Full wwPDB X-ray Structure Validation Report (i)

Nov 16, 2023 – 12:41 AM JST

PDB ID	:	6KL6
Title	:	Crystal structure of MERS-CoV N-NTD complexed with 5-Benzyloxygramine
Authors	:	Hou, M.H.; Lin, S.M.; Wang, Y.S.; Hsu, J.N.
Deposited on	:	2019-07-29
Resolution	:	2.77 Å(reported)

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

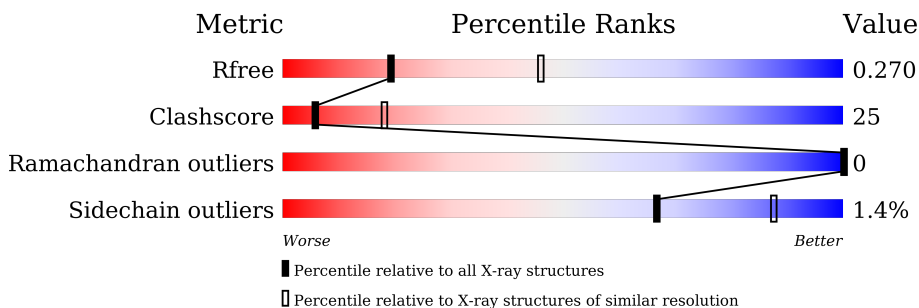|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.77 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	Percentile Ranks	Value
Rfree		0.270
Clashscore		25
Ramachandran outliers		0
Sidechain outliers		1.4%

Worse　　　　　　　　　　　　　　　　　　　　　　　*Better*

▌Percentile relative to all X-ray structures

◫Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4107 (2.80-2.76)
Clashscore	141614	4575 (2.80-2.76)
Ramachandran outliers	138981	4487 (2.80-2.76)
Sidechain outliers	138945	4489 (2.80-2.76)

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%

Mol	Chain	Length	Quality of chain
1	A	144	49% 30% • 19%
1	B	144	54% 26% • 19%
1	C	144	44% 31% 24%
1	D	144	47% 31% 23%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3700 atoms, of which 20 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	117	Total	C	N	O	S	0	0	0
			930	597	166	166	1			
1	B	116	Total	C	N	O		0	0	0
			908	583	161	164				
1	C	109	Total	C	N	O		0	0	0
			849	546	148	155				
1	D	111	Total	C	N	O		0	0	0
			862	554	151	157				

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	HIS	-	expression tag	UNP A0A0D3MU65
A	23	HIS	-	expression tag	UNP A0A0D3MU65
A	24	HIS	-	expression tag	UNP A0A0D3MU65
A	25	HIS	-	expression tag	UNP A0A0D3MU65
A	26	HIS	-	expression tag	UNP A0A0D3MU65
A	27	HIS	-	expression tag	UNP A0A0D3MU65
A	28	SER	-	expression tag	UNP A0A0D3MU65
A	29	SER	-	expression tag	UNP A0A0D3MU65
A	30	GLY	-	expression tag	UNP A0A0D3MU65
A	31	LEU	-	expression tag	UNP A0A0D3MU65
A	32	VAL	-	expression tag	UNP A0A0D3MU65
A	33	PRO	-	expression tag	UNP A0A0D3MU65
A	34	ARG	-	expression tag	UNP A0A0D3MU65
A	35	GLY	-	expression tag	UNP A0A0D3MU65
A	36	SER	-	expression tag	UNP A0A0D3MU65
A	37	HIS	-	expression tag	UNP A0A0D3MU65
A	38	MET	-	expression tag	UNP A0A0D3MU65
B	22	HIS	-	expression tag	UNP A0A0D3MU65
B	23	HIS	-	expression tag	UNP A0A0D3MU65
B	24	HIS	-	expression tag	UNP A0A0D3MU65
B	25	HIS	-	expression tag	UNP A0A0D3MU65

