wwPDB X-ray Structure Validation Summary Report (i)

Sep 23, 2023 – 02:44 PM EDT

PDB ID	:	5T96
Title	:	Crystal structure of the infectious salmon anemia virus (ISAV) HE viral receptor complex
Authors	:	Cook, J.D.; Sultana, A.; Lee, J.E.
Deposited on	:	2016-09-09
Resolution	:	2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (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:

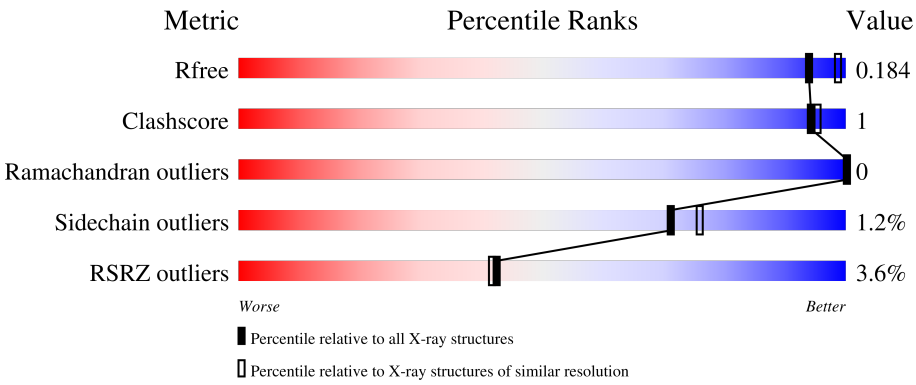
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	342	3%, 92%, • 5%
1	B	342	5%, 92%, 5% •
1	C	342	92%, • 5%
1	D	342	5%, 90%, • 6%
1	E	342	6%, 92%, • 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	342	2% 87% 8%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 30838 atoms, of which 14291 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 HE protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	325	4891	1545	2416	426	486	18	0	0	0
1	B	330	4902	1557	2408	426	493	18	0	0	0
1	C	325	4835	1533	2376	422	486	18	0	0	0
1	D	321	4682	1496	2281	409	479	17	0	0	0
1	E	325	4720	1511	2300	414	478	17	0	0	0
1	F	316	4680	1488	2298	408	468	18	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
A	354	ARG	-	expression tag	UNP Q9J0Y0
A	355	LEU	-	expression tag	UNP Q9J0Y0
A	356	VAL	-	expression tag	UNP Q9J0Y0
A	357	PRO	-	expression tag	UNP Q9J0Y0
A	358	ARG	-	expression tag	UNP Q9J0Y0
B	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
B	354	ARG	-	expression tag	UNP Q9J0Y0
B	355	LEU	-	expression tag	UNP Q9J0Y0
B	356	VAL	-	expression tag	UNP Q9J0Y0
B	357	PRO	-	expression tag	UNP Q9J0Y0
B	358	ARG	-	expression tag	UNP Q9J0Y0
C	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
C	354	ARG	-	expression tag	UNP Q9J0Y0
C	355	LEU	-	expression tag	UNP Q9J0Y0
C	356	VAL	-	expression tag	UNP Q9J0Y0
C	357	PRO	-	expression tag	UNP Q9J0Y0

Continued on next page...

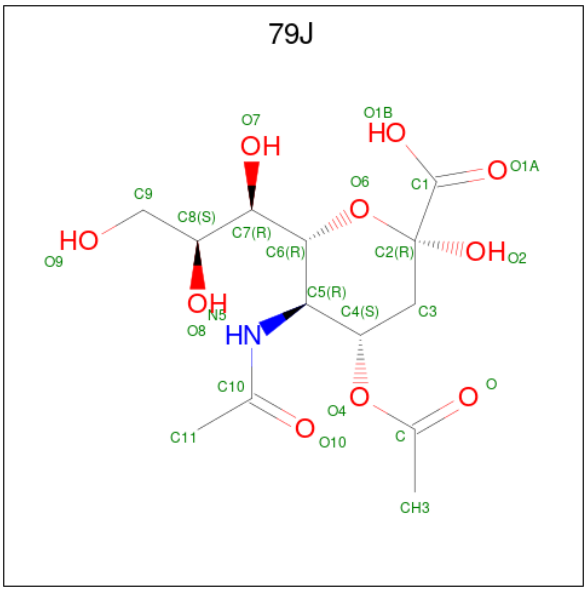
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	358	ARG	-	expression tag	UNP Q9J0Y0
D	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
D	354	ARG	-	expression tag	UNP Q9J0Y0
D	355	LEU	-	expression tag	UNP Q9J0Y0
D	356	VAL	-	expression tag	UNP Q9J0Y0
D	357	PRO	-	expression tag	UNP Q9J0Y0
D	358	ARG	-	expression tag	UNP Q9J0Y0
E	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
E	354	ARG	-	expression tag	UNP Q9J0Y0
E	355	LEU	-	expression tag	UNP Q9J0Y0
E	356	VAL	-	expression tag	UNP Q9J0Y0
E	357	PRO	-	expression tag	UNP Q9J0Y0
E	358	ARG	-	expression tag	UNP Q9J0Y0
F	333	ASP	ASN	engineered mutation	UNP Q9J0Y0
F	354	ARG	-	expression tag	UNP Q9J0Y0
F	355	LEU	-	expression tag	UNP Q9J0Y0
F	356	VAL	-	expression tag	UNP Q9J0Y0
F	357	PRO	-	expression tag	UNP Q9J0Y0
F	358	ARG	-	expression tag	UNP Q9J0Y0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

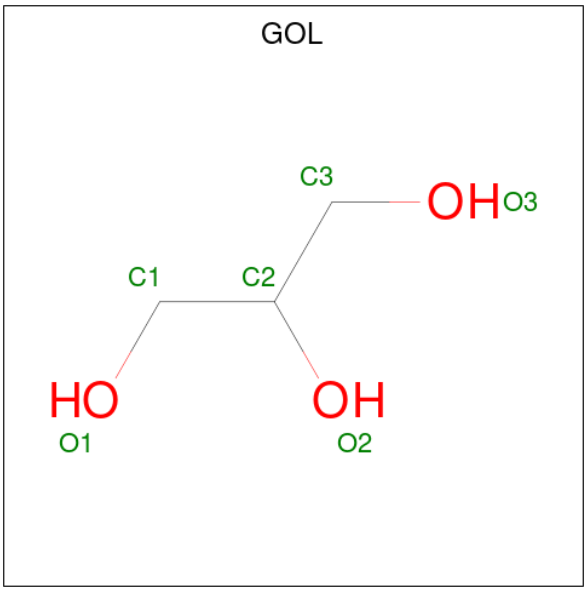
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
2	A	2	2	2	0	0
2	B	1	1	1	0	0
2	D	2	2	2	0	0
2	F	1	1	1	0	0

- Molecule 3 is 4-O-acetyl-5-acetamido-3,5-dideoxy-L-glycero-alpha-D-galacto-non-2-ulopyranosonic acid (three-letter code: 79J) (formula: $C_{13}H_{21}NO_{10}$).



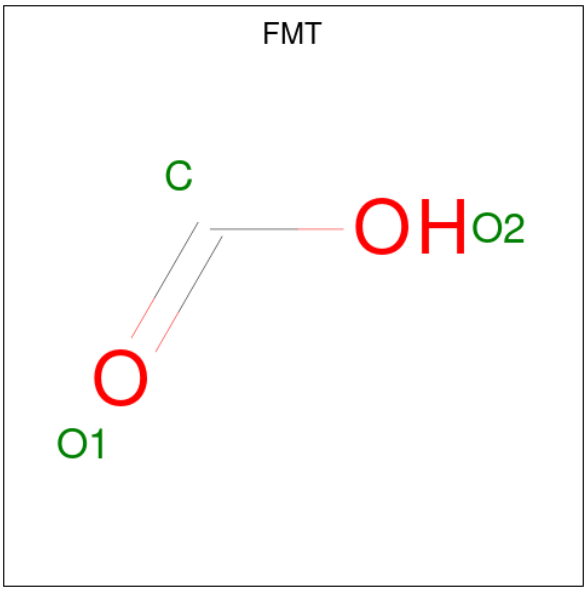
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			44	13	20	1	10		
3	B	1	Total	C	H	N	O	0	0
			44	13	20	1	10		
3	C	1	Total	C	H	N	O	0	0
			44	13	20	1	10		
3	D	1	Total	C	H	N	O	0	0
			44	13	20	1	10		
3	E	1	Total	C	H	N	O	0	0
			44	13	20	1	10		
3	F	1	Total	C	H	N	O	0	0
			44	13	20	1	10		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	A	1	14	3	8	3	0	0
4	B	1	14	3	8	3	0	0
4	B	1	14	3	8	3	0	0
4	C	1	14	3	8	3	0	0
4	D	1	14	3	8	3	0	0
4	D	1	14	3	8	3	0	0
4	E	1	14	3	8	3	0	0
4	F	1	14	3	8	3	0	0

