Full wwPDB X-ray Structure Validation Report (i)

Nov 15, 2023 – 10:19 AM JST

PDB ID	:	6JCM
Title	:	Crystal structure of ligand-free Rv0187.
Authors	:	Kim, J.; Lee, S.
Deposited on	:	2019-01-29
Resolution	:	2.08 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:

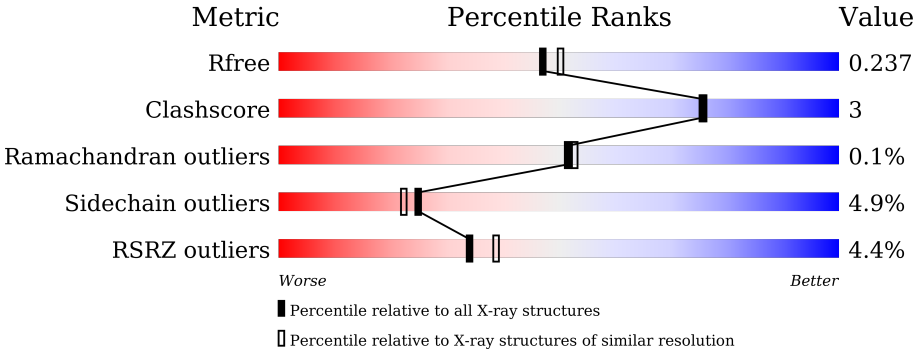
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.08 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	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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	248	4%, 75%, 11%, •, 13%
1	B	248	4%, 80%, 6%, •, 13%
1	C	248	4%, 77%, 8%, •, 13%
1	D	248	3%, 78%, 8%, •, 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6398 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 Probable O-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	1577	994	287	293	3	0	0	0
1	B	215	1570	990	284	293	3	0	0	0
1	C	215	1559	985	283	288	3	0	0	0
1	D	215	1570	991	287	289	3	0	0	0

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP O07431
A	-26	ALA	-	expression tag	UNP O07431
A	-25	GLY	-	expression tag	UNP O07431
A	-24	SER	-	expression tag	UNP O07431
A	-23	HIS	-	expression tag	UNP O07431
A	-22	HIS	-	expression tag	UNP O07431
A	-21	HIS	-	expression tag	UNP O07431
A	-20	HIS	-	expression tag	UNP O07431
A	-19	HIS	-	expression tag	UNP O07431
A	-18	HIS	-	expression tag	UNP O07431
A	-17	GLY	-	expression tag	UNP O07431
A	-16	MET	-	expression tag	UNP O07431
A	-15	ALA	-	expression tag	UNP O07431
A	-14	SER	-	expression tag	UNP O07431
A	-13	MET	-	expression tag	UNP O07431
A	-12	THR	-	expression tag	UNP O07431
A	-11	GLY	-	expression tag	UNP O07431
A	-10	GLY	-	expression tag	UNP O07431
A	-9	GLN	-	expression tag	UNP O07431
A	-8	GLN	-	expression tag	UNP O07431
A	-7	MET	-	expression tag	UNP O07431

