



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 05:49 AM GMT

PDB ID : 2GPY
Title : Crystal structure of putative O-methyltransferase from Bacillus halodurans
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Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2006-04-18
Resolution : 1.90 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

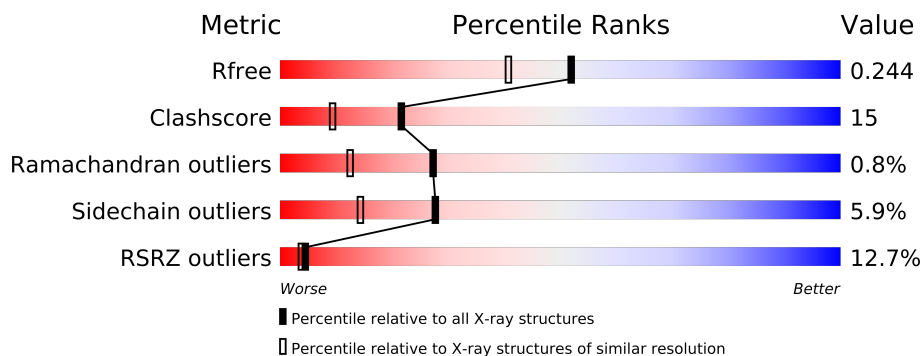
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	233	
1	B	233	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3365 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	185	Total	C	N	O	Se	0	10	0
			1593	1021	277	287	8			
1	B	192	Total	C	N	O	Se	0	2	0
			1583	1012	281	283	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	MODIFIED RESIDUE	GB 10173888
A	2	SER	-	CLONING ARTIFACT	GB 10173888
A	3	LEU	-	CLONING ARTIFACT	GB 10173888
A	26	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	38	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	43	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	52	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	72	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	145	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	149	MSE	MET	MODIFIED RESIDUE	GB 10173888
A	226	GLU	-	CLONING ARTIFACT	GB 10173888
A	227	GLY	-	CLONING ARTIFACT	GB 10173888
A	228	HIS	-	EXPRESSION TAG	GB 10173888
A	229	HIS	-	EXPRESSION TAG	GB 10173888
A	230	HIS	-	EXPRESSION TAG	GB 10173888
A	231	HIS	-	EXPRESSION TAG	GB 10173888
A	232	HIS	-	EXPRESSION TAG	GB 10173888
A	233	HIS	-	EXPRESSION TAG	GB 10173888
B	1	MSE	-	MODIFIED RESIDUE	GB 10173888
B	2	SER	-	CLONING ARTIFACT	GB 10173888
B	3	LEU	-	CLONING ARTIFACT	GB 10173888
B	26	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	38	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	43	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	52	MSE	MET	MODIFIED RESIDUE	GB 10173888

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Chain	Residue	Modelled	Actual	Comment	Reference
B	72	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	145	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	149	MSE	MET	MODIFIED RESIDUE	GB 10173888
B	226	GLU	-	CLONING ARTIFACT	GB 10173888
B	227	GLY	-	CLONING ARTIFACT	GB 10173888
B	228	HIS	-	EXPRESSION TAG	GB 10173888
B	229	HIS	-	EXPRESSION TAG	GB 10173888
B	230	HIS	-	EXPRESSION TAG	GB 10173888
B	231	HIS	-	EXPRESSION TAG	GB 10173888
B	232	HIS	-	EXPRESSION TAG	GB 10173888
B	233	HIS	-	EXPRESSION TAG	GB 10173888

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	5	Total Zn 5 5	0	0
3	A	4	Total Zn 4 4	0	0

- Molecule 4 is water.