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	A	1	4	1	1	2	0	0
			Total	C	H	O		
5	A	1	4	1	1	2	0	0
			Total	C	H	O		
5	A	1	4	1	1	2	0	0
			Total	C	H	O		
5	A	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	B	1	4	1	1	2	0	0
			Total	C	H	O		
5	C	1	4	1	1	2	0	0
			Total	C	H	O		
5	C	1	4	1	1	2	0	0
			Total	C	H	O		
5	C	1	4	1	1	2	0	0
			Total	C	H	O		
5	C	1	4	1	1	2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
5	C	1	4	1	1	2	0	0
			Total	C	H	O		
5	C	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	D	1	4	1	1	2	0	0
			Total	C	H	O		
5	E	1	4	1	1	2	0	0
			Total	C	H	O		
5	E	1	4	1	1	2	0	0
			Total	C	H	O		
5	F	1	4	1	1	2	0	0
			Total	C	H	O		
5	F	1	4	1	1	2	0	0
			Total	C	H	O		
5	F	1	4	1	1	2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	285	285	285	0	0
			Total	O		
6	B	272	272	272	0	0
			Total	O		
6	C	310	310	310	0	0
			Total	O		
6	D	269	269	269	0	0
			Total	O		
6	E	188	188	188	0	0

Continued on next page...

Continued from previous page...

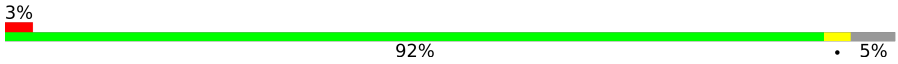
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	F	310	310	310	0	0

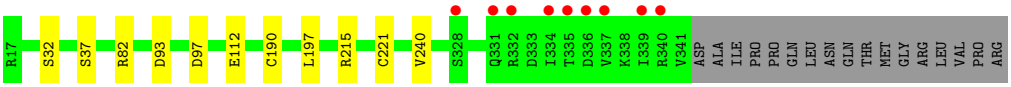
3 Residue-property plots (i)

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: HE protein

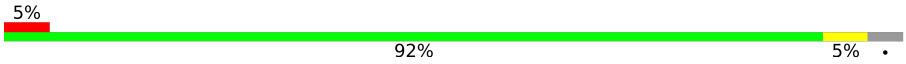
Chain A:

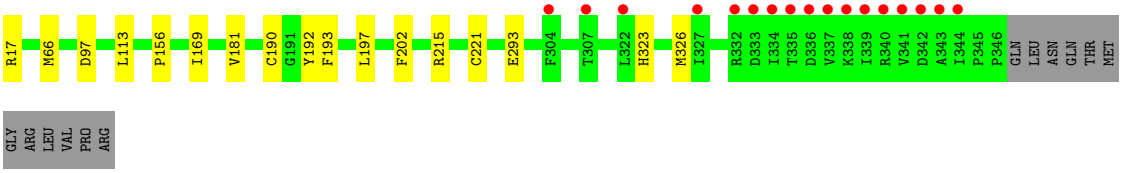




• Molecule 1: HE protein

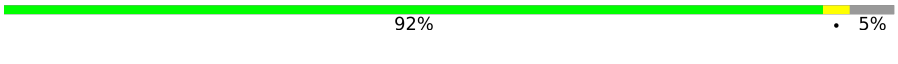
Chain B:





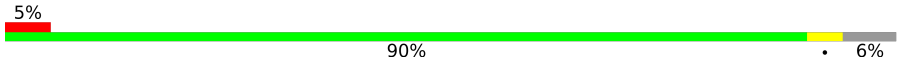
• Molecule 1: HE protein

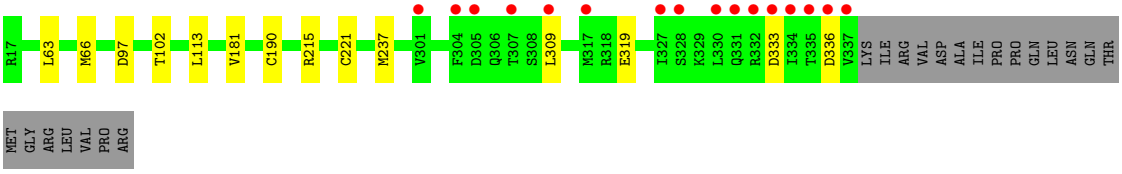
Chain C:



• Molecule 1: HE protein

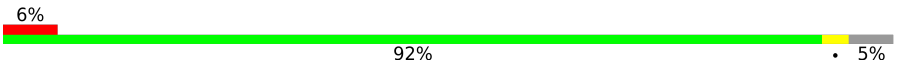
Chain D:

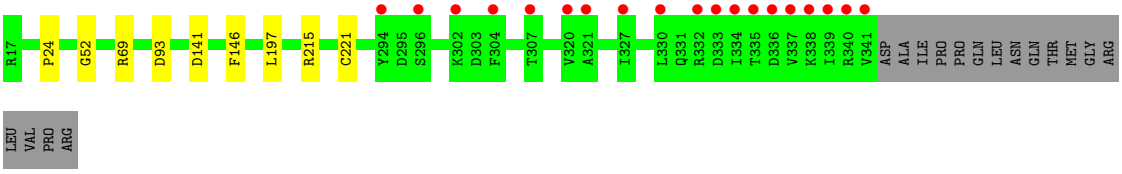




• Molecule 1: HE protein

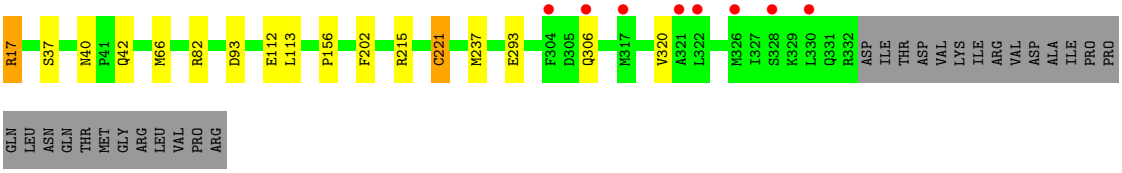
Chain E:





• Molecule 1: HE protein

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	82.48Å 87.57Å 95.53Å 97.14° 113.50° 114.68°	Depositor
Resolution (Å)	48.40 – 2.00 48.39 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.9 (48.40-2.00) 97.9 (48.39-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.50 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.139 , 0.183 0.140 , 0.184	Depositor DCC
R_{free} test set	2000 reflections (1.45%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 52.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	30838	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.24% 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: FMT, 79J, MG, GOL

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	0/2520	0.66	1/3425 (0.0%)
1	B	0.49	0/2540	0.65	0/3457
1	C	0.50	0/2504	0.65	0/3406
1	D	0.47	0/2446	0.65	0/3331
1	E	0.43	0/2465	0.62	0/3357
1	F	0.55	2/2427 (0.1%)	0.71	1/3303 (0.0%)
All	All	0.49	2/14902 (0.0%)	0.66	2/20279 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	17	ARG	CZ-NH1	7.25	1.42	1.33
1	F	17	ARG	CZ-NH2	6.55	1.41	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	17	ARG	NE-CZ-NH1	-5.28	117.66	120.30
1	A	82	ARG	NE-CZ-NH1	5.01	122.80	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	2475	2416	2416	5	0
1	B	2494	2408	2408	10	0
1	C	2459	2376	2376	4	0
1	D	2401	2281	2281	10	0
1	E	2420	2300	2300	4	0
1	F	2382	2298	2298	8	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
2	D	2	0	0	0	0
2	F	1	0	0	0	0
3	A	24	20	0	0	0
3	B	24	20	0	0	0
3	C	24	20	0	0	0
3	D	24	20	0	0	0
3	E	24	20	0	1	0
3	F	24	20	0	0	0
4	A	6	8	8	0	0
4	B	12	16	16	0	0
4	C	6	8	8	0	0
4	D	12	16	16	1	0
4	E	6	8	8	0	0
4	F	6	8	8	0	0
5	A	12	4	4	1	0
5	B	18	6	6	0	0
5	C	18	6	6	0	0
5	D	21	7	7	0	0
5	E	6	2	2	0	0
5	F	9	3	3	0	0
6	A	285	0	0	2	0
6	B	272	0	0	0	0
6	C	310	0	0	0	0
6	D	269	0	0	1	0
6	E	188	0	0	0	0
6	F	310	0	0	1	0
All	All	16547	14291	14171	39	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 1.

