Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2023 – 02:37 AM EDT

PDB ID	:	4S2M
Title	:	Crystal Structure of OXA-163 complexed with iodide in the active site
Authors	:	Stojanoski, V.; Hu, L.; Palzkill, T.G.; Prasad, B.
Deposited on	:	2015-01-21
Resolution	:	2.87 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 ⓘ symbol.

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

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

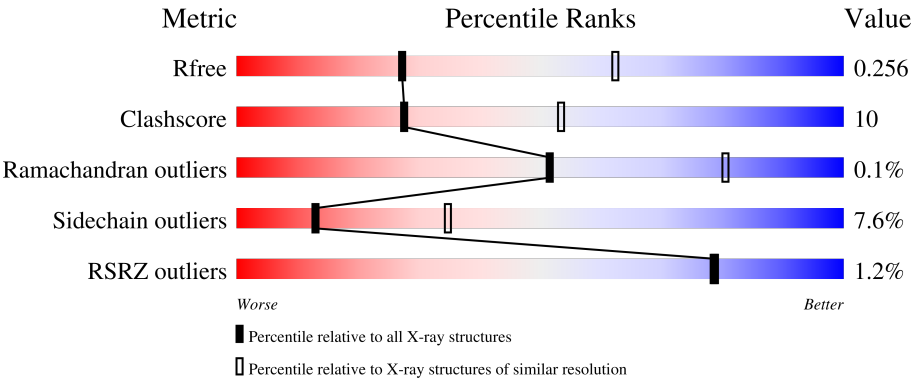
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.87 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)

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	237	70% 24%
1	B	237	2% 74% 23%
1	C	237	% 71% 25%
1	D	237	2% 73% 24%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	A	304	-	-	X	-
2	IOD	A	307	-	-	X	-
2	IOD	D	303	-	-	X	-
2	IOD	D	305	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 7742 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1904	1216	336	345	7			
1	B	234	Total	C	N	O	S	0	0	0
			1916	1224	338	347	7			
1	C	234	Total	C	N	O	S	0	0	0
			1916	1224	338	347	7			
1	D	234	Total	C	N	O	S	0	0	0
			1917	1223	338	349	7			

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	I	0	0
			7	7		
2	B	4	Total	I	0	0
			4	4		
2	C	4	Total	I	0	0
			4	4		
2	D	5	Total	I	0	0
			5	5		

- Molecule 3 is water.

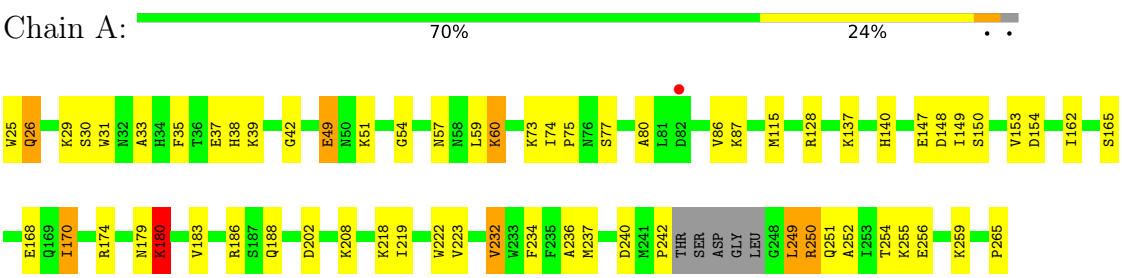
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		
3	B	15	Total	O	0	0
			15	15		
3	C	20	Total	O	0	0
			20	20		
3	D	15	Total	O	0	0
			15	15		

