Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 11:37 am BST

PDB ID	:	6CMJ
Title	:	Human CAMKK2 with GSK650393
Authors	:	Williams, S.P.; Reid, R.A.; Price, D.J.; Drewry, D.H.
Deposited on	:	2018-03-05
Resolution	:	2.40 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 following versions of software and data (see references ⓘ) were used in the production of this report:

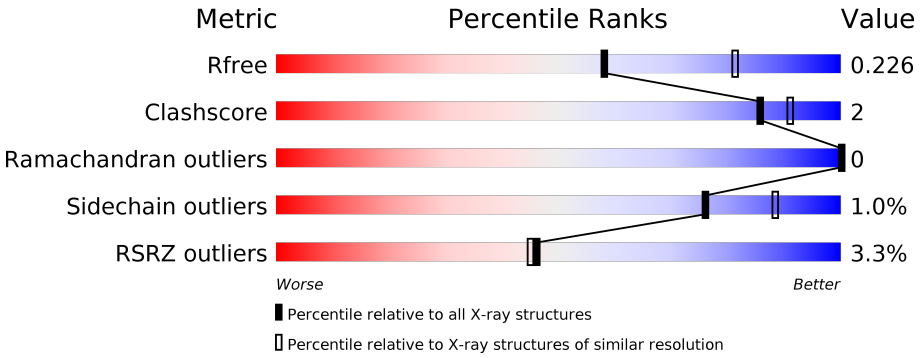
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	321	2% 84% 5% • 10%
1	B	321	4% 83% 6% • 11%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4861 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 Calcium/calmodulin-dependent protein kinase kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	P	S	0	1	0
			2294	1462	373	443	3	13			
1	B	287	Total	C	N	O	P	S	0	0	0
			2252	1436	366	434	3	13			

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	130	MET	-	expression tag	UNP Q96RR4
A	131	ASN	-	expression tag	UNP Q96RR4
A	132	ALA	-	expression tag	UNP Q96RR4
A	133	HIS	-	expression tag	UNP Q96RR4
A	134	HIS	-	expression tag	UNP Q96RR4
A	135	HIS	-	expression tag	UNP Q96RR4
A	136	HIS	-	expression tag	UNP Q96RR4
A	137	HIS	-	expression tag	UNP Q96RR4
A	138	HIS	-	expression tag	UNP Q96RR4
A	139	GLY	-	expression tag	UNP Q96RR4
A	140	SER	-	expression tag	UNP Q96RR4
A	141	ALA	-	expression tag	UNP Q96RR4
A	142	GLU	-	expression tag	UNP Q96RR4
A	143	ASN	-	expression tag	UNP Q96RR4
A	144	LEU	-	expression tag	UNP Q96RR4
A	145	TYR	-	expression tag	UNP Q96RR4
A	146	PHE	-	expression tag	UNP Q96RR4
A	147	GLN	-	expression tag	UNP Q96RR4
A	148	GLY	-	expression tag	UNP Q96RR4
A	163	ASP	ASN	conflict	UNP Q96RR4
A	?	-	GLY	deletion	UNP Q96RR4
A	?	-	PHE	deletion	UNP Q96RR4
A	?	-	PRO	deletion	UNP Q96RR4
A	?	-	ARG	deletion	UNP Q96RR4
A	?	-	ARG	deletion	UNP Q96RR4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP Q96RR4
A	?	-	PRO	deletion	UNP Q96RR4
A	?	-	PRO	deletion	UNP Q96RR4
A	?	-	ARG	deletion	UNP Q96RR4
A	?	-	GLY	deletion	UNP Q96RR4
A	?	-	THR	deletion	UNP Q96RR4
A	?	-	ARG	deletion	UNP Q96RR4
A	?	-	PRO	deletion	UNP Q96RR4
A	?	-	ALA	deletion	UNP Q96RR4
A	?	-	PRO	deletion	UNP Q96RR4
B	130	MET	-	expression tag	UNP Q96RR4
B	131	ASN	-	expression tag	UNP Q96RR4
B	132	ALA	-	expression tag	UNP Q96RR4
B	133	HIS	-	expression tag	UNP Q96RR4
B	134	HIS	-	expression tag	UNP Q96RR4
B	135	HIS	-	expression tag	UNP Q96RR4
B	136	HIS	-	expression tag	UNP Q96RR4
B	137	HIS	-	expression tag	UNP Q96RR4
B	138	HIS	-	expression tag	UNP Q96RR4
B	139	GLY	-	expression tag	UNP Q96RR4
B	140	SER	-	expression tag	UNP Q96RR4
B	141	ALA	-	expression tag	UNP Q96RR4
B	142	GLU	-	expression tag	UNP Q96RR4
B	143	ASN	-	expression tag	UNP Q96RR4
B	144	LEU	-	expression tag	UNP Q96RR4
B	145	TYR	-	expression tag	UNP Q96RR4
B	146	PHE	-	expression tag	UNP Q96RR4
B	147	GLN	-	expression tag	UNP Q96RR4
B	148	GLY	-	expression tag	UNP Q96RR4
B	163	ASP	ASN	conflict	UNP Q96RR4
B	?	-	GLY	deletion	UNP Q96RR4
B	?	-	PHE	deletion	UNP Q96RR4
B	?	-	PRO	deletion	UNP Q96RR4
B	?	-	ARG	deletion	UNP Q96RR4
B	?	-	ARG	deletion	UNP Q96RR4
B	?	-	PRO	deletion	UNP Q96RR4
B	?	-	PRO	deletion	UNP Q96RR4
B	?	-	PRO	deletion	UNP Q96RR4
B	?	-	ARG	deletion	UNP Q96RR4
B	?	-	GLY	deletion	UNP Q96RR4
B	?	-	THR	deletion	UNP Q96RR4
B	?	-	ARG	deletion	UNP Q96RR4

