wwPDB X-ray Structure Validation Summary Report (i)

Nov 11, 2026 – 07:11 PM JST

PDB ID	:	25UD / pdb_000025ud
Title	:	Crystal structure of SktA in complex with 5,7-dibromo-L-tryptophan and Fe2+
Authors	:	Li, H.; Liu, J.; Huang, J.-W.; Chen, C.-C.; Guo, R.-T.
Deposited on	:	2026-04-17
Resolution	:	2.50 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:

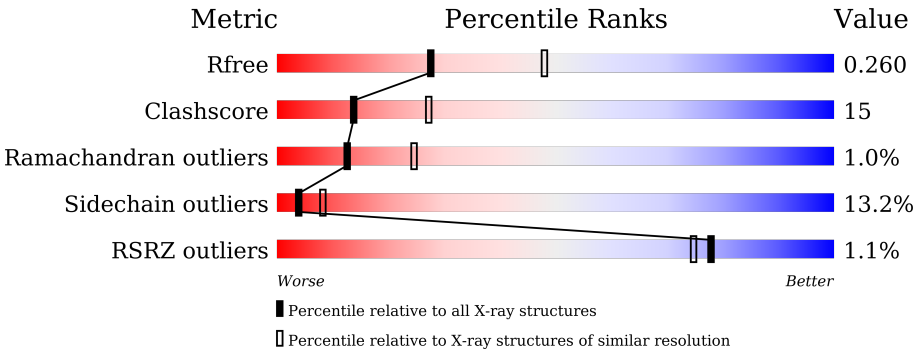
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	248	65% 23% 5% 7%
1	B	248	66% 16% • 13%
1	C	248	51% 31% 6% 12%
1	D	248	46% 35% 5% • 13%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7534 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 Iron-containing redox enzyme family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	0	0
			1916	1232	317	359	8			
1	B	215	Total	C	N	O	S	0	0	0
			1802	1164	298	333	7			
1	C	218	Total	C	N	O	S	0	0	0
			1826	1178	301	340	7			
1	D	216	Total	C	N	O	S	0	0	0
			1794	1153	297	336	8			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP A0A367RF96
A	-9	ALA	-	expression tag	UNP A0A367RF96
A	-8	GLY	-	expression tag	UNP A0A367RF96
A	-7	ALA	-	expression tag	UNP A0A367RF96
A	-6	GLY	-	expression tag	UNP A0A367RF96
A	-5	ALA	-	expression tag	UNP A0A367RF96
A	-4	GLY	-	expression tag	UNP A0A367RF96
A	-3	ALA	-	expression tag	UNP A0A367RF96
A	-2	GLY	-	expression tag	UNP A0A367RF96
A	-1	ALA	-	expression tag	UNP A0A367RF96
A	0	GLY	-	expression tag	UNP A0A367RF96
B	-10	GLY	-	expression tag	UNP A0A367RF96
B	-9	ALA	-	expression tag	UNP A0A367RF96
B	-8	GLY	-	expression tag	UNP A0A367RF96
B	-7	ALA	-	expression tag	UNP A0A367RF96
B	-6	GLY	-	expression tag	UNP A0A367RF96
B	-5	ALA	-	expression tag	UNP A0A367RF96
B	-4	GLY	-	expression tag	UNP A0A367RF96
B	-3	ALA	-	expression tag	UNP A0A367RF96
B	-2	GLY	-	expression tag	UNP A0A367RF96
B	-1	ALA	-	expression tag	UNP A0A367RF96

Continued on next page...

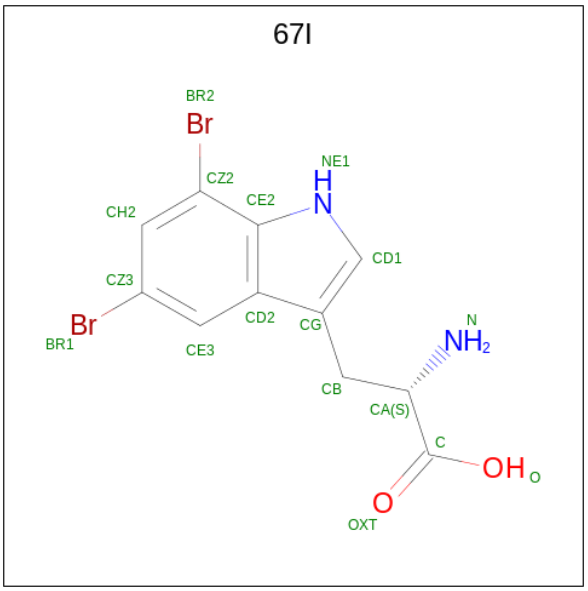
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP A0A367RF96
C	-10	GLY	-	expression tag	UNP A0A367RF96
C	-9	ALA	-	expression tag	UNP A0A367RF96
C	-8	GLY	-	expression tag	UNP A0A367RF96
C	-7	ALA	-	expression tag	UNP A0A367RF96
C	-6	GLY	-	expression tag	UNP A0A367RF96
C	-5	ALA	-	expression tag	UNP A0A367RF96
C	-4	GLY	-	expression tag	UNP A0A367RF96
C	-3	ALA	-	expression tag	UNP A0A367RF96
C	-2	GLY	-	expression tag	UNP A0A367RF96
C	-1	ALA	-	expression tag	UNP A0A367RF96
C	0	GLY	-	expression tag	UNP A0A367RF96
D	-10	GLY	-	expression tag	UNP A0A367RF96
D	-9	ALA	-	expression tag	UNP A0A367RF96
D	-8	GLY	-	expression tag	UNP A0A367RF96
D	-7	ALA	-	expression tag	UNP A0A367RF96
D	-6	GLY	-	expression tag	UNP A0A367RF96
D	-5	ALA	-	expression tag	UNP A0A367RF96
D	-4	GLY	-	expression tag	UNP A0A367RF96
D	-3	ALA	-	expression tag	UNP A0A367RF96
D	-2	GLY	-	expression tag	UNP A0A367RF96
D	-1	ALA	-	expression tag	UNP A0A367RF96
D	0	GLY	-	expression tag	UNP A0A367RF96

- Molecule 2 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Fe 2 2	0	0
2	C	2	Total Fe 2 2	0	0

- Molecule 3 is (2S)-2-azanyl-3-[5,7-bis(bromanyl)-1H-indol-3-yl]propanoic acid (CCD ID: 67I) (formula: $C_{11}H_{10}Br_2N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	Br	C	N	O	0	0
			17	2	11	2	2		
3	B	1	Total	Br	C	N	O	0	0
			17	2	11	2	2		
3	C	1	Total	Br	C	N	O	0	0
			17	2	11	2	2		

- Molecule 4 is water.

