



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:56 AM UTC

PDB ID : 5DYO / pdb_00005dyo
Title : Fab43.1 complex with flourescein
Authors : Longenecker, K.L.; Judge, R.A.
Deposited on : 2015-09-25
Resolution : 2.36 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
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 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

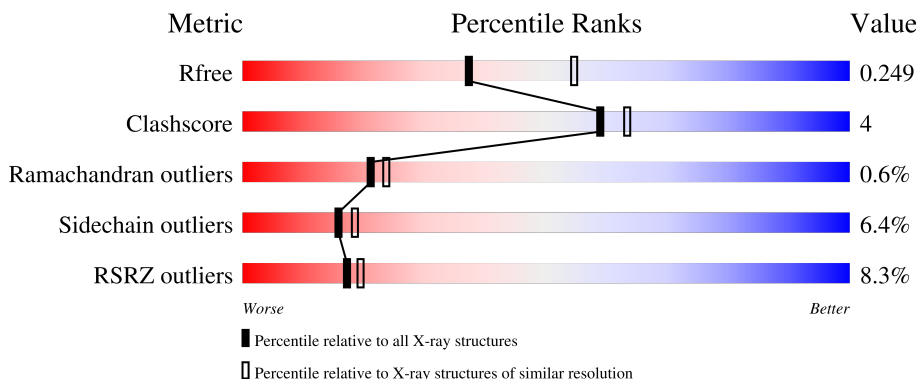
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	212	25% 79% 15% • •
1	H	212	3% 84% 15%
2	B	218	4% 82% 17% •
2	L	218	% 84% 14% •

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6955 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.

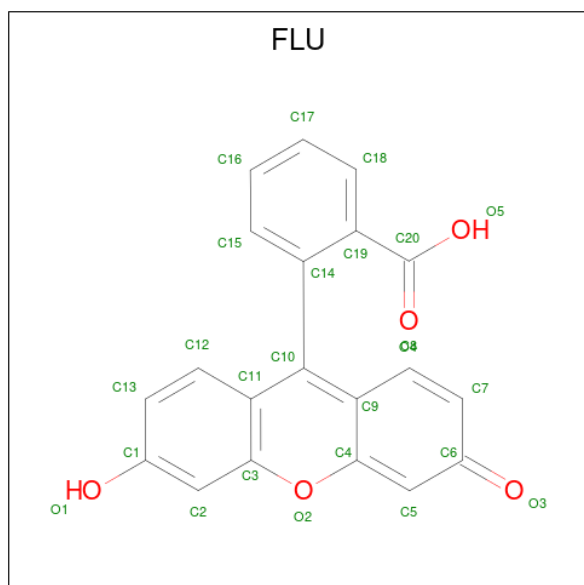
- Molecule 1 is a protein called Fab 43.1 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	0	0	0
			1544	980	248	310	6			
1	H	212	Total	C	N	O	S	0	0	0
			1591	1005	258	321	7			

- Molecule 2 is a protein called Fab 43.1 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	0	0
			1695	1060	286	343	6			
2	L	216	Total	C	N	O	S	0	0	0
			1678	1051	283	338	6			

- Molecule 3 is 2-(6-HYDROXY-3-OXO-3H-XANTHEN-9-YL)-BENZOIC ACID (CCD ID: FLU) (formula: C₂₀H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			25	20	5		
3	H	1	Total	C	O	0	0
			25	20	5		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		
4	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	47	Total	O	0	0
			47	47		
5	B	67	Total	O	0	0
			67	67		
5	H	107	Total	O	0	0
			107	107		

Continued on next page...

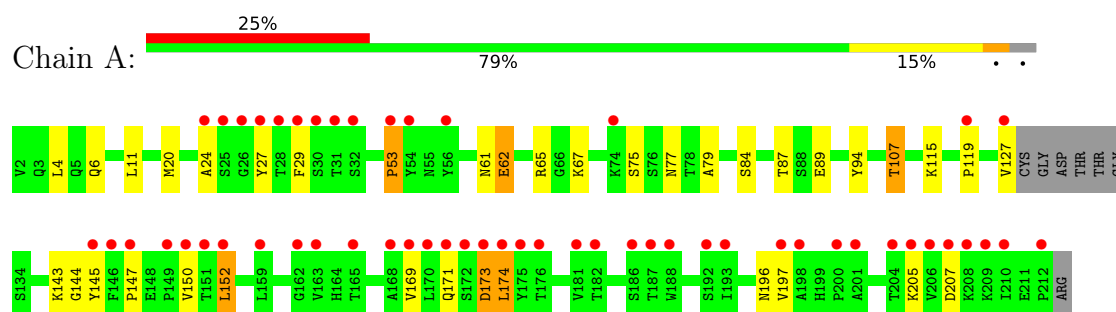
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	L	151	Total	O	0	0
			151	151		

