Full wwPDB X-ray Structure Validation Report (i)

Jun 23, 2024 – 03:25 AM EDT

PDB ID	:	5HR6
Title	:	X-ray crystal structure of C118A RlmN with cross-linked tRNA purified from Escherichia coli
Authors	:	Schwalm, E.L.; Grove, T.L.; Booker, S.J.; Boal, A.K.
Deposited on	:	2016-01-22
Resolution	:	2.88 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

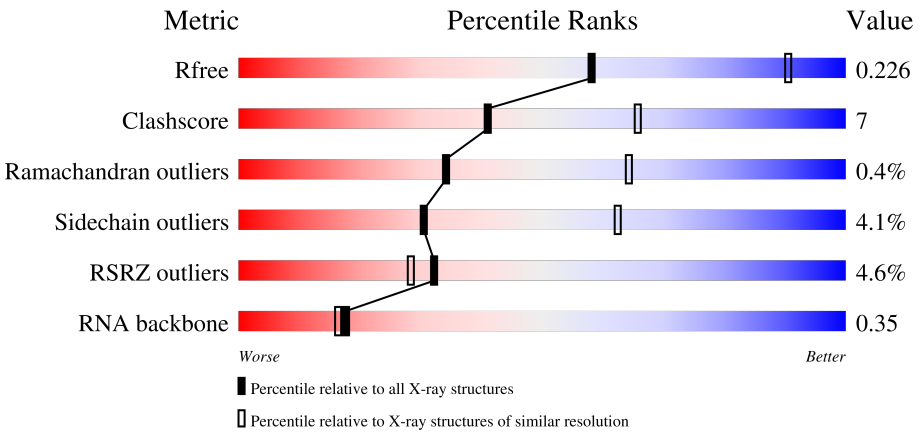
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.88 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)
RNA backbone	3102	1121 (3.16-2.60)

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	404	2% 70% 17% • 12%
1	B	404	7% 70% 16% • 12%
2	C	68	57% 29% 12% •
2	D	68	% 46% 44% 7% •

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8539 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 RlmN methylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	354	2786	1747	498	522	19	0	0	0
1	B	354	2786	1747	498	522	19	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	118	ALA	CYS	engineered mutation	UNP A7ZPW0
A	385	GLY	-	expression tag	UNP A7ZPW0
A	386	ASN	-	expression tag	UNP A7ZPW0
A	387	SER	-	expression tag	UNP A7ZPW0
A	388	SER	-	expression tag	UNP A7ZPW0
A	389	SER	-	expression tag	UNP A7ZPW0
A	390	VAL	-	expression tag	UNP A7ZPW0
A	391	ASP	-	expression tag	UNP A7ZPW0
A	392	LYS	-	expression tag	UNP A7ZPW0
A	393	LEU	-	expression tag	UNP A7ZPW0
A	394	ALA	-	expression tag	UNP A7ZPW0
A	395	ALA	-	expression tag	UNP A7ZPW0
A	396	ALA	-	expression tag	UNP A7ZPW0
A	397	LEU	-	expression tag	UNP A7ZPW0
A	398	GLU	-	expression tag	UNP A7ZPW0
A	399	HIS	-	expression tag	UNP A7ZPW0
A	400	HIS	-	expression tag	UNP A7ZPW0
A	401	HIS	-	expression tag	UNP A7ZPW0
A	402	HIS	-	expression tag	UNP A7ZPW0
A	403	HIS	-	expression tag	UNP A7ZPW0
A	404	HIS	-	expression tag	UNP A7ZPW0
B	118	ALA	CYS	engineered mutation	UNP A7ZPW0
B	385	GLY	-	expression tag	UNP A7ZPW0
B	386	ASN	-	expression tag	UNP A7ZPW0
B	387	SER	-	expression tag	UNP A7ZPW0

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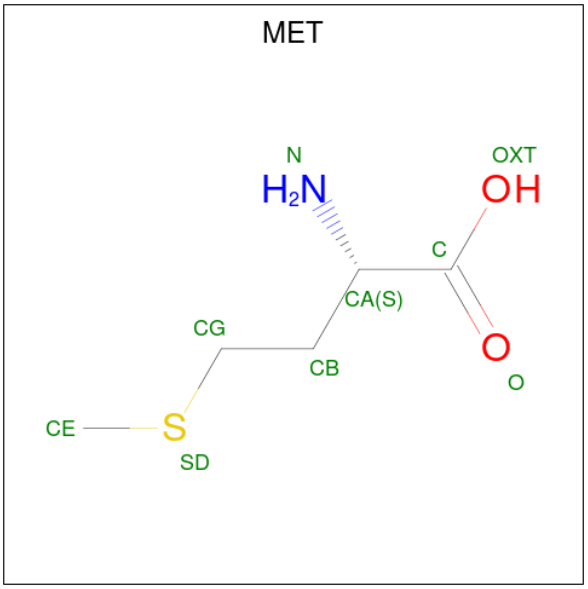
Chain	Residue	Modelled	Actual	Comment	Reference
B	388	SER	-	expression tag	UNP A7ZPW0
B	389	SER	-	expression tag	UNP A7ZPW0
B	390	VAL	-	expression tag	UNP A7ZPW0
B	391	ASP	-	expression tag	UNP A7ZPW0
B	392	LYS	-	expression tag	UNP A7ZPW0
B	393	LEU	-	expression tag	UNP A7ZPW0
B	394	ALA	-	expression tag	UNP A7ZPW0
B	395	ALA	-	expression tag	UNP A7ZPW0
B	396	ALA	-	expression tag	UNP A7ZPW0
B	397	LEU	-	expression tag	UNP A7ZPW0
B	398	GLU	-	expression tag	UNP A7ZPW0
B	399	HIS	-	expression tag	UNP A7ZPW0
B	400	HIS	-	expression tag	UNP A7ZPW0
B	401	HIS	-	expression tag	UNP A7ZPW0
B	402	HIS	-	expression tag	UNP A7ZPW0
B	403	HIS	-	expression tag	UNP A7ZPW0
B	404	HIS	-	expression tag	UNP A7ZPW0

- Molecule 2 is a RNA chain called tRNA Glu.

