Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 01:41 AM JST

PDB ID	:	6IMC
Title	:	Crystal Structure of ALKBH1 in complex with Mn(II) and N-Oxalylglycine
Authors	:	Zhang, M.; Yang, S.; Zhao, W.; Li, H.
Deposited on	:	2018-10-22
Resolution	:	2.51 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:

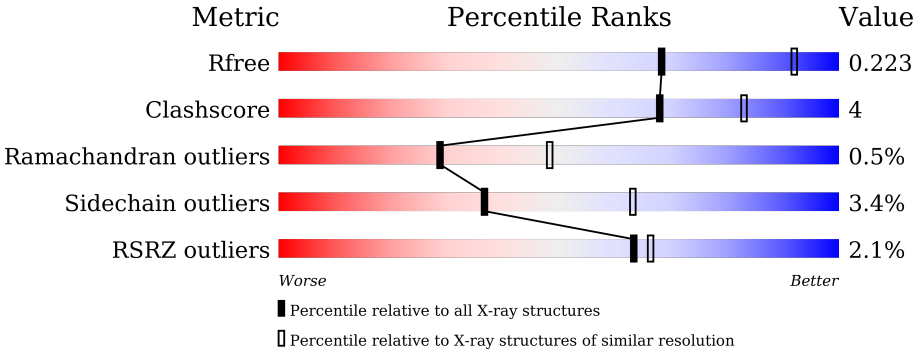
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA,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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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	361	2% 81% 12% • 6%
1	B	361	3% 81% 11% • 6%
1	C	361	2% 80% 14% 6%
1	D	361	% 84% 10% 6%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11238 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 Nucleic acid dioxygenase ALKBH1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	339	2708	1729	477	488	14	0	0	0
1	B	339	2708	1729	477	488	14	0	0	0
1	C	339	2708	1729	477	488	14	0	0	0
1	D	340	2719	1735	481	489	14	0	0	0

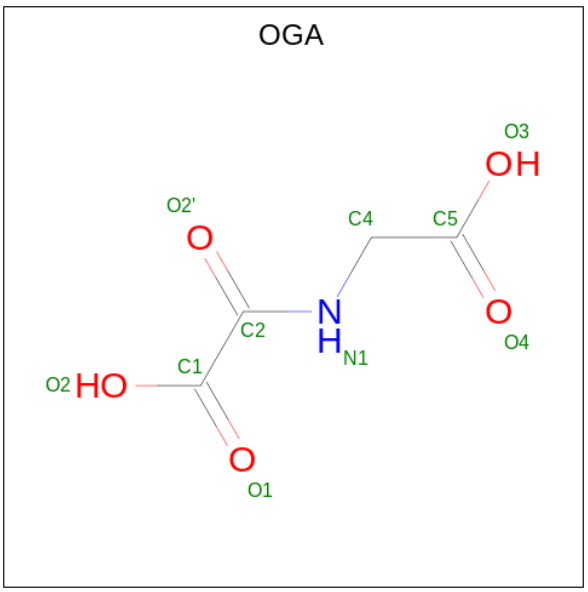
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P0CB42
A	0	PRO	-	expression tag	UNP P0CB42
B	-1	GLY	-	expression tag	UNP P0CB42
B	0	PRO	-	expression tag	UNP P0CB42
C	-1	GLY	-	expression tag	UNP P0CB42
C	0	PRO	-	expression tag	UNP P0CB42
D	-1	GLY	-	expression tag	UNP P0CB42
D	0	PRO	-	expression tag	UNP P0CB42

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0
2	D	1	1	1	0	0

- Molecule 3 is N-OXALYLGLYCINE (three-letter code: OGA) (formula: $C_4H_5NO_5$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	10	4	1	5	0	0
3	B	1	10	4	1	5	0	0
3	C	1	10	4	1	5	0	0
3	D	1	10	4	1	5	0	0

- Molecule 4 is water.

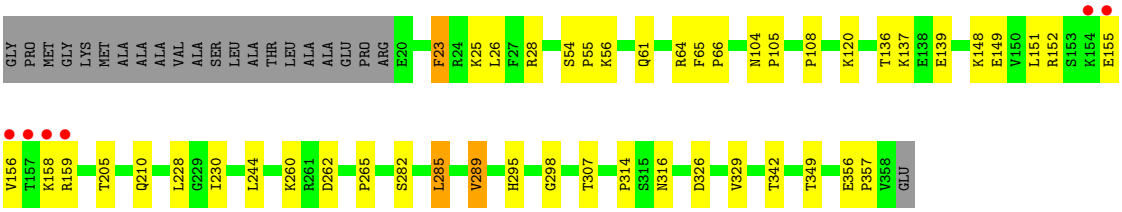
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	106	106	106	0	0
4	B	82	82	82	0	0
4	C	74	74	74	0	0
4	D	89	89	89	0	0

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.