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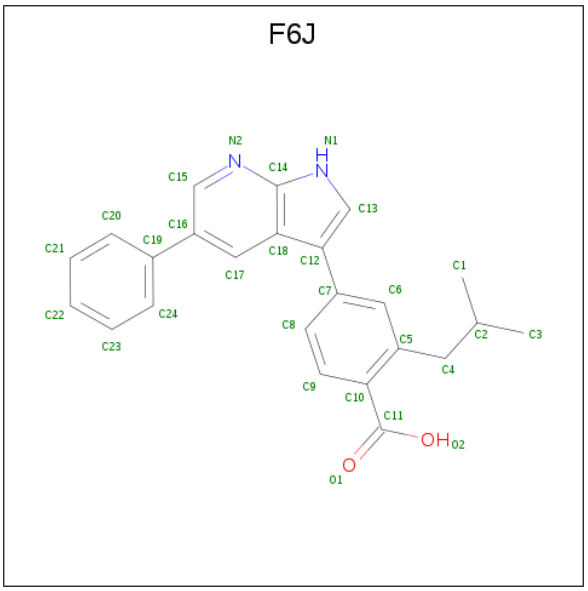
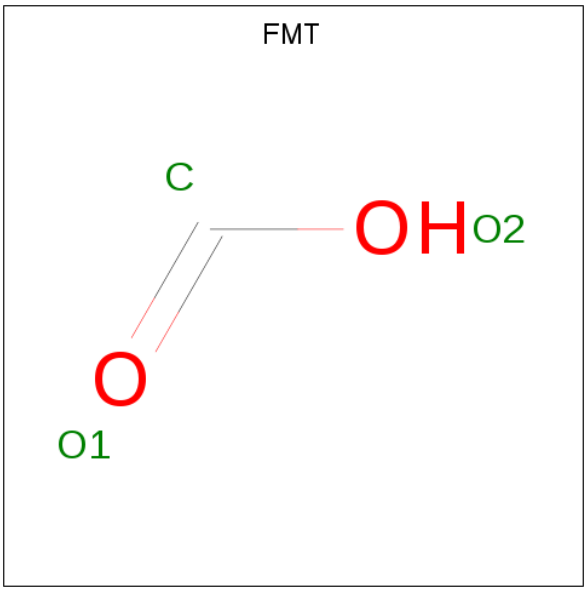
Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	PRO	deletion	UNP Q96RR4
B	?	-	ALA	deletion	UNP Q96RR4
B	?	-	PRO	deletion	UNP Q96RR4

- Molecule 2 is 2-(2-methylpropyl)-4-(5-phenyl-1H-pyrrolo[2,3-b]pyridin-3-yl)benzoic acid (three-letter code: F6J) (formula: $C_{24}H_{22}N_2O_2$).



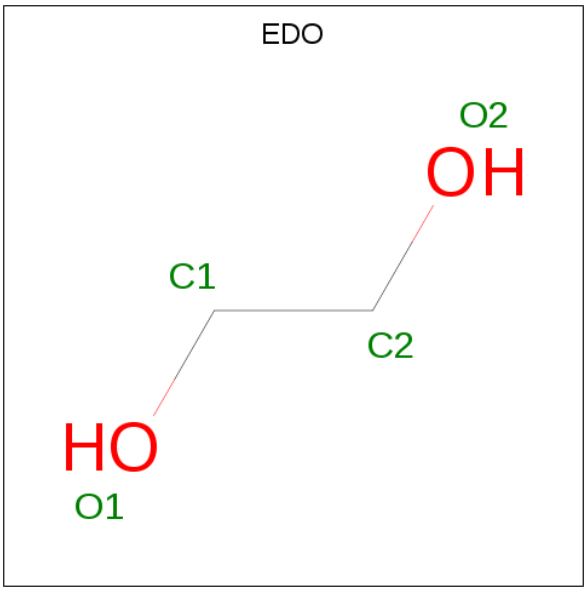
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			28	24	2	2		
2	B	1	Total	C	N	O	0	0
			28	24	2	2		

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 3 1 2	0	0
3	A	1	Total C O 3 1 2	0	0
3	A	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0
3	B	1	Total C O 3 1 2	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 5 is water.