The worst 5 of 39 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:B:66:MET:HE1	1:B:113:LEU:HD21	1.72	0.71
1:B:169:ILE:HD11	1:B:192:TYR:HB3	1.81	0.62
1:B:66:MET:CE	1:B:113:LEU:HD21	2.31	0.61
1:D:66:MET:HE3	1:D:113:LEU:HD21	1.83	0.58
1:E:141:ASP:OD1	3:E:401:79J:O9	2.24	0.55

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	323/342 (94%)	318 (98%)	5 (2%)	0	100	100
1	B	328/342 (96%)	323 (98%)	5 (2%)	0	100	100
1	C	323/342 (94%)	319 (99%)	4 (1%)	0	100	100
1	D	319/342 (93%)	312 (98%)	7 (2%)	0	100	100
1	E	323/342 (94%)	316 (98%)	7 (2%)	0	100	100
1	F	314/342 (92%)	310 (99%)	4 (1%)	0	100	100
All	All	1930/2052 (94%)	1898 (98%)	32 (2%)	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	278/298 (93%)	274 (99%)	4 (1%)	67	72
1	B	277/298 (93%)	275 (99%)	2 (1%)	84	88
1	C	274/298 (92%)	271 (99%)	3 (1%)	73	78
1	D	263/298 (88%)	261 (99%)	2 (1%)	81	86
1	E	262/298 (88%)	259 (99%)	3 (1%)	73	78
1	F	264/298 (89%)	259 (98%)	5 (2%)	57	61
All	All	1618/1788 (90%)	1599 (99%)	19 (1%)	71	76

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	37	SER
1	F	221	CYS
1	F	237	MET
1	F	215	ARG
1	C	221	CYS

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 48 ligands modelled in this entry, 6 are monoatomic - leaving 42 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	$\#\|Z\| > 2$
3	79J	C	402	-	24,24,24	1.80	7 (29%)	29,35,35	2.64	10 (34%)
5	FMT	C	408	-	2,2,2	0.67	0	1,1,1	0.41	0
3	79J	A	403	-	24,24,24	1.63	6 (25%)	29,35,35	2.47	9 (31%)
4	GOL	F	403	-	5,5,5	0.46	0	5,5,5	0.57	0
5	FMT	B	410	-	2,2,2	0.66	0	1,1,1	0.36	0
5	FMT	A	407	-	2,2,2	0.69	0	1,1,1	0.48	0
5	FMT	D	407	-	2,2,2	0.68	0	1,1,1	0.38	0
5	FMT	F	406	-	2,2,2	0.73	0	1,1,1	0.44	0
5	FMT	C	406	-	2,2,2	0.69	0	1,1,1	0.42	0
5	FMT	E	404	-	2,2,2	0.67	0	1,1,1	0.41	0
5	FMT	D	409	-	2,2,2	0.70	0	1,1,1	0.39	0
4	GOL	A	404	-	5,5,5	0.36	0	5,5,5	0.56	0
5	FMT	D	412	-	2,2,2	0.73	0	1,1,1	0.38	0
5	FMT	F	404	-	2,2,2	0.71	0	1,1,1	0.50	0
5	FMT	C	404	-	2,2,2	0.61	0	1,1,1	0.36	0
4	GOL	D	404	-	5,5,5	0.52	0	5,5,5	0.58	0
5	FMT	B	407	-	2,2,2	0.69	0	1,1,1	0.47	0
4	GOL	D	405	-	5,5,5	0.32	0	5,5,5	0.41	0
3	79J	B	402	-	24,24,24	1.45	4 (16%)	29,35,35	2.10	11 (37%)
5	FMT	D	411	-	2,2,2	0.72	0	1,1,1	0.45	0
4	GOL	B	404	-	5,5,5	0.38	0	5,5,5	0.47	0
3	79J	E	401	-	24,24,24	2.24	11 (45%)	29,35,35	2.65	14 (48%)
3	79J	F	402	-	24,24,24	1.79	9 (37%)	29,35,35	3.01	10 (34%)
5	FMT	C	405	-	2,2,2	0.62	0	1,1,1	0.39	0
5	FMT	C	407	-	2,2,2	0.63	0	1,1,1	0.37	0
5	FMT	D	408	-	2,2,2	0.57	0	1,1,1	0.33	0
5	FMT	A	405	-	2,2,2	0.67	0	1,1,1	0.32	0
4	GOL	C	403	-	5,5,5	0.57	0	5,5,5	0.52	0
5	FMT	E	403	-	2,2,2	0.66	0	1,1,1	0.37	0
5	FMT	A	406	-	2,2,2	0.74	0	1,1,1	0.40	0
5	FMT	F	405	-	2,2,2	0.67	0	1,1,1	0.64	0
3	79J	D	403	-	24,24,24	1.54	5 (20%)	29,35,35	2.11	9 (31%)
5	FMT	D	406	-	2,2,2	0.62	0	1,1,1	0.33	0
5	FMT	B	408	-	2,2,2	0.73	0	1,1,1	0.48	0
5	FMT	B	409	-	2,2,2	0.78	0	1,1,1	0.35	0
5	FMT	B	405	-	2,2,2	0.73	0	1,1,1	0.36	0
4	GOL	E	402	-	5,5,5	0.21	0	5,5,5	0.71	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	FMT	C	401	-	2,2,2	0.67	0	1,1,1	0.30	0
4	GOL	B	403	-	5,5,5	0.35	0	5,5,5	0.38	0
5	FMT	A	408	-	2,2,2	0.72	0	1,1,1	0.51	0
5	FMT	B	406	-	2,2,2	0.68	0	1,1,1	0.30	0
5	FMT	D	410	-	2,2,2	0.63	0	1,1,1	0.37	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
3	79J	C	402	-	-	7/24/42/42	0/1/1/1
3	79J	A	403	-	-	5/24/42/42	0/1/1/1
4	GOL	D	404	-	-	3/4/4/4	-
4	GOL	F	403	-	-	2/4/4/4	-
4	GOL	C	403	-	-	1/4/4/4	-
4	GOL	E	402	-	-	4/4/4/4	-
4	GOL	D	405	-	-	0/4/4/4	-
3	79J	B	402	-	-	8/24/42/42	0/1/1/1
3	79J	D	403	-	-	6/24/42/42	0/1/1/1
4	GOL	B	403	-	-	0/4/4/4	-
4	GOL	A	404	-	-	0/4/4/4	-
4	GOL	B	404	-	-	1/4/4/4	-
3	79J	E	401	-	-	7/24/42/42	0/1/1/1
3	79J	F	402	-	-	4/24/42/42	0/1/1/1

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	401	79J	C3-C2	5.22	1.58	1.51
3	C	402	79J	O2-C2	3.86	1.44	1.39
3	E	401	79J	O2-C2	3.81	1.44	1.39
3	A	403	79J	O4-C4	-3.79	1.39	1.46
3	C	402	79J	O4-C4	-3.63	1.40	1.46

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	402	79J	O2-C2-C1	-8.26	93.97	110.76

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	401	79J	C4-O4-C	6.38	127.47	117.46
3	C	402	79J	O2-C2-C1	-6.24	98.07	110.76
3	F	402	79J	O2-C2-C3	6.15	118.29	109.40
3	A	403	79J	O2-C2-C1	-6.14	98.28	110.76

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	402	79J	C7-C8-C9-O9
3	B	402	79J	O8-C8-C9-O9
3	C	402	79J	C6-C7-C8-O8
3	C	402	79J	O7-C7-C8-C9
3	C	402	79J	O7-C7-C8-O8

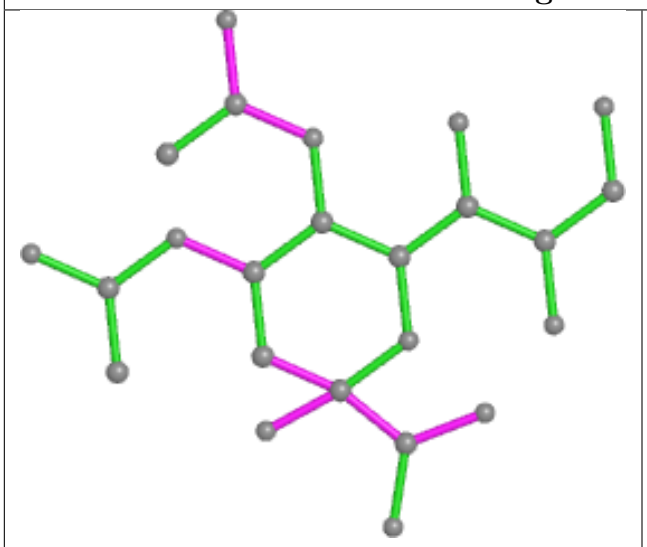
There are no ring outliers.

