



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 05:38 PM UTC

PDB ID : 8SQ7 / pdb_00008sq7
Title : X-ray crystal structure of Acinetobacter baumannii beta-lactamase variant OXA-82 K83D in complex with doripenem
Authors : Powers, R.A.; Leonard, D.A.; June, C.M.; Szarecka, A.; Wawrzak, Z.
Deposited on : 2023-05-04
Resolution : 1.78 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 ⓘ 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

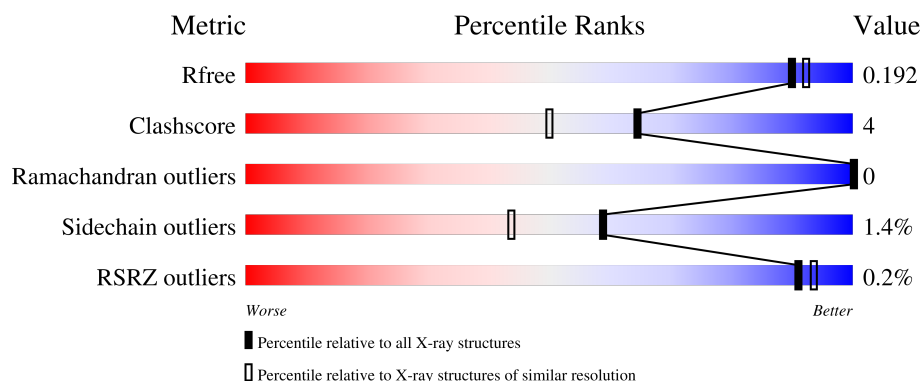
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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.



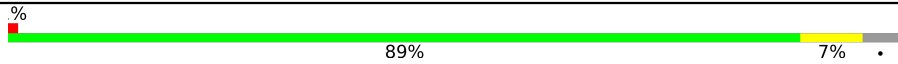
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	250	
1	B	250	
1	C	250	
1	D	250	
1	E	250	

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Mol	Chain	Length	Quality of chain
1	F	250	
1	G	250	
1	H	250	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	H	303	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17045 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 Beta-lactamase OXA-82.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	3	0
			1924	1231	325	362	6			
1	B	240	Total	C	N	O	S	0	3	0
			1886	1206	322	352	6			
1	C	241	Total	C	N	O	S	0	3	0
			1916	1227	323	360	6			
1	D	241	Total	C	N	O	S	0	1	0
			1910	1222	324	358	6			
1	E	240	Total	C	N	O	S	0	1	0
			1893	1215	317	355	6			
1	F	241	Total	C	N	O	S	0	2	0
			1888	1206	319	357	6			
1	G	240	Total	C	N	O	S	0	3	0
			1881	1203	321	351	6			
1	H	240	Total	C	N	O	S	0	2	0
			1898	1214	321	357	6			

There are 16 discrepancies between the modelled and reference sequences:

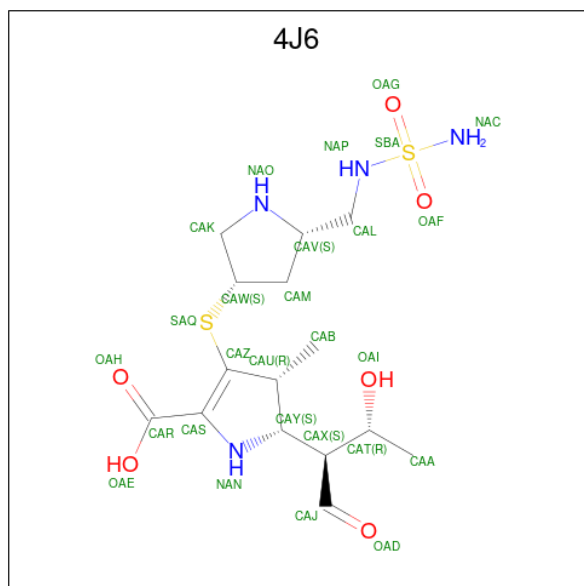
Chain	Residue	Modelled	Actual	Comment	Reference
A	25	MET	-	initiating methionine	UNP A8HDA9
A	83	ASP	LYS	engineered mutation	UNP A8HDA9
B	25	MET	-	initiating methionine	UNP A8HDA9
B	83	ASP	LYS	engineered mutation	UNP A8HDA9
C	25	MET	-	initiating methionine	UNP A8HDA9
C	83	ASP	LYS	engineered mutation	UNP A8HDA9
D	25	MET	-	initiating methionine	UNP A8HDA9
D	83	ASP	LYS	engineered mutation	UNP A8HDA9
E	25	MET	-	initiating methionine	UNP A8HDA9
E	83	ASP	LYS	engineered mutation	UNP A8HDA9
F	25	MET	-	initiating methionine	UNP A8HDA9
F	83	ASP	LYS	engineered mutation	UNP A8HDA9
G	25	MET	-	initiating methionine	UNP A8HDA9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	83	ASP	LYS	engineered mutation	UNP A8HDA9
H	25	MET	-	initiating methionine	UNP A8HDA9
H	83	ASP	LYS	engineered mutation	UNP A8HDA9

- Molecule 2 is (4R,5S)-5-[(2S,3R)-3-hydroxy-1-oxobutan-2-yl]-4-methyl-3-({(3S,5S)-5-[(sulfa moylamino)methyl]pyrrolidin-3-yl}sulfanyl)-4,5-dihydro-1H-pyrrole-2-carboxylic acid (CCD ID: 4J6) (formula: C₁₅H₂₆N₄O₆S₂) (labeled as "Ligand of Interest" by depositor).



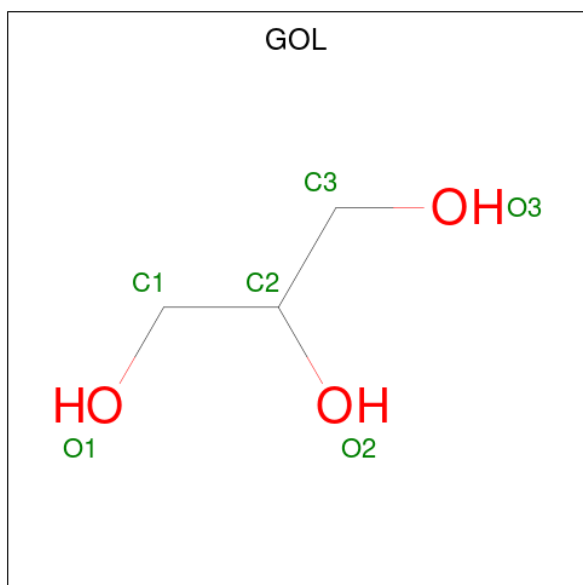
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	B	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	C	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	D	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	E	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	F	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	G	1	Total	C	N	O	S	0	0
			27	15	4	6	2		
2	H	1	Total	C	N	O	S	0	0
			27	15	4	6	2		

- Molecule 3 is CITRATE ANION (CCD ID: FLC) (formula: C₆H₅O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		
3	E	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	F	1	Total	C	O	0	0
			6	3	3		
4	G	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		
4	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	234	Total	O	0	7
			241	241		
5	B	172	Total	O	0	7
			179	179		
5	C	223	Total	O	0	2
			225	225		
5	D	204	Total	O	0	8
			212	212		
5	E	196	Total	O	0	3
			199	199		
5	F	157	Total	O	0	2
			159	159		
5	G	166	Total	O	0	4
			170	170		
5	H	149	Total	O	0	5
			154	154		

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: Beta-lactamase OXA-82

Chain A: 



- Molecule 1: Beta-lactamase OXA-82

Chain B: 



- Molecule 1: Beta-lactamase OXA-82

Chain C: 



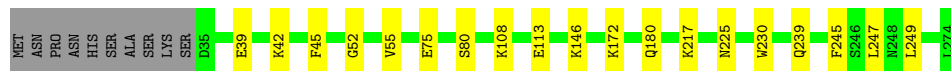
- Molecule 1: Beta-lactamase OXA-82

Chain D: 



- Molecule 1: Beta-lactamase OXA-82

Chain E: 

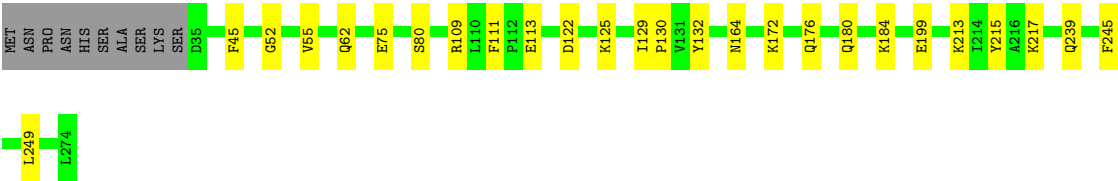
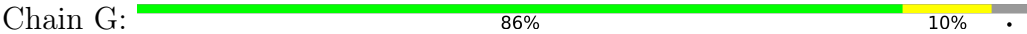