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Chain	Residue	Modelled	Actual	Comment	Reference
B	26	HIS	-	expression tag	UNP A0A0D3MU65
B	27	HIS	-	expression tag	UNP A0A0D3MU65
B	28	SER	-	expression tag	UNP A0A0D3MU65
B	29	SER	-	expression tag	UNP A0A0D3MU65
B	30	GLY	-	expression tag	UNP A0A0D3MU65
B	31	LEU	-	expression tag	UNP A0A0D3MU65
B	32	VAL	-	expression tag	UNP A0A0D3MU65
B	33	PRO	-	expression tag	UNP A0A0D3MU65
B	34	ARG	-	expression tag	UNP A0A0D3MU65
B	35	GLY	-	expression tag	UNP A0A0D3MU65
B	36	SER	-	expression tag	UNP A0A0D3MU65
B	37	HIS	-	expression tag	UNP A0A0D3MU65
B	38	MET	-	expression tag	UNP A0A0D3MU65
C	22	HIS	-	expression tag	UNP A0A0D3MU65
C	23	HIS	-	expression tag	UNP A0A0D3MU65
C	24	HIS	-	expression tag	UNP A0A0D3MU65
C	25	HIS	-	expression tag	UNP A0A0D3MU65
C	26	HIS	-	expression tag	UNP A0A0D3MU65
C	27	HIS	-	expression tag	UNP A0A0D3MU65
C	28	SER	-	expression tag	UNP A0A0D3MU65
C	29	SER	-	expression tag	UNP A0A0D3MU65
C	30	GLY	-	expression tag	UNP A0A0D3MU65
C	31	LEU	-	expression tag	UNP A0A0D3MU65
C	32	VAL	-	expression tag	UNP A0A0D3MU65
C	33	PRO	-	expression tag	UNP A0A0D3MU65
C	34	ARG	-	expression tag	UNP A0A0D3MU65
C	35	GLY	-	expression tag	UNP A0A0D3MU65
C	36	SER	-	expression tag	UNP A0A0D3MU65
C	37	HIS	-	expression tag	UNP A0A0D3MU65
C	38	MET	-	expression tag	UNP A0A0D3MU65
D	22	HIS	-	expression tag	UNP A0A0D3MU65
D	23	HIS	-	expression tag	UNP A0A0D3MU65
D	24	HIS	-	expression tag	UNP A0A0D3MU65
D	25	HIS	-	expression tag	UNP A0A0D3MU65
D	26	HIS	-	expression tag	UNP A0A0D3MU65
D	27	HIS	-	expression tag	UNP A0A0D3MU65
D	28	SER	-	expression tag	UNP A0A0D3MU65
D	29	SER	-	expression tag	UNP A0A0D3MU65
D	30	GLY	-	expression tag	UNP A0A0D3MU65
D	31	LEU	-	expression tag	UNP A0A0D3MU65
D	32	VAL	-	expression tag	UNP A0A0D3MU65
D	33	PRO	-	expression tag	UNP A0A0D3MU65

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Chain	Residue	Modelled	Actual	Comment	Reference
D	34	ARG	-	expression tag	UNP A0A0D3MU65
D	35	GLY	-	expression tag	UNP A0A0D3MU65
D	36	SER	-	expression tag	UNP A0A0D3MU65
D	37	HIS	-	expression tag	UNP A0A0D3MU65
D	38	MET	-	expression tag	UNP A0A0D3MU65

- Molecule 2 is N,N-dimethyl-1-(5-phenylmethoxy-1H-indol-3-yl)methanamine (three-letter code: DJU) (formula: $C_{18}H_{20}N_2O$) (labeled as "Ligand of Interest" by depositor).

DJU
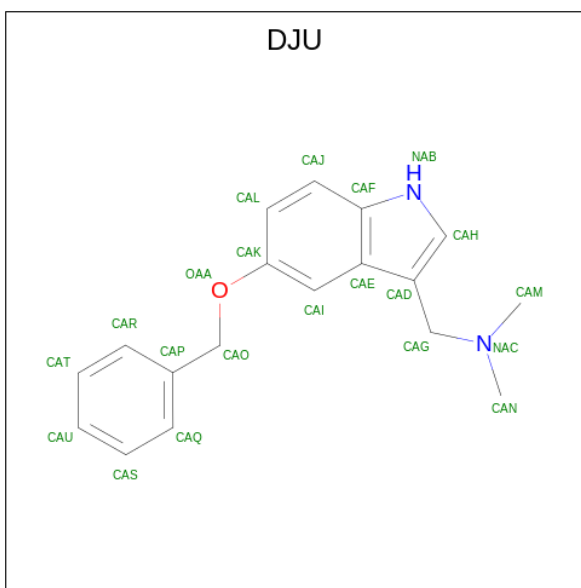
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	D	1	41	18	20	2	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	34	Total	O	0	0
			34	34		
3	B	25	Total	O	0	0
			25	25		
3	C	23	Total	O	0	0
			23	23		
3	D	28	Total	O	0	0
			28	28		

