



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:21 PM GMT

PDB ID : 3R3H
Title : Crystal structure of O-methyltransferase from Legionella pneumophila
Authors : Agarwal, R.; Almo, S.C.; Swaminathan, S.; New York Structural Genomics Research Consortium (NYSGRC)
Deposited on : 2011-03-15
Resolution : 2.65 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

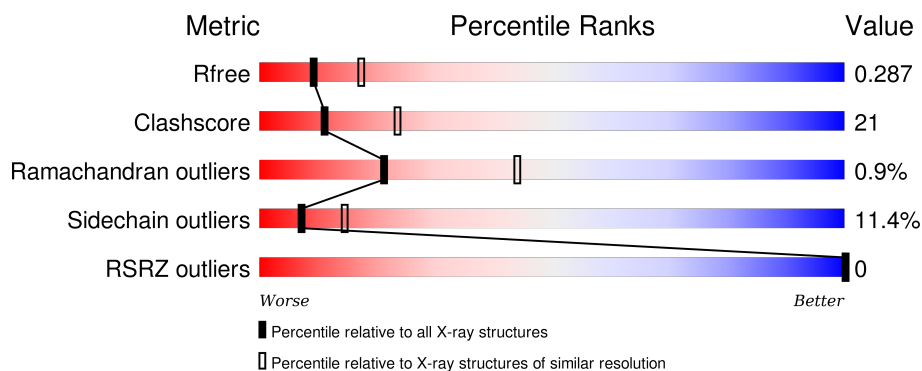
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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	242	
1	B	242	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3452 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 O-methyltransferase, SAM-dependent.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1718	1104	291	316	7			
1	B	217	Total	C	N	O	S	0	0	0
			1726	1110	292	317	7			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q5ZT85
A	2	VAL	-	EXPRESSION TAG	UNP Q5ZT85
A	221	ALA	-	EXPRESSION TAG	UNP Q5ZT85
A	222	GLU	-	EXPRESSION TAG	UNP Q5ZT85
A	223	ASN	-	EXPRESSION TAG	UNP Q5ZT85
A	224	LEU	-	EXPRESSION TAG	UNP Q5ZT85
A	225	TYR	-	EXPRESSION TAG	UNP Q5ZT85
A	226	PHE	-	EXPRESSION TAG	UNP Q5ZT85
A	227	GLN	-	EXPRESSION TAG	UNP Q5ZT85
A	228	SER	-	EXPRESSION TAG	UNP Q5ZT85
A	229	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	230	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	231	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	232	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	233	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	234	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	235	TRP	-	EXPRESSION TAG	UNP Q5ZT85
A	236	SER	-	EXPRESSION TAG	UNP Q5ZT85
A	237	HIS	-	EXPRESSION TAG	UNP Q5ZT85
A	238	PRO	-	EXPRESSION TAG	UNP Q5ZT85
A	239	GLN	-	EXPRESSION TAG	UNP Q5ZT85
A	240	PHE	-	EXPRESSION TAG	UNP Q5ZT85
A	241	GLU	-	EXPRESSION TAG	UNP Q5ZT85
A	242	LYS	-	EXPRESSION TAG	UNP Q5ZT85
B	1	MET	-	EXPRESSION TAG	UNP Q5ZT85