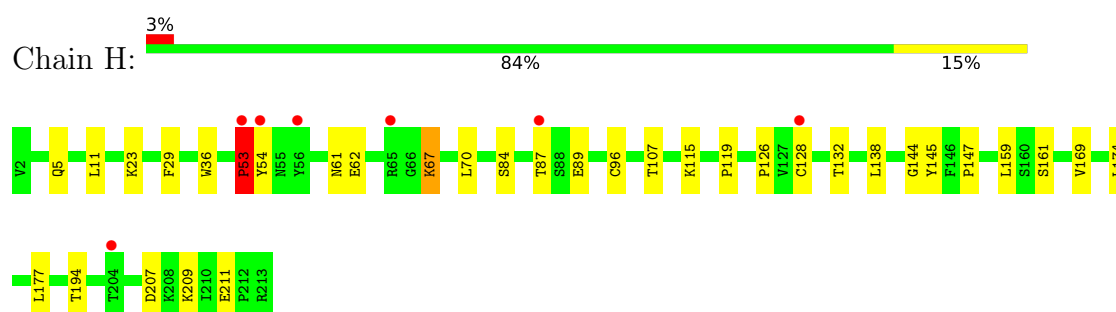
3 Residue-property plots [i](#)

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.

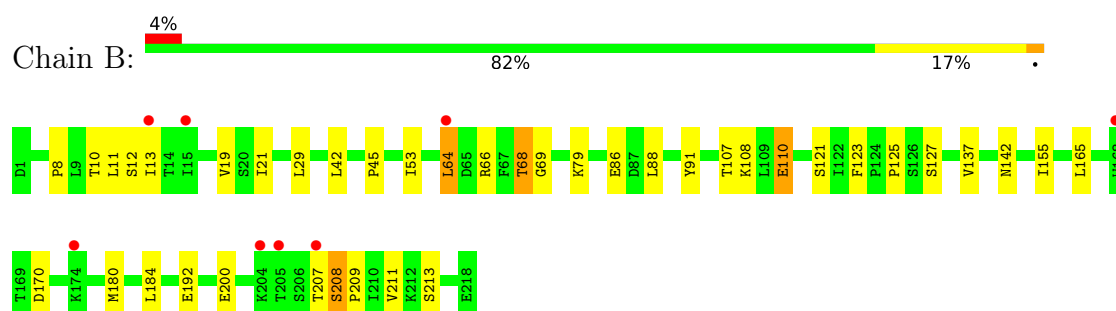
• Molecule 1: Fab 43.1 Heavy Chain



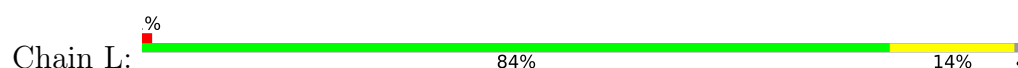
• Molecule 1: Fab 43.1 Heavy Chain



• Molecule 2: Fab 43.1 Light Chain



• Molecule 2: Fab 43.1 Light Chain





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.23Å 105.40Å 109.06Å 90.00° 102.73° 90.00°	Depositor
Resolution (Å)	47.20 – 2.36 47.20 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.20-2.36) 99.8 (47.20-2.36)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.37Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.11.6	Depositor
R, R_{free}	0.193 , 0.239 0.201 , 0.249	Depositor DCC
R_{free} test set	2468 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	37.1	Xtriage
Anisotropy	0.418	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 59.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.029 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6955	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, FLU

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	0.81	0/1585	1.25	5/2166 (0.2%)
1	H	0.85	0/1633	1.20	4/2232 (0.2%)
2	B	0.79	0/1732	1.17	4/2353 (0.2%)
2	L	0.85	0/1715	1.19	6/2330 (0.3%)
All	All	0.83	0/6665	1.20	19/9081 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	ASP	CA-C-N	11.57	142.52	121.70
1	A	173	ASP	C-N-CA	11.57	142.52	121.70
1	H	53	PRO	CA-C-N	7.06	132.00	120.63
1	H	53	PRO	C-N-CA	7.06	132.00	120.63
1	A	27	TYR	CA-C-N	6.35	131.28	121.19
1	A	27	TYR	C-N-CA	6.35	131.28	121.19
2	L	21	ILE	CB-CA-C	6.25	120.12	110.50
2	L	127	SER	CA-C-N	6.11	128.79	120.54
2	L	127	SER	C-N-CA	6.11	128.79	120.54
1	A	61	ASN	N-CA-C	-5.74	100.64	109.76
2	L	210	ILE	N-CA-C	-5.51	100.38	108.54
2	B	142	ASN	CA-C-N	5.39	129.84	122.34
2	B	142	ASN	C-N-CA	5.39	129.84	122.34
1	H	61	ASN	N-CA-C	-5.33	101.28	109.76
1	H	96	CYS	N-CA-C	-5.21	101.66	109.95
2	L	119	THR	N-CA-C	-5.21	100.03	108.41
2	L	99	PHE	CA-CB-CG	-5.17	108.64	113.80
2	B	127	SER	CA-C-N	5.02	126.97	120.44
2	B	127	SER	C-N-CA	5.02	126.97	120.44

