



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:40 PM UTC

PDB ID : 1B9M / pdb_00001b9m
Title : REGULATOR FROM ESCHERICHIA COLI
Authors : Hall, D.R.; Gourley, D.G.; Hunter, W.N.
Deposited on : 1999-02-12
Resolution : 1.75 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

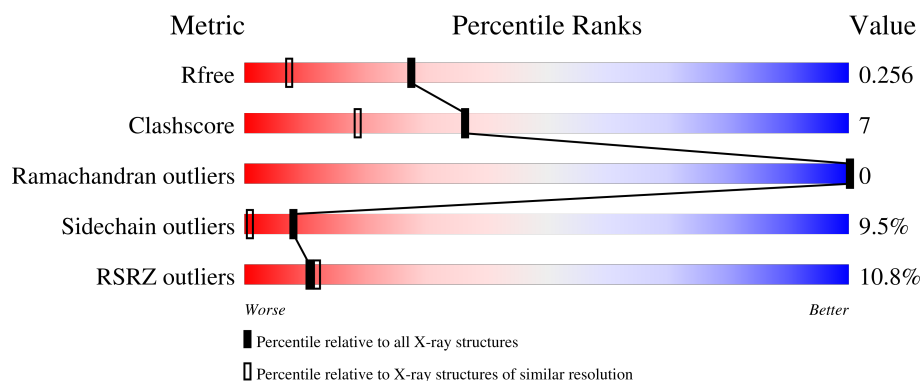
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	180053	3183 (1.76-1.76)
Clashscore	190562	3299 (1.76-1.76)
Ramachandran outliers	187476	3274 (1.76-1.76)
Sidechain outliers	187428	3274 (1.76-1.76)
RSRZ outliers	180081	3183 (1.76-1.76)

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 $\leq 5\%$. 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	265	11% 71% 19% 6% • •
1	B	265	9% 71% 18% • • 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4284 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 PROTEIN (MODE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	Se	0	2	0
			1976	1238	350	382	3	3			
1	B	247	Total	C	N	O	S	Se	0	2	0
			1881	1184	326	365	3	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	SEE REMARK 999	UNP P0A9G8
A	-2	SER	-	SEE REMARK 999	UNP P0A9G8
A	-1	HIS	-	SEE REMARK 999	UNP P0A9G8
A	1	MSE	MET	modified residue	UNP P0A9G8
A	55	MSE	MET	modified residue	UNP P0A9G8
A	221	MSE	MET	modified residue	UNP P0A9G8
B	-3	GLY	-	SEE REMARK 999	UNP P0A9G8
B	-2	SER	-	SEE REMARK 999	UNP P0A9G8
B	-1	HIS	-	SEE REMARK 999	UNP P0A9G8
B	1	MSE	MET	modified residue	UNP P0A9G8
B	55	MSE	MET	modified residue	UNP P0A9G8
B	221	MSE	MET	modified residue	UNP P0A9G8

- Molecule 2 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ni	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	240	Total	O	0	0
			240	240		

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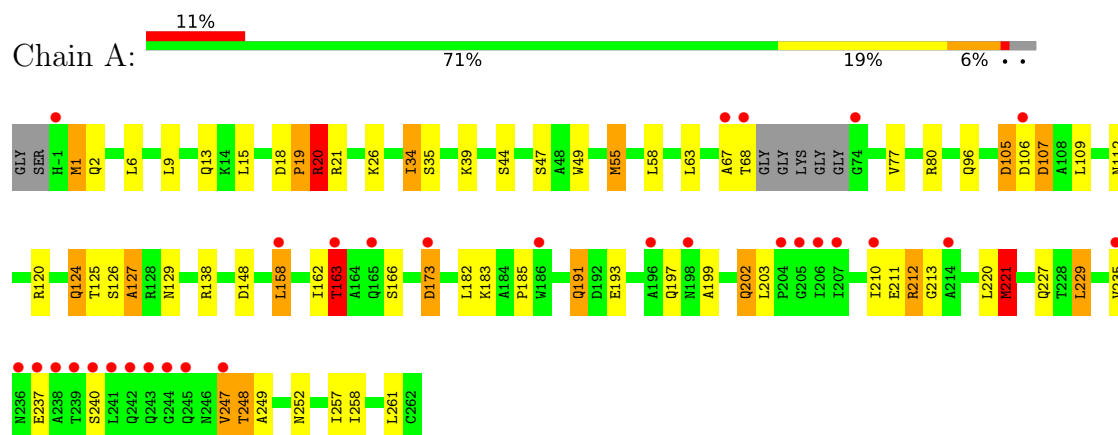
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	186	Total 186	O 186	0	0