- Molecule 1: Beta-lactamase OXA-82

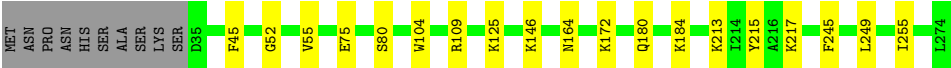
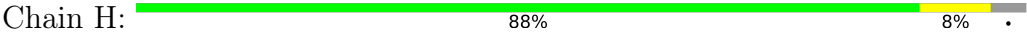
Chain F: 



● Molecule 1: Beta-lactamase OXA-82



● Molecule 1: Beta-lactamase OXA-82



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	70.28Å 70.28Å 448.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.58 – 1.78 38.58 – 1.78	Depositor EDS
% Data completeness (in resolution range)	87.6 (38.58-1.78) 87.7 (38.58-1.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.86 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.155 , 0.181 0.167 , 0.192	Depositor DCC
R_{free} test set	10377 reflections (4.38%)	wwPDB-VP
Wilson B-factor (Å ²)	17.9	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 32.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.487 for -h,-k,l 0.487 for h,-h-k,-l 0.488 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	17045	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.62% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, GOL, 4J6

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	0.92	0/1968	1.14	0/2661
1	B	0.94	1/1930 (0.1%)	1.15	0/2618
1	C	0.92	0/1966	1.14	0/2660
1	D	0.92	0/1951	1.14	0/2638
1	E	0.92	0/1937	1.14	0/2622
1	F	0.94	1/1932 (0.1%)	1.15	0/2620
1	G	0.94	1/1931 (0.1%)	1.15	0/2620
1	H	0.93	1/1942 (0.1%)	1.14	0/2630
All	All	0.93	4/15557 (0.0%)	1.14	0/21069

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	E	0	1
1	G	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	164	ASN	N-CA	5.34	1.51	1.46
1	B	164	ASN	N-CA	5.29	1.51	1.46
1	F	164	ASN	N-CA	5.25	1.50	1.46
1	G	164	ASN	N-CA	5.13	1.50	1.46

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	230	TRP	Peptide
1	E	230	TRP	Mainchain
1	G	132	TYR	Sidechain

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	1924	0	1912	19	0
1	B	1886	0	1839	12	0
1	C	1916	0	1910	17	0
1	D	1910	0	1904	16	0
1	E	1893	0	1869	9	0
1	F	1888	0	1839	16	0
1	G	1881	0	1841	20	0
1	H	1898	0	1874	18	0
2	A	27	0	24	0	0
2	B	27	0	24	0	0
2	C	27	0	24	0	0
2	D	27	0	24	0	0
2	E	27	0	24	0	0
2	F	27	0	24	0	0
2	G	27	0	24	0	0
2	H	27	0	24	0	0
3	A	13	0	5	0	0
3	C	13	0	5	0	0
3	D	13	0	5	0	0
3	E	13	0	5	0	0
4	B	18	0	24	1	0
4	F	6	0	8	2	0
4	G	6	0	8	2	0
4	H	12	0	16	11	0
5	A	241	0	0	3	0
5	B	179	0	0	4	0
5	C	225	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	212	0	0	2	0
5	E	199	0	0	2	0
5	F	159	0	0	5	0
5	G	170	0	0	6	0
5	H	154	0	0	2	0
All	All	17045	0	15256	119	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.

The worst 5 of 119 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:H:104:TRP:HA	4:H:303:GOL:H12	1.50	0.93
1:D:266[B]:LYS:HE3	1:G:199:GLU:OE2	1.70	0.90
1:F:109[B]:ARG:NH2	5:F:401:HOH:O	1.65	0.89
1:C:146:LYS:NZ	5:C:401:HOH:O	2.09	0.85
4:G:302:GOL:O1	5:G:420[B]:HOH:O	1.98	0.81

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	242/250 (97%)	236 (98%)	6 (2%)	0	100	100
1	B	241/250 (96%)	236 (98%)	5 (2%)	0	100	100
1	C	242/250 (97%)	237 (98%)	5 (2%)	0	100	100
1	D	240/250 (96%)	234 (98%)	6 (2%)	0	100	100
1	E	239/250 (96%)	234 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	241/250 (96%)	237 (98%)	4 (2%)	0	100	100
1	G	241/250 (96%)	236 (98%)	5 (2%)	0	100	100
1	H	240/250 (96%)	235 (98%)	5 (2%)	0	100	100
All	All	1926/2000 (96%)	1885 (98%)	41 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	204/213 (96%)	203 (100%)	1 (0%)	81	73
1	B	194/213 (91%)	192 (99%)	2 (1%)	68	55
1	C	204/213 (96%)	200 (98%)	4 (2%)	48	29
1	D	203/213 (95%)	199 (98%)	4 (2%)	48	29
1	E	197/213 (92%)	193 (98%)	4 (2%)	48	29
1	F	196/213 (92%)	194 (99%)	2 (1%)	68	55
1	G	195/213 (92%)	193 (99%)	2 (1%)	68	55
1	H	200/213 (94%)	196 (98%)	4 (2%)	48	29
All	All	1593/1704 (94%)	1570 (99%)	23 (1%)	59	44

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	247	LEU
1	G	125	LYS
1	F	255	ILE
1	G	213	LYS
1	C	266[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	225	ASN
1	E	161	GLN
1	H	180	GLN
1	E	58	GLN
1	E	180	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](#)

19 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$
3	FLC	C	302	-	12,12,12	1.14	1 (8%)	17,17,17	1.13	2 (11%)
3	FLC	E	302	-	12,12,12	1.14	0	17,17,17	1.09	2 (11%)
4	GOL	B	304	-	5,5,5	0.08	0	5,5,5	0.25	0
2	4J6	B	301	1	22,28,28	1.47	4 (18%)	17,41,41	1.73	3 (17%)
3	FLC	A	302	-	12,12,12	1.15	1 (8%)	17,17,17	1.14	2 (11%)
2	4J6	E	301	1	22,28,28	1.56	3 (13%)	17,41,41	2.16	5 (29%)
2	4J6	A	301	1	22,28,28	1.47	3 (13%)	17,41,41	1.93	5 (29%)
4	GOL	B	303	-	5,5,5	0.09	0	5,5,5	0.26	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	4J6	H	301	1	22,28,28	1.52	4 (18%)	17,41,41	1.56	3 (17%)
3	FLC	D	302	-	12,12,12	1.18	1 (8%)	17,17,17	1.10	2 (11%)
2	4J6	G	301	1	22,28,28	1.61	3 (13%)	17,41,41	1.96	4 (23%)
4	GOL	H	302	-	5,5,5	0.09	0	5,5,5	0.27	0
4	GOL	B	302	-	5,5,5	0.09	0	5,5,5	0.29	0
4	GOL	H	303	-	5,5,5	0.12	0	5,5,5	0.36	0
2	4J6	F	301	1	22,28,28	1.60	4 (18%)	17,41,41	2.12	6 (35%)
2	4J6	C	301	1	22,28,28	1.57	3 (13%)	17,41,41	2.03	4 (23%)
2	4J6	D	301	1	22,28,28	1.56	3 (13%)	17,41,41	2.25	5 (29%)
4	GOL	G	302	-	5,5,5	0.07	0	5,5,5	0.25	0
4	GOL	F	302	-	5,5,5	0.08	0	5,5,5	0.24	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	FLC	C	302	-	-	9/16/16/16	-
3	FLC	E	302	-	-	3/16/16/16	-
4	GOL	B	304	-	-	0/4/4/4	-
2	4J6	B	301	1	-	5/20/49/49	0/2/2/2
3	FLC	A	302	-	-	7/16/16/16	-
2	4J6	E	301	1	-	4/20/49/49	0/2/2/2
2	4J6	A	301	1	-	4/20/49/49	0/2/2/2
4	GOL	B	303	-	-	2/4/4/4	-
2	4J6	H	301	1	-	5/20/49/49	0/2/2/2
3	FLC	D	302	-	-	3/16/16/16	-
2	4J6	G	301	1	-	5/20/49/49	0/2/2/2
4	GOL	H	302	-	-	2/4/4/4	-
4	GOL	B	302	-	-	2/4/4/4	-
4	GOL	H	303	-	-	2/4/4/4	-
2	4J6	F	301	1	-	5/20/49/49	0/2/2/2
2	4J6	C	301	1	-	5/20/49/49	0/2/2/2
2	4J6	D	301	1	-	5/20/49/49	0/2/2/2
4	GOL	G	302	-	-	2/4/4/4	-
4	GOL	F	302	-	-	0/4/4/4	-

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	4J6	OAH-CAR	4.39	1.33	1.22
2	F	301	4J6	OAH-CAR	4.38	1.33	1.22
2	E	301	4J6	OAH-CAR	4.38	1.33	1.22
2	G	301	4J6	OAH-CAR	4.35	1.33	1.22
2	D	301	4J6	OAH-CAR	4.31	1.33	1.22

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	4J6	CAU-CAY-NAN	-5.62	100.73	105.07
2	C	301	4J6	CAU-CAY-NAN	-5.55	100.78	105.07
2	D	301	4J6	CAU-CAY-NAN	-5.55	100.78	105.07
2	G	301	4J6	CAU-CAY-NAN	-5.06	101.16	105.07
2	F	301	4J6	CAU-CAY-NAN	-5.04	101.18	105.07

There are no chirality outliers.