3 Residue-property plots ⓘ

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. 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. 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.
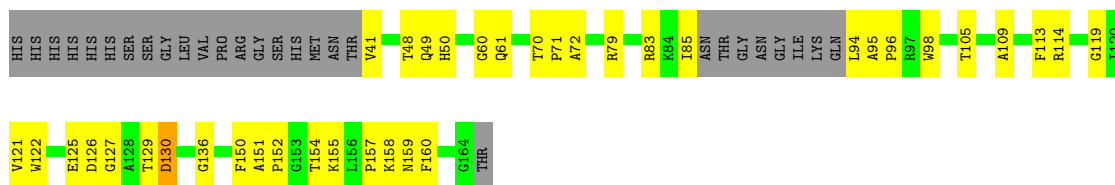
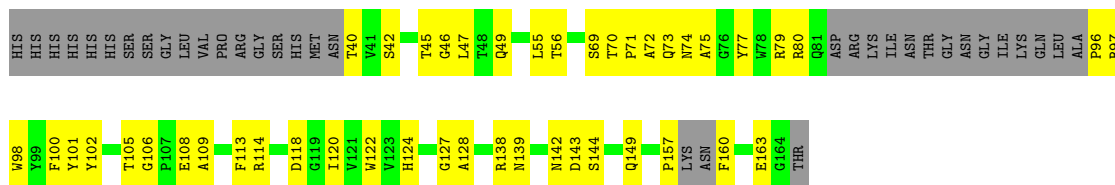- Molecule 1: Nucleoprotein

Chain A:
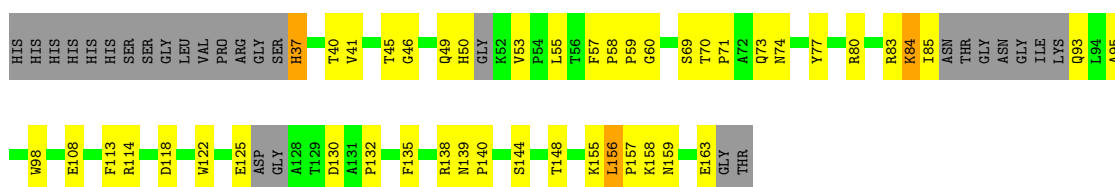
- Molecule 1: Nucleoprotein

Chain B:

- Molecule 1: Nucleoprotein

Chain C:

- Molecule 1: Nucleoprotein

Chain D:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	35.49Å 108.48Å 91.59Å 90.00° 101.16° 90.00°	Depositor
Resolution (Å)	29.39 – 2.77 29.39 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.39-2.77) 99.0 (29.39-2.76)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	7.62 (at 2.76Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.232 , 0.271 0.232 , 0.270	Depositor DCC
R_{free} test set	1742 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å^2)	44.0	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 16.5	EDS
L-test for twinning[2]	$<|L|> = 0.40, <L^2> = 0.22$	Xtriage
Estimated twinning fraction	0.370 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3700	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.96% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: DJU

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	0.42	0/961	0.55	0/1313
1	B	0.24	0/940	0.56	1/1287 (0.1%)
1	C	0.51	0/880	0.64	1/1206 (0.1%)
1	D	0.44	0/894	0.61	0/1227
All	All	0.41	0/3675	0.59	2/5033 (0.0%)

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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	127	GLY	N-CA-C	6.05	128.22	113.10
1	B	157	PRO	C-N-CA	-5.22	108.66	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	130	ASP	Mainchain

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	930	0	888	55	1
1	B	908	0	866	35	0
1	C	849	0	796	44	1
1	D	862	0	813	44	0
2	D	21	20	0	2	0
3	A	34	0	0	6	0
3	B	25	0	0	5	0
3	C	23	0	0	7	0
3	D	28	0	0	7	0
All	All	3680	20	3363	175	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 25.