3 Residue-property plots (i)

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

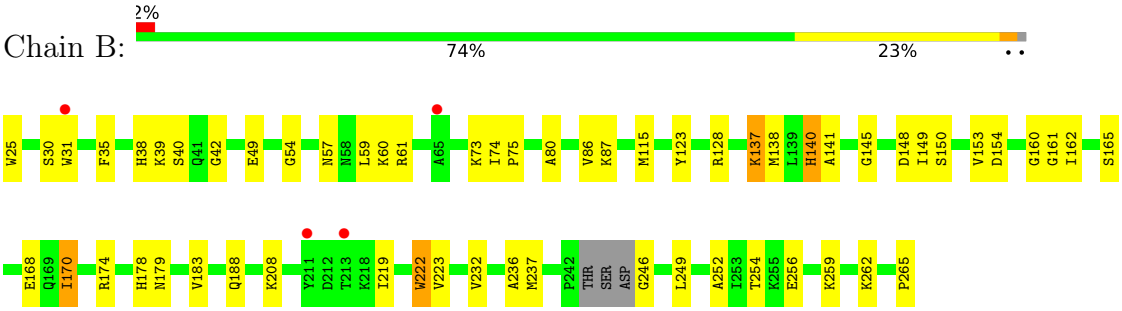
• Molecule 1: Beta-lactamase

Chain A:



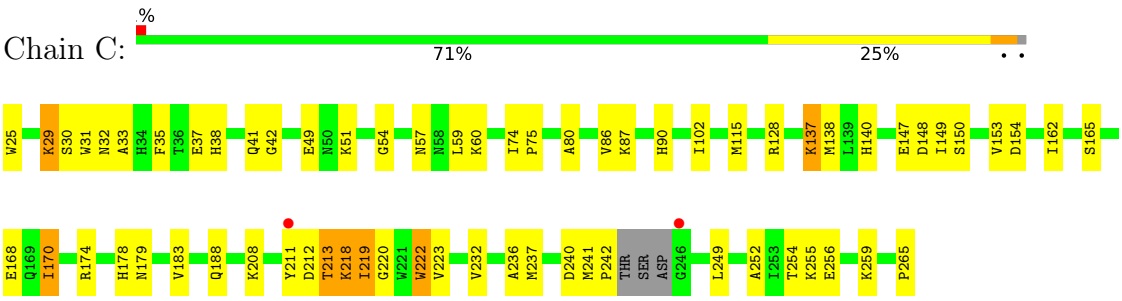
• Molecule 1: Beta-lactamase

Chain B:



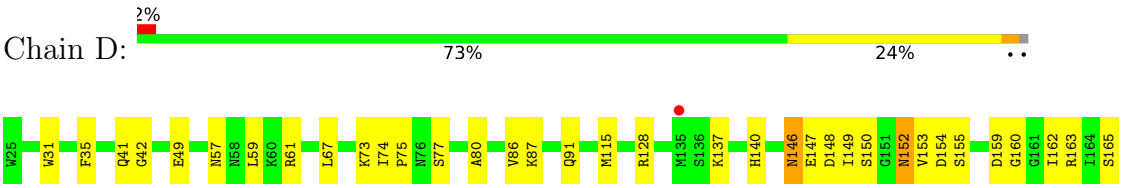
• Molecule 1: Beta-lactamase

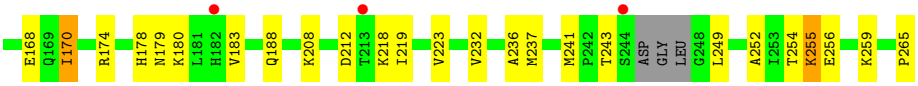
Chain C:



• Molecule 1: Beta-lactamase

Chain D:




E168
Q169
I170
R174
H178
N179
K180
L181
H182
V183
Q188
K208
D212
T213
K218
I219
V223
V232
A236
M237
M241
P242
T243
S244
ASP
GLY
LEU
G248
L249
A252
I253
T254
K255
E256
K259
P265

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	67.63Å 68.41Å 70.22Å 62.20° 68.00° 71.58°	Depositor
Resolution (Å)	59.80 – 2.87 59.80 – 2.87	Depositor EDS
% Data completeness (in resolution range)	95.0 (59.80-2.87) 95.0 (59.80-2.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0049, PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.201 , 0.256 0.207 , 0.256	Depositor DCC
R_{free} test set	1134 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å^2)	51.9	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 61.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	7742	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.75% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IOD