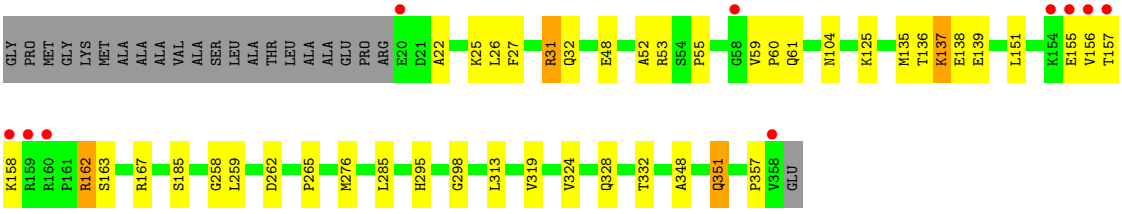
• Molecule 1: Nucleic acid dioxygenase ALKBH1

Chain A:



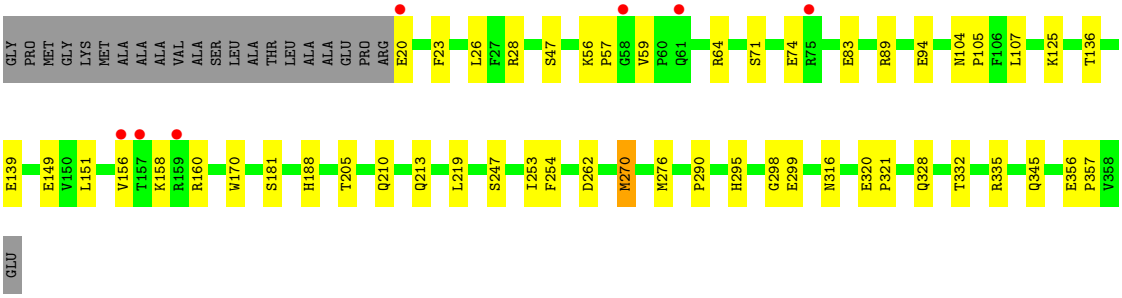
• Molecule 1: Nucleic acid dioxygenase ALKBH1

Chain B:



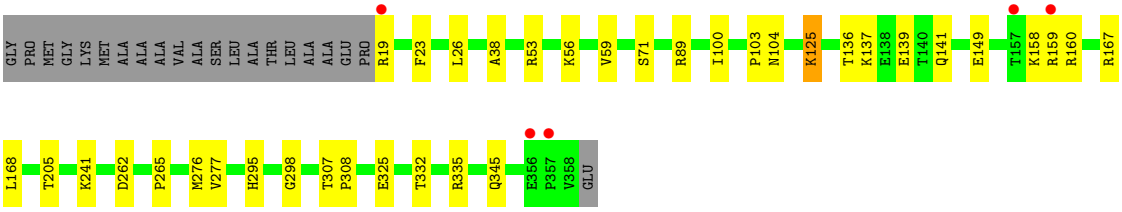
• Molecule 1: Nucleic acid dioxygenase ALKBH1

Chain C:



• Molecule 1: Nucleic acid dioxygenase ALKBH1

Chain D:


GLY
PRO
MET
GLY
LYS
MET
ALA
ALA
ALA
VAL
ALA
SER
LEU
ALA
THR
LEU
ALA
ALA
GLU
PRO
R19
F23
L26
A38
R53
K56
V59
S71
R89
I100
P103
N104
K125
T136
K137
E138
E139
T140
Q141
E149
T157
K158
R159
R160
R167
L168
T205
K241
D262
P265
M276
V277
H295
G298
T307
P308
E325
T332
R335
Q345
E356
P357
V358
GLU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α, β, γ	147.90Å 147.90Å 178.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.16 – 2.51 44.17 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.9 (35.16-2.51) 99.3 (44.17-2.51)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.60 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.14rc3_3206	Depositor
R, R_{free}	0.180 , 0.223 0.181 , 0.223	Depositor DCC
R_{free} test set	3337 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å^2)	41.0	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 46.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.022 for -h,k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	11238	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.05 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8658e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: MN, OGA

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	0/2785	0.57	0/3783
1	B	0.42	0/2785	0.57	0/3783
1	C	0.41	0/2785	0.56	0/3783
1	D	0.43	0/2796	0.57	0/3797
All	All	0.42	0/11151	0.57	0/15146