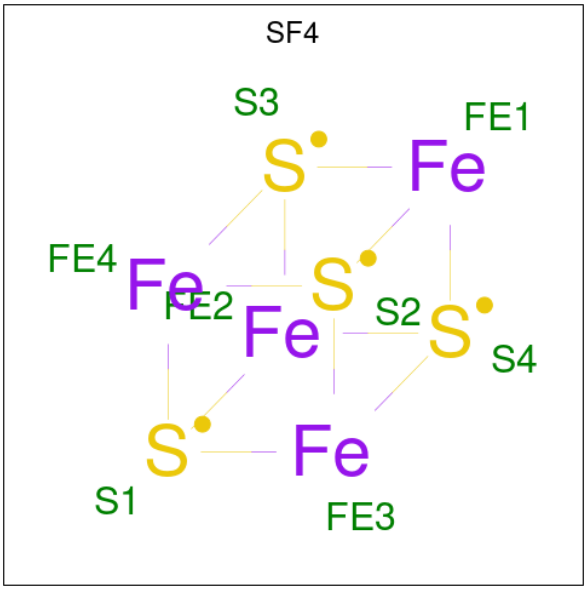
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	68	1444	644	256	476	68	0	0	0
			Total	C	N	O	P			
2	D	66	1401	625	248	462	66	0	0	0

- Molecule 3 is METHIONINE (three-letter code: MET) (formula: $C_5H_{11}NO_2S$).



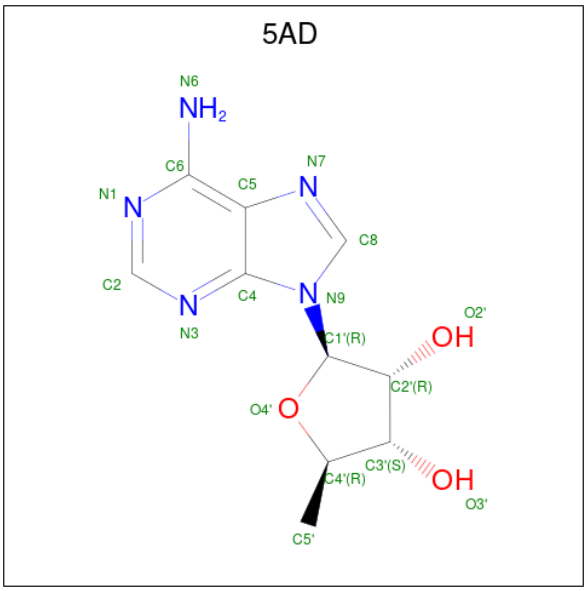
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	9	5	1	2	1	0	0
3	B	1	9	5	1	2	1	0	0

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe	S		
4	A	1	8	4	4	0	0
4	B	1	8	4	4	0	0

- Molecule 5 is 5'-DEOXYADENOSINE (three-letter code: 5AD) (formula: $C_{10}H_{13}N_5O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	18	10	5	3	0	0
5	B	1	18	10	5	3	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	1	1	1	0	0
6	C	3	3	3	0	0
6	B	1	1	1	0	0
6	D	1	1	1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	17	17	17	0	0
7	C	4	4	4	0	0
7	B	20	20	20	0	0

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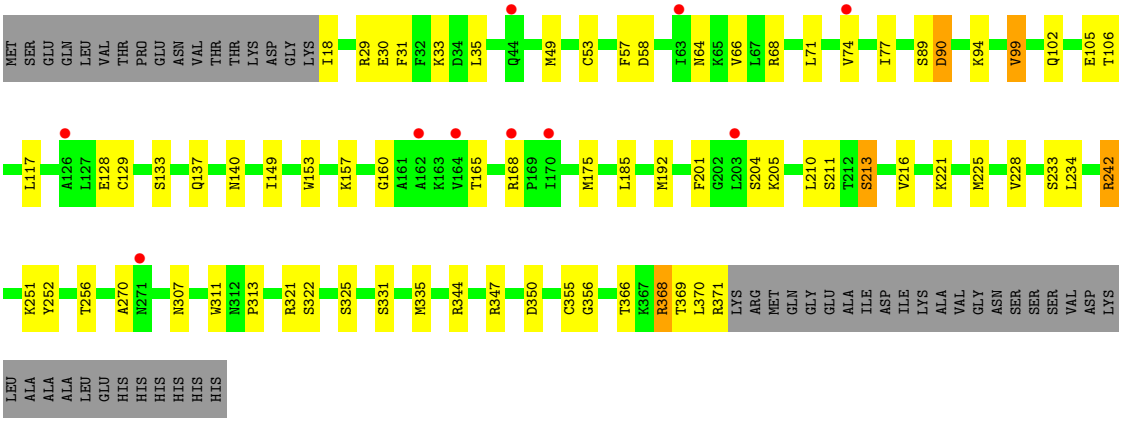
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	D	5	5	5	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