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP O07431
A	-5	ARG	-	expression tag	UNP O07431
A	-4	SER	-	expression tag	UNP O07431
A	-3	GLY	-	expression tag	UNP O07431
A	-2	ASP	-	expression tag	UNP O07431
A	-1	ASP	-	expression tag	UNP O07431
A	0	ASP	-	expression tag	UNP O07431
A	1	ASP	-	expression tag	UNP O07431
A	2	LYS	-	expression tag	UNP O07431
B	-27	MET	-	initiating methionine	UNP O07431
B	-26	ALA	-	expression tag	UNP O07431
B	-25	GLY	-	expression tag	UNP O07431
B	-24	SER	-	expression tag	UNP O07431
B	-23	HIS	-	expression tag	UNP O07431
B	-22	HIS	-	expression tag	UNP O07431
B	-21	HIS	-	expression tag	UNP O07431
B	-20	HIS	-	expression tag	UNP O07431
B	-19	HIS	-	expression tag	UNP O07431
B	-18	HIS	-	expression tag	UNP O07431
B	-17	GLY	-	expression tag	UNP O07431
B	-16	MET	-	expression tag	UNP O07431
B	-15	ALA	-	expression tag	UNP O07431
B	-14	SER	-	expression tag	UNP O07431
B	-13	MET	-	expression tag	UNP O07431
B	-12	THR	-	expression tag	UNP O07431
B	-11	GLY	-	expression tag	UNP O07431
B	-10	GLY	-	expression tag	UNP O07431
B	-9	GLN	-	expression tag	UNP O07431
B	-8	GLN	-	expression tag	UNP O07431
B	-7	MET	-	expression tag	UNP O07431
B	-6	GLY	-	expression tag	UNP O07431
B	-5	ARG	-	expression tag	UNP O07431
B	-4	SER	-	expression tag	UNP O07431
B	-3	GLY	-	expression tag	UNP O07431
B	-2	ASP	-	expression tag	UNP O07431
B	-1	ASP	-	expression tag	UNP O07431
B	0	ASP	-	expression tag	UNP O07431
B	1	ASP	-	expression tag	UNP O07431
B	2	LYS	-	expression tag	UNP O07431
C	-27	MET	-	initiating methionine	UNP O07431
C	-26	ALA	-	expression tag	UNP O07431
C	-25	GLY	-	expression tag	UNP O07431

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-24	SER	-	expression tag	UNP O07431
C	-23	HIS	-	expression tag	UNP O07431
C	-22	HIS	-	expression tag	UNP O07431
C	-21	HIS	-	expression tag	UNP O07431
C	-20	HIS	-	expression tag	UNP O07431
C	-19	HIS	-	expression tag	UNP O07431
C	-18	HIS	-	expression tag	UNP O07431
C	-17	GLY	-	expression tag	UNP O07431
C	-16	MET	-	expression tag	UNP O07431
C	-15	ALA	-	expression tag	UNP O07431
C	-14	SER	-	expression tag	UNP O07431
C	-13	MET	-	expression tag	UNP O07431
C	-12	THR	-	expression tag	UNP O07431
C	-11	GLY	-	expression tag	UNP O07431
C	-10	GLY	-	expression tag	UNP O07431
C	-9	GLN	-	expression tag	UNP O07431
C	-8	GLN	-	expression tag	UNP O07431
C	-7	MET	-	expression tag	UNP O07431
C	-6	GLY	-	expression tag	UNP O07431
C	-5	ARG	-	expression tag	UNP O07431
C	-4	SER	-	expression tag	UNP O07431
C	-3	GLY	-	expression tag	UNP O07431
C	-2	ASP	-	expression tag	UNP O07431
C	-1	ASP	-	expression tag	UNP O07431
C	0	ASP	-	expression tag	UNP O07431
C	1	ASP	-	expression tag	UNP O07431
C	2	LYS	-	expression tag	UNP O07431
D	-27	MET	-	initiating methionine	UNP O07431
D	-26	ALA	-	expression tag	UNP O07431
D	-25	GLY	-	expression tag	UNP O07431
D	-24	SER	-	expression tag	UNP O07431
D	-23	HIS	-	expression tag	UNP O07431
D	-22	HIS	-	expression tag	UNP O07431
D	-21	HIS	-	expression tag	UNP O07431
D	-20	HIS	-	expression tag	UNP O07431
D	-19	HIS	-	expression tag	UNP O07431
D	-18	HIS	-	expression tag	UNP O07431
D	-17	GLY	-	expression tag	UNP O07431
D	-16	MET	-	expression tag	UNP O07431
D	-15	ALA	-	expression tag	UNP O07431
D	-14	SER	-	expression tag	UNP O07431
D	-13	MET	-	expression tag	UNP O07431

