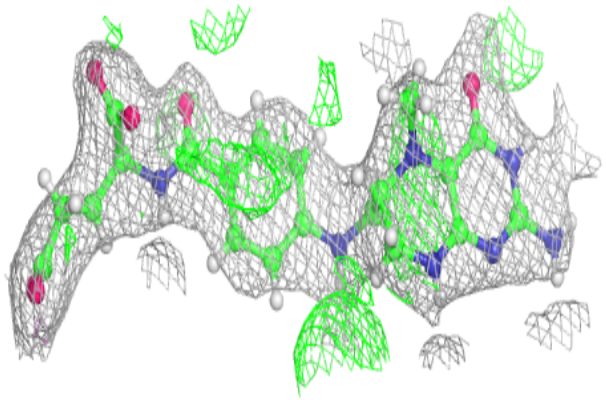


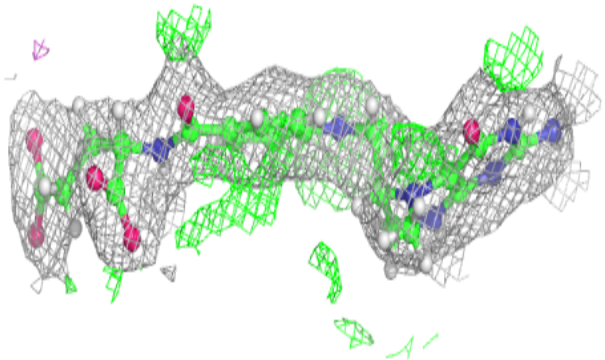


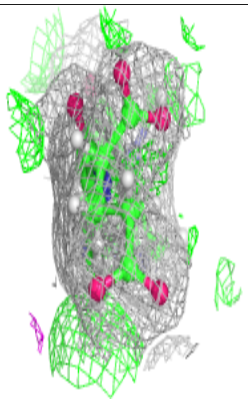


Electron density around C2F E 3001:

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

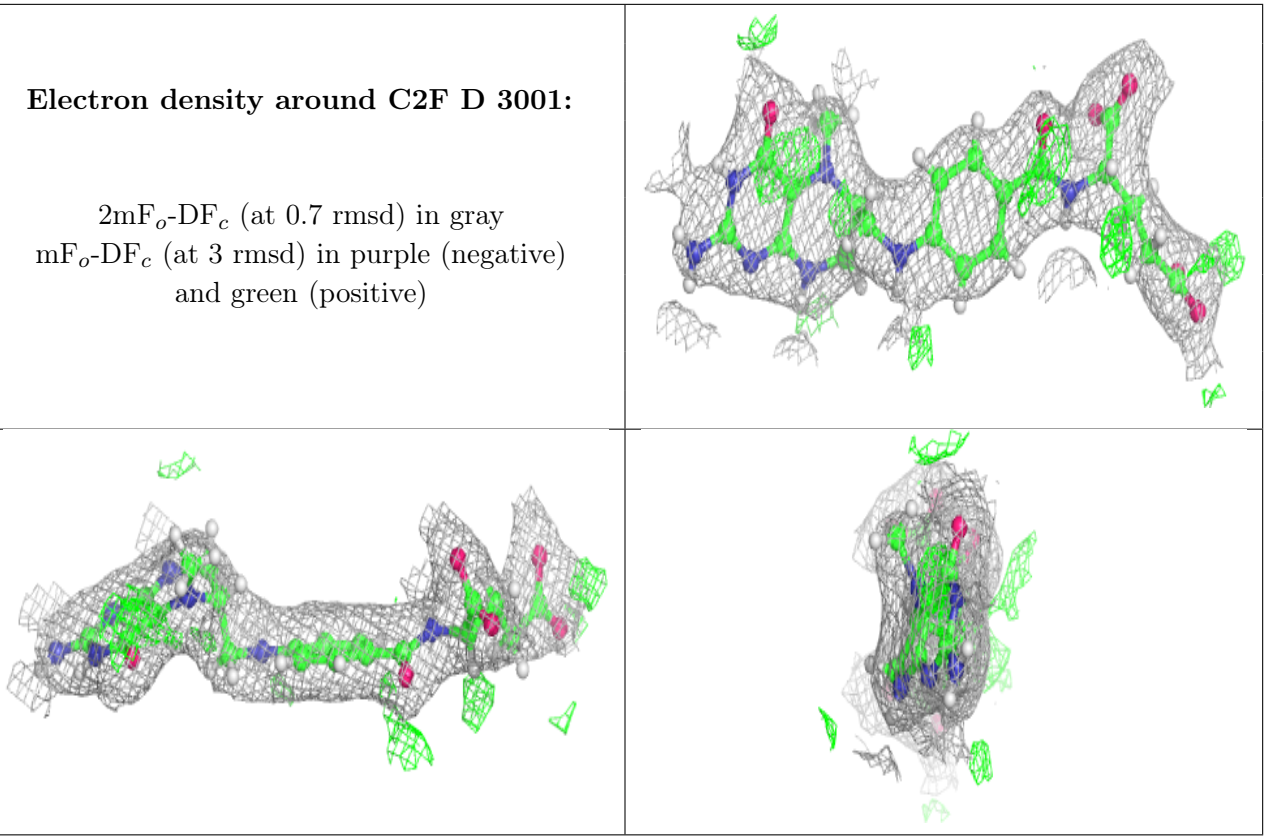






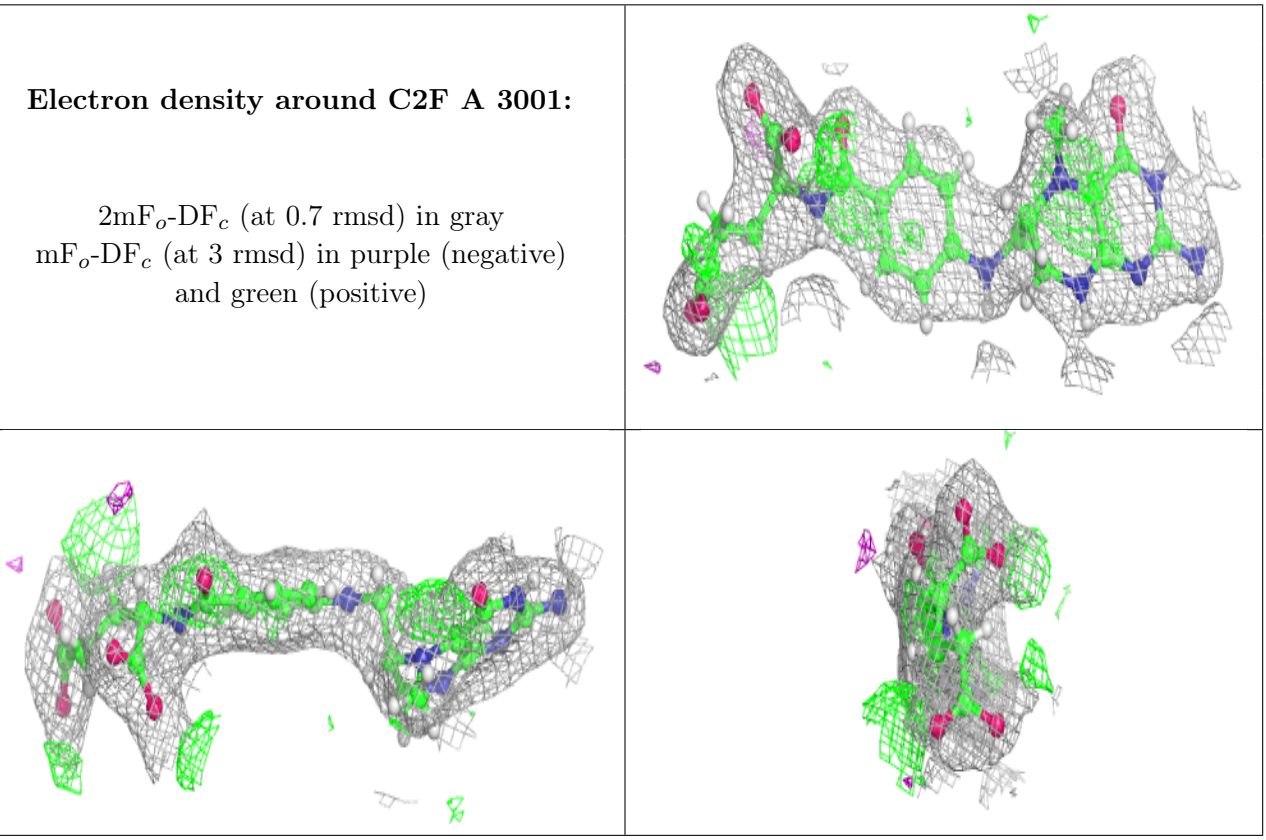
Electron density around C2F D 3001:

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



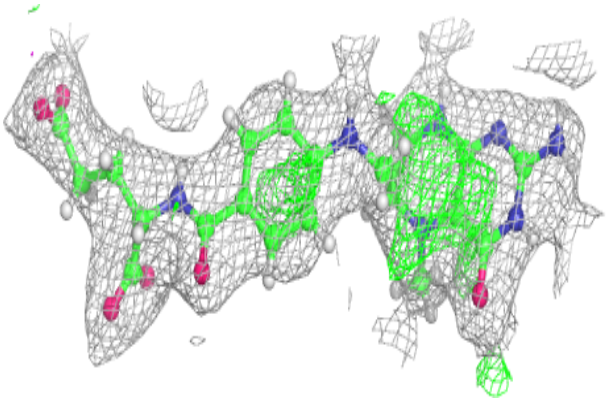
Electron density around C2F A 3001:

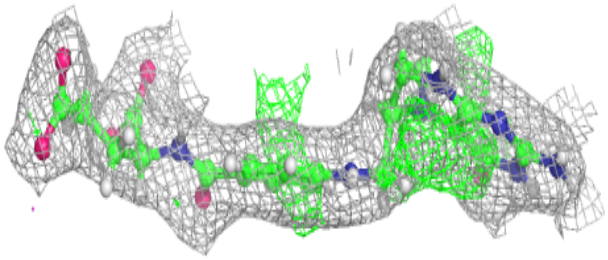
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

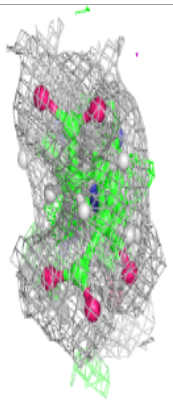


Electron density around C2F B 702:

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

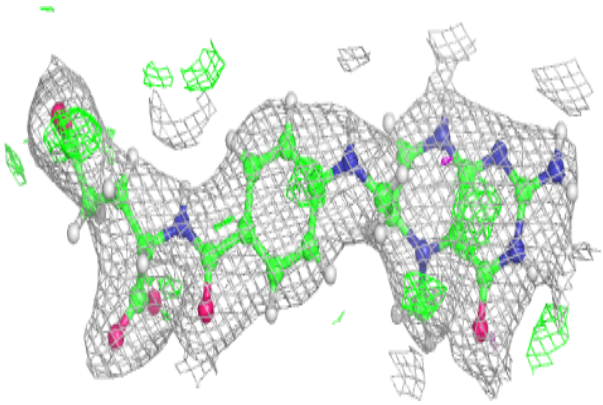


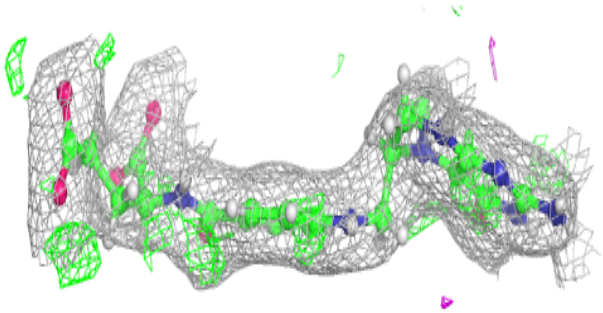


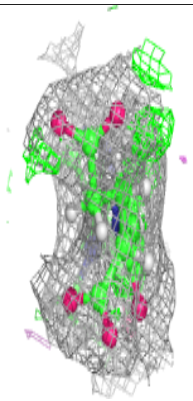


Electron density around C2F C 702:

$2mF_o$-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.