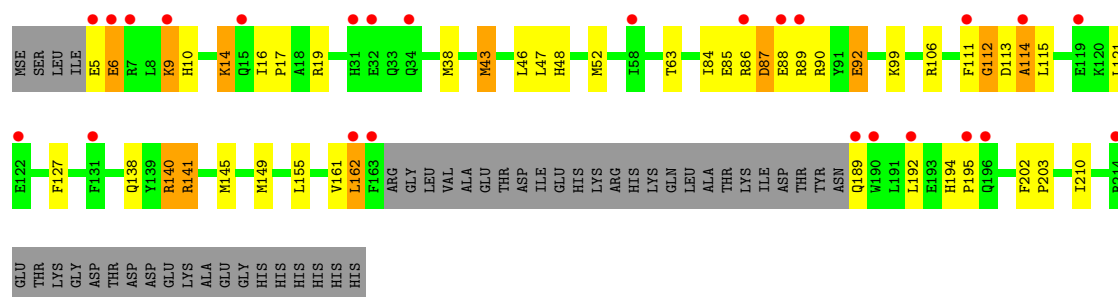
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	71	Total O 71 71	0	0
4	B	108	Total O 108 108	0	0

3 Residue-property plots

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.

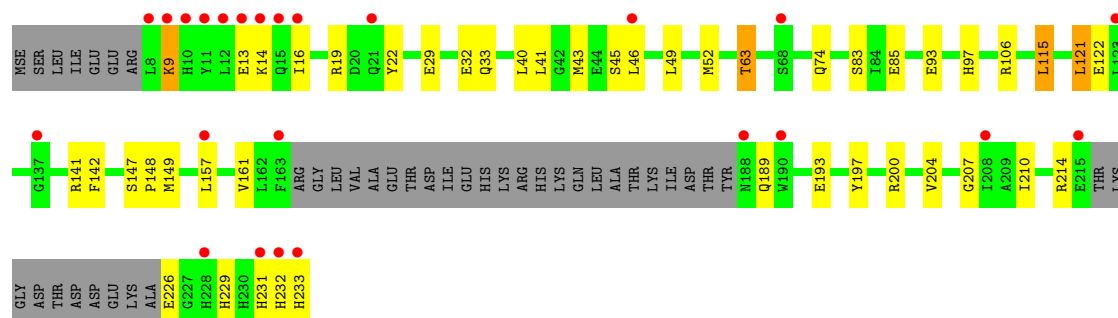
• Molecule 1: O-methyltransferase

Chain A: 



• Molecule 1: O-methyltransferase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.57Å 62.81Å 137.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.44 – 1.90 34.44 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (34.44-1.90) 99.7 (34.44-1.90)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.41 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.206 , 0.248 0.206 , 0.244	Depositor DCC
R_{free} test set	1763 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.400	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 68.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 35168 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3365	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.72	1/1616 (0.1%)	0.75	2/2161 (0.1%)
1	B	0.69	1/1611 (0.1%)	0.73	2/2158 (0.1%)
All	All	0.70	2/3227 (0.1%)	0.74	4/4319 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	43	MSE	SE-CE	-13.14	1.18	1.95
1	B	43	MSE	SE-CE	-9.71	1.38	1.95