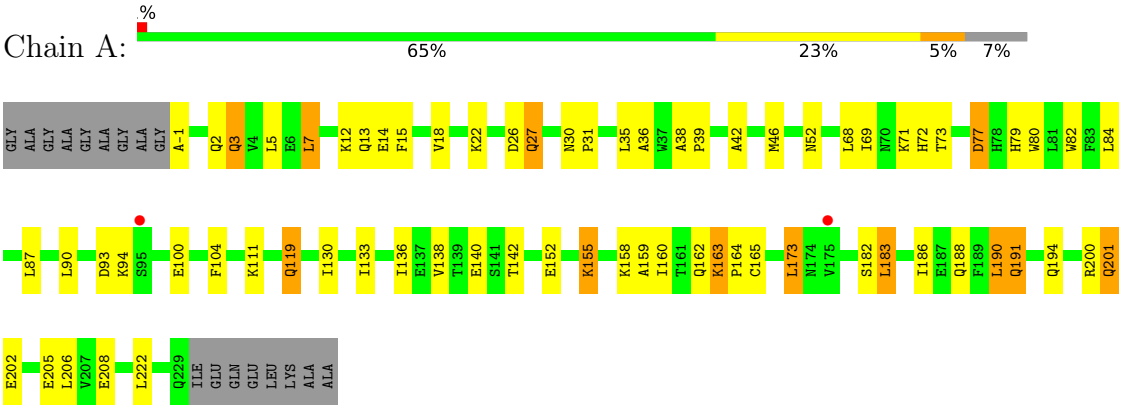
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total	O	0	0
			37	37		
4	B	46	Total	O	0	0
			46	46		
4	C	29	Total	O	0	0
			29	29		
4	D	29	Total	O	0	0
			29	29		

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.

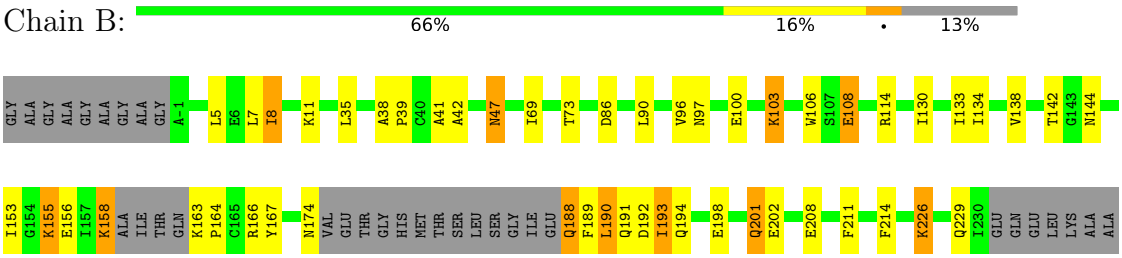
• Molecule 1: Iron-containing redox enzyme family protein

Chain A:



• Molecule 1: Iron-containing redox enzyme family protein

Chain B:



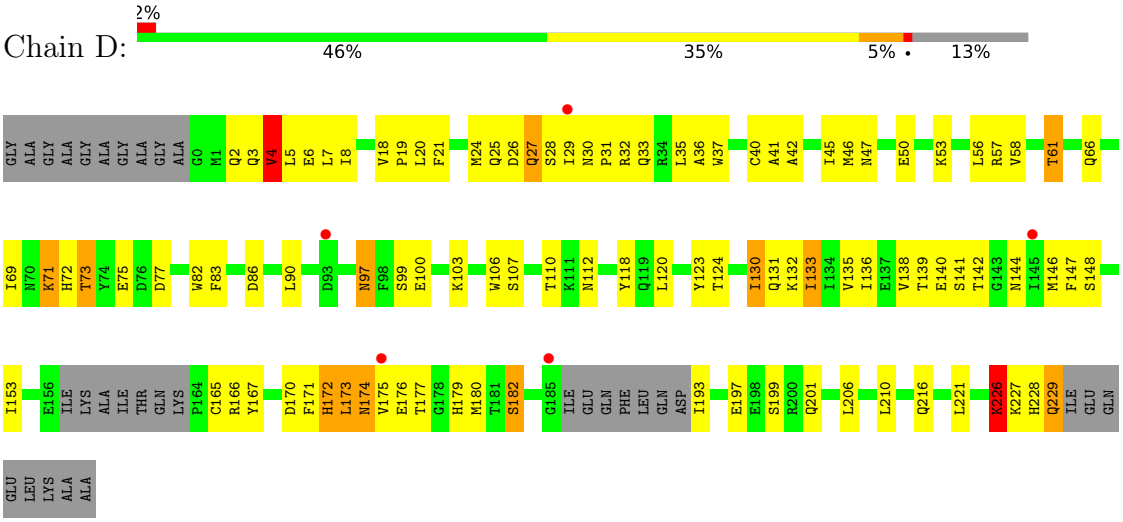
• Molecule 1: Iron-containing redox enzyme family protein

Chain C:



• Molecule 1: Iron-containing redox enzyme family protein

Chain D:


2%
46%
35%
5%
13%
GLY ALA GLY ALA GLY ALA GLY ALA GLY ALA GO M1 Q2 Q3 V4 L5 E6 L7 I8 V18 P19 L20 F21 M24 Q25 D26 Q27 S28 I29 N30 P31 R32 Q33 R34 L35 A36 W37 C40 A41 A42 I45 M46 N47 E50 K53 L56 R57 V58 T61 Q66
I69 N70 K71 H72 T73 Y74 E75 D76 D77 W82 F83 D86 L90 D93 N97 F98 S99 E100 K103 W106 S107 T110 K111 N112 Y118 Q119 L120 Y123 T124 I130 Q131 K132 I133 I134 V135 I136 E137 V138 T139 E140 S141 T142 G143 N144 I145 M146 F147 S148
I153 E156 ILE LYS ALA ILE THR GLN LYS P164 C165 R166 Y167 D170 F171 H172 L173 N174 V175 E176 T177 G178 H179 M180 T181 S182 G185 ILE GLU GLN PHE LEU GLN ASP I193 E197 E198 S199 R200 Q201 L206 L210 Q216 L221 K226 K227 H228 Q229 ILE GLU GLN
GLU LEU LYS ALA ALA