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2	VAL	-	EXPRESSION TAG	UNP Q5ZT85
B	221	ALA	-	EXPRESSION TAG	UNP Q5ZT85
B	222	GLU	-	EXPRESSION TAG	UNP Q5ZT85
B	223	ASN	-	EXPRESSION TAG	UNP Q5ZT85
B	224	LEU	-	EXPRESSION TAG	UNP Q5ZT85
B	225	TYR	-	EXPRESSION TAG	UNP Q5ZT85
B	226	PHE	-	EXPRESSION TAG	UNP Q5ZT85
B	227	GLN	-	EXPRESSION TAG	UNP Q5ZT85
B	228	SER	-	EXPRESSION TAG	UNP Q5ZT85
B	229	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	230	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	231	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	232	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	233	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	234	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	235	TRP	-	EXPRESSION TAG	UNP Q5ZT85
B	236	SER	-	EXPRESSION TAG	UNP Q5ZT85
B	237	HIS	-	EXPRESSION TAG	UNP Q5ZT85
B	238	PRO	-	EXPRESSION TAG	UNP Q5ZT85
B	239	GLN	-	EXPRESSION TAG	UNP Q5ZT85
B	240	PHE	-	EXPRESSION TAG	UNP Q5ZT85
B	241	GLU	-	EXPRESSION TAG	UNP Q5ZT85
B	242	LYS	-	EXPRESSION TAG	UNP Q5ZT85

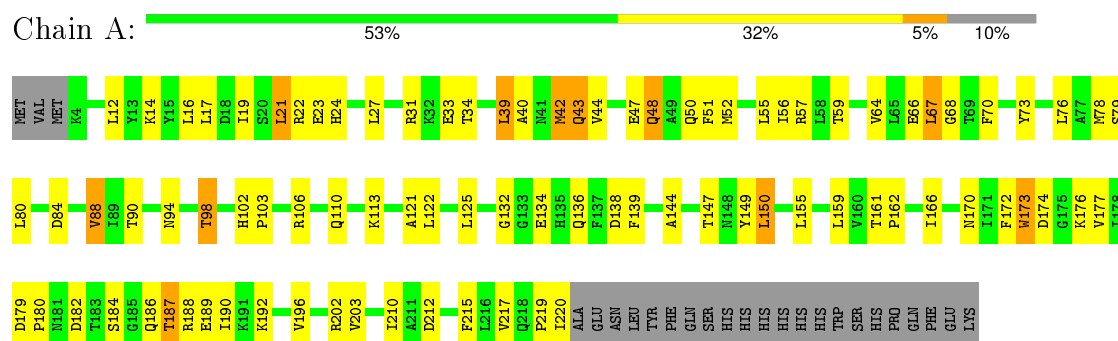
- Molecule 2 is water.

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

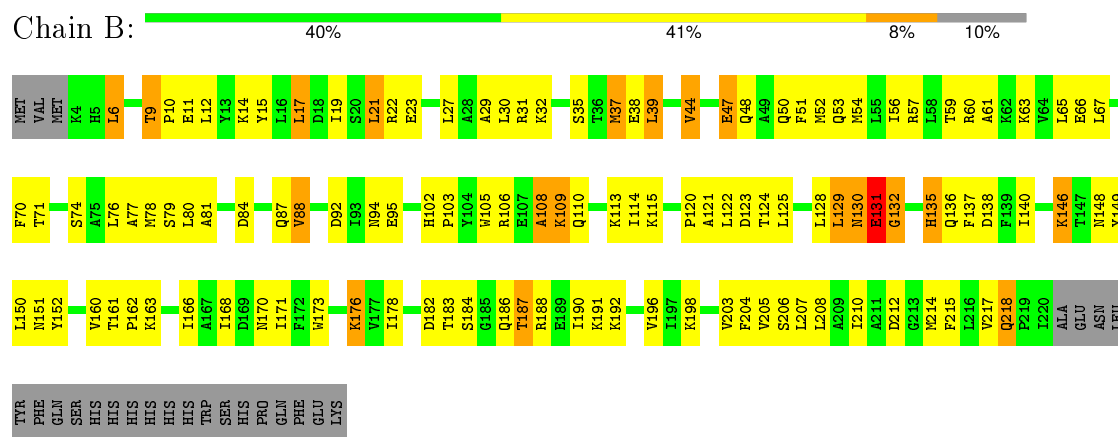
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: O-methyltransferase, SAM-dependent