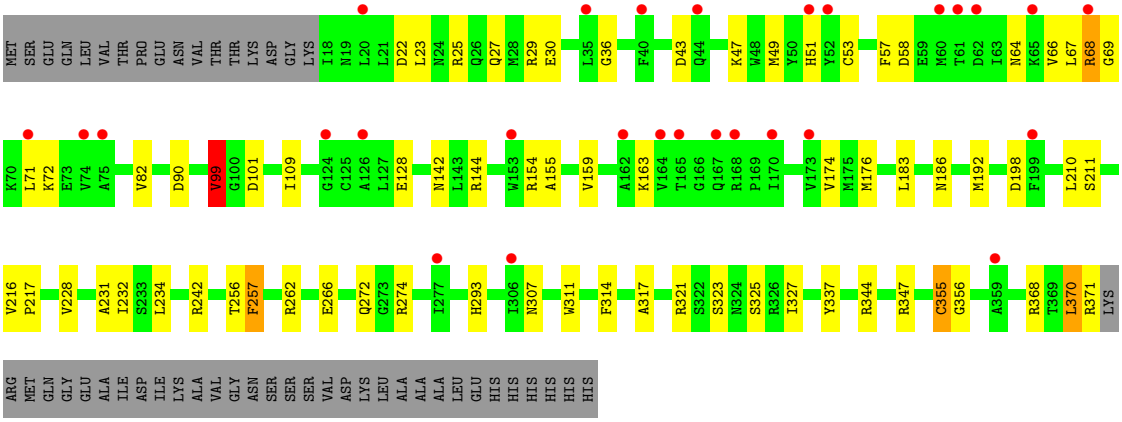
• Molecule 1: RlmN methylase

Chain A:



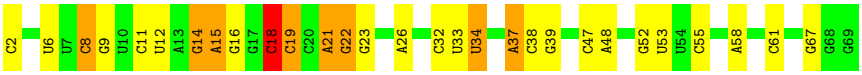
• Molecule 1: RlmN methylase

Chain B:



• Molecule 2: tRNA Glu

Chain C:



• Molecule 2: tRNA Glu

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	88.66Å 69.82Å 149.30Å 90.00° 90.30° 90.00°	Depositor
Resolution (Å)	88.66 – 2.88 49.77 – 2.88	Depositor EDS
% Data completeness (in resolution range)	98.9 (88.66-2.88) 98.2 (49.77-2.88)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.57 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.182 , 0.228 0.186 , 0.226	Depositor DCC
R_{free} test set	1700 reflections (4.10%)	wwPDB-VP
Wilson B-factor (Å^2)	71.2	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 40.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.357 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8539	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.63% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SMC, 5AD, MG, SF4

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	0.68	0/2824	0.88	4/3815 (0.1%)
1	B	0.68	0/2824	0.86	0/3815
2	C	0.49	0/1611	0.87	5/2508 (0.2%)
2	D	0.50	0/1563	0.85	3/2433 (0.1%)
All	All	0.62	0/8822	0.87	12/12571 (0.1%)

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
2	C	0	1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	368	ARG	NE-CZ-NH1	9.23	124.92	120.30
2	C	11	C	O5'-P-OP2	-7.97	98.53	105.70
2	C	32	C	C2'-C3'-O3'	6.45	124.02	113.70
2	C	53	U	O5'-P-OP2	6.14	118.06	110.70
1	A	368	ARG	NE-CZ-NH2	-5.85	117.38	120.30
2	C	18	C	N1-C1'-C2'	5.53	121.18	114.00
2	D	34	U	C2'-C3'-O3'	5.37	122.30	113.70
2	C	14	G	O4'-C1'-N9	5.35	112.48	108.20
1	A	90	ASP	CB-CG-OD1	5.28	123.05	118.30
2	D	53	U	O5'-P-OP1	-5.17	101.05	105.70
2	D	53	U	O5'-P-OP2	5.11	116.83	110.70
1	A	90	ASP	CB-CA-C	-5.11	100.19	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	14	G	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2786	0	2801	45	0
1	B	2786	0	2801	45	0
2	C	1444	0	736	17	0
2	D	1401	0	715	14	0
3	A	9	0	8	0	0
3	B	9	0	8	1	0
4	A	8	0	0	0	0
4	B	8	0	0	0	0
5	A	18	0	13	1	0
5	B	18	0	13	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	3	0	0	0	0
6	D	1	0	0	0	0
7	A	17	0	0	0	0
7	B	20	0	0	0	0
7	C	4	0	0	0	0
7	D	5	0	0	0	0
All	All	8539	0	7095	111	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 7.