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	55.83Å 67.19Å 69.33Å 71.78° 75.95° 74.78°	Depositor
Resolution (Å)	45.25 – 2.50 45.25 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.1 (45.25-2.50) 95.2 (45.25-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	7.21 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.205 , 0.262 0.209 , 0.260	Depositor DCC
R_{free} test set	1506 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å^2)	42.7	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 36.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.039 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7534	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.39% 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: FE2, 67I

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	1.11	0/1962	1.51	6/2653 (0.2%)
1	B	1.10	1/1845 (0.1%)	1.51	4/2491 (0.2%)
1	C	1.03	1/1869 (0.1%)	1.54	2/2523 (0.1%)
1	D	1.05	1/1837 (0.1%)	1.52	3/2481 (0.1%)
All	All	1.07	3/7513 (0.0%)	1.52	15/10148 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	58	VAL	C-O	5.96	1.29	1.24
1	C	19	PRO	C-O	-5.15	1.17	1.24
1	B	108	GLU	C-O	5.02	1.30	1.24

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	77	ASP	CA-CB-CG	6.32	118.92	112.60
1	D	172	HIS	N-CA-C	-6.04	104.03	111.40
1	A	22	LYS	CA-C-N	5.80	128.06	120.28
1	A	22	LYS	C-N-CA	5.80	128.06	120.28
1	B	191	GLN	N-CA-C	-5.74	98.58	110.80

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	1916	0	1868	53	0
1	B	1802	0	1757	37	0
1	C	1826	0	1779	51	0
1	D	1794	0	1737	76	0
2	A	2	0	0	0	0
2	C	2	0	0	0	0
3	A	17	0	0	0	0
3	B	17	0	0	4	0
3	C	17	0	0	2	0
4	A	37	0	0	3	0
4	B	46	0	0	2	0
4	C	29	0	0	1	0
4	D	29	0	0	0	0
All	All	7534	0	7141	211	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 15.

The worst 5 of 211 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)
3:B:301:67I:BR2	3:B:301:67I:CZ2	2.22	1.42
1:D:171:PHE:HA	1:D:174:ASN:HD21	1.26	0.97
1:A:201:GLN:HG2	4:A:412:HOH:O	1.62	0.97
1:B:201:GLN:HE21	1:B:201:GLN:HA	1.38	0.88
1:B:167:TYR:OH	3:B:301:67I:OXT	1.90	0.87

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	229/248 (92%)	212 (93%)	17 (7%)	0	100 100
1	B	209/248 (84%)	193 (92%)	15 (7%)	1 (0%)	24 43
1	C	212/248 (86%)	173 (82%)	36 (17%)	3 (1%)	9 17
1	D	210/248 (85%)	179 (85%)	26 (12%)	5 (2%)	4 8
All	All	860/992 (87%)	757 (88%)	94 (11%)	9 (1%)	12 24

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	141	SER
1	D	4	VAL
1	D	99	SER
1	D	226	LYS
1	B	8	ILE

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	210/216 (97%)	182 (87%)	28 (13%)	4 8
1	B	197/216 (91%)	178 (90%)	19 (10%)	8 17
1	C	201/216 (93%)	172 (86%)	29 (14%)	3 6
1	D	197/216 (91%)	167 (85%)	30 (15%)	3 5
All	All	805/864 (93%)	699 (87%)	106 (13%)	4 8

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	87	LEU
1	C	205	GLU
1	D	193	ILE
1	C	130	ILE
1	C	174	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	72	HIS
1	D	216	GLN
1	D	78	HIS
1	D	174	ASN
1	B	188	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 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	67I	C	303	2	16,18,18	2.92	8 (50%)	23,26,26	3.05	5 (21%)
3	67I	A	303	2	16,18,18	2.81	9 (56%)	23,26,26	3.06	7 (30%)
3	67I	B	301	-	16,18,18	4.45	6 (37%)	23,26,26	4.29	10 (43%)

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	67I	C	303	2	-	0/8/8/8	0/2/2/2
3	67I	A	303	2	-	2/8/8/8	0/2/2/2
3	67I	B	301	-	-	0/8/8/8	0/2/2/2

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	67I	BR2-CZ2	14.57	2.22	1.89
3	B	301	67I	CB-CG	6.00	1.62	1.50
3	C	303	67I	CD2-CG	-5.67	1.34	1.44
3	B	301	67I	CD2-CG	-5.66	1.34	1.44
3	A	303	67I	CD2-CG	-5.57	1.34	1.44

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	301	67I	BR2-CZ2-CE2	14.75	136.16	119.65
3	C	303	67I	BR2-CZ2-CE2	9.85	130.68	119.65
3	A	303	67I	BR2-CZ2-CE2	9.49	130.28	119.65
3	B	301	67I	CE2-CD2-CG	7.95	111.80	106.53
3	C	303	67I	CE2-CD2-CG	6.25	110.67	106.53

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	67I	N-CA-CB-CG
3	A	303	67I	O-C-CA-N

There are no ring outliers.

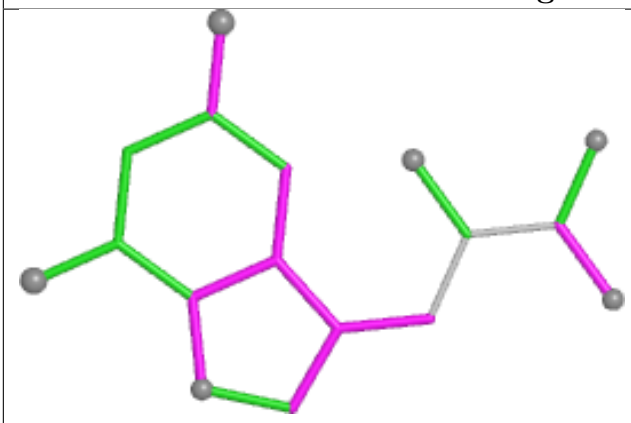
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	303	67I	2	0
3	B	301	67I	4	0

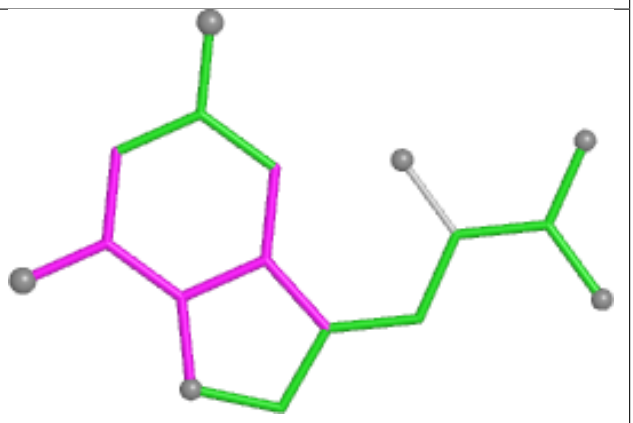
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

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.