All (175) 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:C:102:TYR:O	1:C:105:THR:HG22	1.21	1.33
1:D:48:THR:OG1	1:D:97:ARG:CD	1.77	1.31
1:A:37:HIS:O	1:A:40:THR:CG2	1.88	1.22
1:D:48:THR:OG1	1:D:97:ARG:HD2	1.46	1.16
1:B:155:LYS:HE3	1:B:155:LYS:HA	1.14	1.12
1:D:48:THR:OG1	1:D:97:ARG:HD3	1.43	1.12
1:A:37:HIS:O	1:A:40:THR:HG21	1.56	1.05
1:B:155:LYS:HA	1:B:155:LYS:CE	1.88	1.00
1:A:70:THR:HB	1:A:71:PRO:HD2	1.43	0.98
1:A:37:HIS:O	1:A:40:THR:HG22	1.60	0.96
1:A:40:THR:HG23	1:A:41:VAL:HG23	1.48	0.96
1:C:102:TYR:O	1:C:105:THR:CG2	2.15	0.95
1:A:73:GLN:NE2	3:A:201:HOH:O	1.92	0.94
1:B:155:LYS:HE3	1:B:155:LYS:CA	1.91	0.94
1:A:37:HIS:C	1:A:40:THR:HG21	1.91	0.90
1:C:101:TYR:HB3	1:C:105:THR:HG23	1.57	0.86
1:C:142:ASN:N	3:C:202:HOH:O	2.09	0.85
1:D:70:THR:HG23	1:D:71:PRO:HD2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:164:GLY:O	3:D:301:HOH:O	1.94	0.84
1:D:48:THR:HG1	1:D:97:ARG:HD3	1.42	0.83
1:D:69:SER:HA	2:D:201:DJU:CAT	2.10	0.82
1:A:37:HIS:C	1:A:40:THR:CG2	2.45	0.82
1:B:152:PRO:O	3:B:201:HOH:O	1.98	0.80
1:D:116:VAL:HG12	3:D:304:HOH:O	1.82	0.79
1:A:125:GLU:OE1	3:A:202:HOH:O	2.00	0.78
1:D:102:TYR:O	1:D:105:THR:OG1	2.00	0.77
1:B:136:GLY:O	3:B:202:HOH:O	2.03	0.76
1:D:111:LEU:HG	1:D:115:ALA:HB3	1.66	0.76
1:A:49:GLN:NE2	1:A:53:VAL:O	2.19	0.75
1:A:59:PRO:O	3:A:203:HOH:O	2.04	0.75
1:A:132:PRO:O	3:A:204:HOH:O	2.04	0.75
1:C:114:ARG:HA	1:C:122:TRP:CD1	2.22	0.74
1:C:139:ASN:ND2	3:C:202:HOH:O	2.20	0.74
1:D:47:LEU:CD2	1:D:162:ILE:HG12	2.18	0.73
1:A:156:LEU:HG	1:A:157:PRO:HD2	1.71	0.71
1:D:41:VAL:HG11	1:D:138:ARG:O	1.90	0.71
1:C:42:SER:OG	1:C:100:PHE:O	2.04	0.70
1:C:157:PRO:O	3:C:201:HOH:O	2.08	0.70
1:A:58:PRO:HG2	1:A:155:LYS:HD2	1.74	0.70
1:B:70:THR:HB	1:B:71:PRO:HD2	1.75	0.69
1:C:70:THR:HB	1:C:73:GLN:OE1	1.92	0.69
1:A:37:HIS:CA	1:A:40:THR:HG21	2.22	0.69
1:A:156:LEU:HG	1:A:157:PRO:CD	2.22	0.69
1:B:113:PHE:CE2	1:B:114:ARG:HG3	2.28	0.69
1:B:158:LYS:O	1:B:159:ASN:HB2	1.93	0.68
1:C:70:THR:HG22	1:C:72:ALA:H	1.57	0.67
1:C:70:THR:HG23	1:C:71:PRO:HD2	1.76	0.67
1:D:69:SER:HA	2:D:201:DJU:CAU	2.25	0.67
1:D:151:ALA:O	1:D:154:THR:OG1	2.13	0.66
1:C:46:GLY:O	1:C:163:GLU:OE1	2.14	0.66
1:D:51:GLY:O	3:D:303:HOH:O	2.15	0.64
1:D:70:THR:HG22	1:D:72:ALA:H	1.61	0.64
1:C:40:THR:CG2	1:C:106:GLY:HA2	2.28	0.63
1:D:71:PRO:HA	1:D:125:GLU:OE1	1.99	0.63
1:B:113:PHE:CD2	1:B:114:ARG:HG3	2.33	0.63
1:B:85:ILE:HD11	1:B:94:LEU:HD11	1.79	0.63
1:C:124:HIS:HB2	1:C:128:ALA:HB3	1.81	0.62
1:D:80:ARG:HD2	3:D:302:HOH:O	1.99	0.62