All (111) 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:175:MET:HG3	1:A:192:MET:CE	2.17	0.75
1:A:192:MET:HE1	1:A:210:LEU:HD12	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:ILE:HG22	1:A:74:VAL:O	1.94	0.68
1:A:234:LEU:O	1:A:242:ARG:HD2	1.92	0.68
1:A:94:LYS:HD2	1:A:105:GLU:OE1	1.97	0.65
2:C:18:C:H1'	1:B:142:ASN:ND2	2.13	0.64
1:B:234:LEU:O	1:B:242:ARG:HD2	1.99	0.63
1:A:18:ILE:CG2	1:A:74:VAL:O	2.47	0.62
1:B:370:LEU:O	1:B:371:ARG:O	2.18	0.62
1:A:369:THR:O	1:A:370:LEU:C	2.39	0.61
1:B:210:LEU:C	1:B:210:LEU:HD23	2.22	0.59
1:B:64:ASN:ND2	2:D:68:G:OP1	2.35	0.59
1:B:82:VAL:HG13	1:B:154:ARG:HD2	1.85	0.59
1:B:192:MET:HE2	1:B:228:VAL:HG11	1.83	0.59
1:B:49:MET:O	1:B:53:CYS:HA	2.03	0.58
1:B:99:VAL:HG12	1:B:99:VAL:O	2.03	0.57
2:D:7:U:C2	2:D:14:G:O6	2.58	0.57
1:A:90:ASP:HB3	1:A:347:ARG:HH21	1.70	0.57
1:B:90:ASP:HB3	1:B:347:ARG:HH21	1.70	0.57
1:B:192:MET:CE	1:B:228:VAL:HG11	2.35	0.57
1:B:58:ASP:OD1	1:B:72:LYS:CE	2.55	0.55
1:B:23:LEU:HD22	1:B:27:GLN:HB3	1.89	0.54
1:A:210:LEU:C	1:A:210:LEU:HD23	2.26	0.54
1:A:366:THR:O	1:A:371:ARG:NH1	2.40	0.54
2:C:34:U:C6	2:C:34:U:H5'	2.44	0.52
1:B:216:VAL:HB	1:B:217:PRO:HD3	1.89	0.52
1:B:128:GLU:HG2	1:B:368:ARG:HH12	1.73	0.52
1:B:109:ILE:HD13	2:D:37:A:C5	2.45	0.52
1:A:216:VAL:HG21	1:A:256:THR:HG22	1.91	0.52
1:A:106:THR:CG2	1:A:117:LEU:HD11	2.40	0.51
2:D:62:C:H2'	2:D:63:C:C6	2.45	0.51
2:C:15:A:H5'	2:C:15:A:H8	1.75	0.51
2:C:33:U:C4'	2:C:34:U:H5"	2.41	0.51
1:B:307:ASN:ND2	1:B:344:ARG:HE	2.08	0.51
1:A:185:LEU:HD13	1:A:225:MET:HE1	1.93	0.50
1:A:49:MET:O	1:A:53:CYS:HA	2.11	0.50
2:C:21:A:H5"	2:C:22:G:OP1	2.12	0.50
1:A:106:THR:HG22	1:A:117:LEU:HD11	1.92	0.50
1:B:293:HIS:ND1	1:B:337:TYR:OH	2.37	0.49
1:A:175:MET:HG3	1:A:192:MET:HE2	1.93	0.49
3:B:501:MET:C	3:B:501:MET:SD	2.91	0.48
2:C:33:U:H4'	2:C:34:U:H5"	1.93	0.48
1:A:133:SER:HB3	1:A:356:GLY:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:314:PHE:CZ	1:B:317:ALA:HB2	2.48	0.48
2:D:19:C:H4'	2:D:20:C:OP1	2.14	0.48
1:A:58:ASP:HA	1:A:68:ARG:HD3	1.95	0.47
2:D:21:A:H61	2:D:46:A:H2'	1.79	0.47
1:B:370:LEU:O	1:B:371:ARG:C	2.53	0.47
2:C:33:U:H4'	2:C:34:U:C5'	2.44	0.47
1:B:29:ARG:O	1:B:30:GLU:C	2.53	0.47
1:A:350:ASP:N	1:A:350:ASP:OD1	2.48	0.47
1:B:174:VAL:HG23	1:B:176:MET:HB2	1.97	0.47
1:B:274:ARG:HH12	2:D:32:C:H3'	1.79	0.46
1:B:311:TRP:O	1:B:321:ARG:HD2	2.15	0.46
1:A:307:ASN:ND2	1:A:344:ARG:HE	2.13	0.46
1:B:356:GLY:HA3	5:B:503:5AD:C5	2.46	0.46
1:A:149:ILE:HD11	1:A:201:PHE:HE2	1.81	0.46
1:B:57:PHE:O	1:B:68:ARG:HD2	2.16	0.46
2:C:15:A:H5'	2:C:15:A:C8	2.51	0.46
1:B:211:SER:HA	1:B:231:ALA:O	2.16	0.46
2:D:67:G:H2'	2:D:68:G:C8	2.51	0.46
1:B:216:VAL:HG21	1:B:256:THR:HG22	1.97	0.45
1:A:321:ARG:O	1:A:322:SER:C	2.52	0.45
2:C:18:C:O2	2:C:18:C:H2'	2.15	0.45
2:C:19:C:O2	2:C:21:A:H1'	2.17	0.45
1:B:22:ASP:OD2	1:B:144:ARG:NH2	2.50	0.44
1:A:213:SER:HA	1:A:233:SER:HB2	1.99	0.44
2:C:8:C:H5	2:C:23:G:O6	2.00	0.44
2:C:18:C:H1'	1:B:142:ASN:HD22	1.78	0.44
1:B:57:PHE:CE1	1:B:71:LEU:HD13	2.53	0.44
1:B:183:LEU:HD23	1:B:183:LEU:HA	1.86	0.44
1:A:311:TRP:CH2	1:A:313:PRO:HA	2.53	0.44
1:A:31:PHE:O	1:A:35:LEU:HD13	2.18	0.44
1:B:67:LEU:O	1:B:69:GLY:N	2.50	0.44
1:B:370:LEU:H	1:B:370:LEU:HD23	1.83	0.43
1:A:102:GLN:HE22	1:A:140:ASN:CG	2.22	0.43
1:B:370:LEU:HD23	1:B:370:LEU:N	2.33	0.43
1:A:99:VAL:O	1:A:99:VAL:HG12	2.19	0.43
1:B:323:SER:O	1:B:327:ILE:HG13	2.18	0.43
1:A:185:LEU:HD13	1:A:225:MET:CE	2.48	0.43
2:C:55:C:C6	1:B:371:ARG:HD2	2.54	0.43
1:A:99:VAL:O	1:A:99:VAL:CG1	2.66	0.43
1:A:356:GLY:HA3	5:A:503:5AD:C5	2.48	0.43
2:C:2:C:H6	2:C:2:C:P	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:18:C:O2	1:B:186:ASN:HB2	2.19	0.43
1:A:160:GLY:HA3	1:A:165:THR:HG21	2.01	0.43
2:D:62:C:H2'	2:D:63:C:H6	1.83	0.42
1:B:64:ASN:HB2	1:B:67:LEU:H	1.84	0.42
2:D:29:G:H2'	2:D:30:C:C6	2.54	0.42
1:A:175:MET:HG3	1:A:192:MET:HE3	1.98	0.42
1:A:205:LYS:HB3	1:A:270:ALA:HB2	2.01	0.42
1:A:64:ASN:OD1	1:A:66:VAL:HG12	2.19	0.42
1:A:307:ASN:HD21	2:C:37:A:H5'	1.84	0.42
1:B:47:LYS:O	1:B:51:HIS:HB2	2.18	0.42
1:B:67:LEU:C	1:B:69:GLY:N	2.73	0.42
1:A:204:SER:HB2	2:C:26:A:H5"	2.01	0.41
1:A:251:LYS:HD2	1:A:252:TYR:CE2	2.55	0.41
1:A:331:SER:O	1:A:335:MET:HG3	2.20	0.41
1:A:29:ARG:O	1:A:30:GLU:C	2.58	0.41
1:A:153:TRP:CH2	1:A:157:LYS:HE3	2.55	0.41
1:A:149:ILE:HD11	1:A:201:PHE:CE2	2.56	0.41
1:A:33:LYS:HA	1:A:33:LYS:HE2	2.02	0.41
1:B:155:ALA:O	1:B:159:VAL:HG23	2.21	0.41
1:B:232:ILE:HB	1:B:257:PHE:CZ	2.55	0.41
2:D:31:C:C2'	2:D:32:C:H5'	2.51	0.41
2:D:31:C:H2'	2:D:32:C:H5'	2.03	0.41
1:A:57:PHE:CE1	1:A:71:LEU:HD13	2.55	0.40
1:B:272:GLN:OE1	2:D:30:C:N4	2.53	0.40
1:A:49:MET:HG2	1:A:77:ILE:HD13	2.03	0.40
1:B:355:SMC:SG	2:D:37:A:C6	3.15	0.40
1:A:128:GLU:O	1:A:129:CYS:C	2.59	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	351/404 (87%)	323 (92%)	28 (8%)	0	100	100
1	B	351/404 (87%)	321 (92%)	27 (8%)	3 (1%)	17	45
All	All	702/808 (87%)	644 (92%)	55 (8%)	3 (0%)	34	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	ARG
1	B	99	VAL
1	B	36	GLY