5 of 70 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	4J6	OAE-CAR-CAS-CAZ
2	A	301	4J6	OAH-CAR-CAS-NAN
2	A	301	4J6	OAH-CAR-CAS-CAZ
2	B	301	4J6	OAH-CAR-CAS-NAN
2	C	301	4J6	OAE-CAR-CAS-CAZ

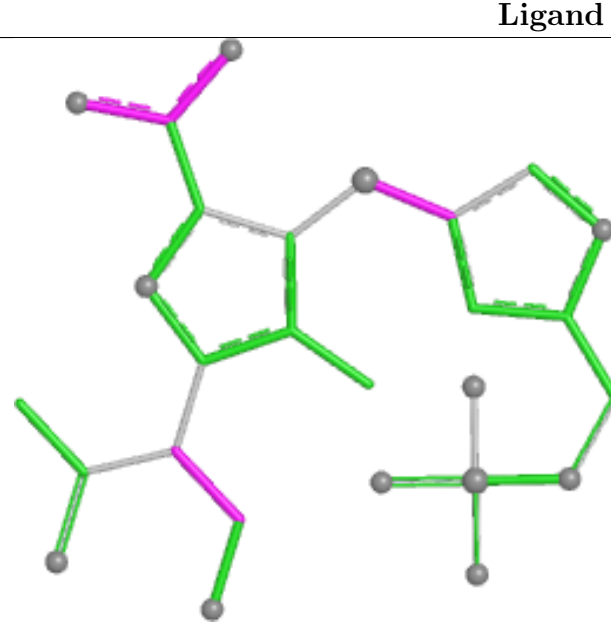
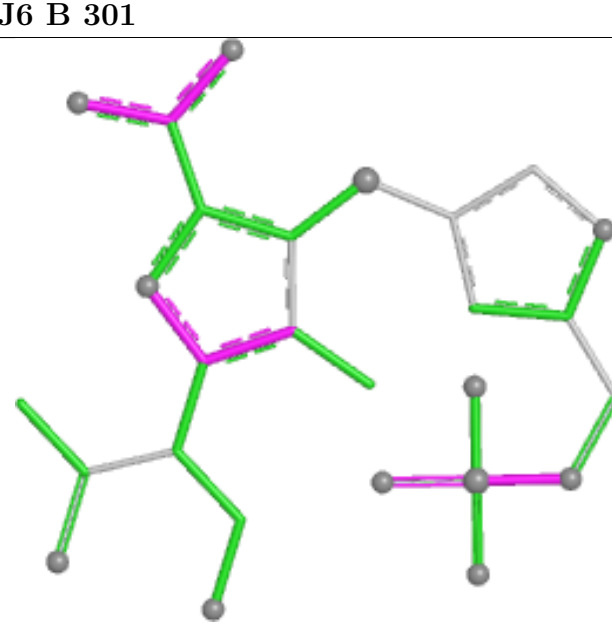
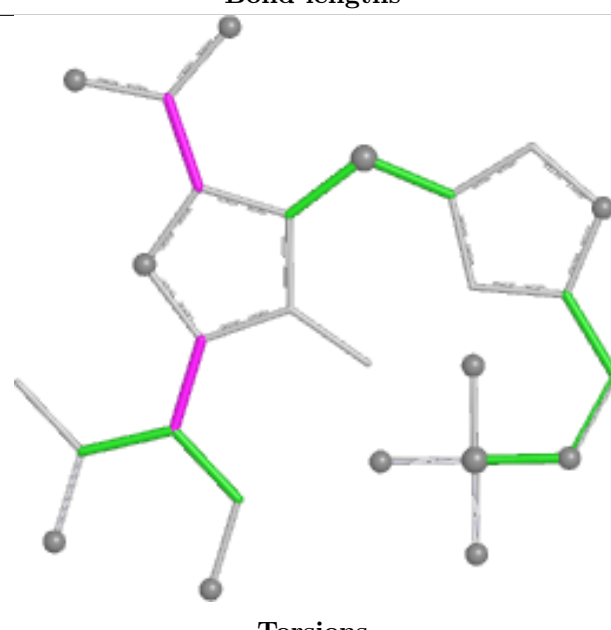
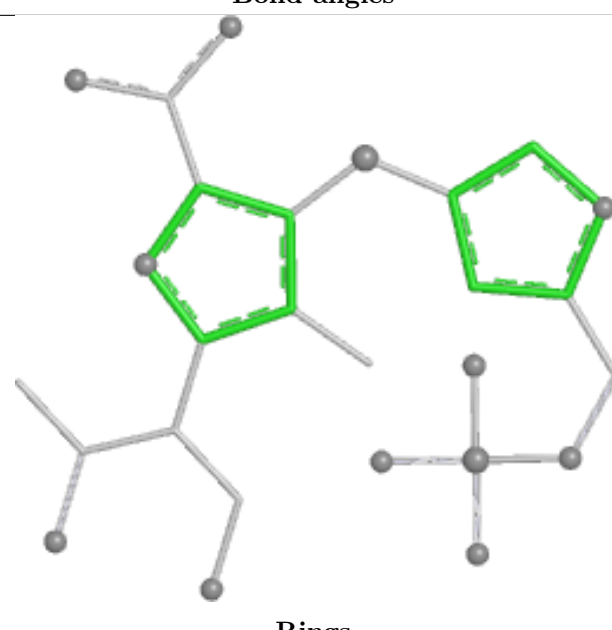
There are no ring outliers.

5 monomers are involved in 16 short contacts:

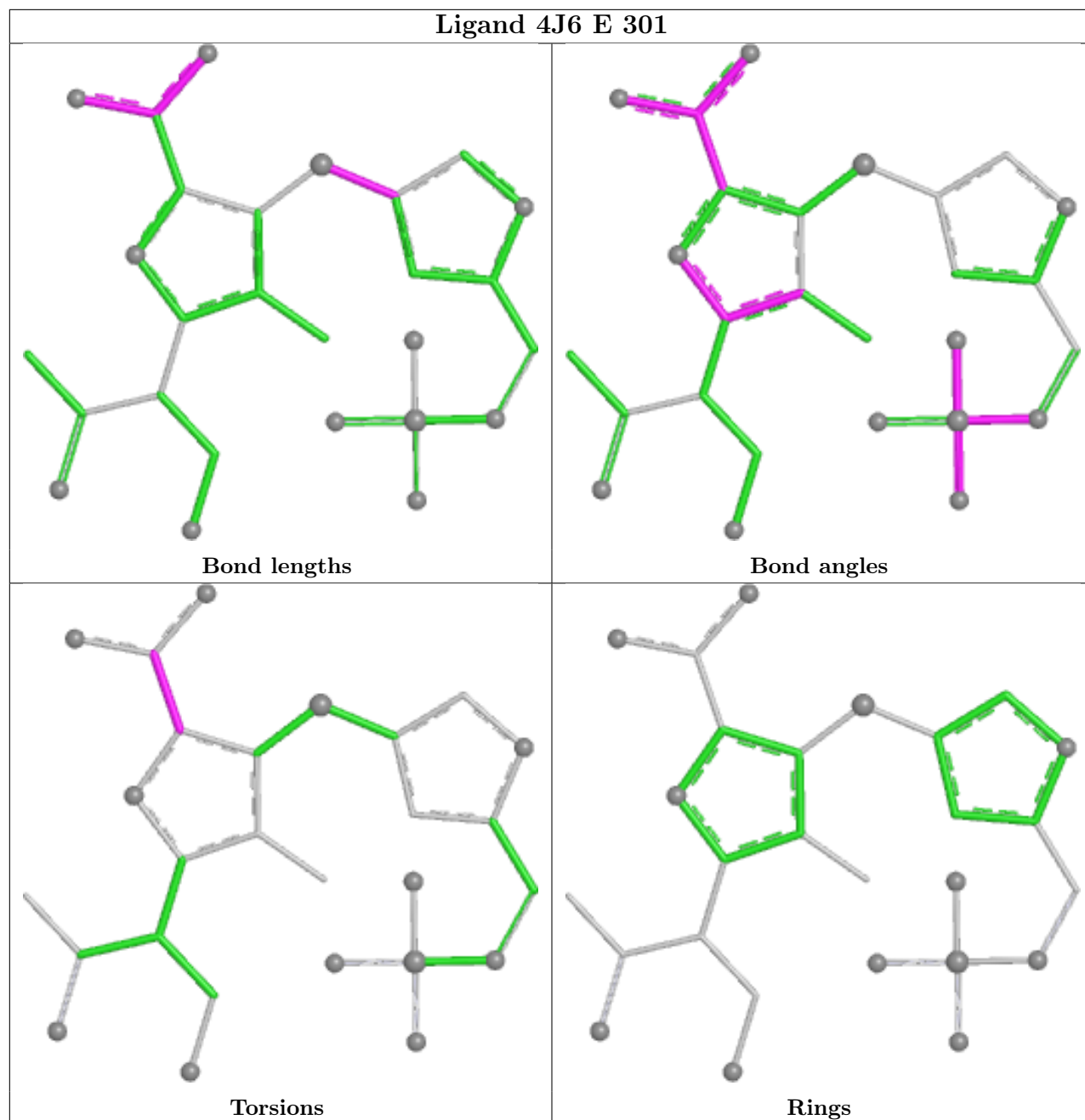
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	H	302	GOL	2	0
4	B	302	GOL	1	0
4	H	303	GOL	9	0
4	G	302	GOL	2	0
4	F	302	GOL	2	0