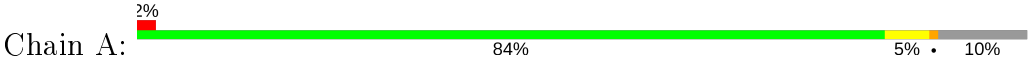
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	123	Total O 123 123	0	0
5	B	106	Total O 106 106	0	0

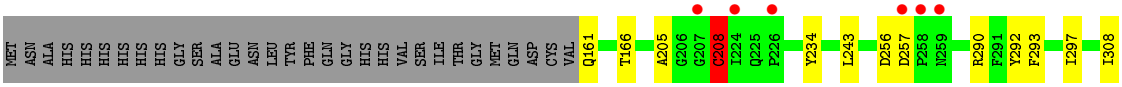
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Calcium/calmodulin-dependent protein kinase kinase 2

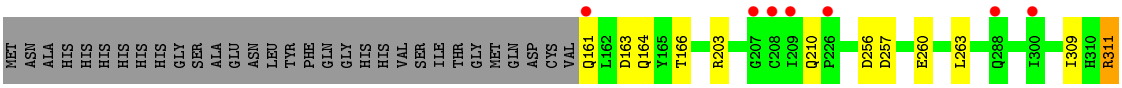
Chain A:

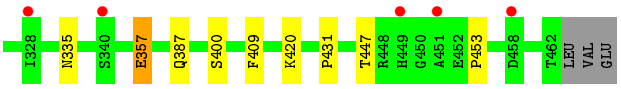




- Molecule 1: Calcium/calmodulin-dependent protein kinase kinase 2

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	89.84Å 89.84Å 181.38Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	27.97 – 2.40 27.97 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.1 (27.97-2.40) 98.2 (27.97-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.05 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.182 , 0.219 0.187 , 0.226	Depositor DCC
R_{free} test set	2334 reflections (7.04%)	wwPDB-VP
Wilson B-factor (Å^2)	41.9	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4861	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: TPO, FMT, EDO, F6J, SEP

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	0.53	1/2314 (0.0%)	0.73	2/3132 (0.1%)
1	B	0.53	1/2270 (0.0%)	0.69	1/3079 (0.0%)
All	All	0.53	2/4584 (0.0%)	0.71	3/6211 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	210	GLN	C-N	9.35	1.52	1.34
1	A	208	CYS	C-N	5.97	1.47	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	311	ARG	NE-CZ-NH2	6.43	123.52	120.30
1	A	257	ASP	CB-CG-OD1	6.14	123.83	118.30
1	A	290	ARG	NE-CZ-NH2	-5.42	117.59	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2294	0	2252	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2252	0	2189	9	1
2	A	28	0	0	0	0
2	B	28	0	0	0	0
3	A	9	0	3	0	0
3	B	9	0	3	0	0
4	A	4	0	6	1	0
4	B	8	0	12	0	0
5	A	123	0	0	2	0
5	B	106	0	0	1	0
All	All	4861	0	4465	20	1

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

All (20) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:TYR:OH	1:A:256:ASP:OD2	1.58	1.21
1:B:161:GLN:OE1	1:B:166:THR:HG23	1.92	0.70
1:A:161:GLN:OE1	1:A:166:THR:HG23	1.94	0.67
1:B:409:PHE:CD2	1:B:420:LYS:HE2	2.33	0.64
1:B:309:ILE:HG22	1:B:311:ARG:HG2	1.81	0.62
1:A:335:ASN:HD22	1:A:335:ASN:C	2.07	0.58
1:A:322:GLU:OE1	5:A:601:HOH:O	2.17	0.56
1:A:243:LEU:HD21	1:A:308:ILE:CD1	2.39	0.53
1:B:447:THR:HG23	1:B:453:PRO:HA	1.91	0.51
1:A:205:ALA:O	1:A:208:CYS:HB2	2.12	0.49
1:A:243:LEU:HD21	1:A:308:ILE:HD13	1.95	0.49
1:A:292:TYR:HB3	1:A:326:ILE:HD12	1.94	0.49
1:B:256:ASP:CG	1:B:263:LEU:HD13	2.34	0.48
1:B:257:ASP:OD2	1:B:260:GLU:HG2	2.15	0.46
4:A:505:EDO:C1	5:A:602:HOH:O	2.64	0.45
1:B:357:GLU:HG2	1:B:431:PRO:HG3	1.98	0.45
1:B:163:ASP:HB3	1:B:164:GLN:OE1	2.20	0.42
1:A:357:GLU:HG2	1:A:431:PRO:HG3	2.01	0.41
1:B:400:SEP:P	5:B:606:HOH:O	2.79	0.41
1:A:293:PHE:CE2	1:A:297:ILE:HD11	2.56	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:203:ARG:NH1	1:B:387:GLN:OE1[5_675]	2.11	0.09