1:A:37:HIS:HA	1:A:40:THR:HG21	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ALA:O	1:B:154:THR:OG1	2.16	0.62
1:D:47:LEU:HD22	1:D:162:ILE:HG12	1.81	0.61
1:D:130:ASP:OD1	1:D:130:ASP:N	2.30	0.61
1:B:105:THR:C	1:B:109:ALA:HB2	2.21	0.61
1:C:160:PHE:N	3:C:207:HOH:O	2.33	0.61
1:D:41:VAL:CG1	1:D:138:ARG:O	2.48	0.61
1:A:74:ASN:ND2	1:A:125:GLU:OE2	2.24	0.60
1:C:97:ARG:HH22	1:C:163:GLU:HG2	1.67	0.60
1:D:111:LEU:HG	1:D:115:ALA:CB	2.33	0.59
1:C:77:TYR:HB3	1:C:122:TRP:CE3	2.37	0.58
1:A:55:LEU:HD11	1:A:57:PHE:CE2	2.38	0.58
1:B:49:GLN:HB3	1:B:96:PRO:HG2	1.86	0.57
1:A:46:GLY:O	1:A:163:GLU:HG2	2.05	0.57
1:A:50:HIS:HB2	1:A:159:ASN:HB3	1.85	0.56
1:A:118:ASP:HA	1:B:114:ARG:HH12	1.71	0.56
1:D:52:LYS:HA	3:D:303:HOH:O	2.05	0.56
1:D:66:ASN:OD1	1:D:68:ASN:HB2	2.06	0.56
1:D:50:HIS:O	1:D:159:ASN:HB2	2.06	0.55
1:C:45:THR:HG21	1:C:163:GLU:O	2.07	0.55
1:D:112:PRO:HG2	1:D:115:ALA:HB2	1.89	0.55
1:A:114:ARG:O	1:B:129:THR:HB	2.06	0.55
1:A:139:ASN:HD22	1:A:140:PRO:HD2	1.71	0.55
1:C:142:ASN:HB2	3:C:202:HOH:O	2.06	0.55
1:D:111:LEU:HD21	1:D:117:LYS:HG2	1.89	0.55
1:B:50:HIS:O	1:B:159:ASN:HB3	2.07	0.55
1:A:93:GLN:N	3:A:205:HOH:O	2.38	0.54
1:B:98:TRP:CZ3	1:B:121:VAL:HG23	2.42	0.54
1:A:113:PHE:CD2	1:A:114:ARG:HG3	2.43	0.54
1:A:41:VAL:HB	1:A:138:ARG:O	2.08	0.54
1:A:55:LEU:HD11	1:A:57:PHE:CZ	2.43	0.54
1:D:41:VAL:HG13	1:D:41:VAL:O	2.06	0.54
1:B:61:GLN:OE1	1:B:155:LYS:HB2	2.08	0.53
1:C:79:ARG:HG3	1:C:120:ILE:HD11	1.90	0.53
1:A:37:HIS:C	1:A:40:THR:HG22	2.21	0.53
1:C:138:ARG:NH1	1:C:143:ASP:O	2.36	0.53
1:B:85:ILE:CG1	1:B:94:LEU:HD11	2.38	0.53
1:A:80:ARG:HB2	1:A:98:TRP:CZ2	2.43	0.53
1:A:70:THR:HB	1:A:71:PRO:CD	2.28	0.53
1:B:41:VAL:HB	3:B:206:HOH:O	2.09	0.52
1:B:113:PHE:O	1:B:114:ARG:HB2	2.09	0.52
1:A:40:THR:HG23	1:A:41:VAL:CG2	2.31	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ARG:HB2	1:A:98:TRP:CE2	2.44	0.52
1:A:60:GLY:HA2	1:A:125:GLU:HA	1.91	0.52
1:C:118:ASP:O	3:C:204:HOH:O	2.19	0.52
1:A:70:THR:CB	1:A:71:PRO:HD2	2.27	0.52
1:C:75:ALA:HB2	1:C:128:ALA:HB1	1.93	0.51
1:B:114:ARG:HA	1:B:122:TRP:CG	2.46	0.51
1:C:70:THR:CG2	1:C:71:PRO:HD2	2.41	0.51
1:B:114:ARG:HA	1:B:122:TRP:CD1	2.46	0.51
1:A:77:TYR:CZ	1:A:108:GLU:HB2	2.47	0.50
1:C:49:GLN:HB3	1:C:96:PRO:HG2	1.94	0.50
1:C:42:SER:HB2	1:C:101:TYR:CE2	2.47	0.49
1:D:111:LEU:HD21	1:D:117:LYS:CG	2.42	0.49
1:D:47:LEU:HG	1:D:78:TRP:CZ3	2.48	0.49
1:A:50:HIS:HB2	1:A:159:ASN:CB	2.43	0.49
1:B:49:GLN:O	1:B:95:ALA:HB1	2.13	0.48
1:D:114:ARG:HA	1:D:122:TRP:CD1	2.48	0.48