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	0/1951	0.74	1/2638 (0.0%)
1	B	0.64	0/1963	0.76	3/2654 (0.1%)
1	C	0.68	0/1963	0.72	1/2654 (0.0%)
1	D	0.62	0/1964	0.73	1/2656 (0.0%)
All	All	0.66	0/7841	0.74	6/10602 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	146	ASN	CB-CA-C	-6.34	97.71	110.40
1	C	222	TRP	CA-CB-CG	6.15	125.39	113.70
1	B	222	TRP	CA-CB-CG	6.14	125.36	113.70
1	B	161	GLY	N-CA-C	-5.62	99.04	113.10
1	B	160	GLY	CA-C-N	5.47	127.14	116.20
1	A	180	LYS	CB-CA-C	5.06	120.53	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1904	0	1859	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1916	0	1873	33	0
1	C	1916	0	1873	35	0
1	D	1917	0	1871	43	0
2	A	7	0	0	5	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	5	0	0	5	0
3	A	19	0	0	3	0
3	B	15	0	0	1	0
3	C	20	0	0	3	0
3	D	15	0	0	0	0
All	All	7742	0	7476	151	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 10.

All (151) 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:140:HIS:HA	1:A:147:GLU:OE1	1.54	1.06
1:A:38:HIS:O	1:A:39:LYS:HG3	1.68	0.93
1:A:51:LYS:HD3	2:A:304:IOD:I	2.40	0.91
1:B:42:GLY:HA2	1:B:61:ARG:NH1	1.87	0.90
1:D:146:ASN:HD21	1:D:163:ARG:HB2	1.34	0.90
1:D:42:GLY:HA2	1:D:61:ARG:NH2	1.90	0.86
1:C:252:ALA:O	1:C:256:GLU:HG3	1.76	0.84
1:D:146:ASN:ND2	1:D:163:ARG:HB2	1.94	0.83
1:A:38:HIS:O	1:A:39:LYS:CG	2.26	0.82
1:D:35:PHE:CE2	1:D:42:GLY:HA3	2.20	0.76
1:A:219:ILE:HD12	1:A:219:ILE:O	1.87	0.75
1:D:41:GLN:HG2	2:D:305:IOD:I	2.57	0.74
1:D:219:ILE:HD12	1:D:219:ILE:O	1.89	0.73
1:D:159:ASP:OD1	1:D:160:GLY:N	2.22	0.72
1:C:102:ILE:HD13	1:C:211:TYR:CE2	2.26	0.70
1:C:165:SER:HB2	1:C:168:GLU:HG3	1.72	0.70
1:A:249:LEU:HD13	1:A:249:LEU:N	2.09	0.67
1:A:249:LEU:O	1:A:250:ARG:HB2	1.94	0.67
1:A:165:SER:OG	1:A:168:GLU:HG3	1.94	0.67
1:B:165:SER:OG	1:B:168:GLU:HG3	1.96	0.65
1:A:33:ALA:O	1:A:37:GLU:HG3	1.98	0.64
1:C:102:ILE:HD13	1:C:211:TYR:HE2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:152:ASN:HD22	1:D:152:ASN:N	1.95	0.61