• Molecule 1: O-methyltransferase, SAM-dependent



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	52.25Å 52.25Å 659.28Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.25 – 2.65 45.25 – 2.34	Depositor EDS
% Data completeness (in resolution range)	98.6 (45.25-2.65) 92.4 (45.25-2.34)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.34Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.265 , 0.290 0.264 , 0.287	Depositor DCC
R_{free} test set	520 reflections (3.07%)	DCC
Wilson B-factor (Å ²)	38.6	Xtriage
Anisotropy	0.622	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	3 of 23465 reflections (0.013%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3452	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.45	0/1754	0.73	0/2379
1	B	0.43	0/1762	0.75	4/2388 (0.2%)
All	All	0.44	0/3516	0.74	4/4767 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	GLY	N-CA-C	-5.80	98.60	113.10
1	B	39	LEU	N-CA-C	-5.23	96.89	111.00
1	B	108	ALA	N-CA-C	-5.22	96.89	111.00
1	B	39	LEU	CA-CB-CG	5.07	126.96	115.30

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	1718	0	1723	57	0
1	B	1726	0	1746	94	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
All	All	3452	0	3469	144	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 21.

All (144) 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:9:THR:HG22	1:B:12:LEU:H	1.35	0.91
1:A:110:GLN:NE2	1:A:113:LYS:HE2	1.87	0.88
1:B:22:ARG:H	1:B:50:GLN:HE22	1.20	0.85
1:A:170:ASN:HA	1:A:212:ASP:HB3	1.58	0.85
1:A:44:VAL:HG22	1:A:48:GLN:HB3	1.61	0.81
1:A:147:THR:HA	1:A:189:GLU:HG3	1.62	0.80
1:A:110:GLN:HE22	1:A:113:LYS:HE2	1.45	0.77
1:B:67:LEU:HD21	1:B:125:LEU:HD11	1.70	0.73
1:B:56:ILE:HD11	1:B:78:MET:HG2	1.70	0.73
1:B:130:ASN:O	1:B:131:GLU:HB2	1.91	0.70
1:B:146:LYS:HG3	1:B:190:ILE:HD11	1.72	0.70
1:B:22:ARG:N	1:B:50:GLN:HE22	1.89	0.70
1:B:160:VAL:HG11	1:B:166:ILE:HD11	1.76	0.68
1:A:22:ARG:H	1:A:50:GLN:HE22	1.42	0.67
1:A:21:LEU:HD22	1:A:23:GLU:HB2	1.77	0.67
1:A:203:VAL:HG12	1:A:219:PRO:HA	1.79	0.65
1:A:52:MET:HA	1:A:55:LEU:HD12	1.79	0.65
1:B:87:GLN:HE21	1:B:115:LYS:HG2	1.62	0.65
1:B:9:THR:HG23	1:B:11:GLU:OE1	1.98	0.64
1:B:205:VAL:HG23	1:B:217:VAL:HG12	1.79	0.64
1:A:186:GLN:O	1:A:190:ILE:HG12	1.98	0.63
1:B:148:ASN:HD22	1:B:151:ASN:HD22	1.43	0.63
1:B:146:LYS:N	1:B:146:LYS:HD2	2.12	0.63
1:A:150:LEU:HD11	1:A:196:VAL:HG21	1.81	0.63
1:A:106:ARG:HG3	1:A:106:ARG:HH11	1.63	0.62
1:A:67:LEU:HD21	1:A:125:LEU:HD11	1.82	0.62
1:B:48:GLN:HE21	1:B:214:MET:HE1	1.65	0.61
1:B:170:ASN:HA	1:B:212:ASP:HB3	1.82	0.61
1:B:184:SER:OG	1:B:187:THR:HG23	2.01	0.60