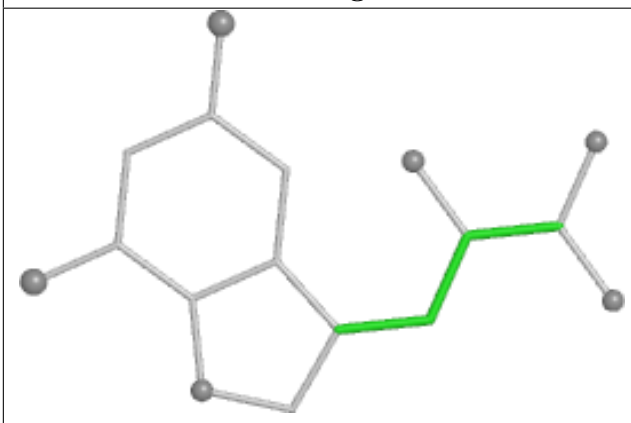
Ligand 67I C 303



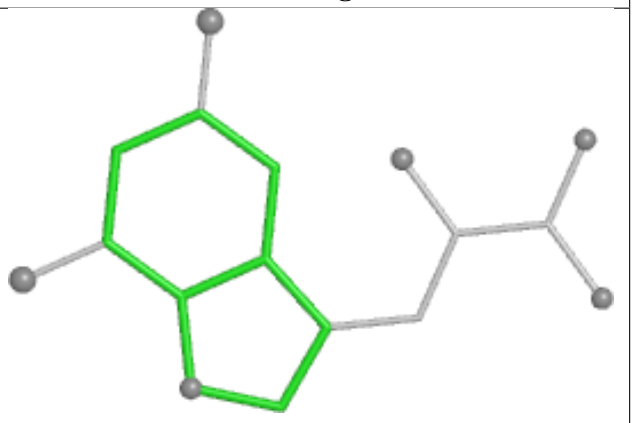
Bond lengths



Bond angles

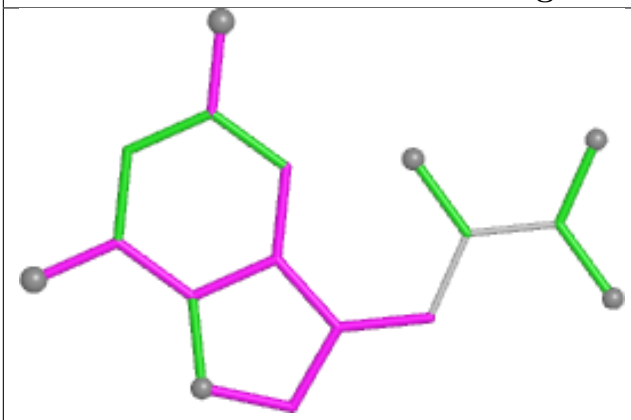


Torsions

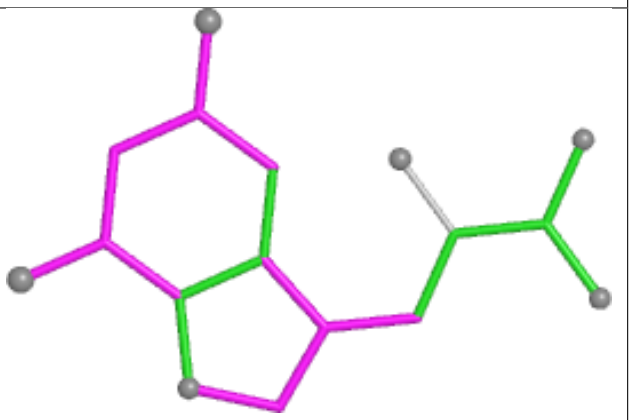


Rings

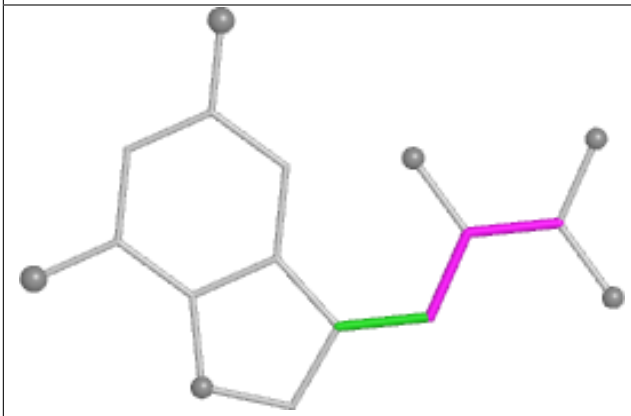
Ligand 67I A 303



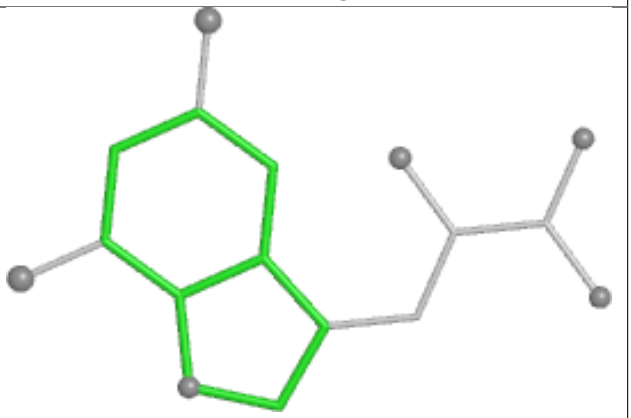
Bond lengths



Bond angles

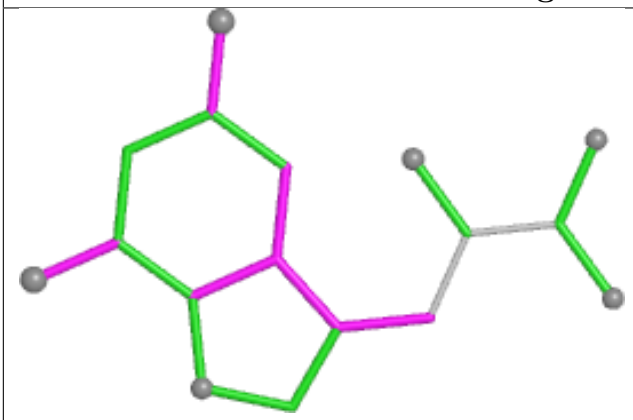


Torsions

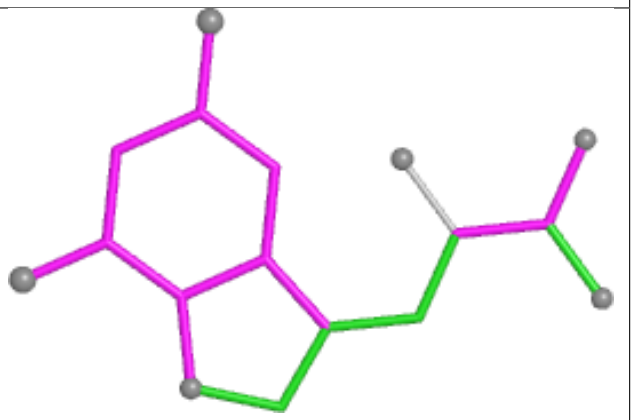


Rings

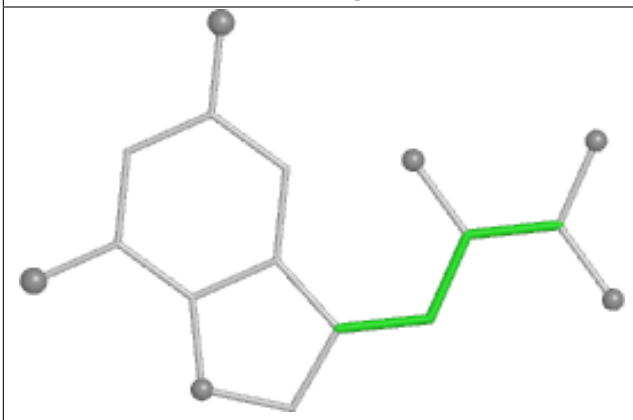
Ligand 67I B 301



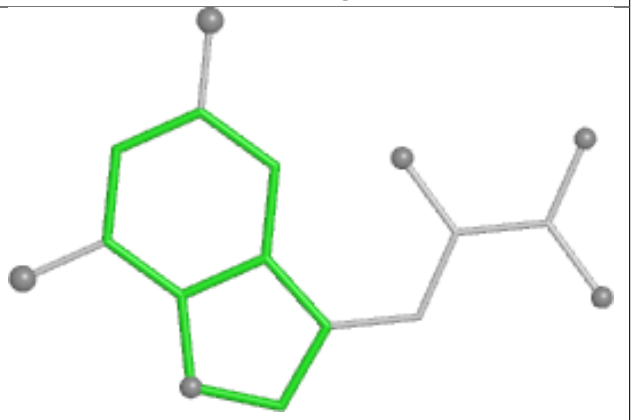
Bond lengths



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	231/248 (93%)	0.05	2 (0%) 81 78	20, 44, 82, 111	0
1	B	215/248 (86%)	-0.08	0 100 100	21, 40, 82, 104	0
1	C	218/248 (87%)	0.29	3 (1%) 73 70	31, 61, 94, 111	0
1	D	216/248 (87%)	0.40	5 (2%) 61 57	29, 60, 95, 136	0