1:C:113:PHE:HZ	1:C:124:HIS:HD2	1.61	0.48
1:A:37:HIS:ND1	1:A:40:THR:HG21	2.28	0.48
1:B:85:ILE:CD1	1:B:94:LEU:HD11	2.43	0.48
1:A:139:ASN:ND2	1:A:140:PRO:HD2	2.29	0.47
1:A:158:LYS:H	1:A:158:LYS:HG2	1.48	0.47
1:D:70:THR:HG23	1:D:71:PRO:CD	2.39	0.47
1:B:98:TRP:HZ3	1:B:121:VAL:HG23	1.79	0.47
1:B:150:PHE:HB2	1:B:154:THR:OG1	2.15	0.47
1:C:80:ARG:HB2	1:C:98:TRP:CH2	2.50	0.47
1:B:60:GLY:N	3:B:210:HOH:O	2.47	0.46
1:A:113:PHE:CE2	1:A:114:ARG:HD2	2.50	0.46
1:D:72:ALA:HA	1:D:128:ALA:HA	1.97	0.46
1:A:85:ILE:N	3:A:205:HOH:O	2.06	0.46
1:D:132:PRO:O	3:D:305:HOH:O	2.21	0.45
1:A:114:ARG:HA	1:A:122:TRP:CD1	2.51	0.45
1:B:83:ARG:NH1	3:B:211:HOH:O	2.48	0.45
1:D:47:LEU:HD21	1:D:162:ILE:HG12	1.96	0.45
1:D:47:LEU:HD22	1:D:162:ILE:CG1	2.45	0.45
1:C:40:THR:HG21	1:C:106:GLY:HA2	1.99	0.45
1:C:80:ARG:HB2	1:C:98:TRP:CZ2	2.52	0.45
1:C:46:GLY:O	1:C:47:LEU:HD23	2.17	0.45
1:C:46:GLY:C	1:C:47:LEU:HD23	2.37	0.44
1:C:70:THR:CB	1:C:73:GLN:OE1	2.64	0.44
1:D:49:GLN:HB3	1:D:96:PRO:HG2	1.98	0.44
1:D:48:THR:CB	1:D:97:ARG:HD2	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:THR:HB	1:A:163:GLU:HB2	2.00	0.44
1:B:79:ARG:HA	1:B:119:GLY:O	2.18	0.44
1:D:143:ASP:OD1	1:D:144:SER:N	2.51	0.44
1:A:69:SER:HB2	1:A:135:PHE:CZ	2.52	0.43
1:C:118:ASP:N	3:C:208:HOH:O	2.39	0.43
1:D:104:GLY:HA2	1:D:109:ALA:O	2.17	0.43
1:C:101:TYR:HB3	1:C:105:THR:CG2	2.39	0.43
1:C:138:ARG:NH1	1:C:144:SER:HA	2.34	0.43
1:A:114:ARG:NE	1:B:130:ASP:OD1	2.52	0.43
1:A:113:PHE:CE2	1:A:114:ARG:HG3	2.53	0.42
1:A:130:ASP:OD1	1:A:130:ASP:N	2.40	0.42
1:C:42:SER:CB	1:C:100:PHE:O	2.67	0.42
1:A:49:GLN:O	1:A:95:ALA:HB1	2.19	0.42
1:C:74:ASN:O	1:C:128:ALA:HB2	2.18	0.42
1:A:84:LYS:HD2	1:A:85:ILE:HG13	2.01	0.42
1:A:139:ASN:HA	1:A:140:PRO:HD2	1.87	0.42
1:D:113:PHE:O	1:D:114:ARG:HB2	2.19	0.42
1:C:113:PHE:CD2	1:C:114:ARG:HG3	2.54	0.42
1:A:113:PHE:O	1:A:114:ARG:HB2	2.20	0.41
1:A:114:ARG:HA	1:A:122:TRP:CG	2.56	0.41
1:A:45:THR:O	1:A:148:THR:OG1	2.35	0.41
1:B:71:PRO:HA	1:B:125:GLU:OE2	2.20	0.41
1:A:83:ARG:HD3	1:A:95:ALA:O	2.20	0.41
1:B:48:THR:O	1:B:160:PHE:HA	2.20	0.41
1:B:49:GLN:HB2	1:B:160:PHE:CE2	2.56	0.41
1:B:72:ALA:HA	1:B:127:GLY:O	2.21	0.41
1:C:69:SER:OG	1:C:70:THR:N	2.54	0.41
1:C:74:ASN:O	1:C:128:ALA:CB	2.69	0.40
1:C:45:THR:CG2	1:C:46:GLY:N	2.83	0.40
1:C:55:LEU:O	1:C:56:THR:CG2	2.69	0.40
1:D:55:LEU:HB3	1:D:121:VAL:HG21	2.03	0.40
1:D:116:VAL:N	3:D:304:HOH:O	2.19	0.40
1:C:108:GLU:O	1:C:109:ALA:C	2.57	0.40
1:D:111:LEU:HA	1:D:111:LEU:HD12	1.78	0.40