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2708	0	2668	21	0
1	B	2708	0	2668	24	0
1	C	2708	0	2668	24	0
1	D	2719	0	2681	16	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	10	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	3	0	0
3	C	10	0	3	0	0
3	D	10	0	3	0	0
4	A	106	0	0	0	0
4	B	82	0	0	2	0
4	C	74	0	0	2	0
4	D	89	0	0	1	0
All	All	11238	0	10697	81	0

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

All (81) 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:137:LYS:HD2	1:A:137:LYS:H	1.55	0.71
1:C:20:GLU:OE1	1:C:28:ARG:NH1	2.26	0.68
1:C:188:HIS:ND1	4:C:602:HOH:O	2.28	0.67
1:B:55:PRO:HG3	1:B:61:GLN:OE1	1.94	0.67
1:D:295:HIS:HB3	1:D:298:GLY:O	1.95	0.66
1:A:108:PRO:HB3	1:A:307:THR:HG21	1.77	0.65
1:C:295:HIS:HB3	1:C:298:GLY:O	1.97	0.65
1:C:74:GLU:OE1	1:D:19:ARG:NH1	2.31	0.64
1:D:71:SER:HB2	1:D:205:THR:HG22	1.82	0.62
1:A:228:LEU:HB3	1:A:289:VAL:HG13	1.82	0.62
1:A:282:SER:HA	1:A:285:LEU:HD22	1.82	0.60
1:B:348:ALA:HB3	1:B:351:GLN:HG3	1.86	0.58
1:B:258:GLY:HA2	1:B:285:LEU:HD22	1.88	0.56
1:A:205:THR:HG23	1:A:210:GLN:HG2	1.89	0.54
1:B:328:GLN:O	1:B:332:THR:HG23	2.07	0.54
1:A:295:HIS:HB3	1:A:298:GLY:O	2.09	0.53
1:C:64:ARG:HH21	1:C:89:ARG:HA	1.72	0.53
1:B:48:GLU:HB3	1:B:53:ARG:HH21	1.74	0.53
1:B:313:LEU:HD13	1:B:319:VAL:O	2.09	0.52
1:B:162:ARG:NH1	4:B:606:HOH:O	2.42	0.51
1:B:27:PHE:O	1:B:31:ARG:HB2	2.10	0.51
1:A:25:LYS:HG3	1:A:28:ARG:HH22	1.75	0.51
1:A:136:THR:OG1	1:A:139:GLU:HG3	2.12	0.49
1:B:295:HIS:HB3	1:B:298:GLY:O	2.13	0.48
1:D:125:LYS:H	1:D:125:LYS:HD2	1.78	0.48
1:D:26:LEU:HD12	1:D:265:PRO:HD2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:213:GLN:HB2	1:C:345:GLN:HG3	1.94	0.47
1:A:155:GLU:HG2	1:A:158:LYS:HE2	1.95	0.47
1:A:244:LEU:O	1:A:342:THR:HA	2.14	0.47
1:D:332:THR:HG22	1:D:335:ARG:NH2	2.29	0.47
1:C:254:PHE:CZ	1:C:276:MET:HE1	2.49	0.47
1:B:155:GLU:HB3	1:B:158:LYS:HE2	1.96	0.47
1:D:89:ARG:O	1:D:103:PRO:HD2	2.15	0.47
1:D:125:LYS:HD3	1:D:137:LYS:HG3	1.96	0.47
1:D:276:MET:HB3	1:D:276:MET:HE3	1.65	0.46
1:C:71:SER:HB2	1:C:205:THR:HG22	1.97	0.46
1:D:241:LYS:HD2	1:D:345:GLN:OE1	2.15	0.46
1:C:170:TRP:HA	1:C:219:LEU:O	2.15	0.46