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	B	106	ARG	NE-CZ-NH1	-6.80	116.90	120.30
1	A	43	MSE	CG-SE-CE	-6.69	84.19	98.90
1	B	121	LEU	CA-CB-CG	-6.14	101.17	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1593	0	1610	62	0
1	B	1583	0	1573	43	0
2	B	1	0	0	0	0
3	A	4	0	0	0	0
3	B	5	0	0	0	0
4	A	71	0	0	2	0
4	B	108	0	0	3	0
All	All	3365	0	3183	97	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (97) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:43:MSE:SE	1:A:43:MSE:CE	1.17	1.37
1:A:43:MSE:CG	1:A:43:MSE:CE	2.19	1.18
1:A:43:MSE:HE1	1:A:43:MSE:SE	1.76	1.04
1:A:43:MSE:SE	1:A:43:MSE:HE2	1.76	1.04
1:A:43:MSE:HE3	1:A:43:MSE:SE	1.76	1.03
1:A:86[B]:ARG:CD	1:A:86[B]:ARG:H	1.75	0.97
1:B:63:THR:HG23	1:B:85:GLU:HB2	1.45	0.96
1:A:86[B]:ARG:HD3	1:A:86[B]:ARG:H	1.30	0.93
1:B:226:GLU:HB2	1:B:229:HIS:HB2	1.62	0.82
1:A:140:ARG:HG3	1:A:140:ARG:HH11	1.45	0.81
1:A:86[A]:ARG:HD2	1:A:87:ASP:HB3	1.68	0.76
1:A:84:ILE:HG21	1:A:114:ALA:HB2	1.68	0.76
1:A:63:THR:HB	1:A:85:GLU:HB2	1.67	0.74
1:A:155:LEU:HD21	1:B:52:MSE:HG3	1.67	0.74
1:B:46:LEU:HD11	1:B:157:LEU:HD13	1.70	0.73
1:A:86[A]:ARG:CD	1:A:87:ASP:HB3	2.21	0.70
1:A:121:LEU:HB3	1:A:149:MSE:HE1	1.74	0.69
1:A:86[B]:ARG:CD	1:A:86[B]:ARG:N	2.52	0.68
1:A:43:MSE:CE	1:A:43:MSE:HG3	2.21	0.68
1:B:63:THR:HB	1:B:83:SER:OG	1.95	0.66
1:A:86[A]:ARG:HH11	1:A:87:ASP:HB3	1.60	0.65
1:A:52[B]:MSE:HE2	1:B:210:ILE:HG21	1.78	0.65
1:B:32:GLU:HG3	1:B:33:GLN:HG2	1.78	0.65
1:B:29:GLU:OE2	1:B:93:GLU:OE2	2.15	0.64
1:A:115:LEU:HD23	1:A:141:ARG:NH1	2.13	0.64
1:A:113:ASP:HB3	4:A:319:HOH:O	1.99	0.61
1:A:38:MSE:HE1	1:A:46:LEU:HD22	1.82	0.61
1:B:226:GLU:HA	1:B:229:HIS:HD2	1.65	0.61
1:A:6:GLU:HA	1:A:9:LYS:HG2	1.82	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:63:THR:HG21	4:B:317:HOH:O	2.00	0.60
1:A:87:ASP:C	1:A:87:ASP:OD1	2.40	0.59
1:A:140:ARG:CG	1:A:140:ARG:HH11	2.16	0.59
1:A:162:LEU:HD23	1:A:162:LEU:H	1.67	0.58
1:A:85:GLU:OE2	1:A:86[A]:ARG:HD2	2.04	0.58
1:A:88:GLU:O	1:A:92:GLU:N	2.29	0.58
1:B:147:SER:HB2	1:B:197:TYR:OH	2.04	0.57
1:B:9:LYS:O	1:B:13:GLU:HG3	2.03	0.57
1:A:43:MSE:HG3	1:A:43:MSE:HE2	1.86	0.57
1:B:231:HIS:O	1:B:233:HIS:N	2.35	0.57
1:B:45:SER:CB	1:B:204:VAL:HG21	2.35	0.56
1:B:49:LEU:HA	1:B:52:MSE:HE3	1.88	0.55
1:A:43:MSE:HE3	1:A:43:MSE:CG	2.14	0.55
1:A:86[A]:ARG:HH11	1:A:87:ASP:CB	2.19	0.55