All	All	880/992 (88%)	0.16	10 (1%) 78 75	20, 51, 91, 136	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	95	SER	2.7
1	C	186	ILE	2.5
1	D	145	ILE	2.5
1	D	185	GLY	2.5
1	C	169	ALA	2.5

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 oligosaccharides in this entry.

6.4 Ligands

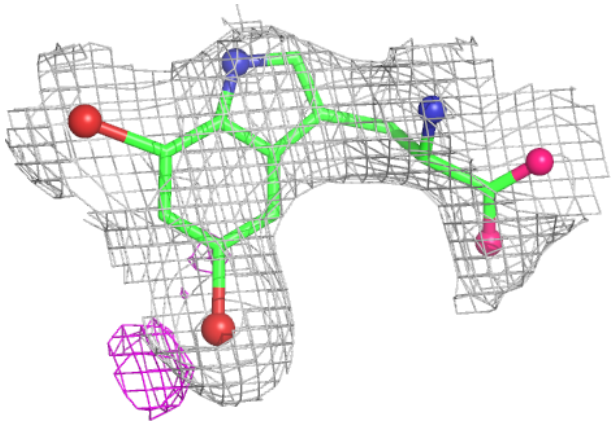
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

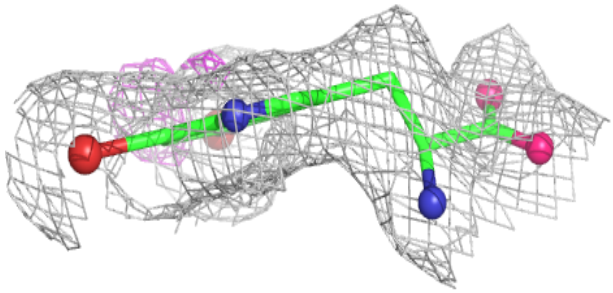
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	67I	C	303	17/17	0.93	0.09	39,56,74,91	0
3	67I	B	301	17/17	0.96	0.08	27,32,42,57	0
2	FE2	C	302	1/1	0.97	0.05	86,86,86,86	0
3	67I	A	303	17/17	0.97	0.07	30,38,49,68	0
2	FE2	A	302	1/1	0.98	0.06	65,65,65,65	0
2	FE2	C	301	1/1	0.98	0.04	75,75,75,75	0
2	FE2	A	301	1/1	1.00	0.02	56,56,56,56	0

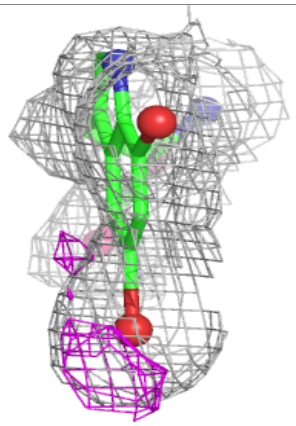
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 67I C 303:

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

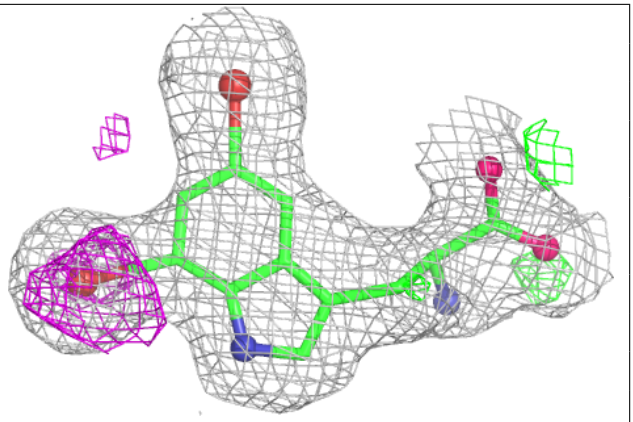


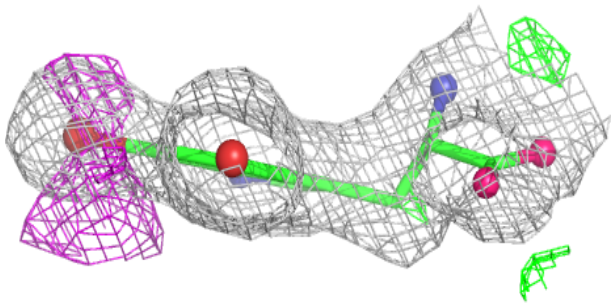


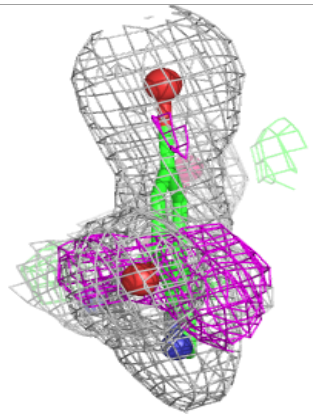


Electron density around 67I B 301:

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

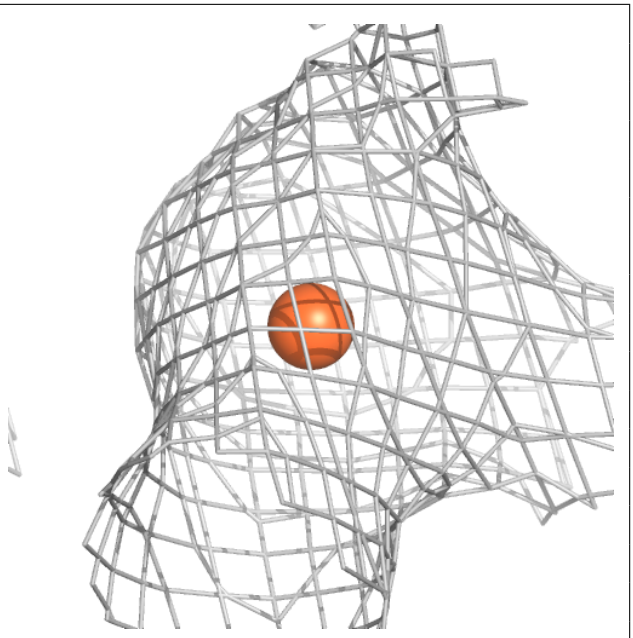


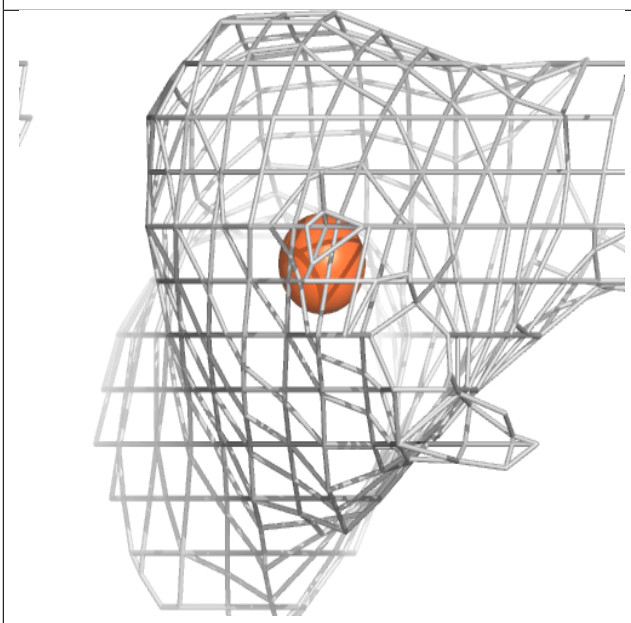


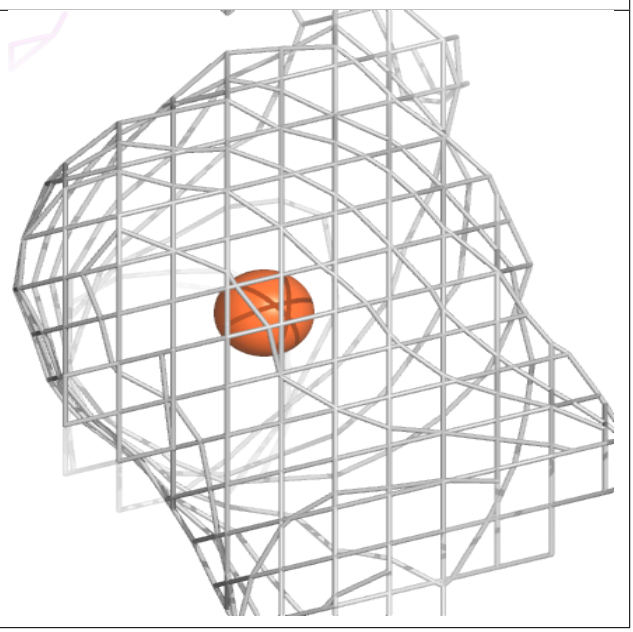


Electron density around FE2 C 302:

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

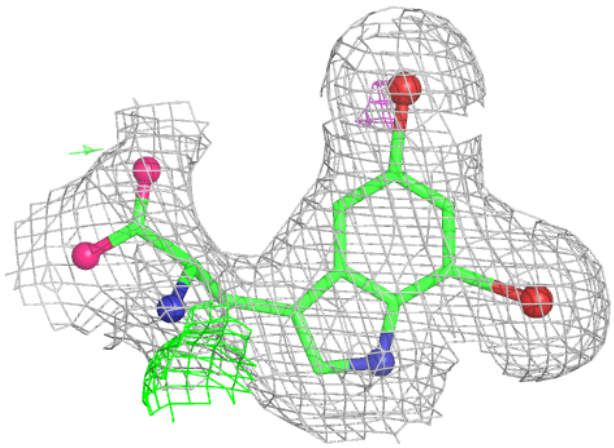


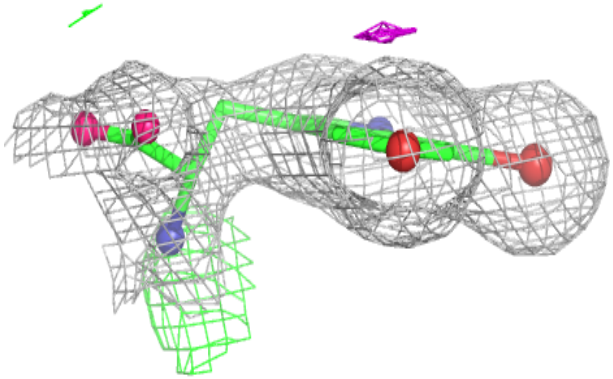


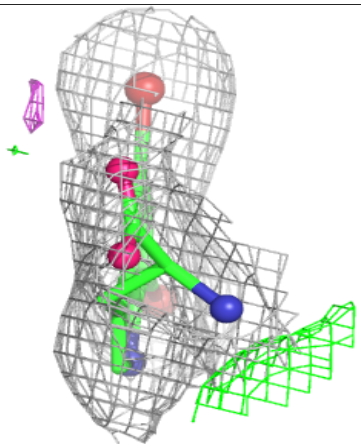


Electron density around 67I A 303:

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

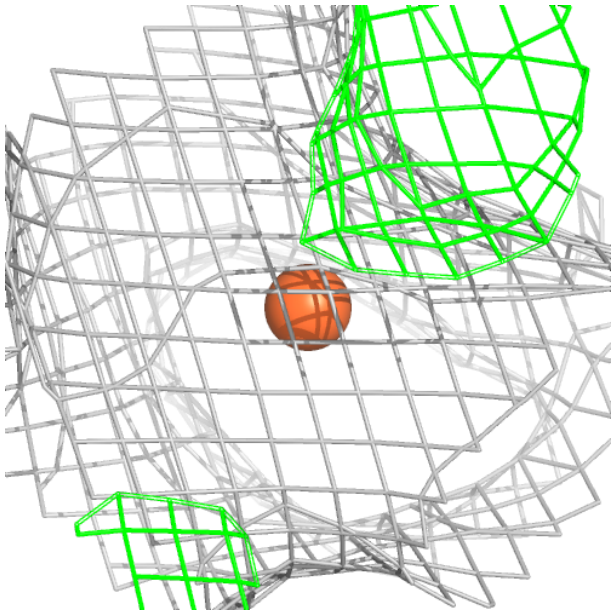


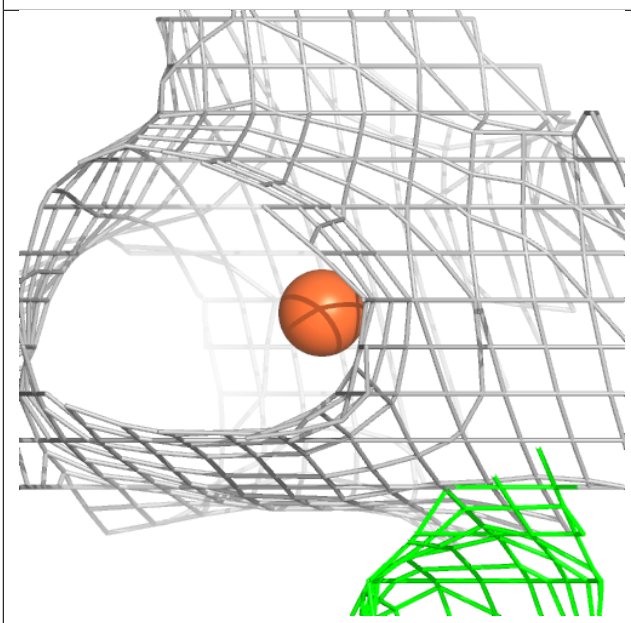


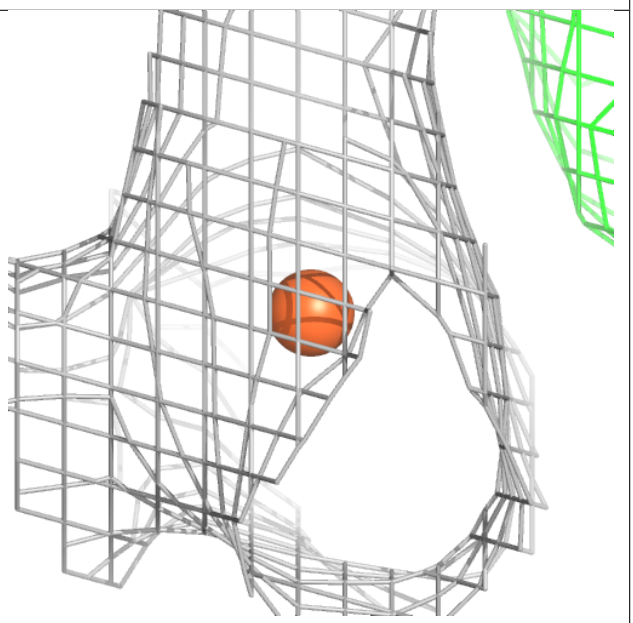


Electron density around FE2 A 302:

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

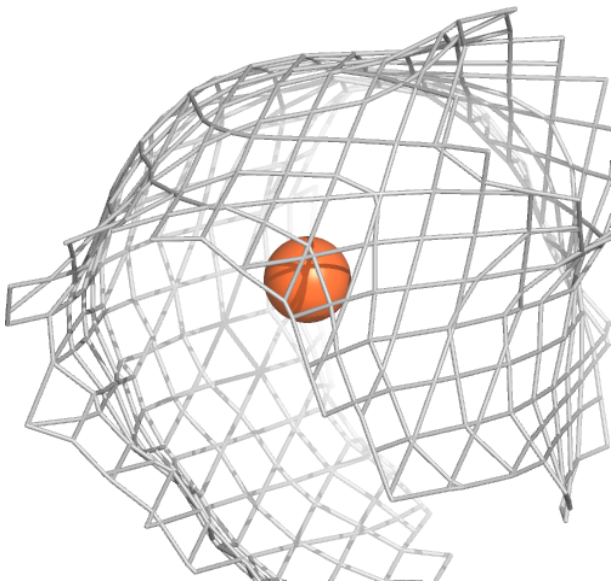


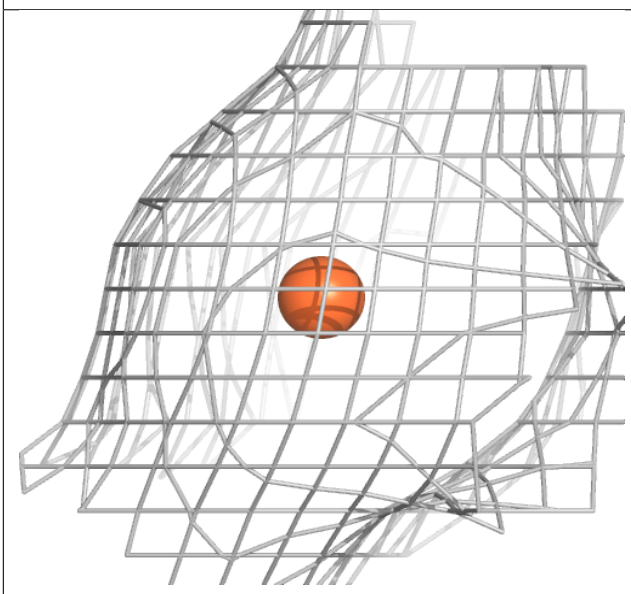


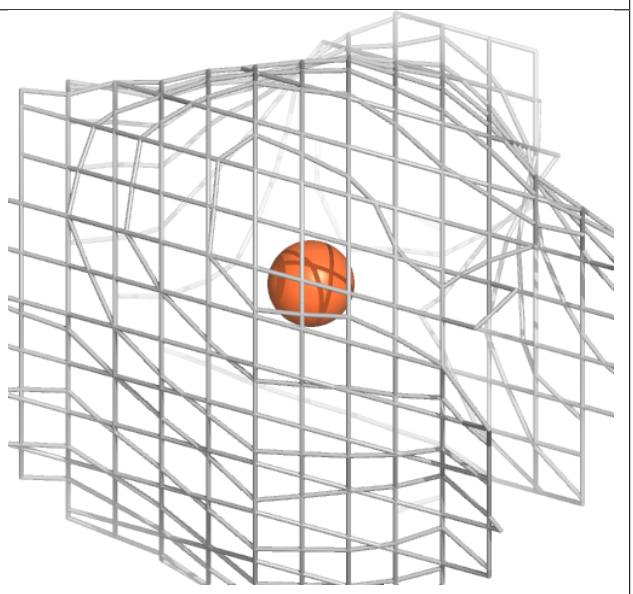


Electron density around FE2 C 301:

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

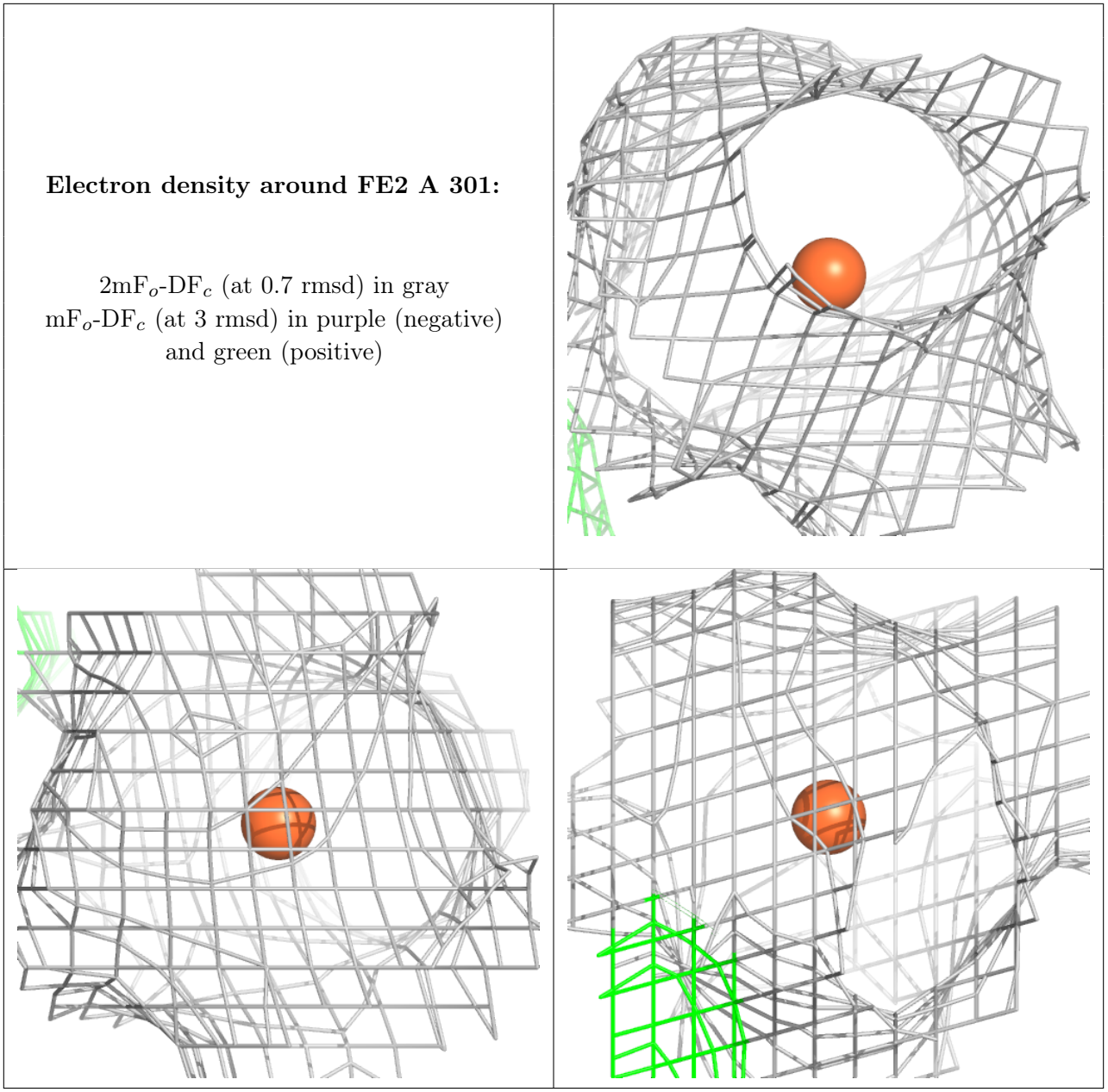






Electron density around FE2 A 301:

$2mF_o$-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

There are no such residues in this entry.