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	284/321 (88%)	279 (98%)	5 (2%)	0	100	100
1	B	283/321 (88%)	278 (98%)	5 (2%)	0	100	100
All	All	567/642 (88%)	557 (98%)	10 (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	250/282 (89%)	247 (99%)	3 (1%)	71	85
1	B	242/282 (86%)	240 (99%)	2 (1%)	81	91
All	All	492/564 (87%)	487 (99%)	5 (1%)	76	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	208	CYS
1	A	335	ASN
1	A	357	GLU

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Mol	Chain	Res	Type
1	B	335	ASN
1	B	357	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	335	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	TPO	B	462	1	8,10,11	1.00	1 (12%)	10,14,16	1.21	1 (10%)
1	TPO	A	462	1	8,10,11	0.90	0	10,14,16	0.96	1 (10%)
1	SEP	B	345	1	8,9,10	0.58	0	8,12,14	1.60	2 (25%)
1	SEP	A	345	1	8,9,10	0.55	0	8,12,14	2.20	2 (25%)
1	SEP	B	400	1	8,9,10	0.82	0	8,12,14	2.13	3 (37%)
1	SEP	A	400	1	8,9,10	0.61	0	8,12,14	1.87	1 (12%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	B	462	1	-	2/9/11/13	-
1	TPO	A	462	1	-	3/9/11/13	-
1	SEP	B	345	1	-	0/5/8/10	-
1	SEP	A	345	1	-	2/5/8/10	-
1	SEP	B	400	1	-	3/5/8/10	-
1	SEP	A	400	1	-	2/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	462	TPO	P-OG1	2.45	1.63	1.59

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	400	SEP	OG-P-O1P	-4.17	94.76	106.47
1	B	400	SEP	O3P-P-OG	-4.08	95.87	106.73
1	A	345	SEP	OG-P-O1P	-3.63	96.29	106.47
1	A	345	SEP	OG-CB-CA	-3.33	104.91	108.14
1	B	400	SEP	O3P-P-O2P	3.31	120.29	107.64
1	B	462	TPO	P-OG1-CB	-2.65	115.20	123.21
1	B	345	SEP	OG-CB-CA	-2.53	105.68	108.14
1	B	345	SEP	O2P-P-OG	-2.50	100.07	106.73
1	B	400	SEP	OG-CB-CA	2.18	110.27	108.14
1	A	462	TPO	P-OG1-CB	-2.13	116.77	123.21

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	462	TPO	N-CA-CB-OG1
1	B	462	TPO	CB-OG1-P-O2P
1	A	462	TPO	N-CA-CB-OG1
1	A	345	SEP	CB-OG-P-O1P
1	B	400	SEP	CA-CB-OG-P
1	A	400	SEP	CA-CB-OG-P
1	B	400	SEP	CB-OG-P-O1P
1	A	345	SEP	CB-OG-P-O2P
1	B	400	SEP	N-CA-CB-OG
1	A	400	SEP	N-CA-CB-OG
1	A	462	TPO	CB-OG1-P-O1P

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Mol	Chain	Res	Type	Atoms
1	A	462	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	400	SEP	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