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:A:144:SER:OG	1:C:149:GLN:NE2[1_655]	1.98	0.22

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	109/144 (76%)	108 (99%)	1 (1%)	0	100	100
1	B	112/144 (78%)	111 (99%)	1 (1%)	0	100	100
1	C	103/144 (72%)	101 (98%)	2 (2%)	0	100	100
1	D	107/144 (74%)	106 (99%)	1 (1%)	0	100	100
All	All	431/576 (75%)	426 (99%)	5 (1%)	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	97/117 (83%)	94 (97%)	3 (3%)	40	71
1	B	93/117 (80%)	92 (99%)	1 (1%)	73	90
1	C	87/117 (74%)	87 (100%)	0	100	100
1	D	88/117 (75%)	87 (99%)	1 (1%)	73	90
All	All	365/468 (78%)	360 (99%)	5 (1%)	67	87

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

Mol	Chain	Res	Type
1	A	37	HIS
1	A	84	LYS

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Mol	Chain	Res	Type
1	A	156	LEU
1	B	126	ASP
1	D	126	ASP

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	81	GLN
1	A	139	ASN
1	C	139	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	#$|Z| > 2$
2	DJU	D	201	-	22,23,23	1.61	3 (13%)	25,31,31	2.01	7 (28%)

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
2	DJU	D	201	-	-	6/8/9/9	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	DJU	CAI-CAE	-3.83	1.34	1.42
2	D	201	DJU	CAI-CAK	3.60	1.43	1.37
2	D	201	DJU	CAG-NAC	-2.75	1.38	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	201	DJU	CAG-CAD-CAH	-5.89	118.30	127.48
2	D	201	DJU	CAD-CAG-NAC	3.96	120.68	112.66
2	D	201	DJU	CAM-NAC-CAG	-3.16	104.18	110.69
2	D	201	DJU	CAJ-CAL-CAK	-2.93	116.24	120.17
2	D	201	DJU	CAO-OAA-CAK	-2.92	110.43	117.65
2	D	201	DJU	CAL-CAJ-CAF	2.05	123.42	120.84
2	D	201	DJU	CAN-NAC-CAM	-2.00	104.56	109.73

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	201	DJU	CAD-CAG-NAC-CAN
2	D	201	DJU	CAL-CAK-OAA-CAO
2	D	201	DJU	CAI-CAK-OAA-CAO
2	D	201	DJU	CAP-CAO-OAA-CAK
2	D	201	DJU	CAH-CAD-CAG-NAC
2	D	201	DJU	CAD-CAG-NAC-CAM

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	201	DJU	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 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 DJU D 201
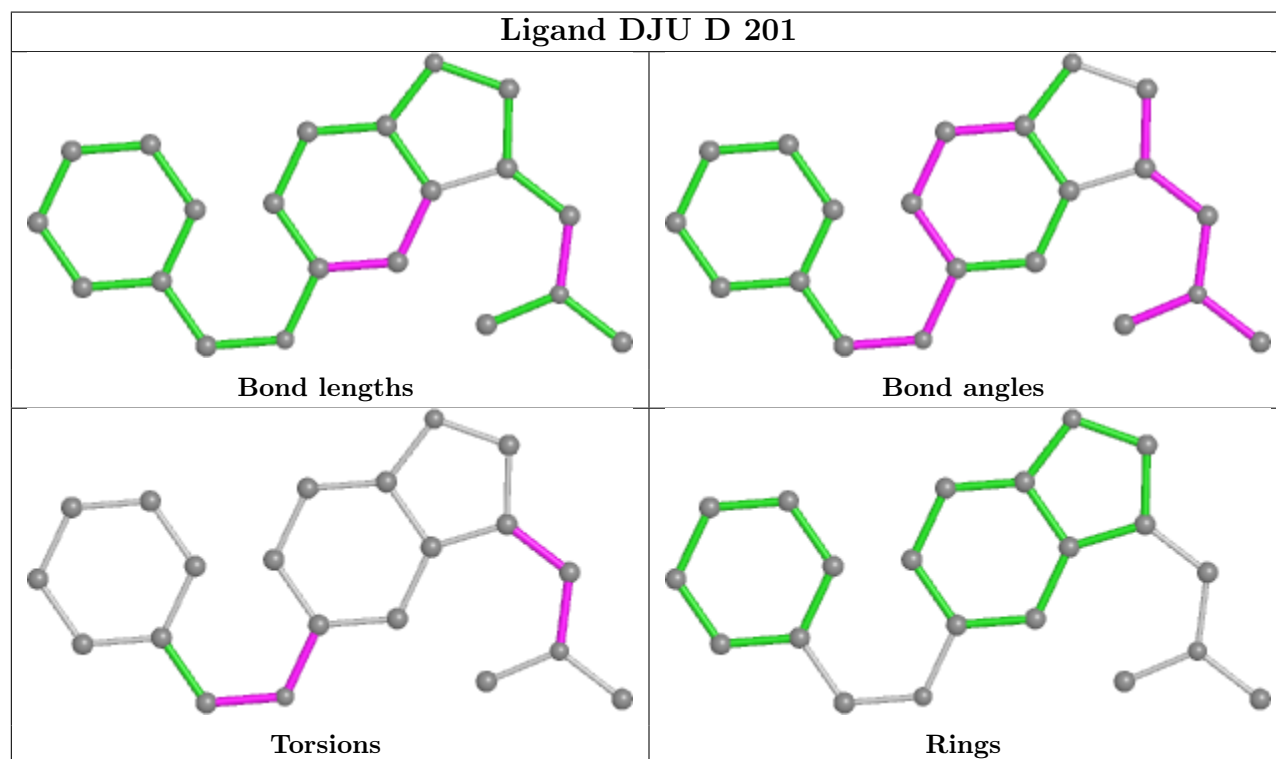
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