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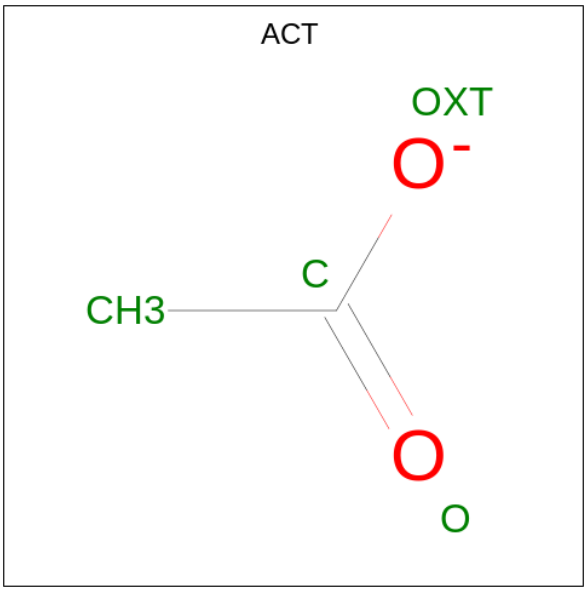
Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	THR	-	expression tag	UNP O07431
D	-11	GLY	-	expression tag	UNP O07431
D	-10	GLY	-	expression tag	UNP O07431
D	-9	GLN	-	expression tag	UNP O07431
D	-8	GLN	-	expression tag	UNP O07431
D	-7	MET	-	expression tag	UNP O07431
D	-6	GLY	-	expression tag	UNP O07431
D	-5	ARG	-	expression tag	UNP O07431
D	-4	SER	-	expression tag	UNP O07431
D	-3	GLY	-	expression tag	UNP O07431
D	-2	ASP	-	expression tag	UNP O07431
D	-1	ASP	-	expression tag	UNP O07431
D	0	ASP	-	expression tag	UNP O07431
D	1	ASP	-	expression tag	UNP O07431
D	2	LYS	-	expression tag	UNP O07431

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 3 is water.

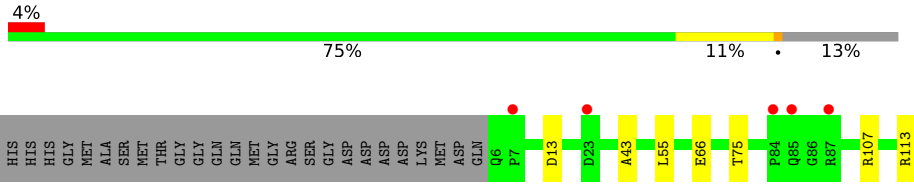
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	26	26	26	0	0
			Total	O		
3	B	24	24	24	0	0
			Total	O		
3	C	25	25	25	0	0
			Total	O		
3	D	31	31	31	0	0

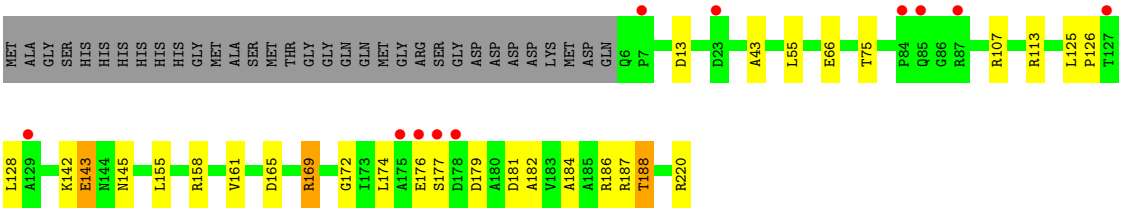
3 Residue-property plots (i)

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: Probable O-methyltransferase

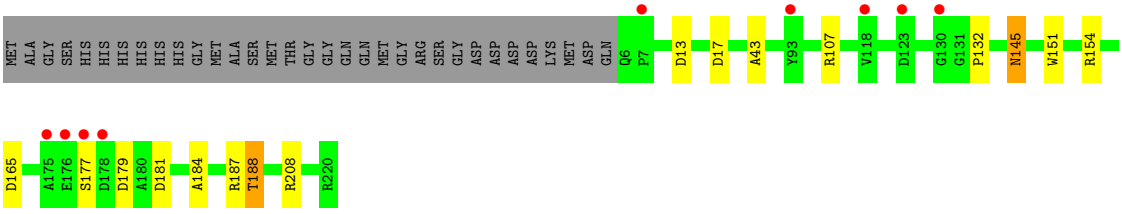
Chain A:





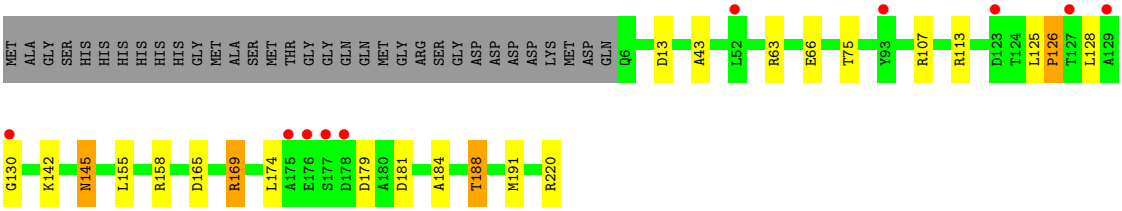
- Molecule 1: Probable O-methyltransferase

Chain B:



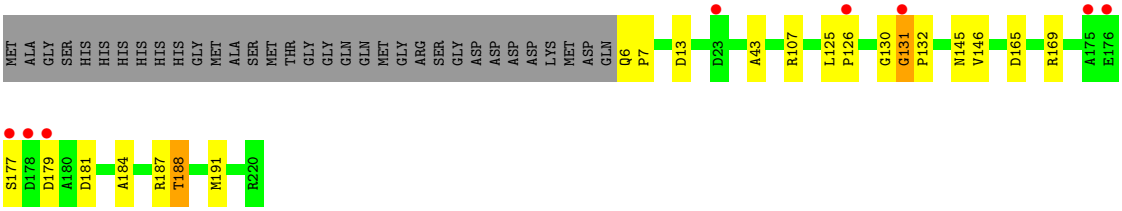
- Molecule 1: Probable O-methyltransferase

Chain C:



- Molecule 1: Probable O-methyltransferase

Chain D:


MET
ALA
GLY
SER
HIS
HIS
HIS
HIS
HIS
HIS
GLY
MET
ALA
SER
MET
THR
GLY
GLY
GLN
GLN
MET
GLY
ARG
SER
GLY
ASP
ASP
ASP
ASP
LYS
MET
ASP
GLN
Q6
P7
D13
D23
A43
R107
L125
P126
G130
G131
P132
N145
V146
D165
R169
A175
E176
S177
D178
D179
A180
D181
A184
R187
T188
M191
R220

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.33Å 94.26Å 125.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.24 – 2.08 29.22 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.6 (29.24-2.08) 98.6 (29.22-2.08)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.38 (at 2.08Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.203 , 0.231 0.211 , 0.237	Depositor DCC
R_{free} test set	2966 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	25.2	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 45.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6398	wwPDB-VP
Average B, all atoms (Å^2)	29.0	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 35.24 % 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 6.0194e-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: ACT

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	0.71	0/1603	0.88	4/2187 (0.2%)
1	B	0.72	0/1596	0.85	3/2179 (0.1%)
1	C	0.72	0/1585	0.87	3/2165 (0.1%)
1	D	0.72	0/1596	0.89	5/2178 (0.2%)
All	All	0.72	0/6380	0.87	15/8709 (0.2%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	169	ARG	NE-CZ-NH2	-7.01	116.79	120.30
1	A	187	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	B	107	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	C	169	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	D	187	ARG	NE-CZ-NH2	6.25	123.42	120.30
1	A	107	ARG	NE-CZ-NH1	-5.87	117.36	120.30
1	B	107	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	D	107	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	D	107	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	D	169	ARG	NE-CZ-NH1	-5.54	117.53	120.30
1	C	169	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	B	187	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	A	186	ARG	NE-CZ-NH1	-5.35	117.62	120.30
1	C	107	ARG	NE-CZ-NH2	5.26	122.93	120.30
1	D	169	ARG	NE-CZ-NH2	5.02	122.81	120.30

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	1577	0	1588	12	0
1	B	1570	0	1575	9	0
1	C	1559	0	1563	10	0
1	D	1570	0	1582	9	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	D	4	0	3	0	0
3	A	26	0	0	0	0
3	B	24	0	0	0	0
3	C	25	0	0	0	0
3	D	31	0	0	0	0
All	All	6398	0	6320	39	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 3.