11 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	EDO	B	506	-	3,3,3	0.95	0	2,2,2	0.71	0
2	F6J	A	501	-	28,31,31	1.13	3 (10%)	31,44,44	1.13	4 (12%)
2	F6J	B	501	-	28,31,31	1.04	3 (10%)	31,44,44	1.21	4 (12%)
3	FMT	A	502	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	A	505	-	3,3,3	0.85	0	2,2,2	0.14	0
3	FMT	B	504	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	A	504	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	A	503	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	503	-	0,2,2	0.00	-	0,1,1	0.00	-
3	FMT	B	502	-	0,2,2	0.00	-	0,1,1	0.00	-
4	EDO	B	505	-	3,3,3	0.50	0	2,2,2	0.35	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
4	EDO	B	506	-	-	0/1/1/1	-
4	EDO	A	505	-	-	0/1/1/1	-
2	F6J	A	501	-	-	2/12/16/16	0/4/4/4
2	F6J	B	501	-	-	1/12/16/16	0/4/4/4
4	EDO	B	505	-	-	1/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	F6J	C10-C11	2.65	1.50	1.47
2	B	501	F6J	C14-N2	-2.55	1.33	1.37
2	A	501	F6J	C14-N2	-2.31	1.33	1.37
2	B	501	F6J	C12-C7	-2.31	1.45	1.49
2	A	501	F6J	C12-C7	-2.12	1.45	1.49
2	B	501	F6J	C10-C11	2.12	1.49	1.47

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	501	F6J	C15-N2-C14	-3.67	113.01	116.69
2	B	501	F6J	C9-C10-C11	-3.17	115.49	120.20
2	A	501	F6J	C15-N2-C14	-3.08	113.61	116.69
2	A	501	F6J	C9-C10-C11	-2.91	115.87	120.20
2	B	501	F6J	C16-C15-N2	2.51	127.87	125.55
2	A	501	F6J	C4-C5-C10	-2.08	120.72	123.65
2	B	501	F6J	C21-C20-C19	2.03	123.11	120.56
2	A	501	F6J	C16-C15-N2	2.00	127.40	125.55

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	505	EDO	O1-C1-C2-O2
2	A	501	F6J	C2-C4-C5-C6
2	B	501	F6J	C2-C4-C5-C6
2	A	501	F6J	C18-C12-C7-C8

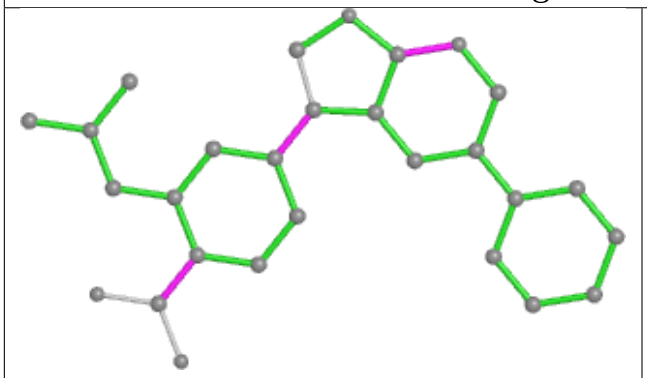
There are no ring outliers.

1 monomer is involved in 1 short contact:

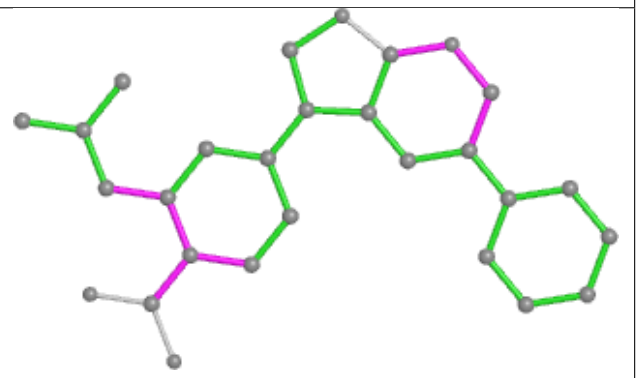
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	505	EDO	1	0

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.