1:C:156:VAL:O	1:C:158:LYS:HG3	2.15	0.46
1:A:314:PRO:HA	1:B:25:LYS:HD2	1.97	0.46
1:A:55:PRO:HG3	1:A:61:GLN:OE1	2.16	0.45
1:B:151:LEU:HD23	1:B:151:LEU:HA	1.69	0.45
1:C:332:THR:HG22	1:C:335:ARG:NH2	2.31	0.45
1:A:56:LYS:HE2	1:C:57:PRO:HG3	1.97	0.45
1:C:47:SER:O	4:C:601:HOH:O	2.21	0.45
1:D:53:ARG:NH2	4:D:607:HOH:O	2.39	0.45
1:B:22:ALA:HB3	1:B:262:ASP:O	2.16	0.45
1:B:259:LEU:HD23	1:B:285:LEU:HD23	1.98	0.44
1:A:26:LEU:HD12	1:A:265:PRO:HD2	1.99	0.44
1:B:135:MET:SD	1:B:167:ARG:NH2	2.90	0.44
1:D:56:LYS:HD3	1:D:59:VAL:HG21	1.99	0.44
1:B:276:MET:HB3	1:B:276:MET:HE3	1.62	0.44
1:C:253:ILE:O	1:C:290:PRO:HD2	2.18	0.43
1:B:137:LYS:HE2	1:B:138:GLU:OE1	2.19	0.43
1:C:356:GLU:HA	1:C:357:PRO:HD3	1.80	0.43
1:C:151:LEU:HA	1:C:151:LEU:HD23	1.86	0.42
1:C:83:GLU:OE2	1:C:107:LEU:HD23	2.19	0.42
1:B:136:THR:OG1	1:B:139:GLU:HG3	2.20	0.42
1:A:120:LYS:NZ	1:A:326:ASP:OD2	2.48	0.42
1:B:26:LEU:HD12	1:B:265:PRO:HD2	2.00	0.42
1:B:59:VAL:HG12	1:B:60:PRO:O	2.20	0.42
1:C:247:SER:HB2	1:C:270:MET:HE1	2.01	0.42
1:A:151:LEU:HD23	1:A:151:LEU:HA	1.89	0.41
1:A:149:GLU:HA	1:A:152:ARG:HG2	2.01	0.41
1:B:52:ALA:HB3	1:D:38:ALA:HB2	2.02	0.41
1:A:148:LYS:HG2	1:A:329:VAL:HG21	2.01	0.41
1:C:136:THR:OG1	1:C:139:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:328:GLN:O	1:C:332:THR:HG23	2.21	0.41
1:C:332:THR:HG22	1:C:335:ARG:HH22	1.85	0.41
1:D:100:ILE:HB	1:D:277:VAL:HB	2.03	0.41
1:B:357:PRO:HG3	4:B:652:HOH:O	2.21	0.41
1:C:26:LEU:HD23	1:C:26:LEU:HA	1.72	0.41
1:C:320:GLU:HB3	1:C:321:PRO:HD2	2.02	0.41
1:B:156:VAL:HG13	1:B:157:THR:HG23	2.02	0.41
1:D:307:THR:HA	1:D:308:PRO:HD3	1.95	0.41
1:A:23:PHE:CE1	1:A:230:ILE:HG12	2.56	0.41
1:B:163:SER:O	1:B:167:ARG:HG3	2.21	0.41
1:D:136:THR:OG1	1:D:139:GLU:HG3	2.20	0.41
1:A:65:PHE:HA	1:A:66:PRO:HD3	1.94	0.40
1:A:356:GLU:HA	1:A:357:PRO:HD3	1.84	0.40
1:C:299:GLU:O	1:C:335:ARG:HD3	2.21	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	337/361 (93%)	326 (97%)	8 (2%)	3 (1%)	17	31
1	B	337/361 (93%)	326 (97%)	10 (3%)	1 (0%)	41	61
1	C	337/361 (93%)	325 (96%)	10 (3%)	2 (1%)	25	43
1	D	338/361 (94%)	331 (98%)	6 (2%)	1 (0%)	41	61
All	All	1349/1444 (93%)	1308 (97%)	34 (2%)	7 (0%)	29	48