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	1544	0	1504	14	0
1	H	1591	0	1547	11	0
2	B	1695	0	1639	21	0
2	L	1678	0	1627	13	0
3	A	25	0	11	0	0
3	H	25	0	11	0	0
4	B	10	0	0	0	0
4	H	5	0	0	0	0
4	L	10	0	0	0	0
5	A	47	0	0	1	0
5	B	67	0	0	0	0
5	H	107	0	0	0	0
5	L	151	0	0	1	0
All	All	6955	0	6339	57	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (57) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:155:ILE:HD11	2:B:184:LEU:HD21	1.67	0.77
1:A:119:PRO:HB3	1:A:145:TYR:HB3	1.66	0.77
2:L:64:LEU:HD12	2:L:66:ARG:HH12	1.56	0.70
1:A:173:ASP:HB2	1:A:174:LEU:HG	1.72	0.70
2:L:21:ILE:HG12	2:L:107:THR:HG21	1.73	0.69
2:L:64:LEU:CD1	2:L:66:ARG:HH12	2.06	0.68
1:H:11:LEU:HB2	1:H:147:PRO:HG3	1.77	0.67
2:B:64:LEU:HD13	2:B:66:ARG:HH12	1.61	0.65
2:B:200:GLU:HG2	2:B:211:VAL:HG22	1.79	0.64
1:H:87:THR:HG22	1:H:89:GLU:H	1.62	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:53:ILE:CD1	2:L:78:LEU:HD13	2.33	0.59
1:A:29:PHE:HE1	1:A:79:ALA:HB2	1.68	0.59
2:L:155:ILE:HD11	2:L:184:LEU:HD21	1.84	0.58
2:B:208:SER:CB	2:B:209:PRO:HD3	2.34	0.58
1:H:29:PHE:O	1:H:53:PRO:HB3	2.04	0.58
1:A:53:PRO:HA	5:A:436:HOH:O	2.04	0.56
2:B:8:PRO:HG3	2:B:11:LEU:HD13	1.88	0.56
1:A:62:GLU:HA	1:A:65:ARG:HG2	1.88	0.56
1:H:53:PRO:HG2	1:H:54:TYR:CD2	2.41	0.56
1:H:169:VAL:HG21	2:L:165:LEU:HB3	1.88	0.55
1:A:152:LEU:HD13	1:A:197:VAL:HG22	1.90	0.54
1:H:67:LYS:HE2	1:H:84:SER:O	2.08	0.53
1:A:169:VAL:HG21	2:B:165:LEU:HB3	1.90	0.53
1:A:6:GLN:NE2	1:A:107:THR:HG22	2.27	0.50
2:B:11:LEU:CD2	2:B:19:VAL:HG13	2.41	0.50
1:A:11:LEU:HB2	1:A:147:PRO:HG3	1.94	0.49
2:B:68:THR:HG22	2:B:79:LYS:HB2	1.94	0.49
2:B:125:PRO:HD3	2:B:137:VAL:HG22	1.95	0.49
2:B:13:ILE:HG13	2:B:19:VAL:HG22	1.94	0.49
2:B:21:ILE:HG12	2:B:107:THR:HG21	1.96	0.47
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.96	0.46
1:A:174:LEU:HD23	1:A:174:LEU:HA	1.86	0.46
2:B:10:THR:HG22	2:B:108:LYS:HB3	1.98	0.45
1:A:87:THR:HG22	1:A:89:GLU:H	1.82	0.45
2:L:13:ILE:HG13	2:L:19:VAL:HG22	1.99	0.44
2:L:21:ILE:HG23	5:L:427:HOH:O	2.16	0.44
2:L:53:ILE:HA	2:L:58:ASN:O	2.18	0.44
1:H:36:TRP:CD1	1:H:70:LEU:HD22	2.53	0.44
1:H:144:GLY:HA2	1:H:174:LEU:HB3	2.00	0.43
2:B:208:SER:HB2	2:B:209:PRO:HD3	2.00	0.43
1:A:4:LEU:HD23	1:A:24:ALA:HB2	2.00	0.43
2:L:64:LEU:HD12	2:L:66:ARG:NH1	2.27	0.43
1:H:209:LYS:HE2	1:H:211:GLU:OE1	2.17	0.43
2:B:42:LEU:HD13	2:B:91:TYR:CZ	2.54	0.43
2:B:64:LEU:HD13	2:B:66:ARG:NH1	2.31	0.43
1:A:20:MET:HE1	1:A:94:TYR:CD2	2.54	0.43
2:B:207:THR:HA	2:B:208:SER:HA	1.60	0.43
2:B:53:ILE:HD13	2:B:69:GLY:HA3	2.00	0.42
2:L:53:ILE:HD11	2:L:78:LEU:HD13	2.00	0.42
2:B:208:SER:HB3	2:B:209:PRO:HD3	2.01	0.42
2:B:12:SER:HA	2:B:110:GLU:O	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:24:LYS:HA	2:L:74:THR:O	2.20	0.41
2:L:4:MET:SD	2:L:25:SER:HB3	2.60	0.41
2:B:121:SER:HB3	2:B:123:PHE:CE1	2.56	0.41
1:A:67:LYS:HE3	1:A:84:SER:O	2.21	0.40
2:B:45:PRO:HB3	2:B:170:ASP:HB2	2.02	0.40
1:H:126:PRO:HD3	1:H:138:LEU:HD23	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	201/212 (95%)	186 (92%)	12 (6%)	3 (2%)	8	7
1	H	210/212 (99%)	205 (98%)	4 (2%)	1 (0%)	24	27
2	B	216/218 (99%)	210 (97%)	5 (2%)	1 (0%)	24	27
2	L	214/218 (98%)	211 (99%)	3 (1%)	0	100	100
All	All	841/860 (98%)	812 (97%)	24 (3%)	5 (1%)	21	24