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 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

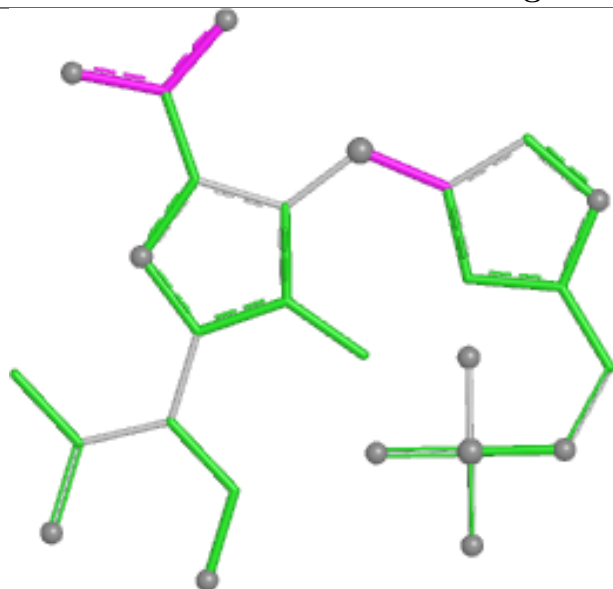
Ligand 4J6 B 301

 Bond lengths	 Bond angles
 Torsions	 Rings

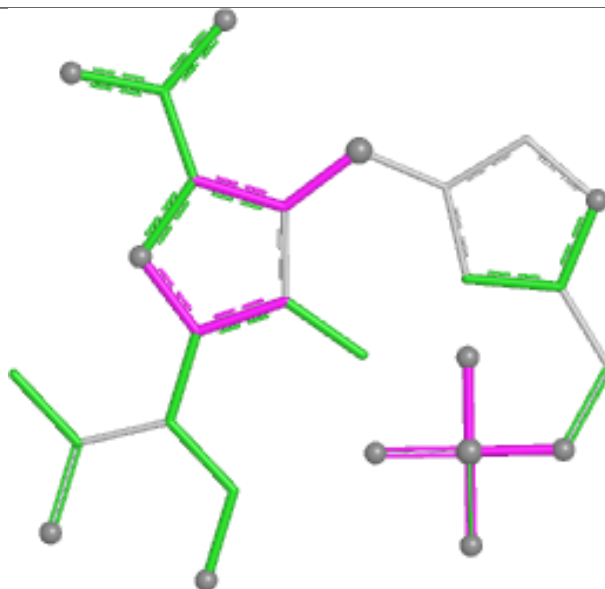
Ligand 4J6 E 301



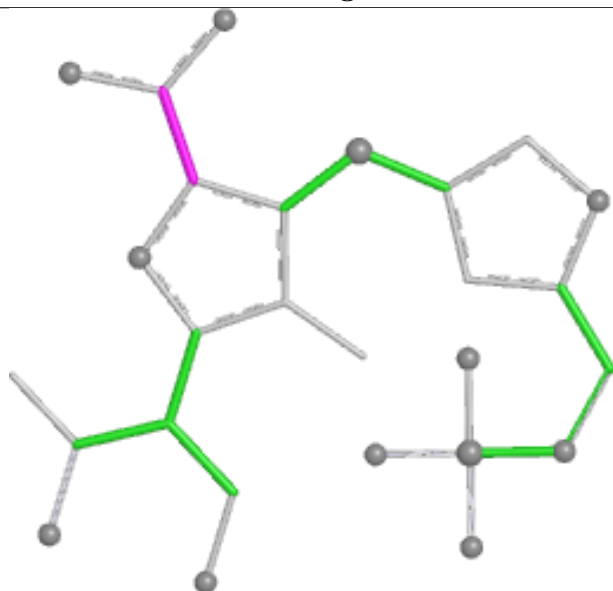
Ligand 4J6 A 301



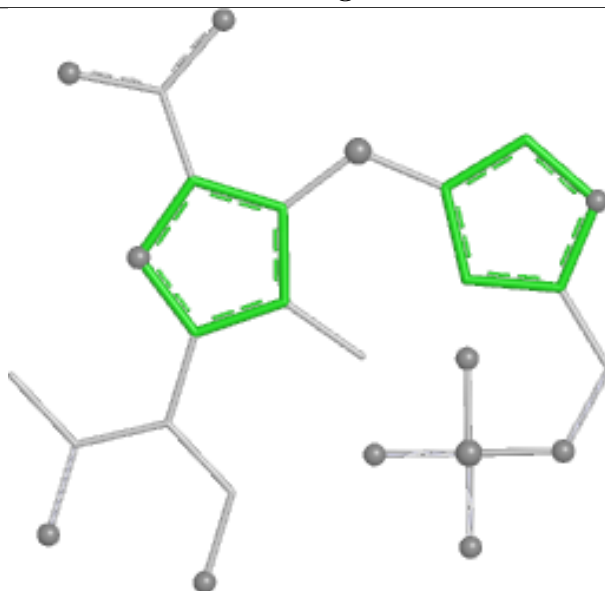
Bond lengths