All (39) 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:B:132:PRO:HG2	1:D:132:PRO:HG3	1.66	0.77
1:A:172:GLY:O	1:A:176:GLU:HB3	1.97	0.64
1:D:6:GLN:CB	1:D:7:PRO:HD3	2.29	0.62
1:D:179:ASP:OD1	1:D:181:ASP:HB3	2.03	0.58
1:C:63:ARG:HD2	1:C:130:GLY:O	2.05	0.56
1:B:151:TRP:CZ3	1:B:154:ARG:HD2	2.42	0.55
1:C:179:ASP:OD1	1:C:181:ASP:HB3	2.08	0.54
1:B:151:TRP:CE3	1:B:154:ARG:HD2	2.44	0.53
1:B:179:ASP:OD1	1:B:181:ASP:HB3	2.09	0.53
1:D:43:ALA:HB1	1:D:165:ASP:OD2	2.12	0.50
1:D:130:GLY:O	1:D:131:GLY:O	2.30	0.49
1:B:184:ALA:O	1:B:188:THR:CG2	2.61	0.49
1:C:184:ALA:O	1:C:188:THR:CG2	2.60	0.49
1:D:146:VAL:HA	1:D:191:MET:CE	2.43	0.49
1:A:172:GLY:O	1:A:176:GLU:CB	2.59	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:ASP:OD1	1:A:181:ASP:HB2	2.13	0.48
1:C:66:GLU:OE1	1:C:75:THR:OG1	2.23	0.48
1:A:158:ARG:HG3	1:A:220:ARG:O	2.14	0.48
1:A:176:GLU:HB2	1:A:182:ALA:CB	2.43	0.48
1:D:184:ALA:O	1:D:188:THR:CG2	2.62	0.47
1:A:184:ALA:O	1:A:188:THR:CG2	2.62	0.47
1:A:43:ALA:HB1	1:A:165:ASP:OD2	2.15	0.46
1:C:43:ALA:HB1	1:C:165:ASP:OD2	2.15	0.46
1:B:43:ALA:HB1	1:B:165:ASP:OD2	2.15	0.46
1:A:143:GLU:CD	1:A:143:GLU:H	2.20	0.44
1:B:145:ASN:HD22	1:B:145:ASN:HA	1.61	0.44
1:C:184:ALA:O	1:C:188:THR:HG23	2.18	0.43
1:B:184:ALA:O	1:B:188:THR:HG23	2.19	0.43
1:D:184:ALA:O	1:D:188:THR:HG23	2.19	0.42
1:A:66:GLU:OE1	1:A:75:THR:OG1	2.23	0.42
1:B:17:ASP:OD2	1:B:208:ARG:NH2	2.52	0.42
1:A:55:LEU:HD21	1:A:161:VAL:HG11	2.02	0.42
1:C:184:ALA:O	1:C:188:THR:HG22	2.20	0.42
1:C:125:LEU:N	1:C:126:PRO:HD2	2.36	0.41
1:C:145:ASN:HD22	1:C:145:ASN:HA	1.63	0.41
1:C:158:ARG:HG3	1:C:220:ARG:O	2.20	0.41
1:A:184:ALA:O	1:A:188:THR:HG23	2.20	0.40
1:D:125:LEU:N	1:D:126:PRO:HD2	2.36	0.40
1:A:125:LEU:N	1:A:126:PRO:HD2	2.37	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	213/248 (86%)	207 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	213/248 (86%)	205 (96%)	8 (4%)	0	100	100
1	C	213/248 (86%)	207 (97%)	6 (3%)	0	100	100
1	D	213/248 (86%)	205 (96%)	7 (3%)	1 (0%)	29	25
All	All	852/992 (86%)	824 (97%)	27 (3%)	1 (0%)	51	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	131	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	154/182 (85%)	143 (93%)	11 (7%)	14	11
1	B	153/182 (84%)	149 (97%)	4 (3%)	46	49
1	C	150/182 (82%)	139 (93%)	11 (7%)	14	10
1	D	152/182 (84%)	148 (97%)	4 (3%)	46	49
All	All	609/728 (84%)	579 (95%)	30 (5%)	25	22