1:A:127:PHE:HE2	1:A:149:MSE:CE	2.20	0.55
1:A:202:PHE:CD1	1:A:210:ILE:HD12	2.42	0.54
1:A:155:LEU:CD2	1:B:52:MSE:HG3	2.36	0.54
1:A:43:MSE:CG	1:A:43:MSE:HE2	2.14	0.53
1:B:29:GLU:HA	1:B:32:GLU:HG2	1.90	0.53
1:B:74:GLN:NE2	4:B:418:HOH:O	2.41	0.53
1:B:49:LEU:HD23	1:B:52:MSE:HE1	1.90	0.52
1:A:87:ASP:OD1	1:A:88:GLU:N	2.43	0.52
1:B:226:GLU:CB	1:B:229:HIS:HB2	2.38	0.51
1:A:149:MSE:HE3	4:A:348:HOH:O	2.11	0.51
1:B:16:ILE:CG2	1:B:40:LEU:HD22	2.41	0.51
1:B:16:ILE:HG21	1:B:40:LEU:HD22	1.92	0.51
1:B:22:TYR:OH	1:B:97:HIS:HD2	1.93	0.50
1:B:115:LEU:HD21	1:B:141:ARG:HD3	1.94	0.50
1:A:63:THR:CB	1:A:85:GLU:HB2	2.37	0.50
1:B:189:GLN:O	1:B:193:GLU:HG2	2.13	0.49
1:A:43:MSE:CE	1:A:47[B]:LEU:HD13	2.44	0.48
1:A:38:MSE:HE1	1:A:46:LEU:CD2	2.44	0.47
1:A:88:GLU:O	1:A:92:GLU:HB2	2.14	0.47
1:B:49:LEU:HD23	1:B:52:MSE:CE	2.45	0.47
1:B:45:SER:OG	1:B:204:VAL:HG21	2.16	0.46
1:A:10:HIS:O	1:A:14[B]:LYS:HG3	2.15	0.46
1:A:48:HIS:O	1:A:52[A]:MSE:HG3	2.15	0.46
1:A:189:GLN:HA	1:A:192:LEU:HD12	1.97	0.46
1:A:115:LEU:HA	1:A:145:MSE:HE1	1.98	0.45
1:A:48:HIS:CE1	1:B:200[A]:ARG:HG3	2.51	0.45
1:A:111:PHE:HA	1:A:112:GLY:HA2	1.55	0.45
1:A:17:PRO:HD3	1:B:200[B]:ARG:HH21	1.80	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:140:ARG:CG	1:A:140:ARG:NH1	2.77	0.45
1:B:231:HIS:C	1:B:233:HIS:H	2.21	0.45
1:A:99:LYS:HB3	1:A:99:LYS:HE3	1.78	0.45
1:B:122:GLU:HG3	1:B:149:MSE:HE2	1.99	0.44
1:A:115:LEU:HD21	1:A:138:GLN:HE22	1.82	0.44
1:B:93:GLU:HG3	4:B:330:HOH:O	2.17	0.43
1:B:147:SER:N	1:B:148:PRO:CD	2.81	0.43
1:A:115:LEU:HD21	1:A:141:ARG:HD3	2.01	0.43
1:B:63:THR:HG23	1:B:85:GLU:CB	2.33	0.43
1:B:161:VAL:HG22	1:B:207:GLY:C	2.39	0.43
1:A:43:MSE:HE2	1:A:47[B]:LEU:HD13	2.01	0.43
1:A:87:ASP:OD1	1:A:89:ARG:N	2.52	0.43
1:B:93:GLU:OE2	1:B:97:HIS:HE1	2.01	0.43
1:B:197:TYR:O	1:B:214:ARG:NH1	2.53	0.42
1:B:14:LYS:HE2	1:B:14:LYS:HA	2.02	0.42
1:B:16:ILE:O	1:B:16:ILE:HG13	2.19	0.42
1:A:52[B]:MSE:CE	1:B:210:ILE:HD13	2.50	0.41
1:A:140:ARG:HG3	1:A:140:ARG:NH1	2.23	0.41
1:A:17:PRO:HD3	1:B:200[B]:ARG:NH2	2.36	0.41
1:A:48:HIS:ND1	1:B:200[A]:ARG:HG3	2.36	0.41
1:B:115:LEU:HD13	1:B:142:PHE:CD1	2.54	0.41
1:A:86[B]:ARG:N	1:A:86[B]:ARG:HD2	2.34	0.41
1:A:194:HIS:HA	1:A:195:PRO:HD3	1.94	0.41
1:A:16:ILE:HA	1:A:17:PRO:HD3	1.96	0.40
1:A:86[A]:ARG:HD3	1:A:87:ASP:HB3	2.01	0.40