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	PRO
1	A	174	LEU
2	B	208	SER
1	H	53	PRO
1	A	144	GLY

5.3.2 Protein sidechains ⓘ

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	178/183 (97%)	165 (93%)	13 (7%)	13	14
1	H	183/183 (100%)	170 (93%)	13 (7%)	13	15
2	B	195/195 (100%)	186 (95%)	9 (5%)	24	31
2	L	193/195 (99%)	180 (93%)	13 (7%)	15	17
All	All	749/756 (99%)	701 (94%)	48 (6%)	16	18

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	62	GLU
1	A	75	SER
1	A	77	ASN
1	A	107	THR
1	A	115	LYS
1	A	127	VAL
1	A	143	LYS
1	A	150	VAL
1	A	152	LEU
1	A	171	GLN
1	A	196	ASN
1	A	205	LYS
1	A	207	ASP
2	B	29	LEU
2	B	64	LEU
2	B	68	THR
2	B	86	GLU
2	B	88	LEU
2	B	110	GLU
2	B	180	MET
2	B	192	GLU
2	B	213	SER
1	H	5	GLN
1	H	23	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	H	62	GLU
1	H	67	LYS
1	H	107	THR
1	H	115	LYS
1	H	128	CYS
1	H	132	THR
1	H	159	LEU
1	H	161	SER
1	H	177	LEU
1	H	194	THR
1	H	207	ASP
2	L	21	ILE
2	L	29	LEU
2	L	50	GLU
2	L	75	ASP
2	L	83	VAL
2	L	86	GLU
2	L	88	LEU
2	L	149	ILE
2	L	151	VAL
2	L	158	SER
2	L	186	LEU
2	L	192	GLU
2	L	203	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	43	GLN
1	A	59	GLN
1	A	191	GLN
2	B	27	GLN
2	B	43	GLN
2	B	58	ASN
1	H	39	GLN
1	H	164	HIS
2	L	43	GLN
2	L	142	ASN
2	L	143	ASN
2	L	162	ASN
2	L	215	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
4	SO4	L	301	-	4,4,4	0.29	0	6,6,6	0.20	0
3	FLU	H	901	-	28,28,28	0.93	2 (7%)	41,41,41	0.61	1 (2%)
4	SO4	H	902	-	4,4,4	0.34	0	6,6,6	0.29	0
3	FLU	A	301	-	28,28,28	0.48	0	41,41,41	0.39	0
4	SO4	B	901	-	4,4,4	0.24	0	6,6,6	0.63	0
4	SO4	L	302	-	4,4,4	0.28	0	6,6,6	0.09	0
4	SO4	B	902	-	4,4,4	0.25	0	6,6,6	0.14	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	FLU	H	901	-	-	4/6/12/12	0/4/4/4
3	FLU	A	301	-	-	4/6/12/12	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	901	FLU	O5-C20	-3.27	1.20	1.30
3	H	901	FLU	O4-C20	2.66	1.30	1.22

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	901	FLU	O4-C20-C19	-2.22	116.67	121.97

There are no chirality outliers.