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	104	ASN

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Mol	Chain	Res	Type
1	D	104	ASN
1	B	104	ASN
1	C	104	ASN
1	A	156	VAL
1	C	105	PRO
1	A	105	PRO

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	297/310 (96%)	287 (97%)	10 (3%)	37	63
1	B	297/310 (96%)	289 (97%)	8 (3%)	44	71
1	C	297/310 (96%)	285 (96%)	12 (4%)	31	56
1	D	298/310 (96%)	287 (96%)	11 (4%)	34	60
All	All	1189/1240 (96%)	1148 (97%)	41 (3%)	37	63

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	PHE
1	A	54	SER
1	A	64	ARG
1	A	159	ARG
1	A	260	LYS
1	A	262	ASP
1	A	285	LEU
1	A	289	VAL
1	A	316	ASN
1	A	349	THR
1	B	31	ARG
1	B	32	GLN
1	B	125	LYS
1	B	137	LYS
1	B	162	ARG

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Mol	Chain	Res	Type
1	B	185	SER
1	B	324	VAL
1	B	351	GLN
1	C	23	PHE
1	C	56	LYS
1	C	59	VAL
1	C	94	GLU
1	C	125	LYS
1	C	149	GLU
1	C	160	ARG
1	C	181	SER
1	C	210	GLN
1	C	262	ASP
1	C	270	MET
1	C	316	ASN
1	D	23	PHE
1	D	125	LYS
1	D	141	GLN
1	D	149	GLU
1	D	158	LYS
1	D	159	ARG
1	D	160	ARG
1	D	167	ARG
1	D	168	LEU
1	D	262	ASP
1	D	325	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
3	OGA	D	502	2	9,9,9	2.54	3 (33%)	10,11,11	1.04	1 (10%)
3	OGA	A	502	2	9,9,9	2.49	1 (11%)	10,11,11	1.45	1 (10%)
3	OGA	C	502	2	9,9,9	2.51	1 (11%)	10,11,11	1.42	1 (10%)
3	OGA	B	502	2	9,9,9	2.46	1 (11%)	10,11,11	1.38	1 (10%)

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	OGA	D	502	2	-	2/8/9/9	-
3	OGA	A	502	2	-	1/8/9/9	-
3	OGA	C	502	2	-	2/8/9/9	-
3	OGA	B	502	2	-	2/8/9/9	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	502	OGA	C2-C1	-6.92	1.45	1.54
3	A	502	OGA	C2-C1	-6.85	1.45	1.54
3	D	502	OGA	C2-C1	-6.83	1.45	1.54
3	B	502	OGA	C2-C1	-6.80	1.45	1.54
3	D	502	OGA	O2-C1	-2.13	1.24	1.30
3	D	502	OGA	O3-C5	-2.11	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	502	OGA	O2'-C2-C1	-3.93	115.77	121.32
3	C	502	OGA	O2'-C2-C1	-3.79	115.97	121.32
3	B	502	OGA	O2'-C2-C1	-3.34	116.61	121.32
3	D	502	OGA	O2'-C2-C1	-2.42	117.90	121.32

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	502	OGA	N1-C4-C5-O3
3	D	502	OGA	C1-C2-N1-C4
3	B	502	OGA	N1-C4-C5-O4
3	D	502	OGA	O2'-C2-N1-C4
3	C	502	OGA	C1-C2-N1-C4
3	A	502	OGA	N1-C4-C5-O3
3	C	502	OGA	O2'-C2-N1-C4

There are no ring outliers.

No monomer is involved in short contacts.

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	339/361 (93%)	-0.24	6 (1%)	68	71	25, 42, 69, 110	0
1	B	339/361 (93%)	-0.21	10 (2%)	51	55	27, 43, 73, 113	0
1	C	339/361 (93%)	-0.15	7 (2%)	63	66	29, 46, 72, 100	0
1	D	340/361 (94%)	-0.23	5 (1%)	73	75	28, 43, 66, 87	0
All	All	1357/1444 (93%)	-0.21	28 (2%)	63	66	25, 44, 70, 113	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	156	VAL	6.6
1	A	156	VAL	6.4
1	B	157	THR	5.9
1	B	155	GLU	5.0
1	B	159	ARG	3.9
1	A	159	ARG	3.7
1	A	155	GLU	3.4
1	D	356	GLU	3.2
1	D	19	ARG	3.2
1	D	159	ARG	3.1
1	D	157	THR	2.9
1	A	157	THR	2.7
1	C	58	GLY	2.7
1	A	158	LYS	2.7
1	C	20	GLU	2.6
1	B	160	ARG	2.6
1	C	75	ARG	2.6
1	D	357	PRO	2.6
1	B	58	GLY	2.6
1	C	159	ARG	2.4
1	C	61	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	154	LYS	2.4
1	B	358	VAL	2.3
1	C	156	VAL	2.3
1	C	157	THR	2.3
1	B	158	LYS	2.3
1	B	20	GLU	2.1
1	B	154	LYS	2.0

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 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
3	OGA	B	502	10/10	0.98	0.12	30,34,35,35	0
2	MN	D	501	1/1	0.99	0.14	33,33,33,33	0
3	OGA	A	502	10/10	0.99	0.12	29,32,33,34	0
2	MN	B	501	1/1	0.99	0.16	35,35,35,35	0
3	OGA	C	502	10/10	0.99	0.11	33,36,41,41	0
3	OGA	D	502	10/10	0.99	0.12	30,35,38,43	0
2	MN	C	501	1/1	1.00	0.13	31,31,31,31	0
2	MN	A	501	1/1	1.00	0.15	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.