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	303/345 (88%)	292 (96%)	11 (4%)	35	67
1	B	303/345 (88%)	291 (96%)	12 (4%)	31	63
All	All	606/690 (88%)	583 (96%)	23 (4%)	30	65

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	89	SER
1	A	99	VAL
1	A	137	GLN
1	A	168	ARG
1	A	211	SER
1	A	213	SER
1	A	221	LYS
1	A	228	VAL
1	A	242	ARG
1	A	325	SER
1	A	368	ARG
1	B	25	ARG
1	B	43	ASP

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Mol	Chain	Res	Type
1	B	66	VAL
1	B	99	VAL
1	B	101	ASP
1	B	163	LYS
1	B	198	ASP
1	B	257	PHE
1	B	262	ARG
1	B	266	GLU
1	B	325	SER
1	B	370	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	307	ASN
1	B	64	ASN
1	B	307	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	67/68 (98%)	20 (29%)	4 (5%)
2	D	65/68 (95%)	23 (35%)	4 (6%)
All	All	132/136 (97%)	43 (32%)	8 (6%)

All (43) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	6	U
2	C	8	C
2	C	9	G
2	C	12	U
2	C	15	A
2	C	16	G
2	C	18	C
2	C	19	C
2	C	21	A
2	C	22	G
2	C	34	U
2	C	37	A

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Mol	Chain	Res	Type
2	C	38	C
2	C	39	G
2	C	47	C
2	C	48	A
2	C	52	G
2	C	58	A
2	C	61	C
2	C	67	G
2	D	6	U
2	D	8	C
2	D	9	G
2	D	12	U
2	D	15	A
2	D	16	G
2	D	18	C
2	D	20	C
2	D	26	A
2	D	32	C
2	D	33	U
2	D	34	U
2	D	35	U
2	D	38	C
2	D	39	G
2	D	42	G
2	D	47	C
2	D	52	G
2	D	54	U
2	D	58	A
2	D	61	C
2	D	63	C
2	D	68	G

All (8) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	8	C
2	C	15	A
2	C	16	G
2	C	38	C
2	D	8	C
2	D	33	U
2	D	34	U

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Mol	Chain	Res	Type
2	D	38	C

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

2 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	SMC	B	355	2,1	5,6,7	1.22	1 (20%)	2,6,8	2.16	1 (50%)
1	SMC	A	355	2,1	5,6,7	1.28	1 (20%)	2,6,8	3.12	1 (50%)

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	SMC	B	355	2,1	-	0/3/5/7	-
1	SMC	A	355	2,1	-	0/3/5/7	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	SMC	CB-SG	-2.64	1.77	1.80
1	B	355	SMC	CB-SG	-2.33	1.77	1.80