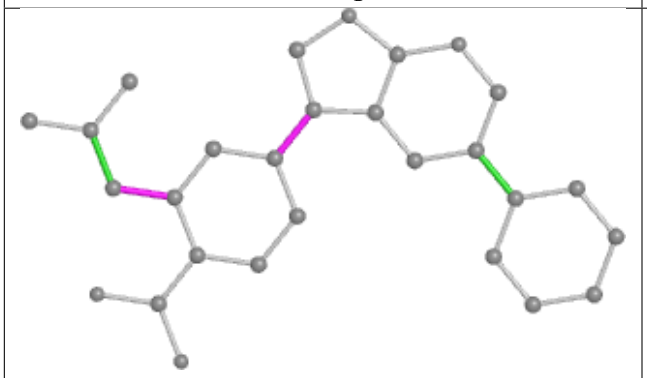
Ligand F6J A 501



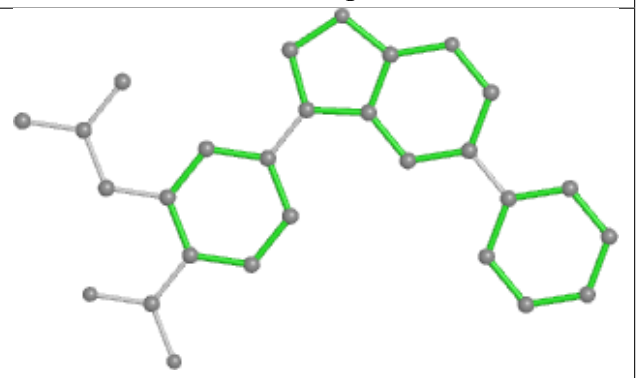
Bond lengths



Bond angles

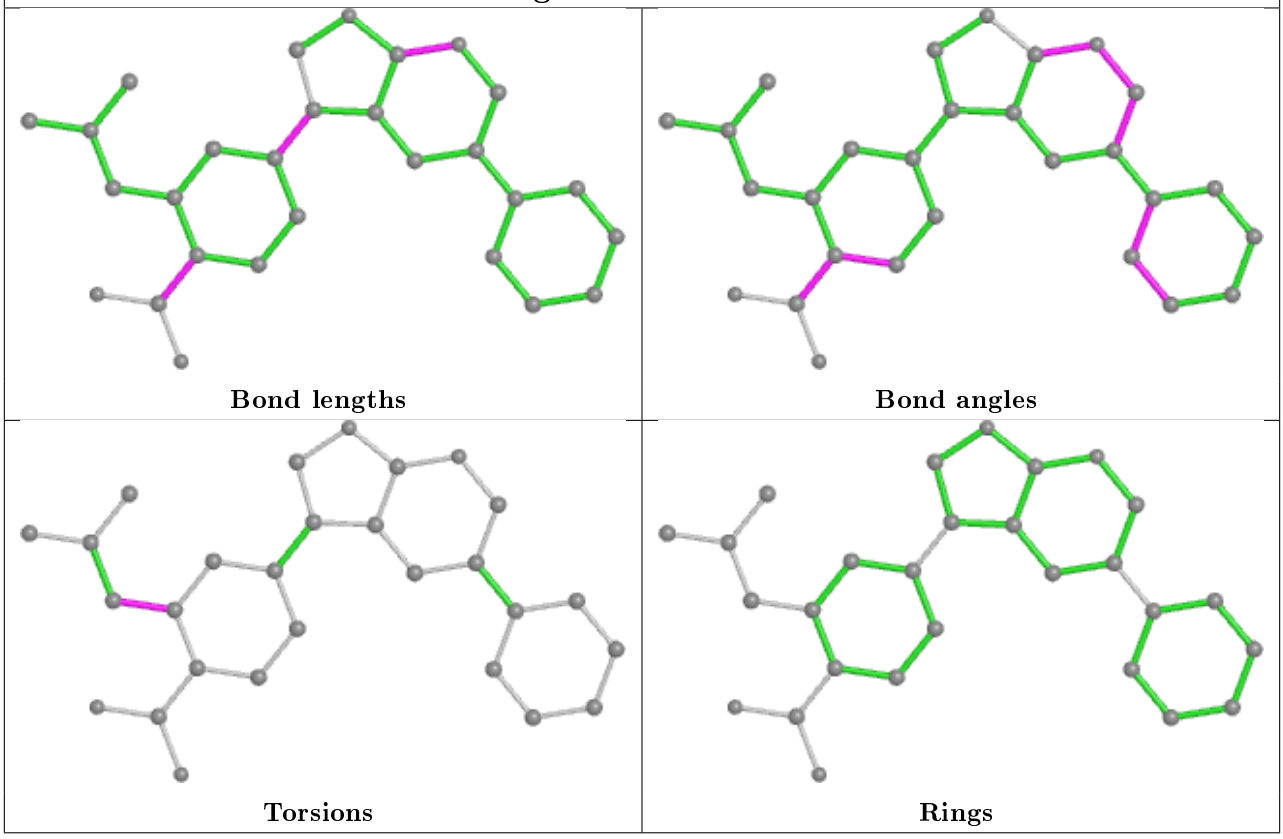


Torsions



Rings

Ligand F6J B 501



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	285/321 (88%)	-0.27	7 (2%) 57 55	29, 40, 65, 99	0
1	B	284/321 (88%)	-0.13	12 (4%) 36 35	31, 43, 69, 104	0
All	All	569/642 (88%)	-0.20	19 (3%) 46 45	29, 42, 69, 104	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	226	PRO	4.6
1	A	259	ASN	4.5
1	A	463	LEU	3.8
1	A	258	PRO	3.6
1	B	451	ALA	3.1
1	B	209	ILE	3.0
1	A	257	ASP	2.9
1	A	207	GLY	2.9
1	B	458	ASP	2.9
1	B	449	HIS	2.8
1	A	226	PRO	2.6
1	B	340	SER	2.5
1	B	208	CYS	2.3
1	A	224	ILE	2.2
1	B	207	GLY	2.2
1	B	328	ILE	2.2
1	B	288	GLN	2.2
1	B	300	ILE	2.1
1	B	161	GLN	2.0