1:B:145:GLY:HA2	1:B:168:GLU:OE2	2.00	0.61
1:C:25:TRP:CE3	1:C:54:GLY:HA3	2.35	0.60
1:D:180:LYS:CD	2:D:303:IOD:I	3.19	0.60
1:A:49:GLU:HG2	1:A:234:PHE:HE1	1.66	0.60
1:D:165:SER:OG	1:D:168:GLU:HG3	2.01	0.60
1:B:219:ILE:O	1:B:219:ILE:HD12	2.01	0.60
1:D:180:LYS:HD2	2:D:303:IOD:I	2.72	0.59
1:D:140:HIS:HA	1:D:147:GLU:OE1	2.04	0.58
1:B:259:LYS:HD3	1:B:265:PRO:C	2.25	0.57
1:D:35:PHE:CE2	1:D:42:GLY:CA	2.88	0.57
1:C:213:THR:OG1	1:C:218:LYS:N	2.36	0.57
1:D:35:PHE:HE2	1:D:42:GLY:HA3	1.69	0.56
1:A:25:TRP:CE3	1:A:54:GLY:HA3	2.42	0.55
1:C:90:HIS:HE1	3:C:409:HOH:O	1.88	0.55
1:D:218:LYS:HA	1:D:218:LYS:HE2	1.88	0.55
1:C:49:GLU:OE1	1:C:178:HIS:NE2	2.29	0.55
1:A:51:LYS:CD	2:A:304:IOD:I	3.23	0.55
1:A:252:ALA:O	1:A:256:GLU:HG3	2.07	0.54
1:A:38:HIS:C	1:A:39:LYS:CG	2.75	0.53
1:D:218:LYS:HA	1:D:218:LYS:CE	2.37	0.53
1:C:137:LYS:HD2	1:C:138:MET:HG2	1.90	0.53
1:B:25:TRP:CE3	1:B:54:GLY:HA3	2.43	0.53
1:B:123:TYR:HB3	3:B:402:HOH:O	2.09	0.53
1:B:137:LYS:HD2	1:B:138:MET:HG2	1.91	0.52
1:C:29:LYS:HG2	1:C:32:ASN:ND2	2.23	0.52
1:D:180:LYS:HD3	2:D:303:IOD:I	2.80	0.52
1:A:249:LEU:N	1:A:249:LEU:CD1	2.73	0.52
1:D:252:ALA:O	1:D:256:GLU:HG3	2.10	0.52
1:B:140:HIS:CE1	1:D:180:LYS:CE	2.93	0.52
1:A:249:LEU:HD13	1:A:249:LEU:H	1.73	0.52
1:C:219:ILE:HD12	1:C:219:ILE:O	2.10	0.51
1:D:179:ASN:HA	1:D:188:GLN:OE1	2.10	0.51
1:A:26:GLN:NE2	3:A:416:HOH:O	2.43	0.51
1:C:115:MET:HG2	1:C:208:LYS:HG3	1.93	0.51
1:B:35:PHE:CE1	1:B:42:GLY:HA3	2.45	0.51
1:B:179:ASN:HA	1:B:188:GLN:OE1	2.11	0.51
1:A:168:GLU:HB3	3:A:406:HOH:O	2.12	0.50
1:B:252:ALA:O	1:B:256:GLU:HG3	2.12	0.50
1:A:115:MET:HG2	1:A:208:LYS:HG3	1.94	0.50
1:C:179:ASN:HA	1:C:188:GLN:OE1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:LYS:HD3	1:A:265:PRO:O	2.12	0.50
1:B:42:GLY:CA	1:B:61:ARG:NH1	2.67	0.50
1:B:115:MET:HG2	1:B:208:LYS:HG3	1.93	0.50
1:A:179:ASN:HA	1:A:188:GLN:OE1	2.12	0.50
1:A:255:LYS:O	1:A:259:LYS:HG3	2.12	0.50