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	355	SMC	CS-SG-CB	4.41	109.41	101.30
1	B	355	SMC	CS-SG-CB	3.00	106.82	101.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	355	SMC	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 6 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
4	SF4	A	502	1,3	0,12,12	-	-	-		
5	5AD	A	503	-	17,20,20	1.06	1 (5%)	15,30,30	2.53	4 (26%)
3	MET	A	501	4	7,8,8	1.01	0	7,9,9	1.47	2 (28%)
4	SF4	B	502	1,3	0,12,12	-	-	-		
5	5AD	B	503	-	17,20,20	1.08	1 (5%)	15,30,30	2.59	4 (26%)
3	MET	B	501	4	7,8,8	1.05	0	7,9,9	1.20	1 (14%)

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	SF4	A	502	1,3	-	-	0/6/5/5
5	5AD	A	503	-	-	0/0/20/20	0/3/3/3
4	SF4	B	502	1,3	-	-	0/6/5/5
3	MET	A	501	4	-	3/8/8/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	5AD	B	503	-	-	0/0/20/20	0/3/3/3
3	MET	B	501	4	-	1/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	503	5AD	C4-N3	-2.21	1.32	1.35
5	A	503	5AD	C6-C5	2.07	1.51	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	503	5AD	C5'-C4'-C3'	-7.86	107.45	115.70
5	A	503	5AD	C5'-C4'-C3'	-6.95	108.40	115.70
5	B	503	5AD	C4-C5-N7	-4.29	104.92	109.40
5	A	503	5AD	C4-C5-N7	-3.82	105.42	109.40
5	A	503	5AD	N3-C2-N1	-3.63	123.01	128.68
5	A	503	5AD	C1'-N9-C4	-2.98	121.40	126.64
5	B	503	5AD	N3-C2-N1	-2.47	124.82	128.68
3	A	501	MET	OXT-C-CA	2.32	121.28	113.38
3	B	501	MET	OXT-C-CA	2.29	121.19	113.38
3	A	501	MET	O-C-CA	-2.20	114.38	122.14
5	B	503	5AD	C1'-N9-C4	-2.10	122.95	126.64

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	MET	CA-CB-CG-SD
3	B	501	MET	CA-CB-CG-SD
3	A	501	MET	N-CA-CB-CG
3	A	501	MET	C-CA-CB-CG

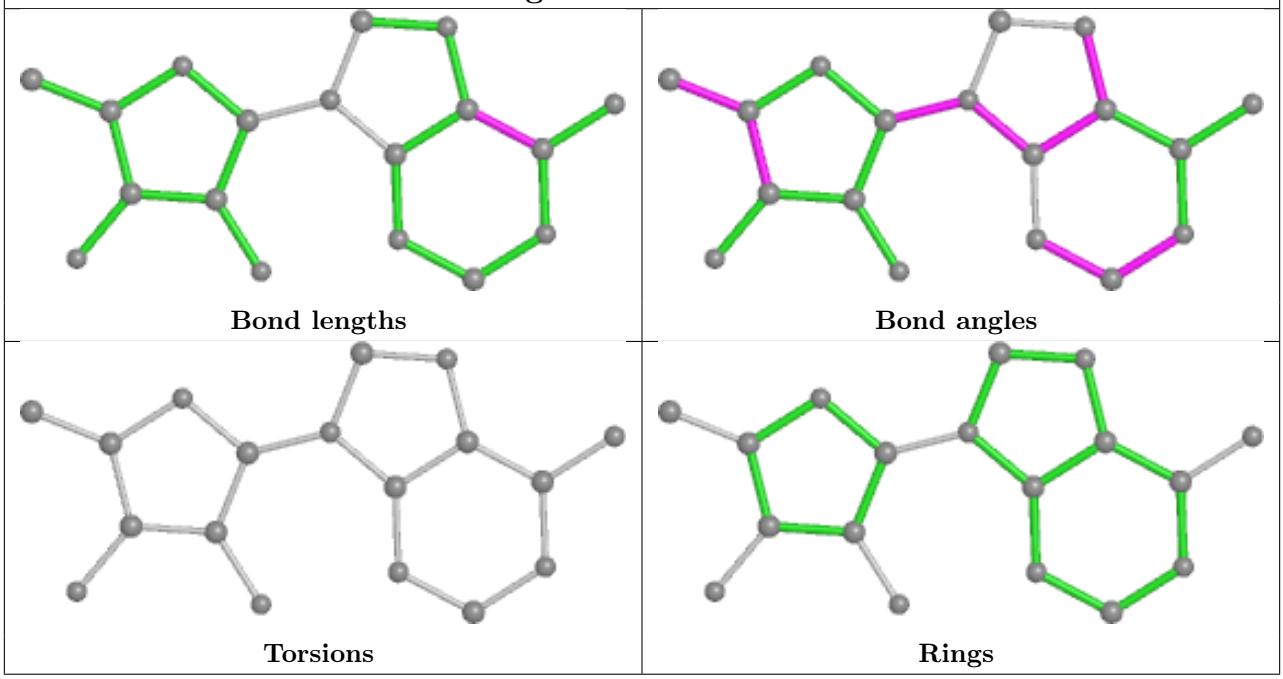
There are no ring outliers.