1:B:39:LEU:HD12	1:B:71:THR:HG22	1.83	0.59
1:B:122:LEU:HD22	1:B:122:LEU:H	1.67	0.59
1:B:102:HIS:HD2	1:B:106:ARG:HH21	1.51	0.59
1:A:79:SER:HB3	1:A:88:VAL:HG11	1.85	0.59
1:A:80:LEU:HD23	1:A:110:GLN:OE1	2.03	0.59
1:A:134:GLU:O	1:A:159:LEU:HA	2.03	0.59
1:B:48:GLN:HE21	1:B:214:MET:CE	2.17	0.58
1:B:124:THR:O	1:B:128:LEU:HG	2.04	0.58
1:A:43:GLN:HE22	1:A:70:PHE:HA	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:6:LEU:HD23	1:B:6:LEU:O	2.03	0.57
1:A:57:ARG:NH1	1:B:204:PHE:HB3	2.19	0.57
1:B:187:THR:O	1:B:191:LYS:HG3	2.06	0.56
1:B:87:GLN:NE2	1:B:115:LYS:HG2	2.21	0.56
1:B:205:VAL:HG22	1:B:206:SER:H	1.69	0.56
1:A:121:ALA:O	1:A:125:LEU:HG	2.06	0.56
1:B:9:THR:HG22	1:B:12:LEU:N	2.15	0.56
1:A:27:LEU:HD23	1:A:76:LEU:HD23	1.87	0.55
1:B:22:ARG:H	1:B:50:GLN:NE2	1.99	0.55
1:B:15:TYR:O	1:B:19:ILE:HG12	2.07	0.54
1:B:53:GLN:HG2	1:B:81:ALA:HB2	1.90	0.54
1:B:53:GLN:O	1:B:57:ARG:HG3	2.07	0.54
1:B:168:ILE:HB	1:B:171:ILE:HD11	1.89	0.53
1:B:176:LYS:HD3	1:B:182:ASP:OD1	2.09	0.53
1:B:44:VAL:HG21	1:B:52:MET:HE3	1.91	0.53
1:B:92:ASP:OD2	1:B:94:ASN:HB2	2.08	0.52
1:B:192:LYS:O	1:B:196:VAL:HG23	2.09	0.52
1:B:125:LEU:O	1:B:129:LEU:HB2	2.10	0.52
1:B:137:PHE:HB2	1:B:140:ILE:HD11	1.92	0.52
1:A:166:ILE:HB	1:A:217:VAL:HG22	1.92	0.52
1:B:87:GLN:HE22	1:B:115:LYS:HE3	1.74	0.52
1:A:24:HIS:O	1:A:27:LEU:HB2	2.11	0.51
1:B:162:PRO:O	1:B:163:LYS:HB2	2.11	0.51
1:A:21:LEU:CD2	1:A:23:GLU:HB2	2.40	0.51
1:B:204:PHE:HB2	1:B:218:GLN:HG2	1.92	0.51
1:B:10:PRO:O	1:B:14:LYS:HG2	2.10	0.50
1:B:166:ILE:N	1:B:166:ILE:HD12	2.27	0.50
1:B:114:ILE:O	1:B:115:LYS:HE2	2.13	0.49
1:A:182:ASP:OD2	1:A:187:THR:HG21	2.13	0.49
1:B:17:LEU:O	1:B:21:LEU:HB2	2.12	0.49
1:B:31:ARG:O	1:B:35:SER:HB2	2.13	0.49
1:A:31:ARG:HG3	1:A:73:TYR:CE2	2.48	0.48
1:B:186:GLN:O	1:B:190:ILE:HG12	2.13	0.48
1:B:105:TRP:O	1:B:108:ALA:O	2.31	0.48
1:B:102:HIS:CD2	1:B:106:ARG:HH21	2.31	0.48
1:B:79:SER:HB2	1:B:88:VAL:HG11	1.95	0.48
1:A:51:PHE:CD2	1:B:208:LEU:HD11	2.49	0.48
1:A:12:LEU:HA	1:B:178:ILE:HD11	1.96	0.48
1:A:56:ILE:HD11	1:A:78:MET:HG2	1.96	0.48
1:B:176:LYS:HE3	1:B:176:LYS:HA	1.95	0.47
1:A:173:TRP:O	1:A:174:ASP:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:LEU:HG	1:B:21:LEU:HD12	1.96	0.47
1:B:21:LEU:HD22	1:B:23:GLU:HB2	1.96	0.47
1:B:66:GLU:HB3	1:B:70:PHE:CZ	2.49	0.47
1:B:129:LEU:C	1:B:131:GLU:H	2.18	0.47
1:A:68:GLY:HA2	1:A:144:ALA:HA	1.96	0.47
1:A:16:LEU:HG	1:B:207:LEU:HD23	1.96	0.46
1:A:161:THR:HG23	1:A:162:PRO:HD2	1.97	0.46
1:B:29:ALA:HA	1:B:32:LYS:HD2	1.97	0.46
1:A:94:ASN:ND2	1:A:98:THR:HG23	2.31	0.46
1:A:67:LEU:N	1:A:67:LEU:HD12	2.31	0.46