1:A:180:LYS:HE2	2:A:307:IOD:I	2.82	0.49
1:C:213:THR:O	1:C:218:LYS:C	2.50	0.49
1:A:49:GLU:HB2	1:A:232:VAL:O	2.11	0.49
1:C:222:TRP:CZ3	3:C:415:HOH:O	2.64	0.49
1:D:259:LYS:HD3	1:D:265:PRO:O	2.12	0.49
1:D:223:VAL:HG12	1:D:236:ALA:HA	1.94	0.49
1:C:148:ASP:O	1:C:162:ILE:HB	2.13	0.49
1:D:115:MET:HG2	1:D:208:LYS:HG3	1.94	0.49
1:A:38:HIS:O	1:A:39:LYS:HG2	2.10	0.48
1:C:223:VAL:HG12	1:C:236:ALA:HA	1.95	0.48
1:A:148:ASP:O	1:A:162:ILE:HB	2.14	0.48
1:B:140:HIS:CE1	1:D:180:LYS:HE3	2.48	0.48
1:B:49:GLU:OE1	1:B:178:HIS:NE2	2.30	0.48
1:D:218:LYS:HE2	1:D:218:LYS:CA	2.42	0.48
1:D:87:LYS:HB2	1:D:91:GLN:OE1	2.13	0.47
1:D:67:LEU:O	1:D:219:ILE:HD11	2.14	0.47
1:B:42:GLY:HA2	1:B:61:ARG:HH12	1.76	0.47
1:C:240:ASP:O	1:C:242:PRO:HD2	2.15	0.47
1:A:223:VAL:HG12	1:A:236:ALA:HA	1.96	0.47
1:B:148:ASP:O	1:B:162:ILE:HB	2.15	0.47
1:C:35:PHE:CE1	1:C:42:GLY:HA3	2.50	0.47
1:C:255:LYS:O	1:C:259:LYS:HG3	2.15	0.47
1:A:49:GLU:HG2	1:A:234:PHE:CE1	2.50	0.46
1:D:41:GLN:CG	2:D:305:IOD:I	3.30	0.46
1:D:212:ASP:HB3	1:D:219:ILE:O	2.14	0.46
1:D:152:ASN:N	1:D:152:ASN:ND2	2.63	0.46
1:B:140:HIS:CG	1:B:141:ALA:N	2.81	0.46
1:C:80:ALA:HB1	1:C:86:VAL:HG23	1.98	0.46
1:C:259:LYS:HD3	1:C:265:PRO:O	2.16	0.46
1:D:148:ASP:O	1:D:162:ILE:HB	2.14	0.46
1:D:255:LYS:O	1:D:259:LYS:HG3	2.15	0.46
1:B:246:GLY:HA2	1:B:249:LEU:HB2	1.98	0.45
1:A:74:ILE:HB	1:A:75:PRO:CD	2.46	0.45
1:D:80:ALA:HB1	1:D:86:VAL:HG23	1.98	0.45
1:A:170:ILE:O	1:A:174:ARG:HG3	2.17	0.45
1:B:140:HIS:CE1	1:D:180:LYS:HE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:ILE:O	1:D:174:ARG:HG3	2.16	0.45
1:A:80:ALA:HB1	1:A:86:VAL:HG23	1.98	0.45
1:A:180:LYS:CE	2:A:307:IOD:I	3.34	0.45
1:A:73:LYS:O	1:A:77:SER:OG	2.27	0.45
1:C:33:ALA:O	1:C:37:GLU:HG3	2.17	0.45
1:D:128:ARG:NH1	1:D:154:ASP:OD2	2.50	0.45
1:D:137:LYS:HE3	1:D:137:LYS:HB2	1.85	0.45
1:A:35:PHE:CE1	1:A:42:GLY:HA3	2.52	0.45
1:A:128:ARG:NH1	1:A:154:ASP:OD2	2.50	0.45
1:C:31:TRP:HB2	1:C:57:ASN:HB3	1.99	0.44