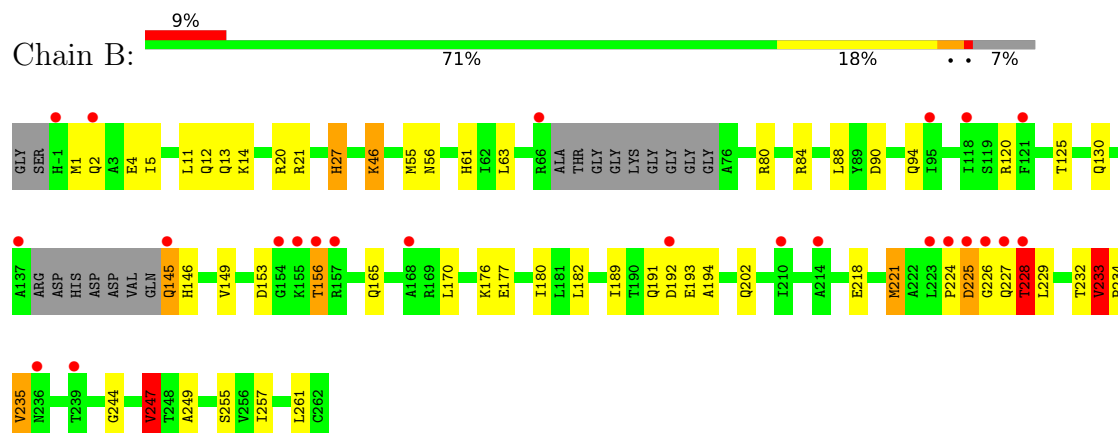
3 Residue-property plots [i](#)

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: PROTEIN (MODE)



• Molecule 1: PROTEIN (MODE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.61Å 127.24Å 62.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.15 – 1.75 24.15 – 1.75	Depositor EDS
% Data completeness (in resolution range)	80.2 (24.15-1.75) 79.8 (24.15-1.75)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 1.75Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.234 , 0.279 0.215 , 0.256	Depositor DCC
R_{free} test set	2663 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4284	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% 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, 0.333 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:
NI

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	1.08	4/2008 (0.2%)	1.77	31/2717 (1.1%)
1	B	0.86	3/1912 (0.2%)	1.69	29/2588 (1.1%)
All	All	0.98	7/3920 (0.2%)	1.74	60/5305 (1.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	55	MSE	SE-CE	-21.03	1.32	1.95
1	A	221	MSE	SE-CE	-6.49	1.75	1.95
1	A	21	ARG	CD-NE	5.89	1.54	1.46
1	B	221	MSE	SE-CE	-5.31	1.79	1.95
1	A	1	MSE	SE-CE	-5.28	1.79	1.95
1	B	1	MSE	SE-CE	-5.13	1.80	1.95
1	B	55	MSE	SE-CE	-5.01	1.80	1.95