3 monomers are involved in 3 short contacts:

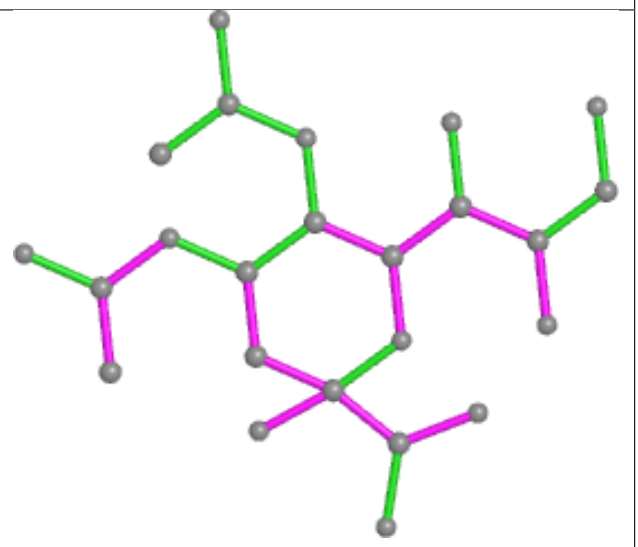
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	407	FMT	1	0
4	D	405	GOL	1	0
3	E	401	79J	1	0

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.