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	113	ARG
1	A	128	LEU
1	A	142	LYS
1	A	143	GLU
1	A	145	ASN
1	A	155	LEU
1	A	169	ARG
1	A	174	LEU
1	A	177	SER

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Mol	Chain	Res	Type
1	A	188	THR
1	B	13	ASP
1	B	145	ASN
1	B	177	SER
1	B	188	THR
1	C	13	ASP
1	C	113	ARG
1	C	126	PRO
1	C	128	LEU
1	C	142	LYS
1	C	145	ASN
1	C	155	LEU
1	C	169	ARG
1	C	174	LEU
1	C	188	THR
1	C	191	MET
1	D	13	ASP
1	D	145	ASN
1	D	177	SER
1	D	188	THR

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)

4 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	$\#\|Z\| > 2$
2	ACT	C	301	-	3,3,3	1.28	0	3,3,3	0.59	0
2	ACT	D	301	-	3,3,3	0.90	0	3,3,3	0.99	0
2	ACT	B	301	-	3,3,3	1.02	0	3,3,3	0.92	0
2	ACT	A	301	-	3,3,3	0.83	0	3,3,3	0.72	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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	215/248 (86%)	0.10	11 (5%)	28	32	16, 27, 46, 69	0
1	B	215/248 (86%)	0.08	9 (4%)	36	41	16, 26, 44, 79	0
1	C	215/248 (86%)	0.16	10 (4%)	31	36	16, 28, 48, 75	0
1	D	215/248 (86%)	0.05	8 (3%)	41	46	16, 26, 48, 72	0
All	All	860/992 (86%)	0.10	38 (4%)	34	39	16, 27, 47, 79	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	175	ALA	7.9
1	B	178	ASP	5.3
1	B	177	SER	5.0
1	B	175	ALA	4.9
1	C	178	ASP	4.9
1	C	129	ALA	4.5
1	D	176	GLU	4.4
1	D	177	SER	4.3
1	D	175	ALA	4.2
1	D	178	ASP	3.9
1	B	176	GLU	3.8
1	A	129	ALA	3.7
1	A	178	ASP	3.6
1	C	176	GLU	3.6
1	C	177	SER	3.5
1	A	177	SER	3.1
1	C	93	TYR	3.0
1	B	130	GLY	2.9
1	B	123	ASP	2.6
1	A	176	GLU	2.5
1	B	7	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	85	GLN	2.4
1	C	127	THR	2.4
1	C	52	LEU	2.3
1	A	7	PRO	2.3
1	D	126	PRO	2.3
1	A	23	ASP	2.3
1	D	23	ASP	2.3
1	B	118	VAL	2.2
1	A	175	ALA	2.2
1	A	127	THR	2.2
1	D	179	ASP	2.1
1	C	130	GLY	2.1
1	A	84	PRO	2.1
1	D	131	GLY	2.1
1	A	87	ARG	2.0
1	C	123	ASP	2.0
1	B	93	TYR	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
2	ACT	B	301	4/4	0.92	0.20	28,31,31,32	0
2	ACT	D	301	4/4	0.93	0.18	24,30,32,34	0
2	ACT	A	301	4/4	0.96	0.12	25,26,26,26	0
2	ACT	C	301	4/4	0.97	0.10	28,28,30,31	0

6.5 Other polymers (i)

There are no such residues in this entry.