All (8) torsion outliers are listed below:

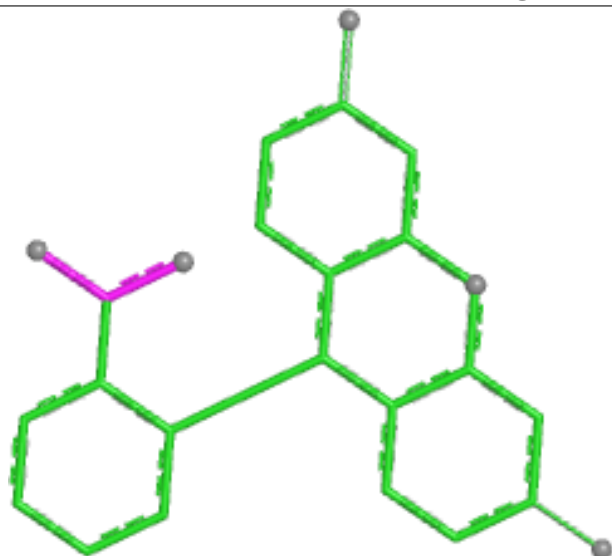
Mol	Chain	Res	Type	Atoms
3	H	901	FLU	C18-C19-C20-O4
3	A	301	FLU	C18-C19-C20-O4
3	A	301	FLU	C18-C19-C20-O5
3	H	901	FLU	C18-C19-C20-O5
3	H	901	FLU	C14-C19-C20-O4
3	A	301	FLU	C14-C19-C20-O5
3	A	301	FLU	C14-C19-C20-O4
3	H	901	FLU	C14-C19-C20-O5

There are no ring outliers.

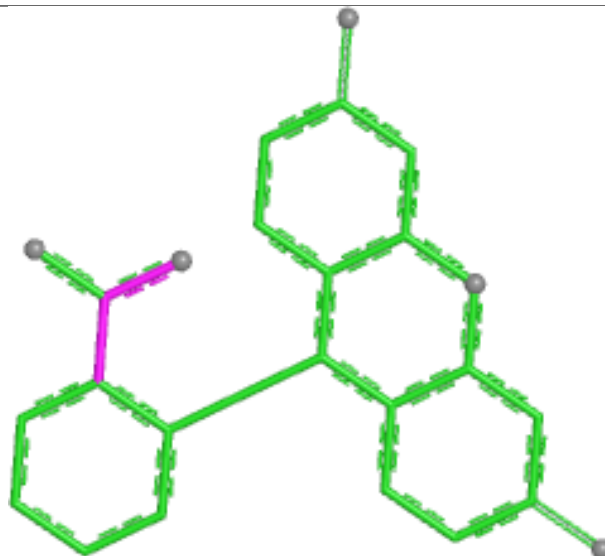
No monomer is involved in short contacts.

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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