1:B:223:VAL:HG12	1:B:236:ALA:HA	1.98	0.44
1:C:128:ARG:NH1	1:C:154:ASP:OD2	2.50	0.44
1:D:237:MET:HG2	1:D:254:THR:OG1	2.17	0.44
1:B:80:ALA:HB1	1:B:86:VAL:HG23	1.98	0.44
1:B:128:ARG:NH1	1:B:154:ASP:OD2	2.50	0.44
1:C:74:ILE:HB	1:C:75:PRO:CD	2.47	0.44
1:C:213:THR:O	1:C:219:ILE:N	2.50	0.44
1:A:237:MET:HG2	1:A:254:THR:OG1	2.18	0.43
1:A:249:LEU:HB3	1:A:252:ALA:HB3	1.99	0.43
1:B:140:HIS:NE2	1:D:180:LYS:HE3	2.33	0.43
1:C:170:ILE:O	1:C:174:ARG:HG3	2.17	0.43
1:D:49:GLU:OE1	1:D:178:HIS:NE2	2.34	0.43
1:C:218:LYS:H	1:C:218:LYS:HG2	1.51	0.43
1:B:31:TRP:HB2	1:B:57:ASN:HB3	2.01	0.43
1:B:73:LYS:HG2	1:B:123:TYR:CE2	2.53	0.43
1:B:170:ILE:O	1:B:174:ARG:HG3	2.18	0.43
1:B:237:MET:HG2	1:B:254:THR:OG1	2.19	0.43
1:A:31:TRP:HB2	1:A:57:ASN:HB3	1.99	0.43
1:A:38:HIS:C	1:A:39:LYS:HG2	2.38	0.42
1:D:73:LYS:O	1:D:77:SER:OG	2.26	0.42
1:B:222:TRP:HB3	1:B:237:MET:HG3	2.02	0.42
1:C:237:MET:HG2	1:C:254:THR:OG1	2.19	0.42
1:D:74:ILE:HB	1:D:75:PRO:CD	2.49	0.42
1:C:218:LYS:O	1:C:241:MET:HB2	2.20	0.42
1:D:31:TRP:HB2	1:D:57:ASN:HB3	2.02	0.42
1:A:186:ARG:HA	2:A:303:IOD:I	2.89	0.41
1:B:38:HIS:CD2	1:B:249:LEU:HD13	2.54	0.41
1:C:38:HIS:CD2	1:C:249:LEU:HD13	2.55	0.41
1:C:90:HIS:CE1	3:C:409:HOH:O	2.68	0.41
1:A:222:TRP:CE2	1:A:251:GLN:HG2	2.55	0.41
1:A:240:ASP:O	1:A:242:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:HB	1:B:75:PRO:CD	2.50	0.41
1:C:212:ASP:CB	1:C:220:GLY:HA2	2.51	0.40
1:B:219:ILE:O	1:B:219:ILE:CD1	2.68	0.40
1:A:60:LYS:HA	1:A:60:LYS:HD3	1.94	0.40
1:A:202:ASP:HA	3:A:405:HOH:O	2.21	0.40
1:C:140:HIS:HA	1:C:147:GLU:OE2	2.22	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	228/237 (96%)	218 (96%)	9 (4%)	1 (0%)	34 64
1	B	230/237 (97%)	220 (96%)	10 (4%)	0	100 100
1	C	230/237 (97%)	219 (95%)	11 (5%)	0	100 100
1	D	230/237 (97%)	222 (96%)	8 (4%)	0	100 100
All	All	918/948 (97%)	879 (96%)	38 (4%)	1 (0%)	51 80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	ARG