Bond angles

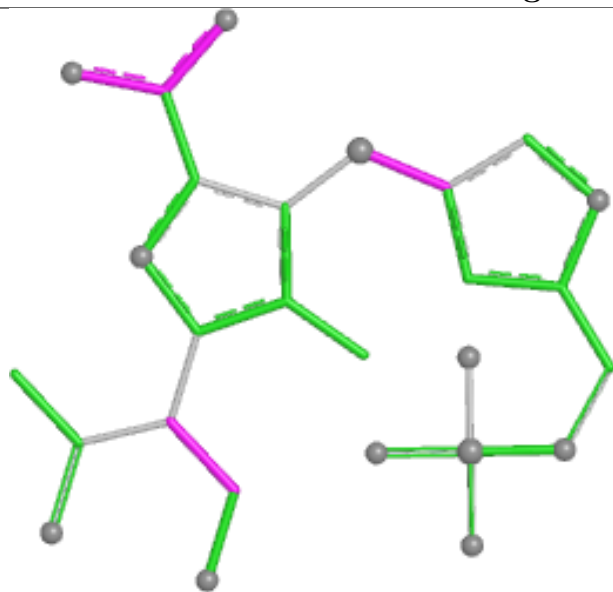


Torsions

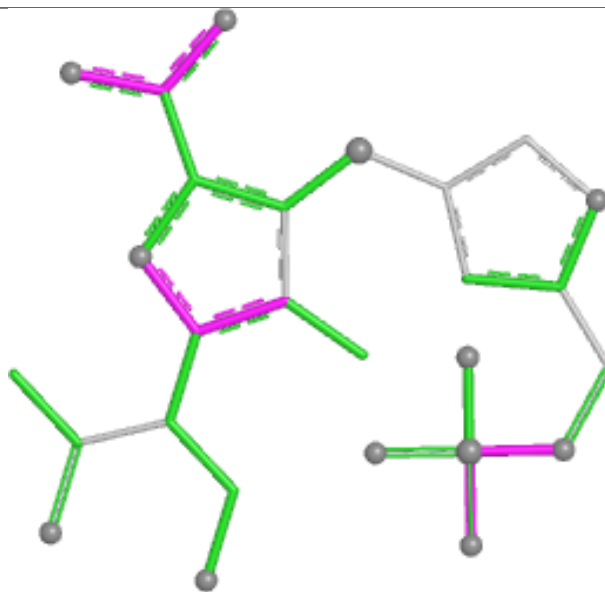


Rings

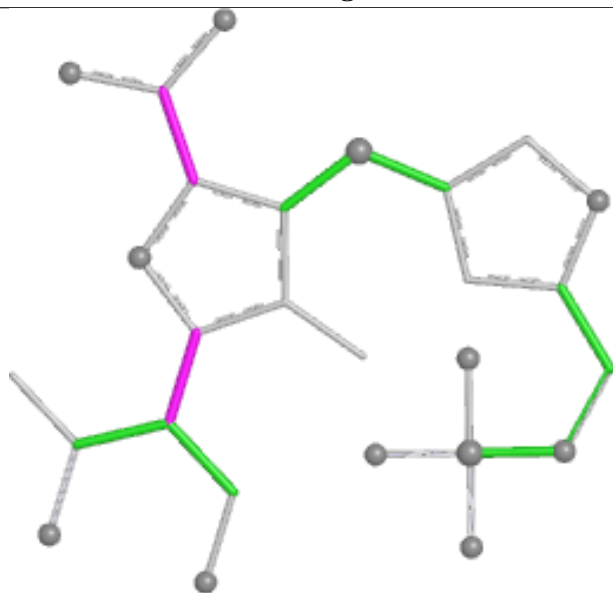
Ligand 4J6 H 301



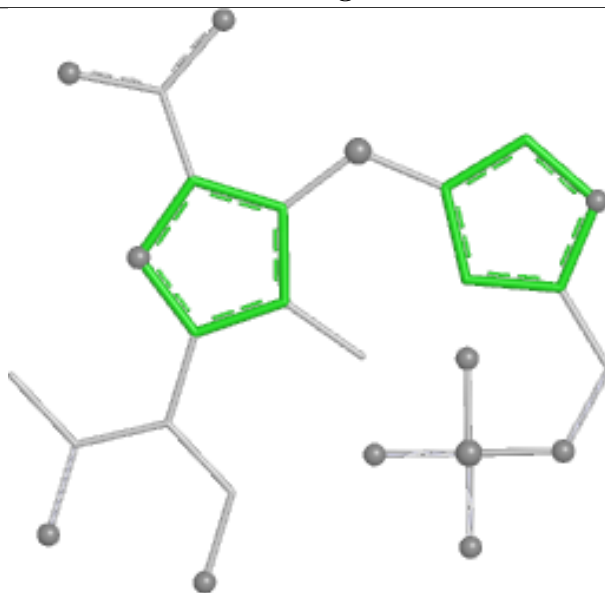
Bond lengths



Bond angles

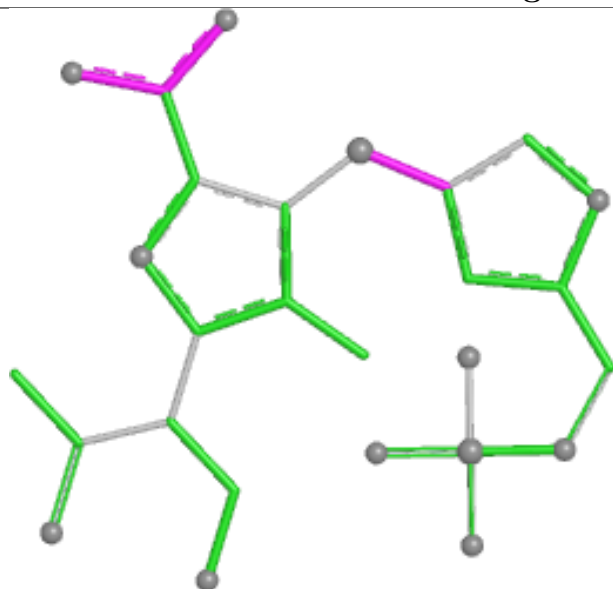


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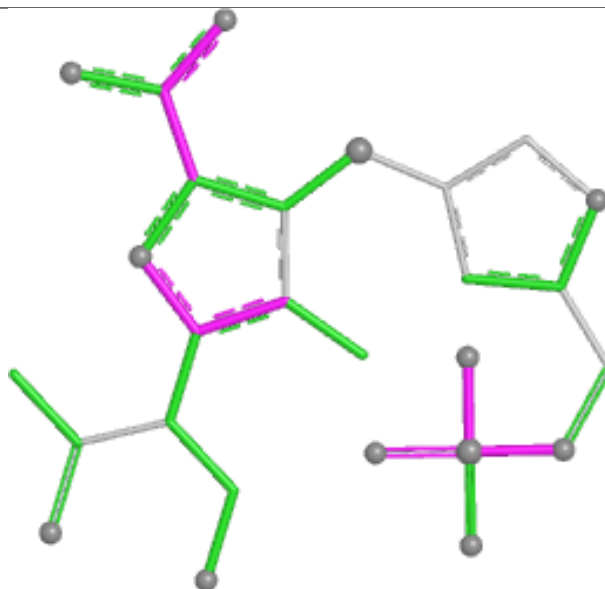