3 monomers are involved in 3 short contacts:

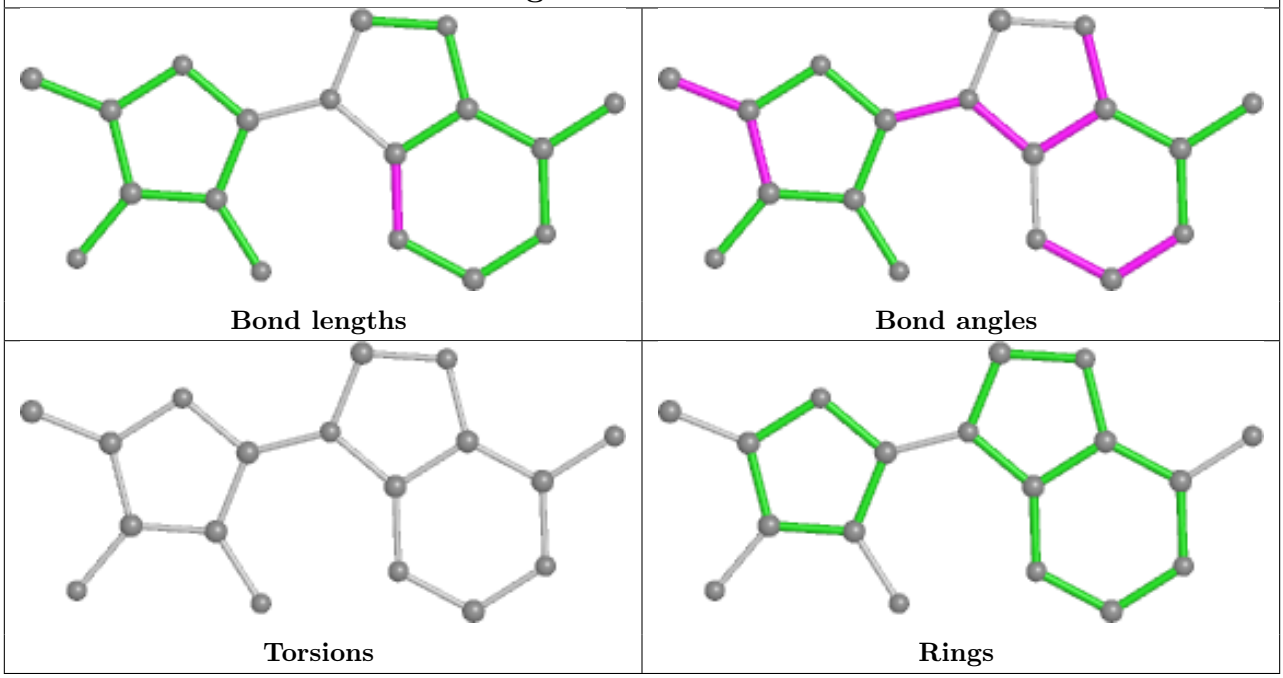
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	503	5AD	1	0
5	B	503	5AD	1	0
3	B	501	MET	1	0

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 5AD A 503



Ligand 5AD B 503



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	353/404 (87%)	0.65	10 (2%) 53 50	46, 61, 97, 112	0
1	B	353/404 (87%)	0.75	28 (7%) 12 9	51, 65, 110, 133	0
2	C	68/68 (100%)	0.17	0 100 100	55, 73, 109, 128	0
2	D	66/68 (97%)	-0.06	1 (1%) 73 73	61, 87, 126, 135	0
All	All	840/944 (88%)	0.59	39 (4%) 32 28	46, 65, 110, 135	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	162	ALA	5.7
1	B	71	LEU	5.5
1	B	167	GLN	4.4
1	B	61	THR	4.0
1	A	162	ALA	3.6
1	B	306	ILE	3.5
1	B	44	GLN	3.4
1	B	62	ASP	3.3
1	B	40	PHE	3.3
1	B	359	ALA	3.1
1	B	164	VAL	3.1
1	B	52	TYR	3.0
1	A	63	ILE	3.0
1	B	277	ILE	2.8
1	B	74	VAL	2.8
1	B	199	PHE	2.8
1	B	168	ARG	2.7
1	B	35	LEU	2.7
1	A	168	ARG	2.7
1	A	170	ILE	2.6
1	B	173	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	68	ARG	2.5
1	B	170	ILE	2.4
1	B	124	GLY	2.4
1	B	153	TRP	2.4
1	A	74	VAL	2.4
1	A	44	GLN	2.4
1	B	165	THR	2.3
1	A	126	ALA	2.3
1	B	65	LYS	2.3
1	B	51	HIS	2.3
1	A	164	VAL	2.2
1	B	75	ALA	2.1
1	B	126	ALA	2.1
1	A	271	ASN	2.1
1	A	203	LEU	2.1
2	D	18	C	2.0
1	B	60	MET	2.0
1	B	20	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	SMC	B	355	7/8	0.97	0.15	52,56,57,57	0
1	SMC	A	355	7/8	0.99	0.18	43,49,54,55	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