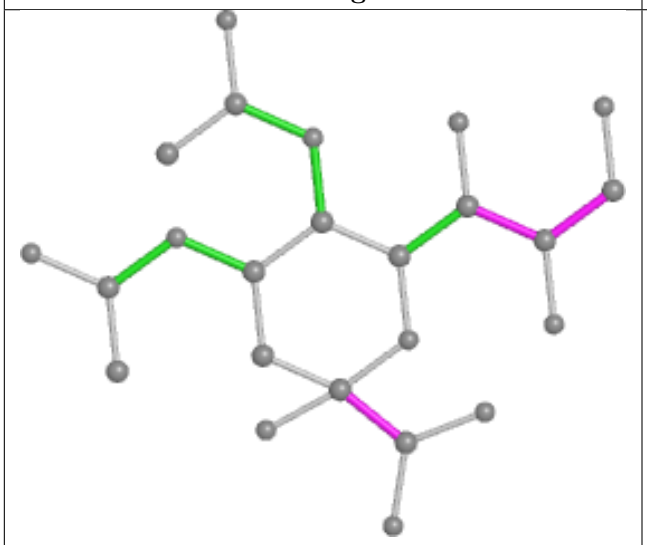
Ligand 79J C 402



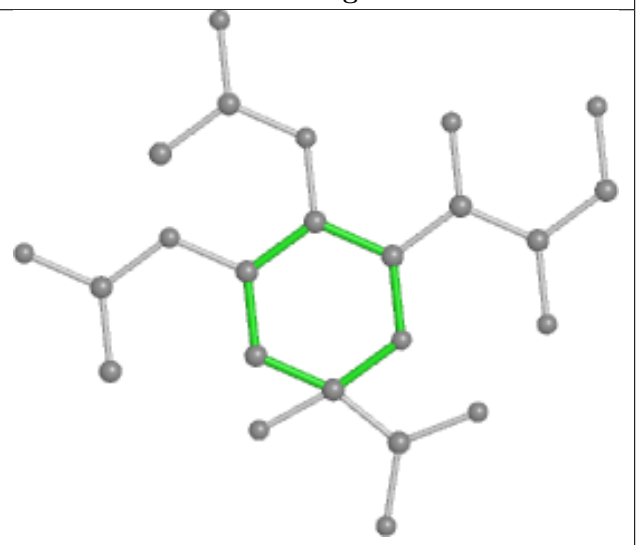
Bond lengths



Bond angles

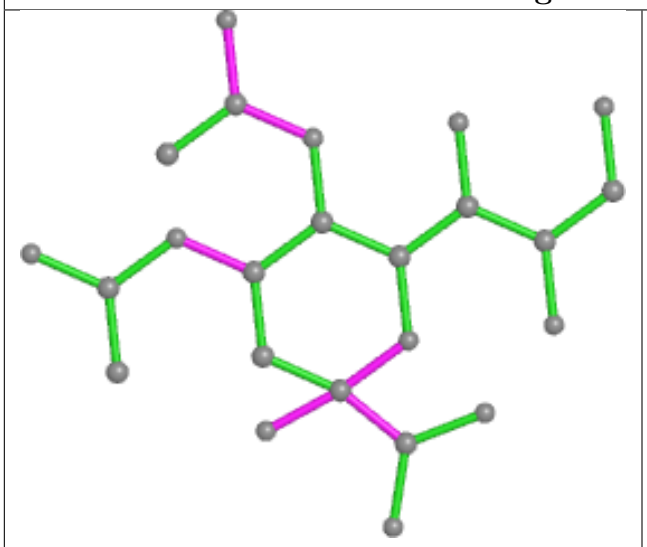


Torsions

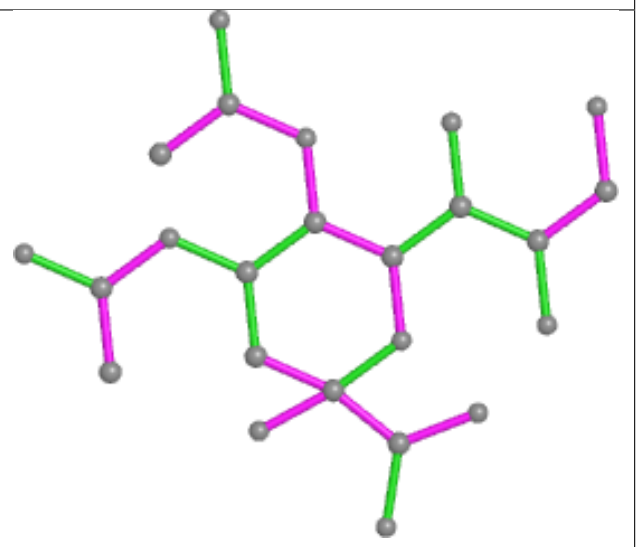


Rings

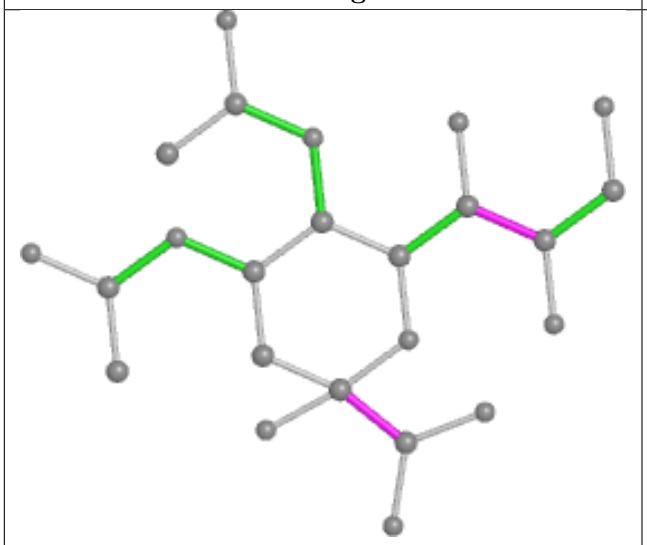
Ligand 79J A 403



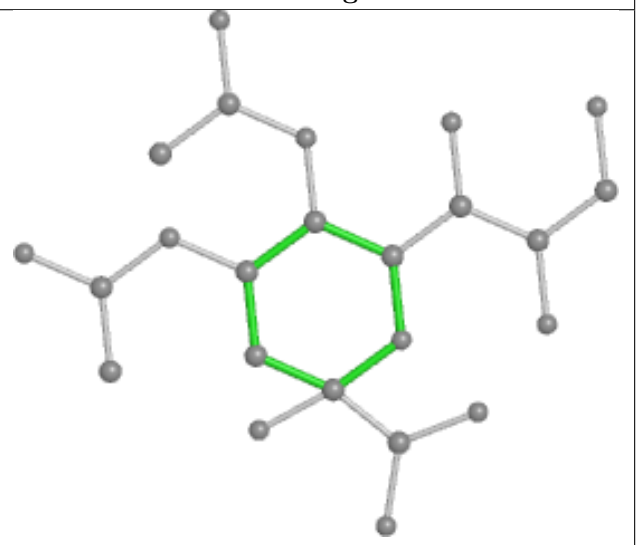
Bond lengths



Bond angles

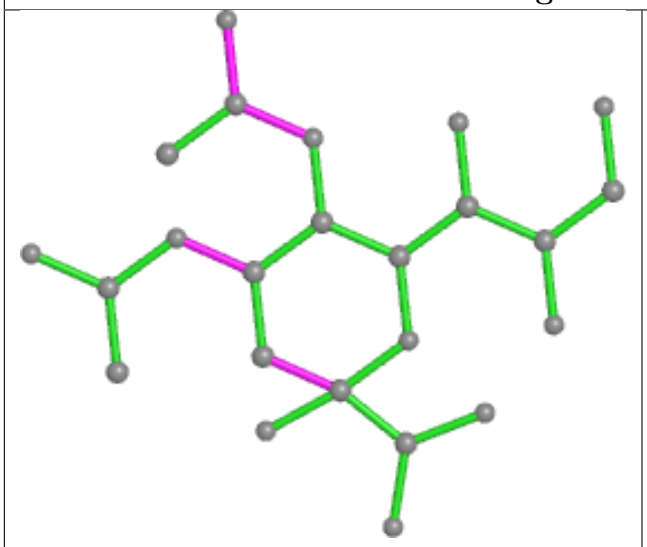


Torsions

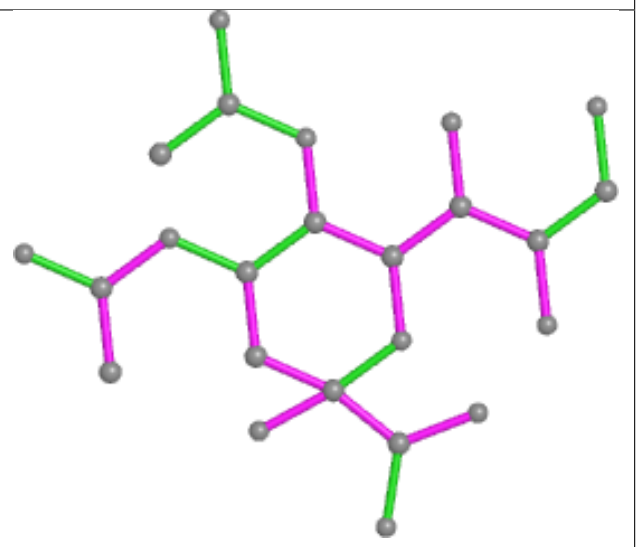


Rings

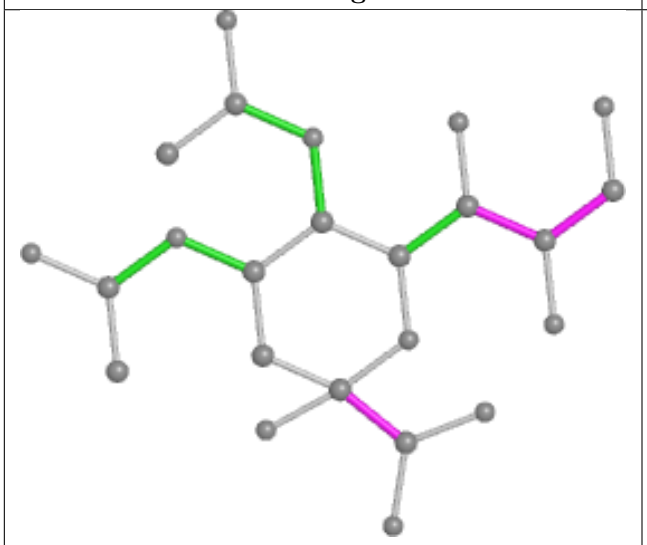
Ligand 79J B 402



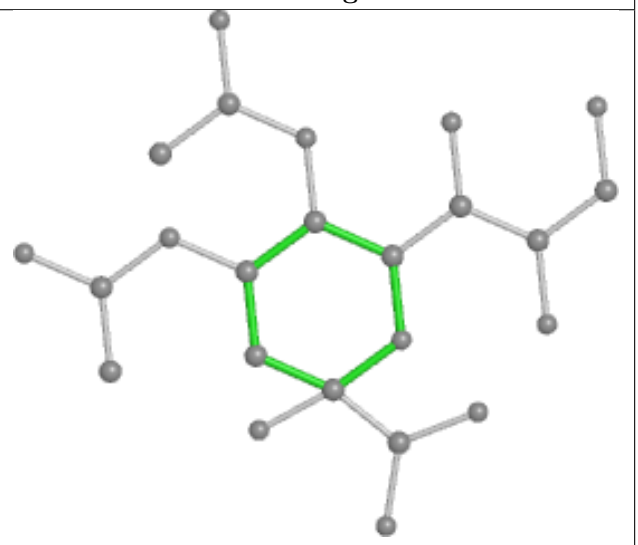
Bond lengths



Bond angles

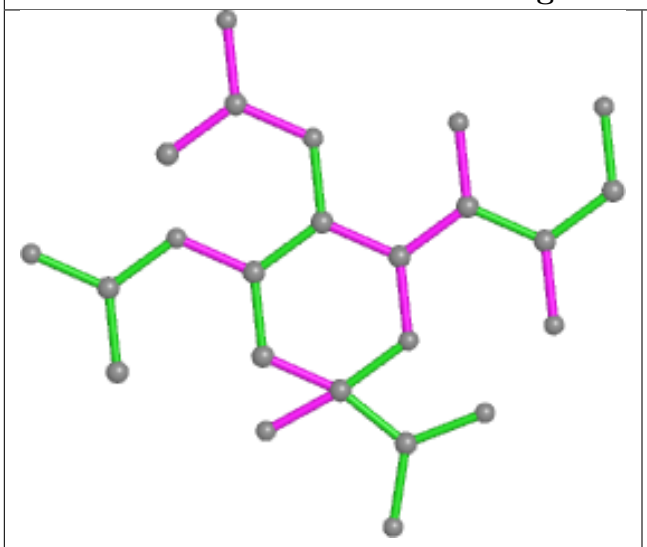


Torsions

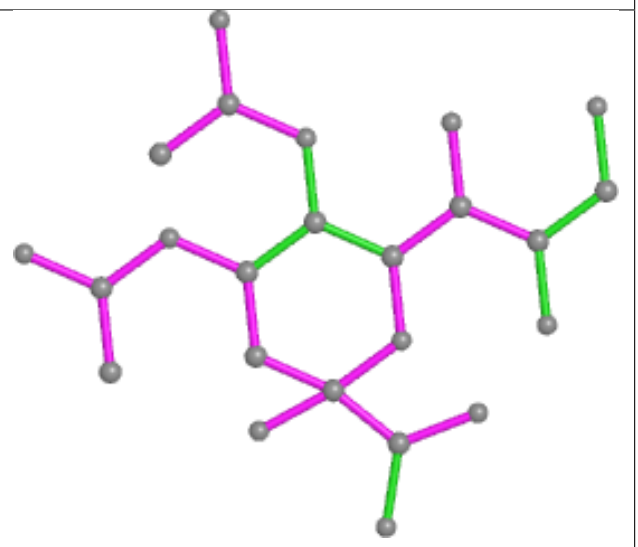


Rings

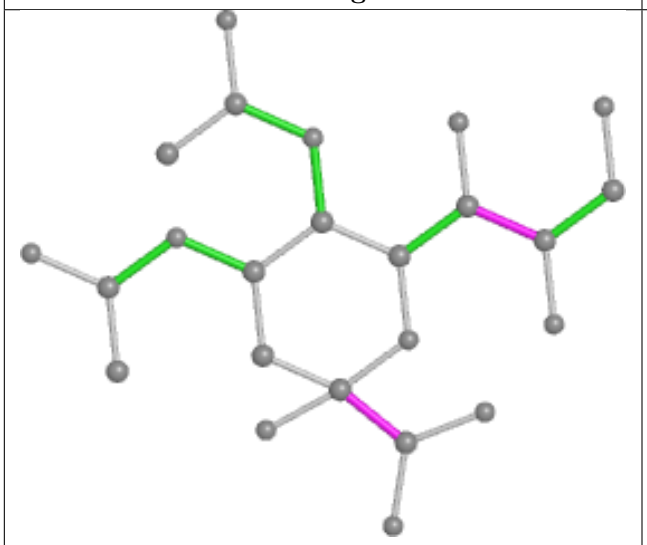
Ligand 79J E 401



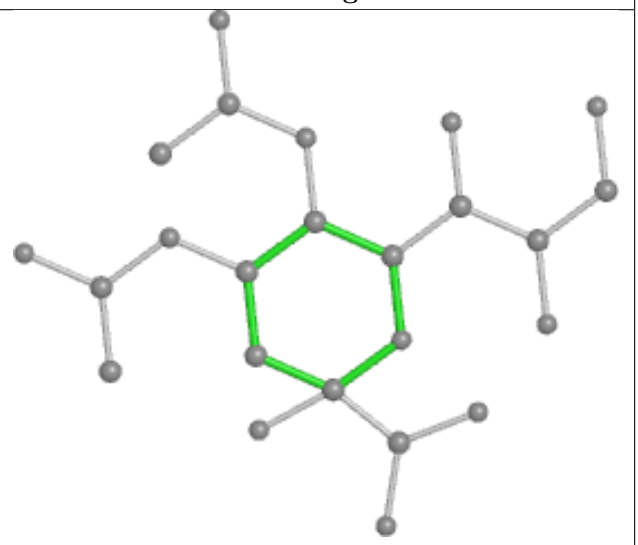
Bond lengths



Bond angles

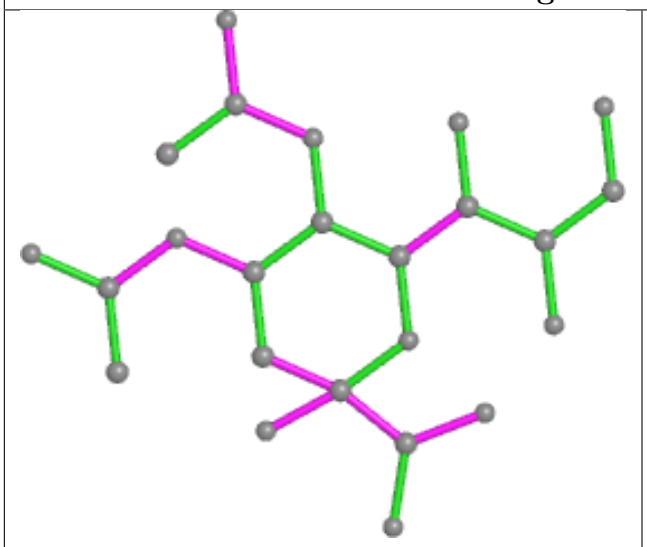