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

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
1	TPO	A	462	11/12	0.79	0.30	78,89,99,101	0
1	TPO	B	462	11/12	0.84	0.36	78,88,98,104	0
1	SEP	B	345	10/11	0.85	0.19	52,63,83,86	0
1	SEP	A	345	10/11	0.89	0.17	51,60,83,84	0
1	SEP	A	400	10/11	0.90	0.14	36,46,66,68	0
1	SEP	B	400	10/11	0.91	0.12	37,48,65,68	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

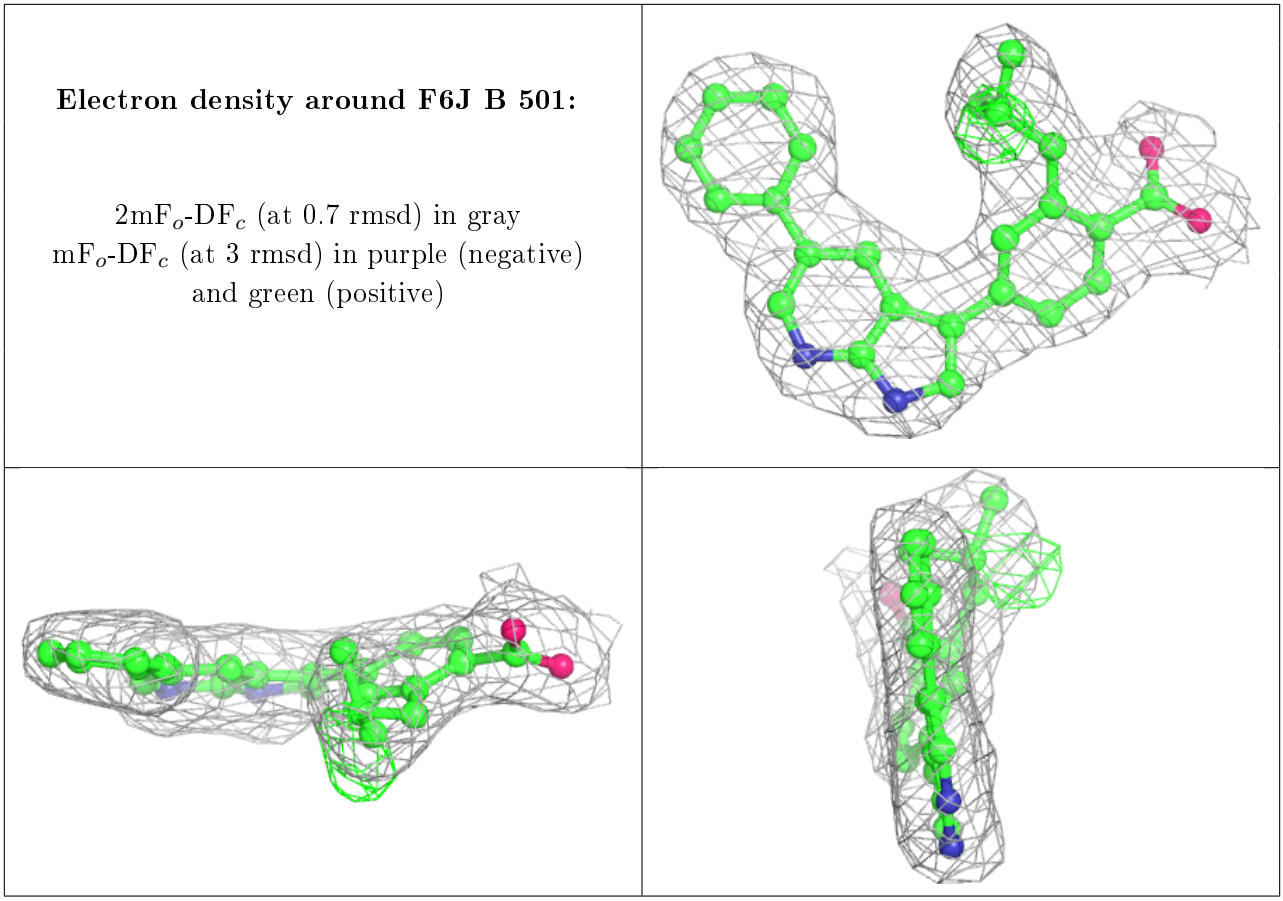
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	EDO	B	506	4/4	0.79	0.27	38,41,47,49	0
4	EDO	A	505	4/4	0.87	0.15	35,35,36,37	0
4	EDO	B	505	4/4	0.92	0.11	59,61,62,63	0
2	F6J	B	501	28/28	0.94	0.12	34,36,42,47	0
3	FMT	B	504	3/3	0.95	0.12	41,41,46,47	0
2	F6J	A	501	28/28	0.95	0.13	31,34,40,41	0
3	FMT	A	502	3/3	0.96	0.10	30,30,33,38	0
3	FMT	A	504	3/3	0.97	0.11	36,36,39,47	0
3	FMT	B	503	3/3	0.98	0.08	39,39,41,43	0
3	FMT	B	502	3/3	0.98	0.08	38,38,39,44	0
3	FMT	A	503	3/3	0.98	0.13	43,43,44,44	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.