There are no symmetry-related clashes.

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	191/233 (82%)	186 (97%)	3 (2%)	2 (1%)	22	8
1	B	188/233 (81%)	183 (97%)	4 (2%)	1 (0%)	38	23
All	All	379/466 (81%)	369 (97%)	7 (2%)	3 (1%)	27	12

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	GLY
1	B	232	HIS
1	A	114	ALA

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	168/192 (88%)	154 (92%)	14 (8%)	16	6
1	B	166/192 (86%)	160 (96%)	6 (4%)	47	33
All	All	334/384 (87%)	314 (94%)	20 (6%)	28	13

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	6	GLU
1	A	9	LYS
1	A	14[A]	LYS
1	A	14[B]	LYS
1	A	19	ARG
1	A	87	ASP
1	A	90	ARG
1	A	92	GLU
1	A	140	ARG
1	A	141	ARG
1	A	161	VAL
1	A	162	LEU
1	A	203	PRO
1	B	9	LYS
1	B	19	ARG
1	B	41	LEU
1	B	63	THR
1	B	115	LEU
1	B	121	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	138	GLN
1	B	34	GLN
1	B	229	HIS

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 10 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.

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 ⓘ

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	185/233 (79%)	0.95	25 (13%) 4 3	33, 42, 56, 64	0
1	B	192/233 (82%)	0.93	24 (12%) 5 4	31, 41, 52, 74	0
All	All	377/466 (80%)	0.94	49 (12%) 4 3	31, 41, 56, 74	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	LEU	8.1
1	A	114	ALA	7.4
1	B	163	PHE	6.8
1	B	11	TYR	6.2
1	B	8	LEU	6.0
1	B	231	HIS	5.9
1	A	89	ARG	5.5
1	A	111	PHE	5.1
1	B	16	ILE	5.1
1	A	119	GLU	4.8
1	B	232	HIS	4.5
1	B	228	HIS	4.5
1	A	163	PHE	4.4
1	B	137	GLY	4.3
1	A	9	LYS	4.2
1	A	195	PRO	4.2
1	A	88	GLU	4.0
1	B	9	LYS	3.9
1	B	215	GLU	3.8
1	B	10	HIS	3.7
1	A	6	GLU	3.7
1	B	233	HIS	3.6
1	A	34	GLN	3.6
1	A	31	HIS	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	5	GLU	3.5
1	A	192	LEU	3.2
1	A	86[A]	ARG	3.1
1	B	190	TRP	3.1
1	A	58	ILE	3.1
1	B	14	LYS	2.9
1	A	32	GLU	2.9
1	A	15	GLN	2.9
1	B	13	GLU	2.8
1	B	208	ILE	2.7
1	A	189	GLN	2.7
1	A	7	ARG	2.7
1	B	157	LEU	2.5
1	B	15	GLN	2.5
1	A	131	PHE	2.4
1	B	46	LEU	2.4
1	A	162	LEU	2.3
1	A	196	GLN	2.3
1	B	68[A]	SER	2.3
1	A	214	ARG	2.3
1	A	190	TRP	2.2
1	B	21	GLN	2.2
1	B	188	ASN	2.1
1	B	123	LEU	2.1
1	A	122	GLU	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 carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	ZN	B	310	1/1	0.13	0.35	55,55,55,55	1
3	ZN	B	302	1/1	0.06	-1.35	41,41,41,41	1
3	ZN	B	305	1/1	0.06	-1.35	38,38,38,38	1
3	ZN	A	308	1/1	0.06	-1.48	44,44,44,44	1
3	ZN	B	309	1/1	0.10	-1.63	45,45,45,45	1
2	MG	B	301	1/1	0.07	-2.09	35,35,35,35	0
3	ZN	A	304	1/1	0.04	-2.38	41,41,41,41	1
3	ZN	B	303	1/1	0.07	-3.58	42,42,42,42	1
3	ZN	A	306	1/1	0.07	-27.50	34,34,34,34	1
3	ZN	A	307	1/1	0.06	-	46,46,46,46	1

6.5 Other polymers ⓘ

There are no such residues in this entry.