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	202/206 (98%)	185 (92%)	17 (8%)	11	30
1	B	203/206 (98%)	188 (93%)	15 (7%)	13	36
1	C	203/206 (98%)	186 (92%)	17 (8%)	11	30
1	D	204/206 (99%)	191 (94%)	13 (6%)	17	43
All	All	812/824 (98%)	750 (92%)	62 (8%)	13	35

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	29	LYS
1	A	30	SER
1	A	49	GLU
1	A	59	LEU
1	A	60	LYS
1	A	87	LYS
1	A	137	LYS
1	A	149	ILE
1	A	150	SER
1	A	153	VAL
1	A	170	ILE
1	A	180	LYS
1	A	183	VAL
1	A	218	LYS
1	A	232	VAL
1	A	249	LEU
1	B	30	SER
1	B	39	LYS
1	B	40	SER
1	B	59	LEU
1	B	60	LYS
1	B	87	LYS
1	B	137	LYS
1	B	140	HIS
1	B	149	ILE
1	B	150	SER
1	B	153	VAL
1	B	170	ILE
1	B	183	VAL
1	B	232	VAL

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Mol	Chain	Res	Type
1	B	262	LYS
1	C	29	LYS
1	C	30	SER
1	C	41	GLN
1	C	51	LYS
1	C	59	LEU
1	C	60	LYS
1	C	87	LYS
1	C	137	LYS
1	C	149	ILE
1	C	150	SER
1	C	153	VAL
1	C	170	ILE
1	C	183	VAL
1	C	213	THR
1	C	218	LYS
1	C	219	ILE
1	C	232	VAL
1	D	59	LEU
1	D	149	ILE
1	D	150	SER
1	D	152	ASN
1	D	153	VAL
1	D	155	SER
1	D	170	ILE
1	D	183	VAL
1	D	232	VAL
1	D	241	MET
1	D	243	THR
1	D	249	LEU
1	D	255	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	129	GLN
1	B	53	GLN
1	B	129	GLN
1	C	26	GLN
1	C	38	HIS
1	C	41	GLN

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Mol	Chain	Res	Type
1	C	53	GLN
1	C	90	HIS
1	C	129	GLN
1	D	129	GLN
1	D	146	ASN
1	D	152	ASN
1	D	260	GLN

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

Of 20 ligands modelled in this entry, 20 are monoatomic - leaving 0 for Mogul analysis.

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

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

6.1 Protein, DNA and RNA chains

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, 95^{th} 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	232/237 (97%)	-0.40	1 (0%)	92	92	22, 46, 72, 95	0
1	B	234/237 (98%)	-0.24	4 (1%)	70	70	31, 55, 86, 97	0
1	C	234/237 (98%)	-0.34	2 (0%)	84	84	22, 52, 85, 103	0
1	D	234/237 (98%)	-0.08	4 (1%)	70	70	30, 61, 97, 118	0
All	All	934/948 (98%)	-0.27	11 (1%)	79	78	22, 53, 88, 118	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	213	THR	6.1
1	D	182	HIS	4.2
1	D	135	MET	2.5
1	B	213	THR	2.5
1	A	82	ASP	2.3
1	C	246	GLY	2.3
1	D	244	SER	2.2
1	B	31	TRP	2.2
1	B	65	ALA	2.1
1	C	211	TYR	2.1
1	B	211	TYR	2.0

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

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

6.3 Carbohydrates

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, 95^{th} 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	IOD	D	305	1/1	0.81	0.09	149,149,149,149	0
2	IOD	A	304	1/1	0.88	0.09	154,154,154,154	0
2	IOD	B	303	1/1	0.92	0.09	117,117,117,117	0
2	IOD	D	302	1/1	0.93	0.08	100,100,100,100	0
2	IOD	A	305	1/1	0.95	0.07	97,97,97,97	0
2	IOD	C	303	1/1	0.95	0.09	71,71,71,71	0
2	IOD	A	306	1/1	0.98	0.08	73,73,73,73	0
2	IOD	D	303	1/1	0.98	0.08	83,83,83,83	0
2	IOD	D	304	1/1	0.98	0.06	99,99,99,99	0
2	IOD	C	304	1/1	0.98	0.05	92,92,92,92	0
2	IOD	C	301	1/1	0.99	0.12	57,57,57,57	0
2	IOD	A	302	1/1	0.99	0.10	54,54,54,54	0
2	IOD	A	307	1/1	0.99	0.10	71,71,71,71	0
2	IOD	D	301	1/1	0.99	0.10	59,59,59,59	0
2	IOD	B	301	1/1	0.99	0.11	57,57,57,57	0
2	IOD	B	302	1/1	0.99	0.10	48,48,48,48	0
2	IOD	A	303	1/1	0.99	0.14	48,48,48,48	0
2	IOD	B	304	1/1	0.99	0.09	60,60,60,60	0
2	IOD	C	302	1/1	1.00	0.09	63,63,63,63	0
2	IOD	A	301	1/1	1.00	0.14	57,57,57,57	0

6.5 Other polymers (i)

There are no such residues in this entry.