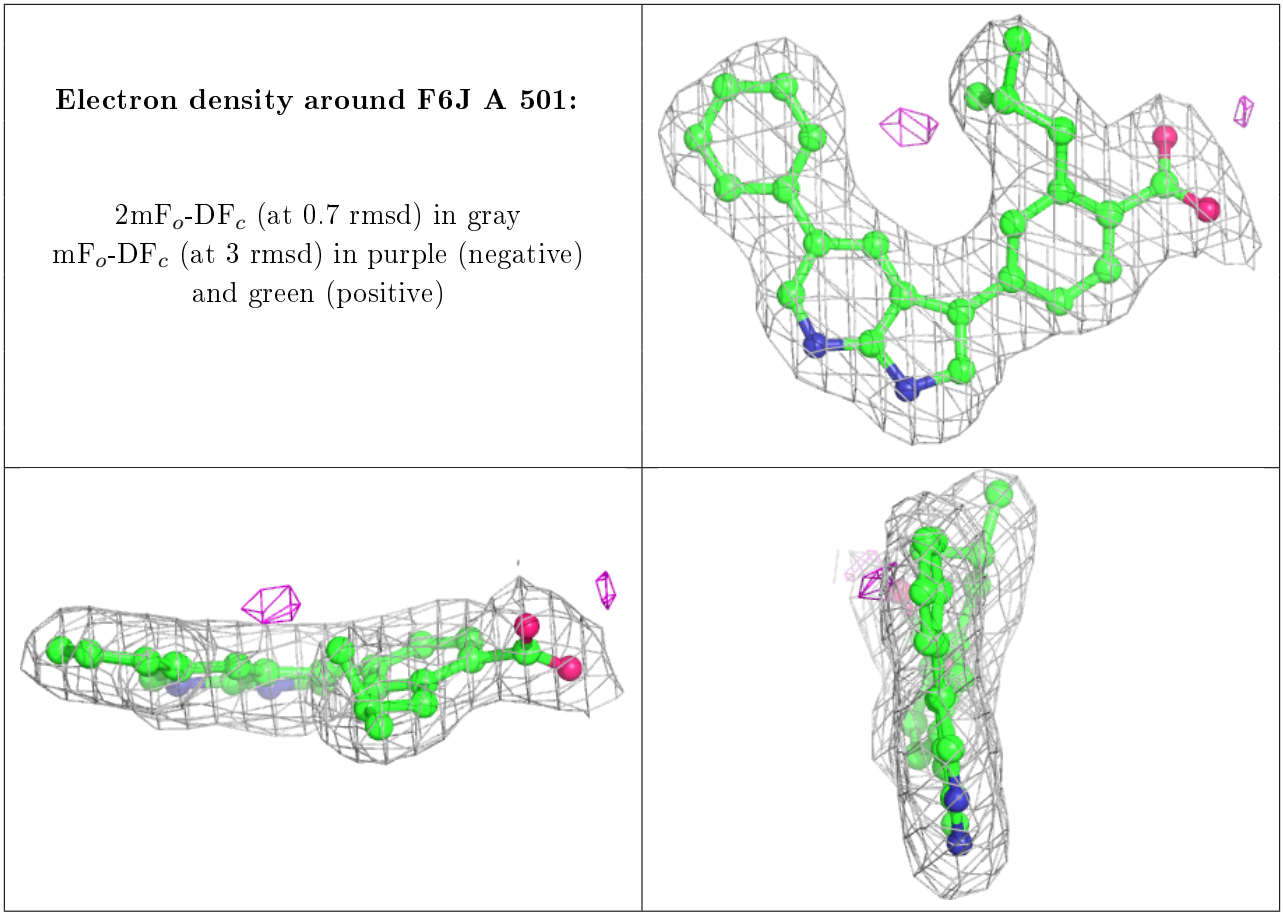
Electron density around F6J B 501:

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



Electron density around F6J A 501:

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



6.5 Other polymers

There are no such residues in this entry.