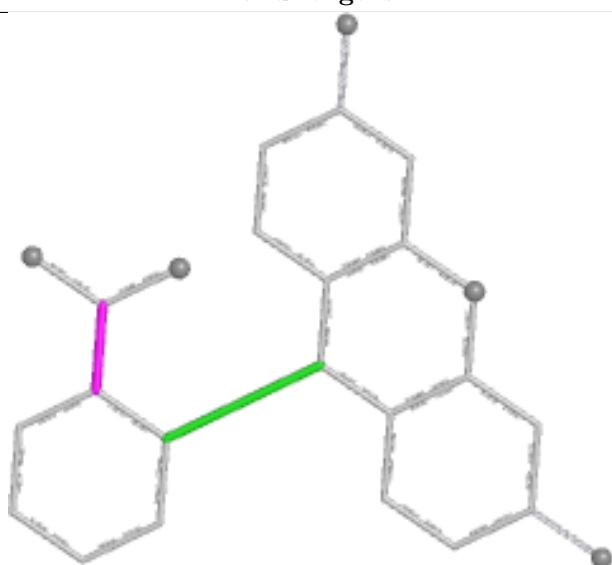
Ligand FLU H 901



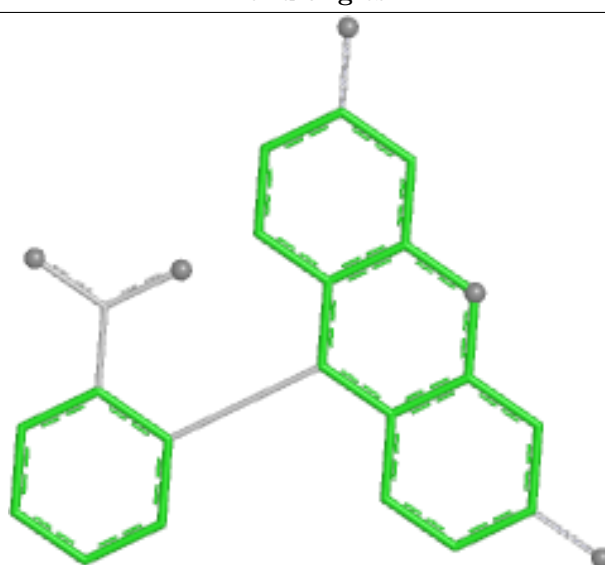
Bond lengths



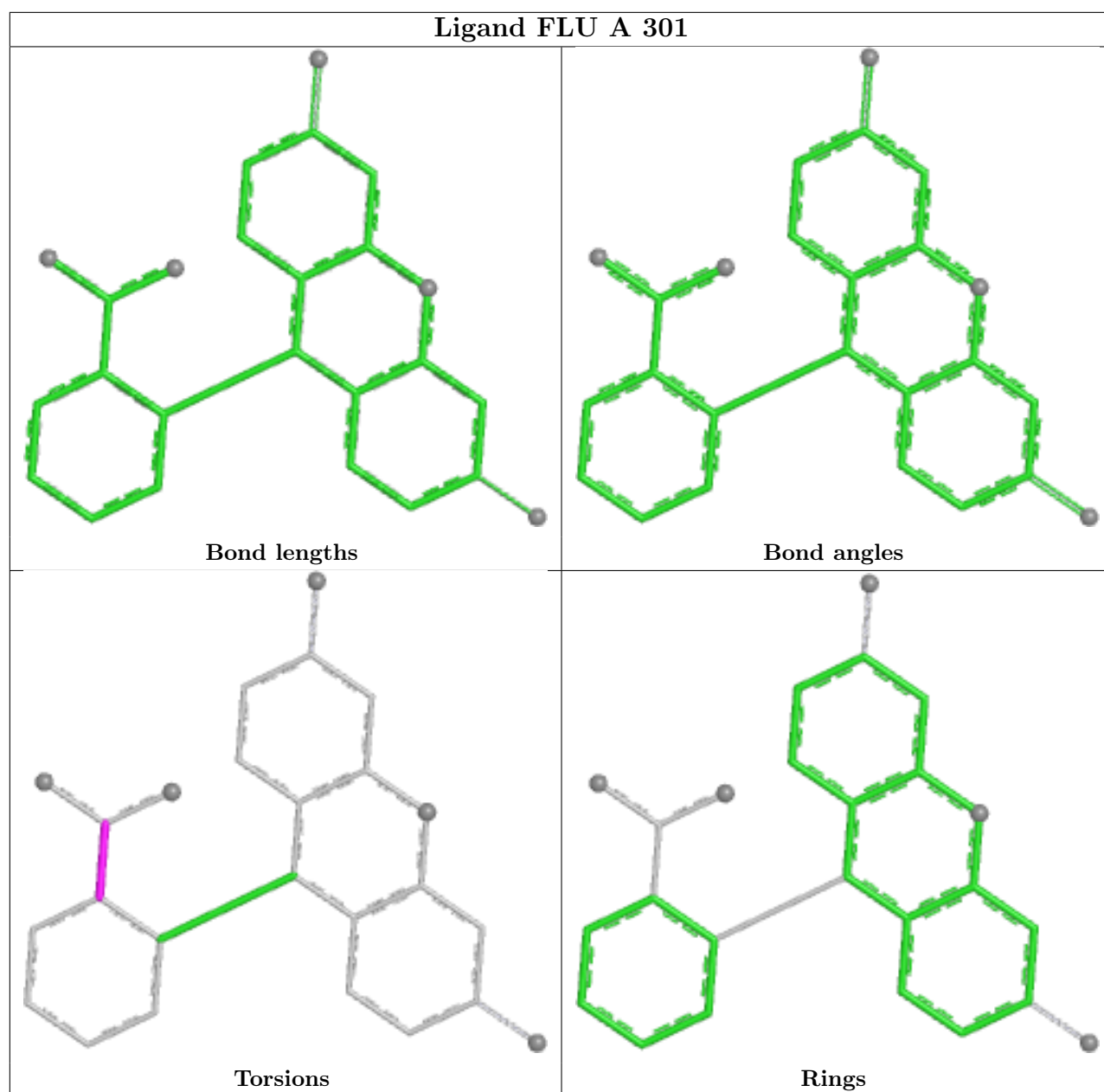
Bond angles



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, 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	205/212 (96%)	1.30	54 (26%) 1 1	30, 66, 105, 120	0
1	H	212/212 (100%)	0.09	7 (3%) 49 56	20, 41, 69, 81	0
2	B	218/218 (100%)	0.48	8 (3%) 45 51	27, 51, 70, 82	0
2	L	216/218 (99%)	-0.23	2 (0%) 81 84	18, 33, 55, 66	0
All	All	851/860 (98%)	0.40	71 (8%) 17 19	18, 45, 91, 120	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	THR	5.9
1	A	29	PHE	5.9
1	A	31	THR	5.9
1	H	54	TYR	5.5
1	A	25	SER	5.2
1	A	200	PRO	4.9
1	A	26	GLY	4.8
1	A	27	TYR	4.7
2	B	64	LEU	4.7
1	A	173	ASP	4.6
2	L	64	LEU	4.3
1	A	53	PRO	4.2
1	A	174	LEU	4.1
1	A	159	LEU	4.0
1	A	54	TYR	3.9
1	A	206	VAL	3.8
1	A	150	VAL	3.8
1	A	56	TYR	3.5
1	A	212	PRO	3.5
1	A	127	VAL	3.5