1:B:65:LEU:HB3	1:B:140:ILE:HG13	1.97	0.46
1:B:135:HIS:O	1:B:161:THR:HG22	2.15	0.46
1:B:56:ILE:HG23	1:B:61:ALA:HB3	1.98	0.46
1:B:114:ILE:C	1:B:115:LYS:HE2	2.35	0.46
1:A:176:LYS:HD3	1:A:182:ASP:OD2	2.15	0.46
1:B:39:LEU:HD12	1:B:71:THR:CG2	2.46	0.46
1:B:102:HIS:N	1:B:103:PRO:CD	2.79	0.46
1:B:129:LEU:C	1:B:131:GLU:N	2.69	0.45
1:A:184:SER:OG	1:A:187:THR:HG23	2.16	0.45
1:B:129:LEU:O	1:B:131:GLU:N	2.49	0.45
1:B:63:LYS:HD2	1:B:87:GLN:HB3	1.98	0.45
1:B:135:HIS:ND1	1:B:135:HIS:N	2.65	0.45
1:B:205:VAL:HG22	1:B:206:SER:N	2.32	0.45
1:A:66:GLU:HG3	1:A:90:THR:HA	1.98	0.45
1:B:11:GLU:CD	1:B:11:GLU:H	2.20	0.45
1:B:120:PRO:HB2	1:B:123:ASP:OD1	2.17	0.45
1:A:188:ARG:O	1:A:192:LYS:HG3	2.16	0.45
1:A:202:ARG:O	1:A:220:ILE:HG12	2.17	0.45
1:A:59:THR:CG2	1:A:138:ASP:HB3	2.47	0.45
1:B:110:GLN:NE2	1:B:113:LYS:HE2	2.32	0.45
1:A:42:MET:HG2	1:A:42:MET:H	1.53	0.45
1:A:64:VAL:HG22	1:A:139:PHE:HB3	1.99	0.45
1:B:44:VAL:HG23	1:B:48:GLN:HB3	1.99	0.44
1:B:51:PHE:O	1:B:54:MET:HB3	2.16	0.44
1:B:47:GLU:H	1:B:47:GLU:HG3	1.48	0.44
1:A:79:SER:HB3	1:A:88:VAL:CG1	2.46	0.44
1:A:22:ARG:NH2	1:B:203:VAL:O	2.50	0.44
1:B:77:ALA:HA	1:B:80:LEU:HD12	1.98	0.44
1:B:188:ARG:O	1:B:192:LYS:HG2	2.17	0.44
1:A:39:LEU:HD23	1:A:42:MET:HG3	2.00	0.44
1:A:48:GLN:O	1:A:52:MET:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:PHE:HA	1:A:177:VAL:HG21	2.00	0.43
1:B:61:ALA:CB	1:B:138:ASP:HB2	2.48	0.43
1:A:102:HIS:CG	1:A:103:PRO:HD3	2.53	0.43
1:A:179:ASP:HA	1:A:180:PRO:HD3	1.88	0.43
1:A:19:ILE:HA	1:B:198:LYS:HG3	2.01	0.43
1:B:87:GLN:NE2	1:B:115:LYS:HE3	2.34	0.42
1:B:208:LEU:HB3	1:B:210:ILE:HG12	2.00	0.42
1:B:27:LEU:HD23	1:B:76:LEU:HD23	2.01	0.42
1:A:172:PHE:O	1:A:174:ASP:N	2.46	0.42
1:A:34:THR:O	1:A:40:ALA:HB2	2.19	0.42
1:B:30:LEU:HD23	1:B:30:LEU:O	2.20	0.42
1:B:121:ALA:HB3	1:B:152:TYR:OH	2.20	0.42
1:A:44:VAL:HG21	1:A:52:MET:CE	2.50	0.42
1:A:132:GLY:HA3	1:A:136:GLN:NE2	2.35	0.41
1:B:37:MET:O	1:B:38:GLU:HG2	2.20	0.41
1:B:140:ILE:HD13	1:B:160:VAL:HB	2.03	0.41
1:B:44:VAL:CG1	1:B:74:SER:HB3	2.51	0.41
1:B:59:THR:O	1:B:60:ARG:HB2	2.19	0.41
1:B:188:ARG:HG3	1:B:188:ARG:NH1	2.36	0.41
1:B:109:LYS:H	1:B:109:LYS:HZ2	1.69	0.41
1:A:182:ASP:CG	1:A:187:THR:HG21	2.41	0.41
1:A:210:ILE:HG23	1:B:210:ILE:HG23	2.02	0.41
1:A:106:ARG:NH1	1:A:106:ARG:HG3	2.33	0.40
1:B:173:TRP:CD1	1:B:187:THR:HG22	2.57	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	215/242 (89%)	206 (96%)	9 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	215/242 (89%)	199 (93%)	12 (6%)	4 (2%)	10	22
All	All	430/484 (89%)	405 (94%)	21 (5%)	4 (1%)	21	44