Rings

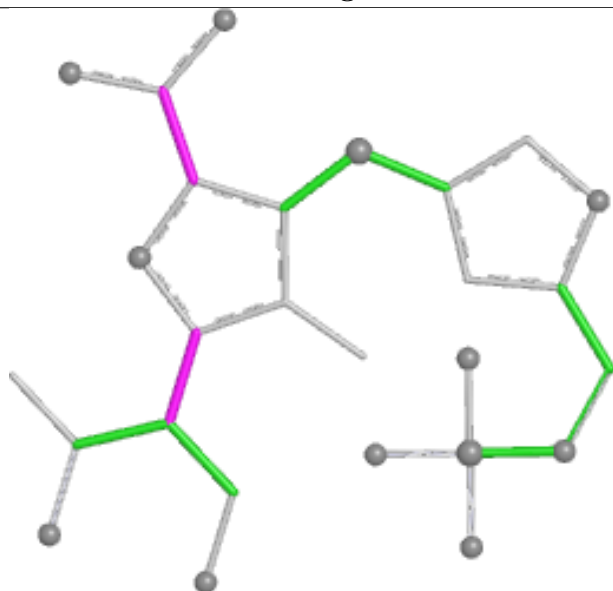
Ligand 4J6 G 301



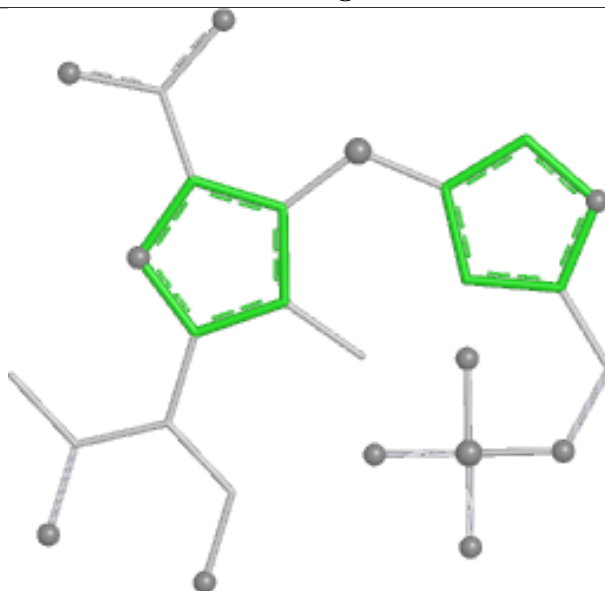
Bond lengths



Bond angles

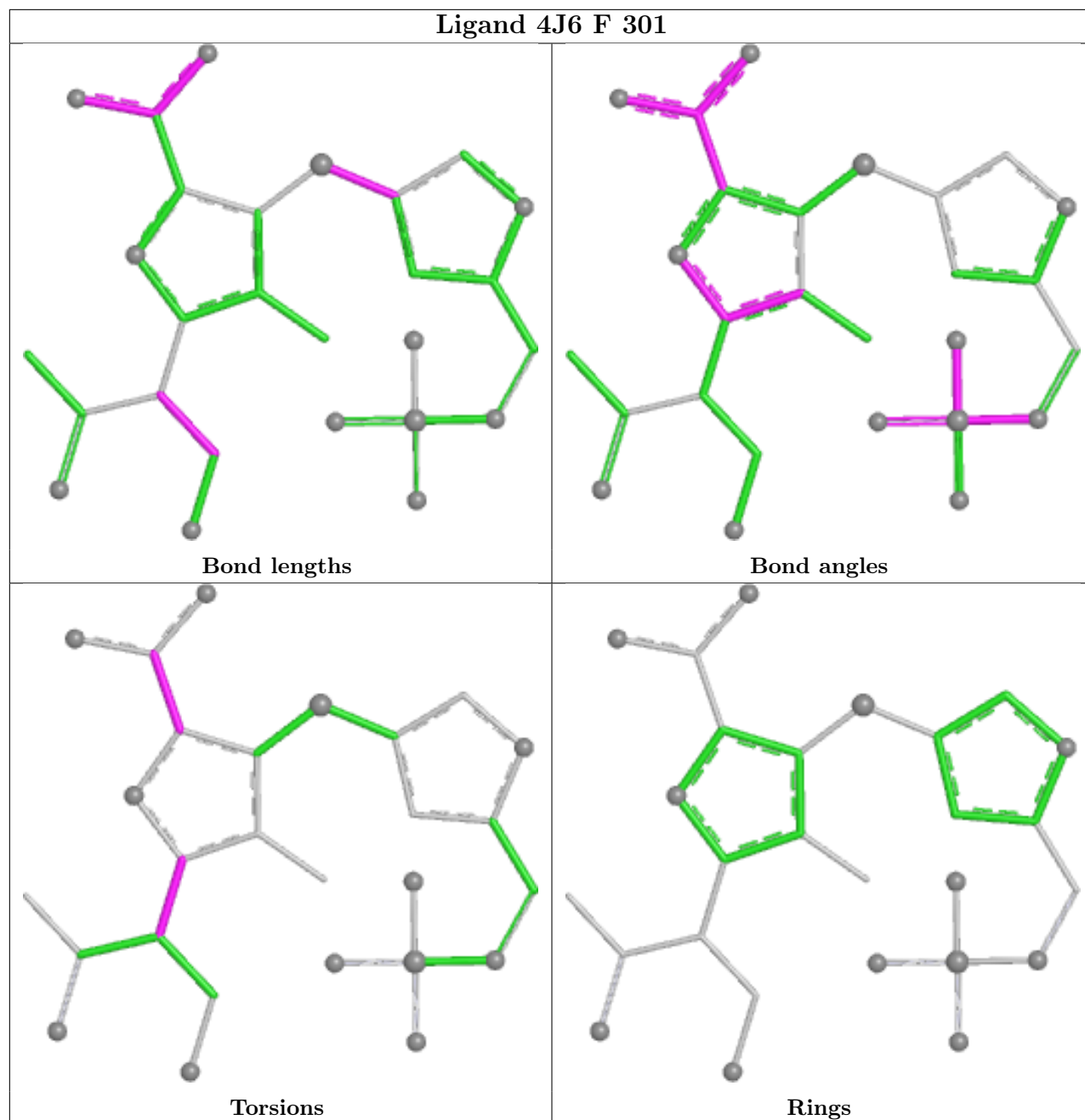


Torsions

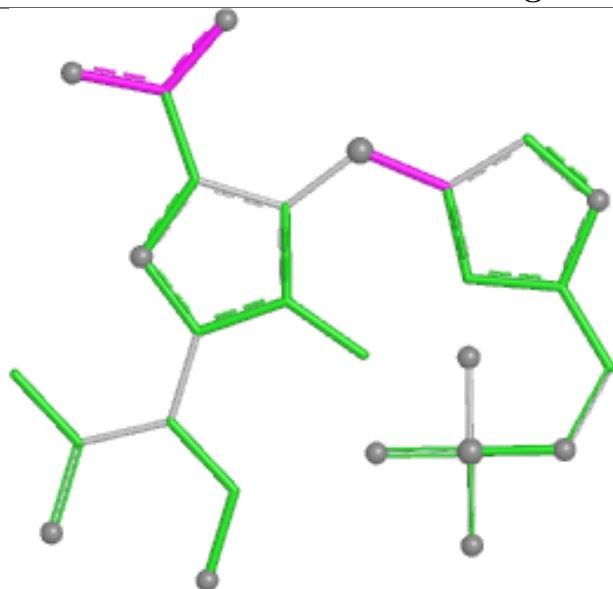


Rings

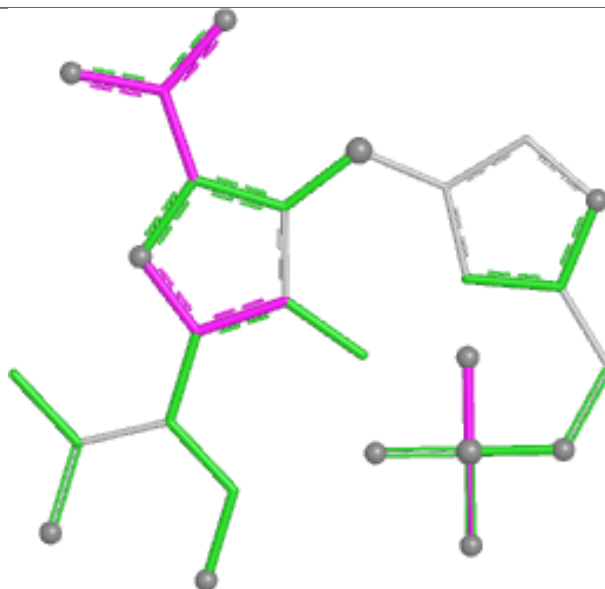
Ligand 4J6 F 301



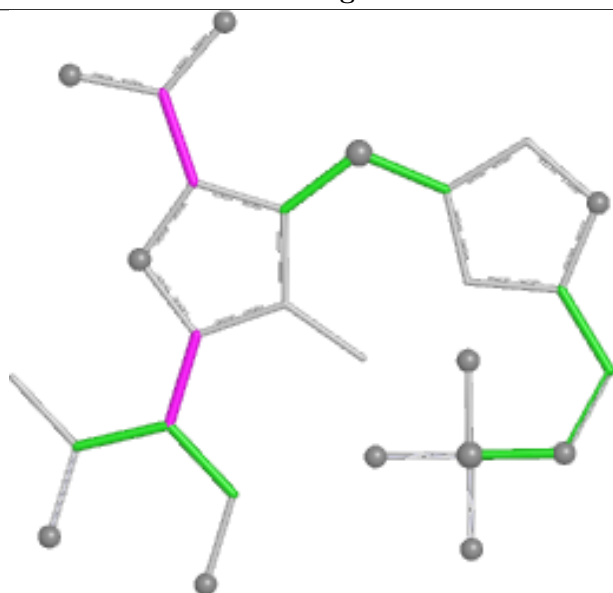
Ligand 4J6 C 301



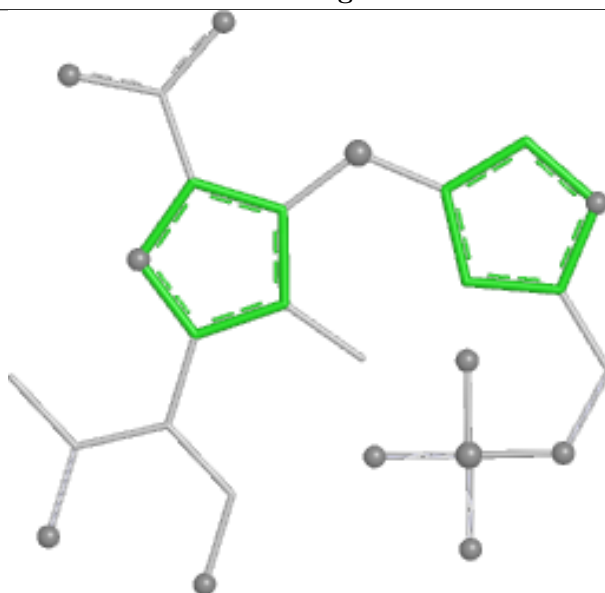
Bond lengths



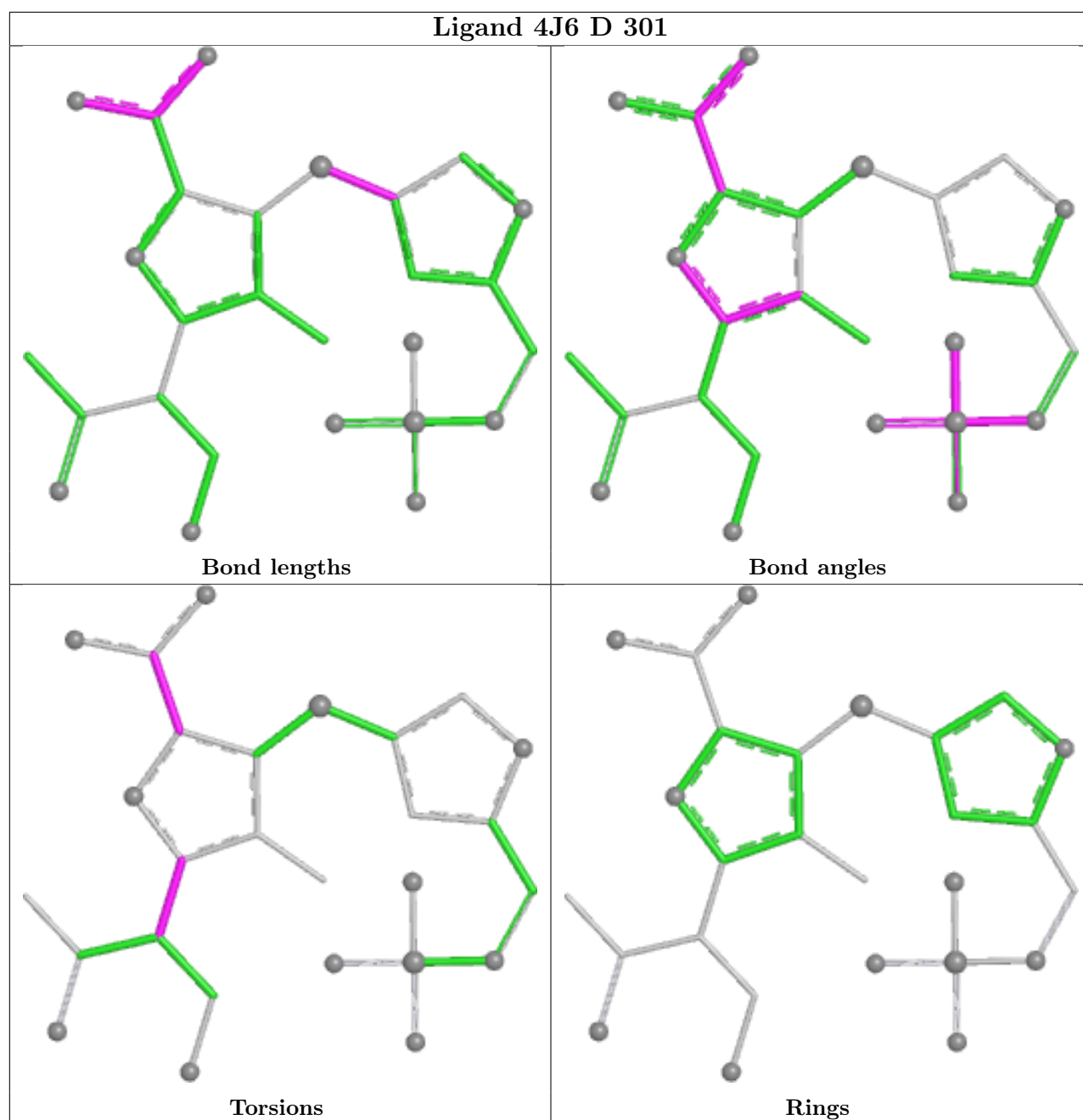
Bond angles



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 [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	241/250 (96%)	-1.28	0 100 100	11, 23, 46, 80	3 (1%)
1	B	240/250 (96%)	-1.09	1 (0%) 88 92	12, 25, 61, 97	3 (1%)
1	C	241/250 (96%)	-1.29	0 100 100	11, 22, 48, 78	3 (1%)
1	D	241/250 (96%)	-1.29	0 100 100	11, 23, 48, 84	1 (0%)
1	E	240/250 (96%)	-1.30	0 100 100	12, 23, 46, 60	1 (0%)
1	F	241/250 (96%)	-1.08	2 (0%) 82 87	12, 25, 62, 99	2 (0%)
1	G	240/250 (96%)	-1.11	0 100 100	13, 25, 61, 87	3 (1%)
1	H	240/250 (96%)	-1.11	0 100 100	13, 25, 63, 96	2 (0%)
All	All	1924/2000 (96%)	-1.20	3 (0%) 91 93	11, 24, 56, 99	18 (0%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	36	VAL	2.7
1	B	35	ASP	2.5
1	F	35	ASP	2.1