Torsions

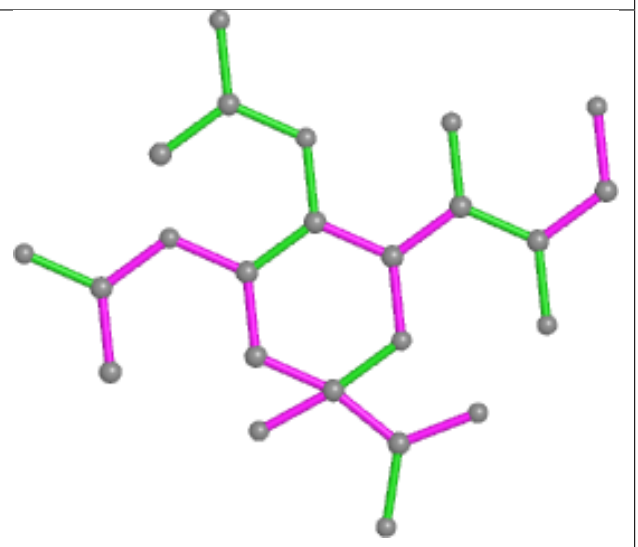


Rings

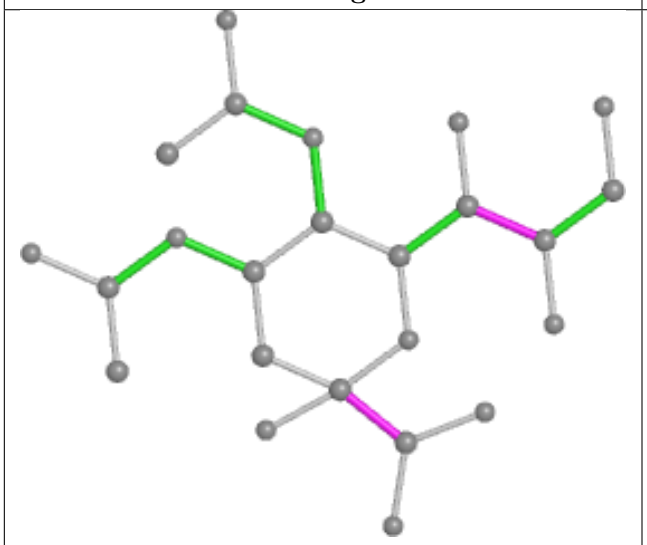
Ligand 79J F 402



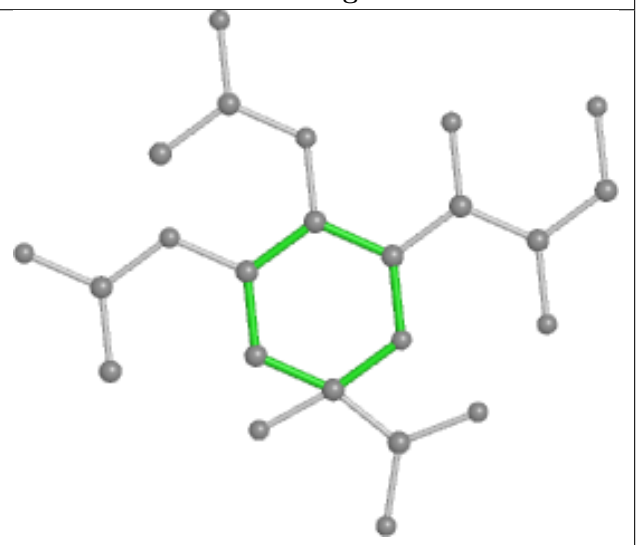
Bond lengths



Bond angles

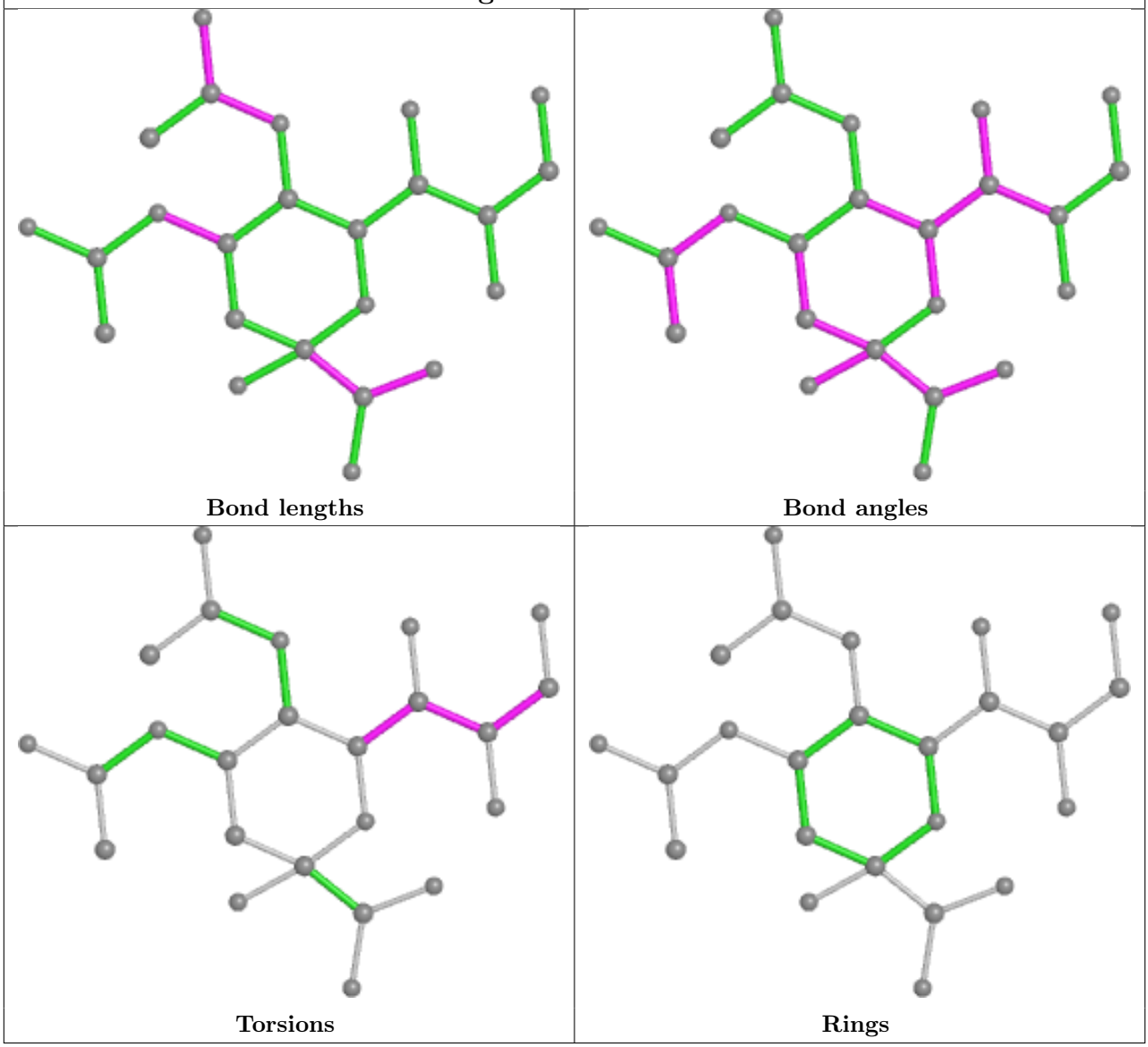


Torsions



Rings

Ligand 79J D 403



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	325/342 (95%)	-0.39	9 (2%)	53	51	19, 29, 55, 109	0
1	B	330/342 (96%)	-0.24	17 (5%)	27	26	19, 28, 66, 93	0
1	C	325/342 (95%)	-0.46	1 (0%)	94	93	17, 26, 52, 112	0
1	D	321/342 (93%)	-0.22	16 (4%)	28	28	19, 29, 75, 110	0
1	E	325/342 (95%)	-0.12	19 (5%)	23	22	22, 37, 71, 104	0
1	F	316/342 (92%)	-0.35	8 (2%)	57	56	17, 26, 62, 117	0
All	All	1942/2052 (94%)	-0.30	70 (3%)	42	42	17, 29, 66, 117	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	335	THR	7.6
1	B	334	ILE	6.6
1	E	339	ILE	6.3
1	B	343	ALA	5.7
1	B	341	VAL	4.9