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	37	MET
1	B	131	GLU
1	B	130	ASN
1	B	132	GLY

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	183/212 (86%)	163 (89%)	20 (11%)	8	16
1	B	186/212 (88%)	164 (88%)	22 (12%)	6	13
All	All	369/424 (87%)	327 (89%)	42 (11%)	7	14

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LYS
1	A	17	LEU
1	A	21	LEU
1	A	33	GLU
1	A	39	LEU
1	A	42	MET
1	A	43	GLN
1	A	47	GLU
1	A	48	GLN
1	A	67	LEU
1	A	84	ASP
1	A	88	VAL

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Mol	Chain	Res	Type
1	A	98	THR
1	A	122	LEU
1	A	149	TYR
1	A	150	LEU
1	A	155	LEU
1	A	173	TRP
1	A	187	THR
1	A	215	PHE
1	B	6	LEU
1	B	9	THR
1	B	17	LEU
1	B	21	LEU
1	B	44	VAL
1	B	47	GLU
1	B	84	ASP
1	B	88	VAL
1	B	95	GLU
1	B	109	LYS
1	B	129	LEU
1	B	131	GLU
1	B	135	HIS
1	B	136	GLN
1	B	146	LYS
1	B	149	TYR
1	B	150	LEU
1	B	176	LYS
1	B	183	THR
1	B	187	THR
1	B	215	PHE
1	B	218	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	50	GLN
1	A	53	GLN
1	A	110	GLN
1	A	135	HIS
1	A	136	GLN
1	A	148	ASN
1	A	151	ASN

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Mol	Chain	Res	Type
1	A	199	ASN
1	B	48	GLN
1	B	50	GLN
1	B	53	GLN
1	B	87	GLN
1	B	102	HIS
1	B	110	GLN
1	B	136	GLN
1	B	148	ASN
1	B	218	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	217/242 (89%)	-0.22	0 100 100	24, 43, 61, 71	0
1	B	217/242 (89%)	-0.10	0 100 100	35, 51, 68, 77	0
All	All	434/484 (89%)	-0.16	0 100 100	24, 47, 65, 77	0

There are no RSRZ outliers to report.

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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.