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

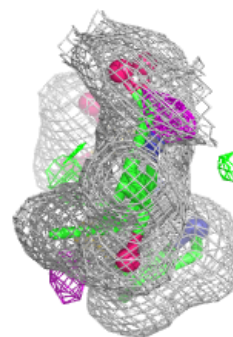
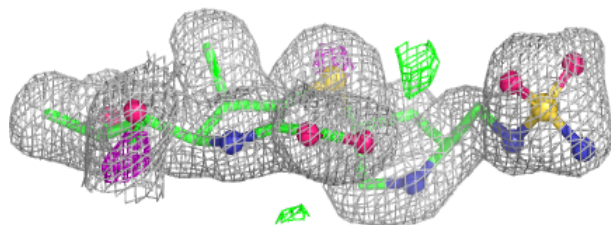
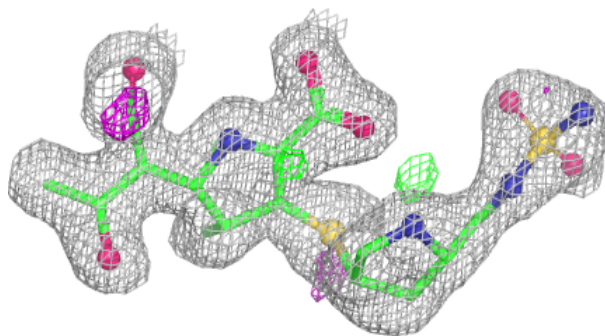
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	GOL	B	303	6/6	0.97	0.07	43,56,86,89	0
4	GOL	B	304	6/6	0.97	0.08	50,69,89,90	0
4	GOL	B	302	6/6	0.98	0.07	41,65,69,82	0
3	FLC	C	302	13/13	0.98	0.05	32,58,87,99	0
3	FLC	D	302	13/13	0.98	0.05	34,60,83,87	0
4	GOL	F	302	6/6	0.98	0.06	45,65,80,81	0
4	GOL	G	302	6/6	0.98	0.07	48,54,66,78	0
4	GOL	H	302	6/6	0.98	0.07	45,63,76,77	0
2	4J6	G	301	27/27	0.99	0.03	14,23,34,48	0
2	4J6	H	301	27/27	0.99	0.03	15,23,34,39	0
3	FLC	A	302	13/13	0.99	0.04	33,60,85,93	0
2	4J6	E	301	27/27	0.99	0.03	10,16,23,26	0
2	4J6	F	301	27/27	0.99	0.03	15,23,35,48	0
3	FLC	E	302	13/13	0.99	0.05	33,60,86,86	0
4	GOL	H	303	6/6	0.99	0.06	32,37,45,49	0
2	4J6	D	301	27/27	1.00	0.03	11,16,25,30	0
2	4J6	A	301	27/27	1.00	0.03	11,16,24,29	0
2	4J6	B	301	27/27	1.00	0.03	14,23,34,42	0
2	4J6	C	301	27/27	1.00	0.02	10,16,23,28	0

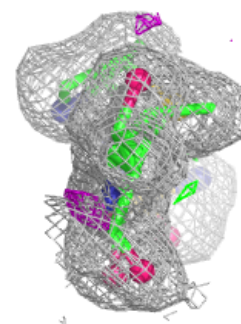
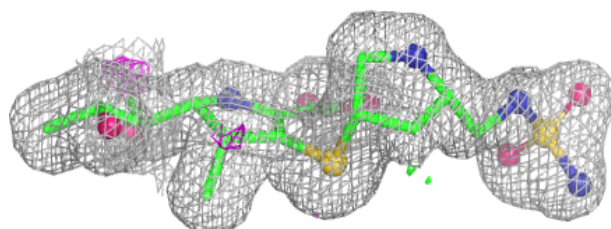
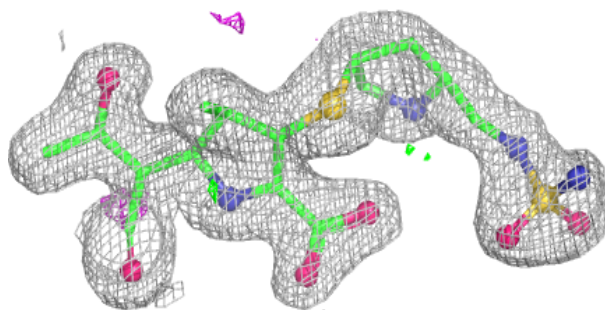
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 4J6 G 301:

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

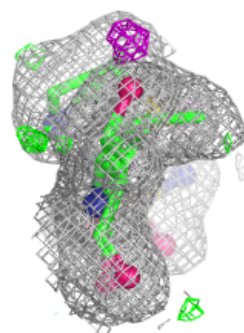
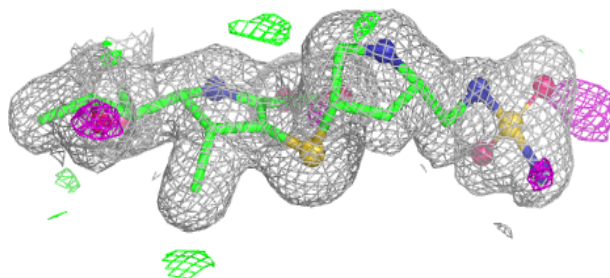
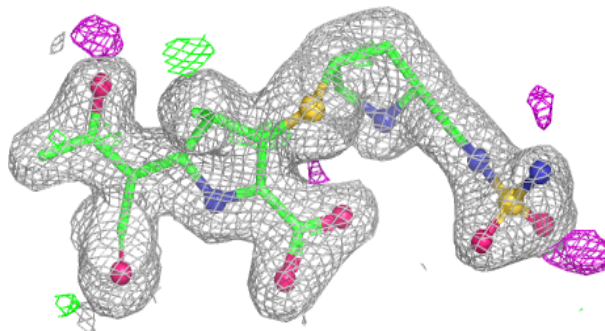
**Electron density around 4J6 H 301:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

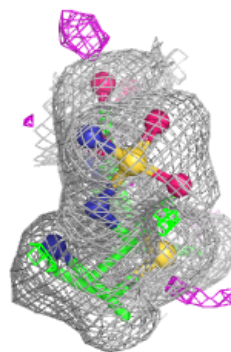
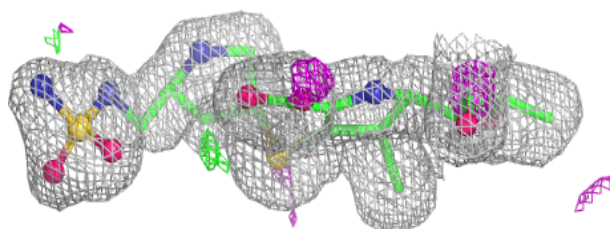
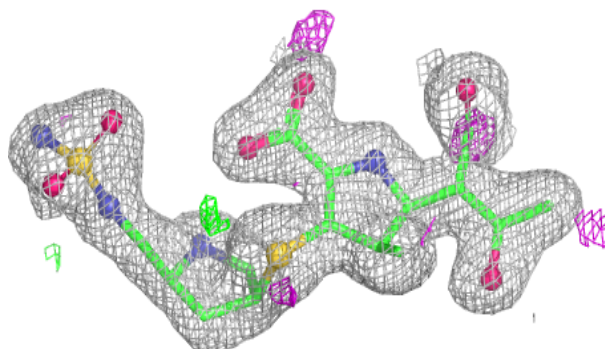


Electron density around 4J6 E 301:

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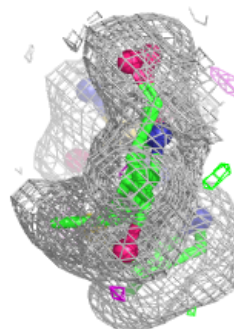
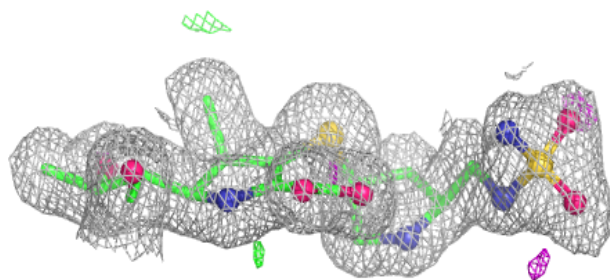
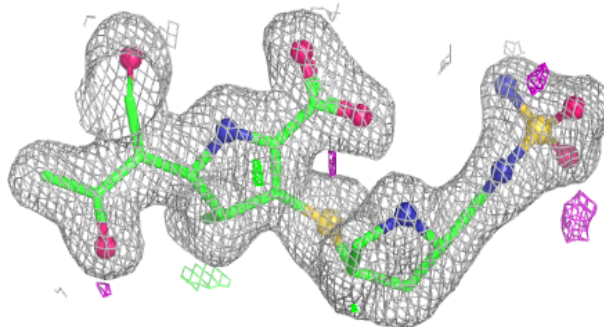
**Electron density around 4J6 F 301:**

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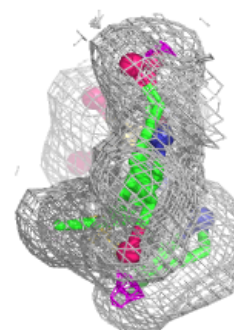
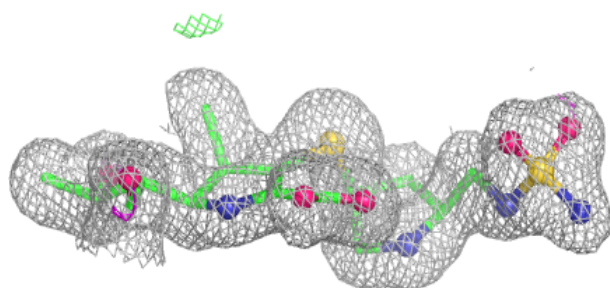
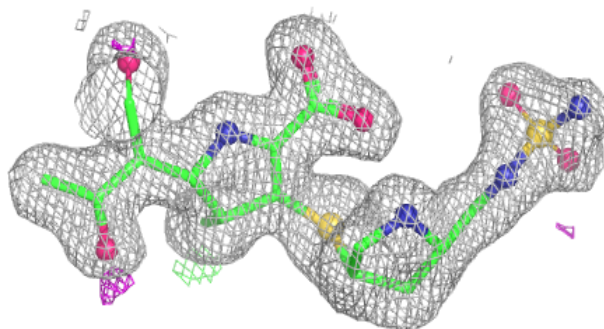


Electron density around 4J6 D 301:

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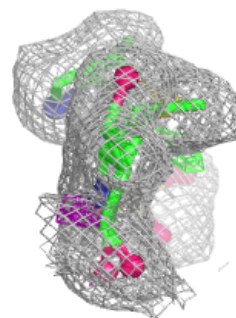
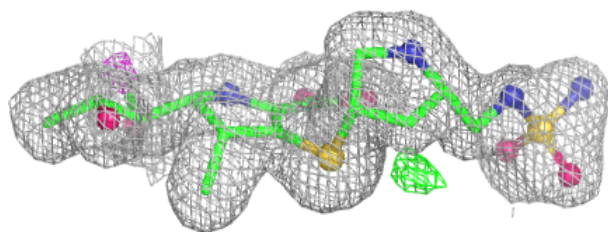
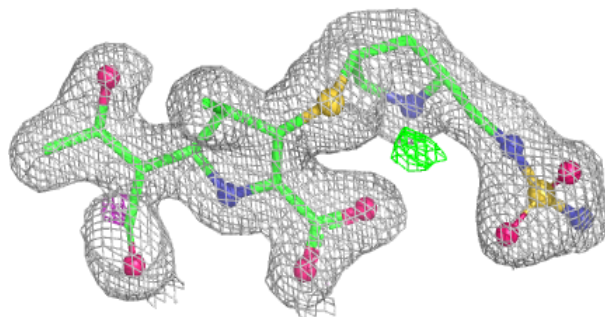
**Electron density around 4J6 A 301:**

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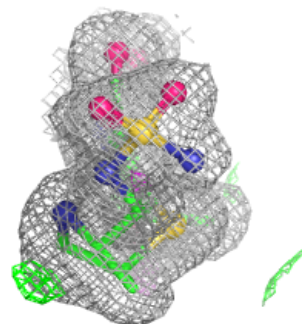
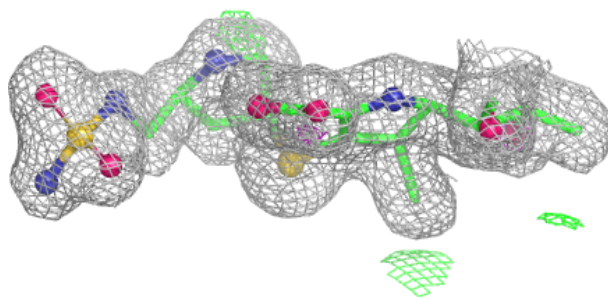
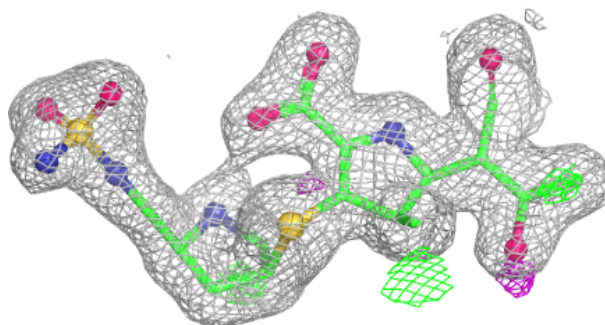


Electron density around 4J6 B 301:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around 4J6 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.