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
5	FMT	C	407	3/3	0.70	0.17	63,65,68,79	0
5	FMT	C	406	3/3	0.78	0.13	54,58,63,70	0
5	FMT	A	405	3/3	0.78	0.14	51,59,62,70	0
5	FMT	D	410	3/3	0.79	0.19	62,62,65,79	0
5	FMT	B	410	3/3	0.81	0.26	57,65,69,83	0
5	FMT	D	407	3/3	0.84	0.10	56,59,62,75	0
5	FMT	D	408	3/3	0.85	0.17	40,57,57,69	0
5	FMT	C	405	3/3	0.86	0.11	54,57,59,71	0
5	FMT	B	406	3/3	0.86	0.12	57,58,64,77	0
2	MG	A	402	1/1	0.86	0.10	57,57,57,57	0
5	FMT	B	407	3/3	0.87	0.14	73,76,79,91	0
2	MG	D	402	1/1	0.87	0.11	72,72,72,72	0
5	FMT	B	409	3/3	0.88	0.20	46,73,80,88	0
5	FMT	D	409	3/3	0.89	0.14	54,70,75,84	0
5	FMT	B	408	3/3	0.90	0.14	66,70,71,85	0
5	FMT	A	406	3/3	0.90	0.22	57,61,65,78	0
5	FMT	C	404	3/3	0.91	0.11	51,59,62,74	0
2	MG	B	401	1/1	0.91	0.05	65,65,65,65	0
5	FMT	E	403	3/3	0.91	0.12	37,49,50,59	0
5	FMT	F	404	3/3	0.91	0.35	59,63,68,76	0
5	FMT	F	406	3/3	0.91	0.69	90,96,98,117	0
5	FMT	D	406	3/3	0.92	0.19	39,44,46,55	0
3	79J	E	401	24/24	0.92	0.10	26,48,76,91	0
4	GOL	B	404	6/6	0.92	0.18	28,42,91,92	0
5	FMT	A	408	3/3	0.92	0.12	29,45,54,54	0
4	GOL	E	402	6/6	0.93	0.14	32,60,74,74	0
5	FMT	D	411	3/3	0.93	0.14	35,53,63,64	0
3	79J	B	402	24/24	0.93	0.12	23,39,63,78	0
4	GOL	D	405	6/6	0.93	0.11	28,65,76,88	0
5	FMT	C	401	3/3	0.93	0.18	40,48,55,66	0
3	79J	F	402	24/24	0.94	0.10	22,38,53,59	0
3	79J	C	402	24/24	0.94	0.09	22,35,57,68	0
5	FMT	E	404	3/3	0.94	0.14	43,71,77,85	0
5	FMT	C	408	3/3	0.94	0.12	31,53,58,64	0
3	79J	A	403	24/24	0.94	0.12	24,39,64,77	0
4	GOL	C	403	6/6	0.95	0.12	16,37,50,60	0
4	GOL	B	403	6/6	0.95	0.11	29,50,61,63	0

Continued on next page...

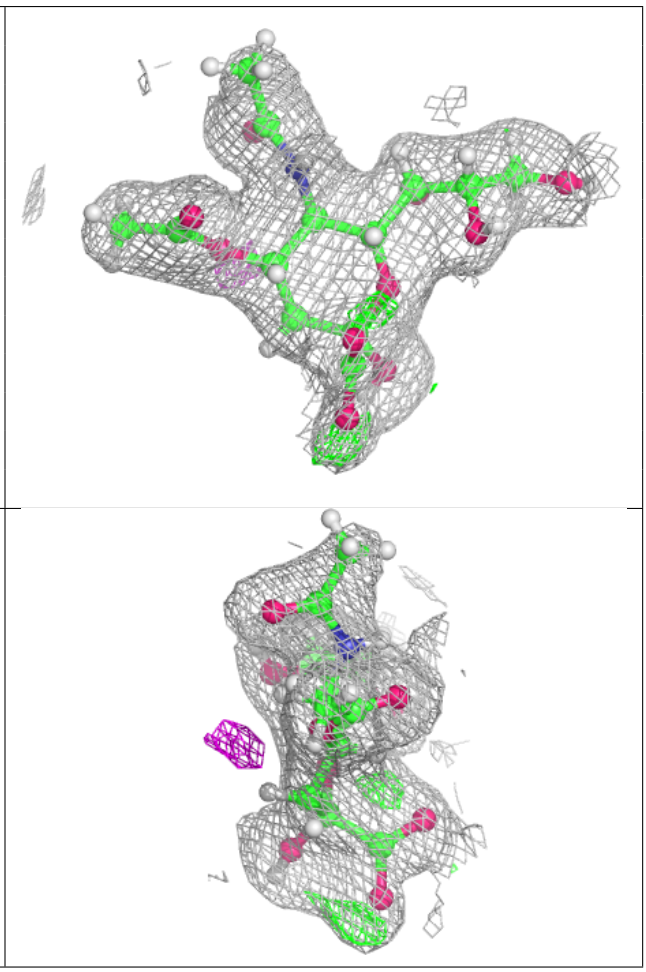
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	79J	D	403	24/24	0.95	0.14	28,46,61,73	0
5	FMT	B	405	3/3	0.96	0.10	30,42,43,52	0
4	GOL	D	404	6/6	0.96	0.10	30,50,63,63	0
5	FMT	A	407	3/3	0.97	0.12	37,56,57,69	0
4	GOL	F	403	6/6	0.97	0.10	27,52,63,63	0
2	MG	F	401	1/1	0.97	0.03	60,60,60,60	0
5	FMT	F	405	3/3	0.97	0.13	30,50,55,60	0
4	GOL	A	404	6/6	0.97	0.09	26,43,53,53	0
2	MG	D	401	1/1	0.98	0.03	41,41,41,41	0
5	FMT	D	412	3/3	0.99	0.11	28,42,45,50	0
2	MG	A	401	1/1	0.99	0.04	26,26,26,26	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.

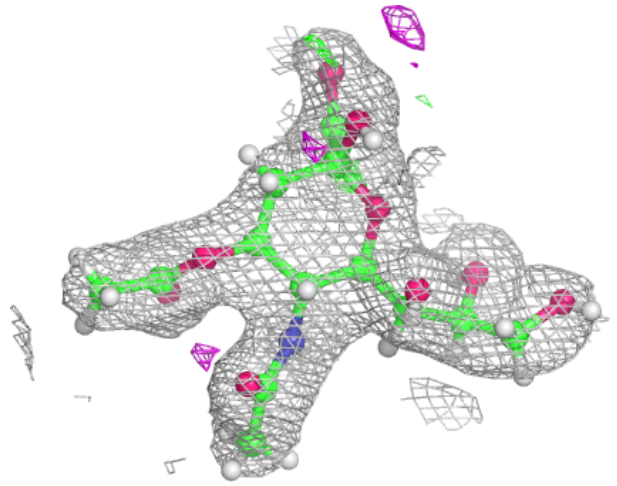
Electron density around 79J E 401:

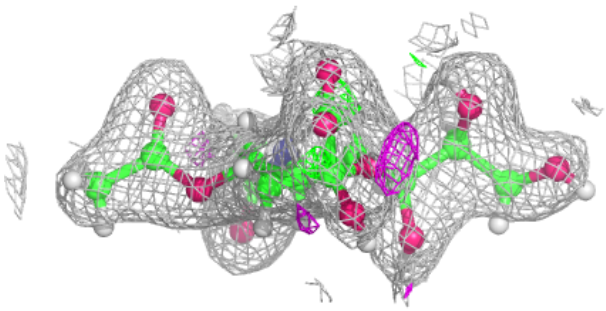
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)

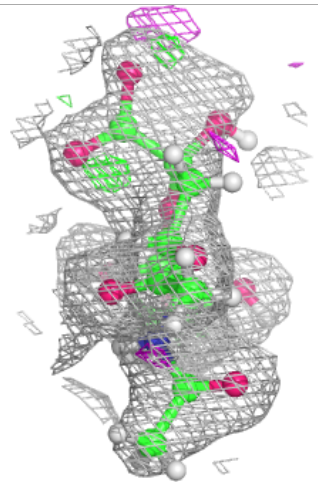


Electron density around 79J B 402:

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

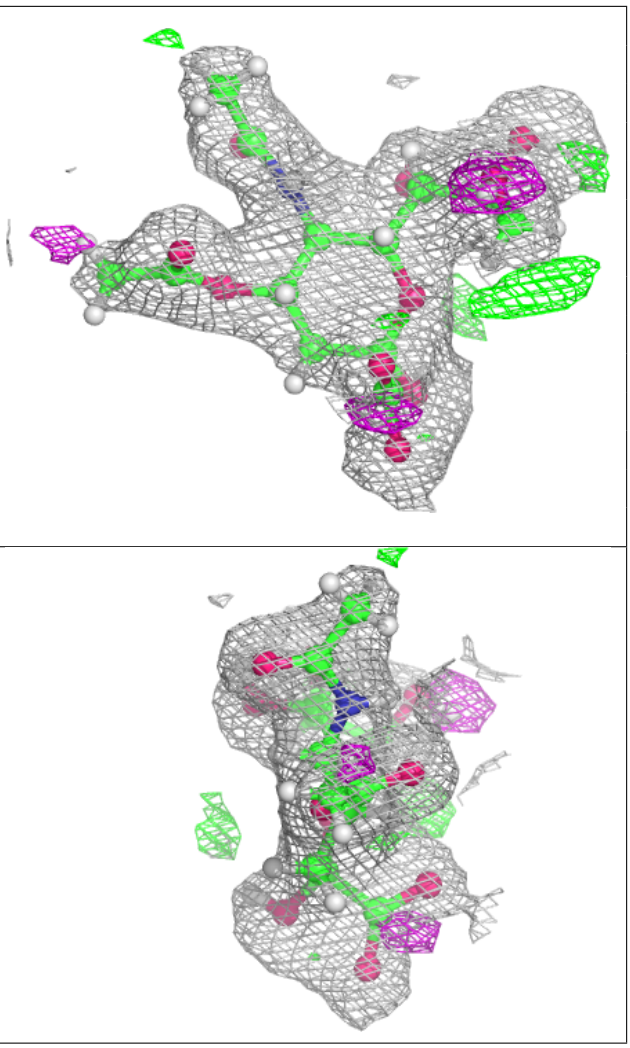






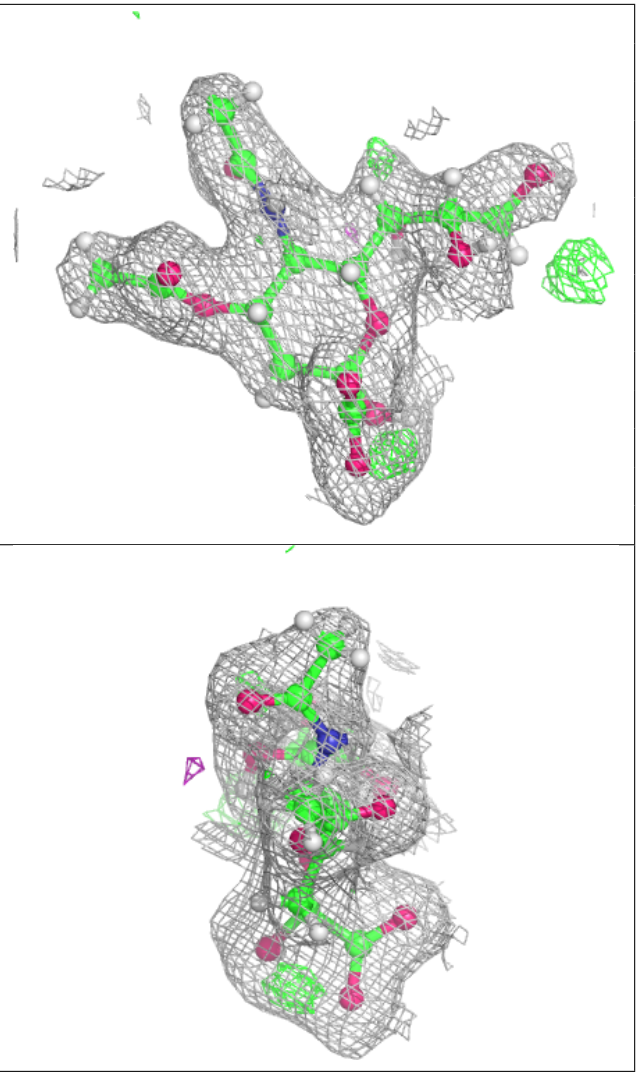
Electron density around 79J F 402:

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



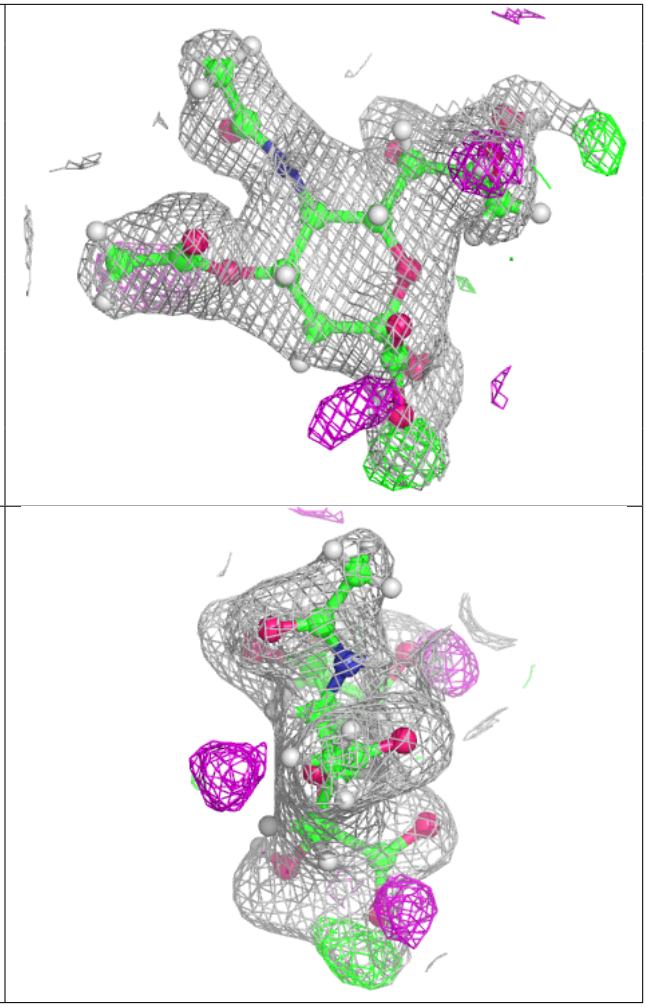
Electron density around 79J C 402:

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



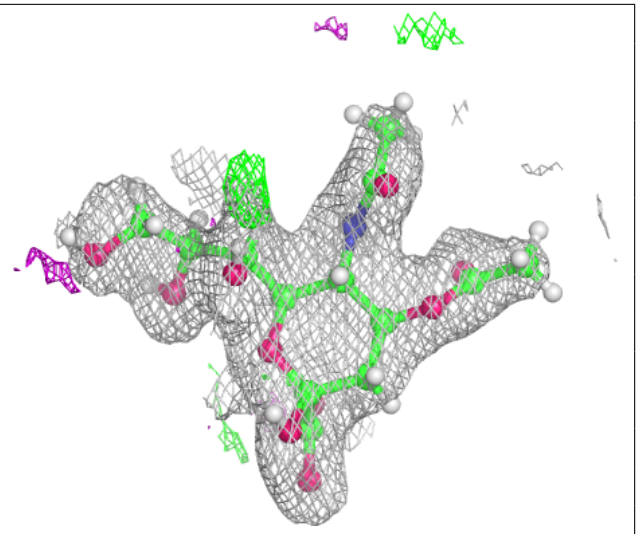
Electron density around 79J A 403:

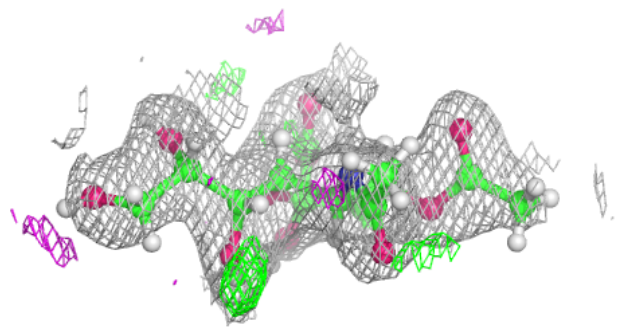
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

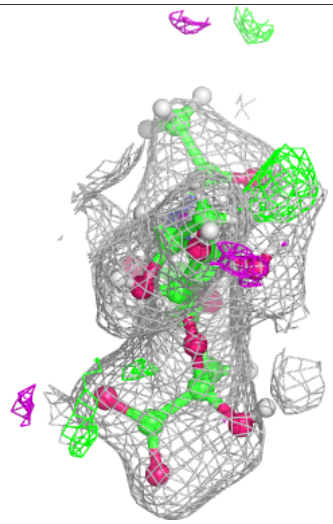


Electron density around 79J D 403:

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.