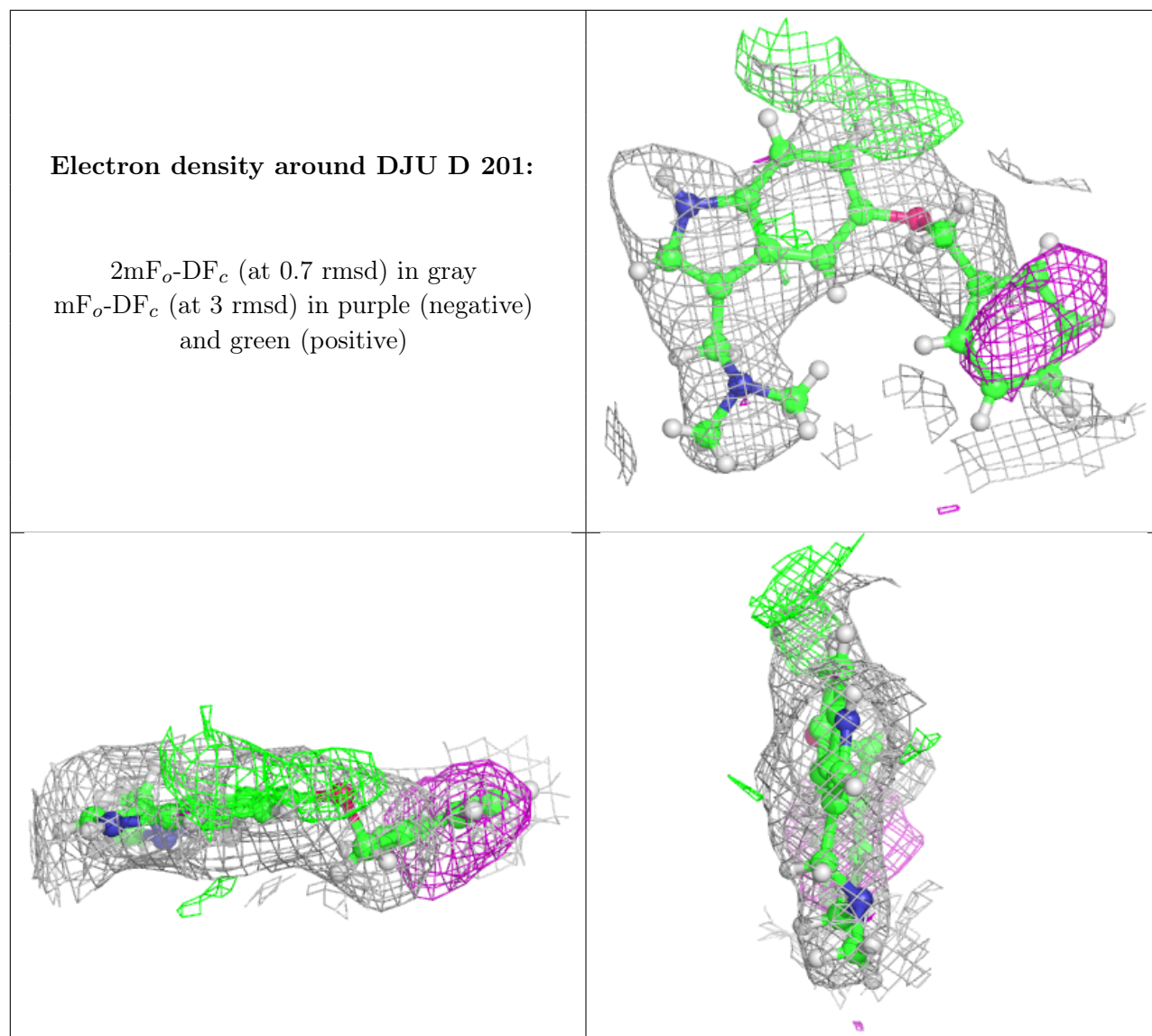Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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 DJU D 201:

$2mF_o$-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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.