1	A	149	PRO	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	207	THR	3.4
1	A	201	ALA	3.4
1	A	175	TYR	3.3
1	A	152	LEU	3.2
1	A	162	GLY	3.2
2	B	168	TRP	3.2
1	A	145	TYR	3.1
1	A	197	VAL	3.1
1	A	119	PRO	3.0
1	A	210	ILE	3.0
1	H	128	CYS	2.9
1	A	30	SER	2.9
1	A	32	SER	2.9
1	H	53	PRO	2.8
1	A	198	ALA	2.7
1	A	193	ILE	2.7
1	A	170	LEU	2.7
1	A	74	LYS	2.6
2	B	174	LYS	2.6
1	A	24	ALA	2.6
1	A	172	SER	2.6
1	A	147	PRO	2.5
2	B	205	THR	2.5
1	A	181	VAL	2.5
1	A	182	THR	2.4
2	B	13	ILE	2.4
1	A	151	THR	2.3
1	H	87	THR	2.3
2	L	99	PHE	2.3
1	A	205	LYS	2.3
1	A	208	LYS	2.3
1	A	209	LYS	2.3
1	A	168	ALA	2.3
1	H	56	TYR	2.2
1	A	192	SER	2.2
1	A	207	ASP	2.1
1	A	176	THR	2.1
1	A	204	THR	2.1
1	A	163	VAL	2.1
1	A	171	GLN	2.1
1	A	165	THR	2.1
1	A	187	THR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	204	LYS	2.1
1	A	169	VAL	2.1
1	A	188	TRP	2.1
2	B	15	ILE	2.0
1	H	65	ARG	2.0
1	A	146	PHE	2.0
1	A	186	SER	2.0
1	H	204	THR	2.0