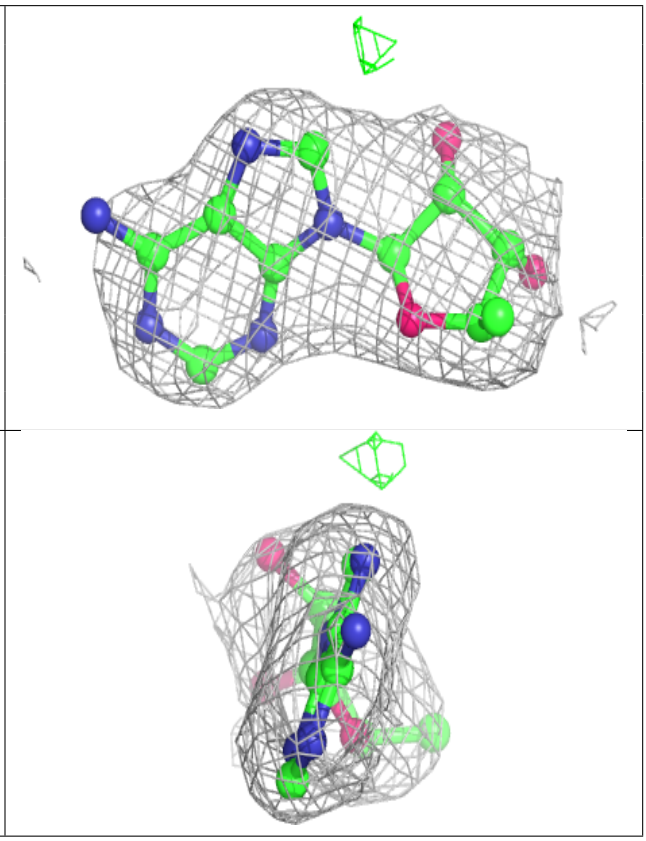
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	MG	C	103	1/1	0.45	0.31	88,88,88,88	0
6	MG	A	504	1/1	0.81	0.22	56,56,56,56	0
6	MG	C	102	1/1	0.93	0.29	70,70,70,70	0
3	MET	A	501	9/9	0.98	0.23	60,66,69,72	0
6	MG	C	101	1/1	0.98	0.31	29,29,29,29	0
5	5AD	A	503	18/18	0.98	0.31	53,59,69,73	0
5	5AD	B	503	18/18	0.98	0.28	54,60,68,68	0
6	MG	D	101	1/1	0.98	0.14	41,41,41,41	0
4	SF4	A	502	8/8	0.99	0.22	40,44,55,55	0
4	SF4	B	502	8/8	0.99	0.22	42,43,57,59	0
6	MG	B	504	1/1	0.99	0.14	67,67,67,67	0
3	MET	B	501	9/9	0.99	0.22	56,62,68,69	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.

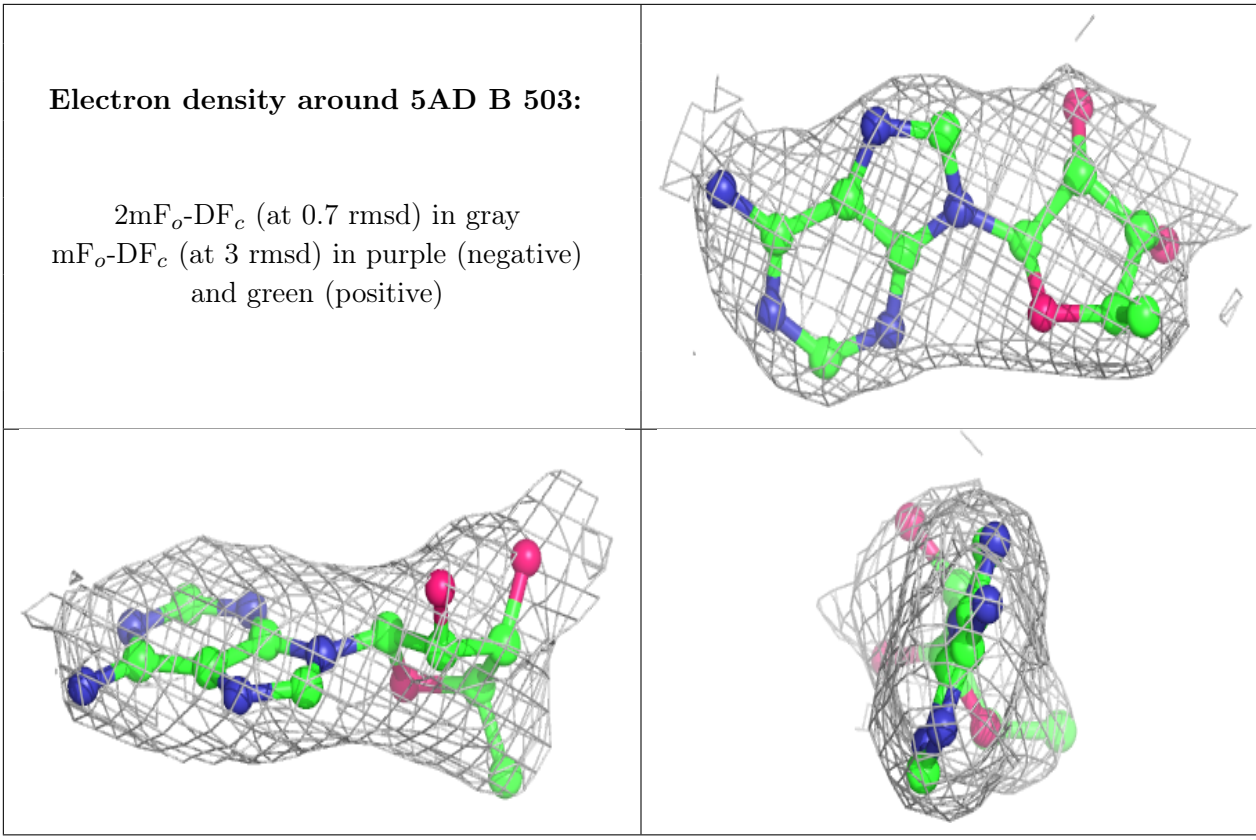
Electron density around 5AD A 503:

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 5AD B 503:

$2mF_o$-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.