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 ⓘ

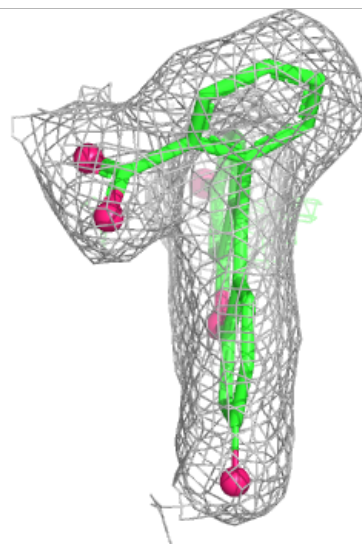
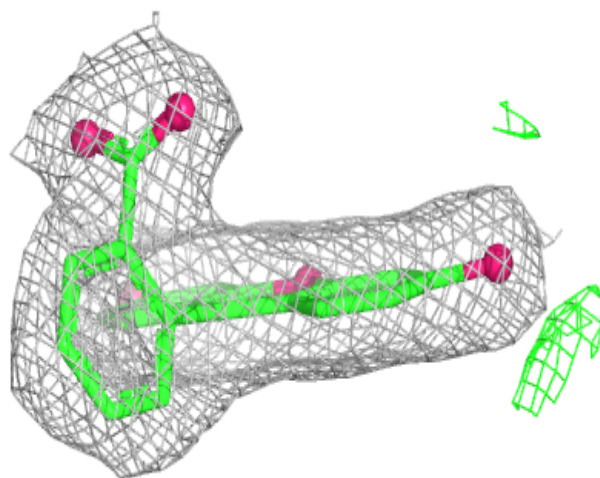
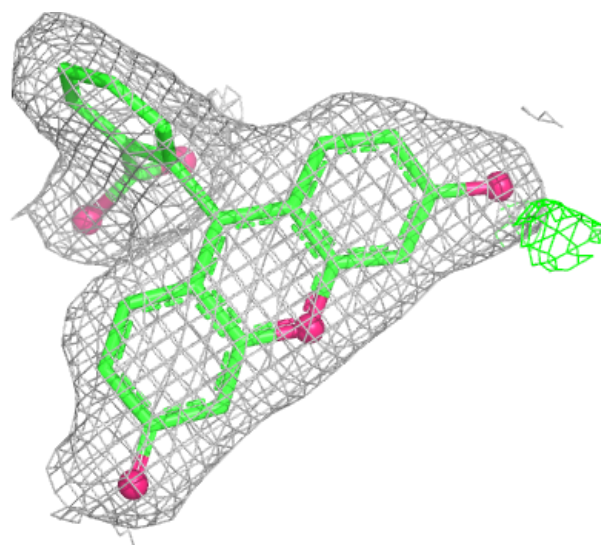
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	L	302	5/5	0.81	0.10	100,101,102,102	0
4	SO4	B	902	5/5	0.84	0.09	97,97,98,98	0
4	SO4	L	301	5/5	0.91	0.14	75,75,76,79	0
4	SO4	B	901	5/5	0.95	0.09	54,57,58,59	0
4	SO4	H	902	5/5	0.97	0.10	50,52,54,56	0
3	FLU	A	301	25/25	0.97	0.05	25,31,34,37	0
3	FLU	H	901	25/25	0.97	0.06	11,24,30,34	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.

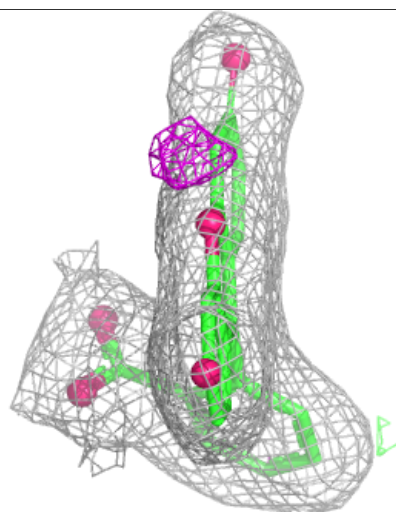
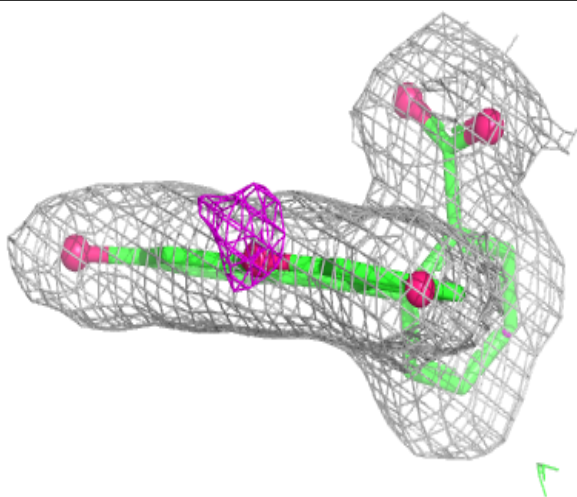
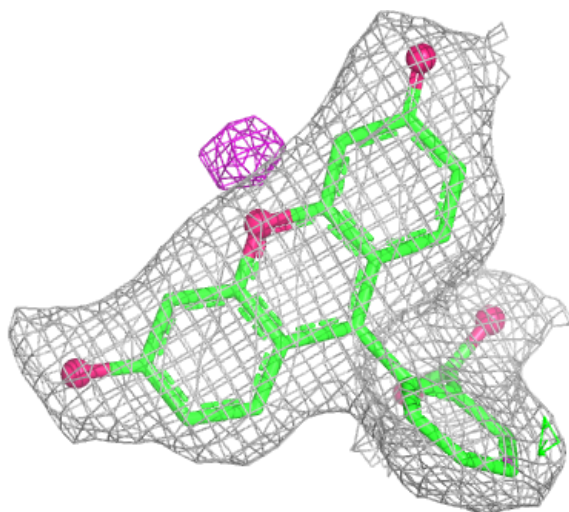
Electron density around FLU A 301:

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



Electron density around FLU H 901:

$2mF_o-DF_c$ (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.