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ASP	CA-CB-CG	12.08	124.68	112.60
1	B	233	VAL	N-CA-CB	-11.02	95.79	111.21
1	B	247	VAL	N-CA-CB	-10.84	96.20	112.35
1	A	173	ASP	CA-CB-CG	-10.31	102.29	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	235	VAL	CB-CA-C	-10.06	98.86	112.04
1	A	163	THR	N-CA-CB	-9.13	95.85	110.46
1	B	225	ASP	CA-CB-CG	8.73	121.33	112.60
1	A	105	ASP	CA-CB-CG	8.57	121.17	112.60
1	A	220	LEU	CA-C-O	-8.33	111.88	120.71
1	B	90	ASP	CA-CB-CG	8.30	120.90	112.60
1	B	235	VAL	N-CA-CB	7.83	120.26	110.47
1	B	226	GLY	N-CA-C	-7.65	104.48	115.64
1	B	146	HIS	N-CA-C	7.49	118.49	108.38
1	A	126	SER	CA-C-O	7.47	128.57	119.97
1	B	21	ARG	NE-CZ-NH2	7.39	125.85	119.20
1	A	212	ARG	CD-NE-CZ	7.38	134.73	124.40
1	A	227	GLN	OE1-CD-NE2	7.37	129.97	122.60
1	A	126	SER	O-C-N	-6.70	114.03	122.27
1	B	94	GLN	OE1-CD-NE2	6.53	129.13	122.60
1	A	112	ASN	CA-CB-CG	6.44	119.04	112.60
1	A	252	ASN	CA-CB-CG	-6.42	106.18	112.60
1	B	84[A]	ARG	CD-NE-CZ	6.33	133.27	124.40
1	B	84[B]	ARG	CD-NE-CZ	6.33	133.27	124.40
1	A	20[A]	ARG	CD-NE-CZ	6.32	133.25	124.40
1	A	20[B]	ARG	CD-NE-CZ	6.32	133.25	124.40
1	A	248	THR	CA-CB-OG1	6.26	118.99	109.60
1	B	191	GLN	CA-C-O	6.26	126.88	119.56
1	B	145	GLN	CA-C-O	-6.02	110.56	120.80
1	A	80	ARG	NE-CZ-NH2	5.96	124.56	119.20
1	B	228	THR	N-CA-CB	5.93	119.90	110.65
1	A	247	VAL	N-CA-CB	-5.90	101.23	110.96
1	A	129	ASN	CA-CB-CG	-5.83	106.77	112.60
1	B	227	GLN	N-CA-C	-5.77	101.74	110.28
1	B	233	VAL	CA-CB-CG1	5.73	120.14	110.40
1	B	4	GLU	N-CA-CB	-5.71	102.12	111.66
1	B	1	MSE	CB-CA-C	-5.69	99.56	109.64
1	B	261	LEU	CA-C-O	-5.69	114.43	120.40
1	B	146	HIS	CA-CB-CG	-5.65	108.15	113.80
1	B	165	GLN	OE1-CD-NE2	-5.53	117.07	122.60
1	A	96	GLN	CB-CA-C	-5.50	101.50	110.85
1	B	255	SER	N-CA-C	-5.45	106.48	113.23
1	A	127	ALA	N-CA-C	-5.37	102.10	110.10
1	B	27	HIS	CA-CB-CG	-5.37	108.44	113.80
1	B	1	MSE	N-CA-C	5.36	117.21	110.24
1	A	148	ASP	CA-CB-CG	-5.36	107.25	112.60
1	B	14	LYS	CA-C-O	-5.34	115.19	121.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ASP	CA-C-O	-5.24	115.67	121.28
1	A	58	LEU	N-CA-C	5.23	116.98	111.28
1	A	213	GLY	N-CA-C	-5.21	106.54	112.79
1	B	244	GLY	CA-C-O	5.20	124.83	119.27
1	A	182	LEU	CA-C-O	-5.19	113.86	120.20
1	A	193	GLU	CA-C-O	-5.19	115.02	120.63
1	A	120	ARG	CG-CD-NE	5.17	123.37	112.00
1	A	124	GLN	CG-CD-NE2	-5.16	108.67	116.40
1	B	56	ASN	OD1-CG-ND2	-5.11	117.49	122.60
1	B	13	GLN	CB-CA-C	5.08	119.64	111.36
1	A	34	ILE	CB-CG1-CD1	5.08	124.46	113.80
1	A	191	GLN	N-CA-C	-5.03	106.84	113.17
1	A	138	ARG	N-CA-CB	5.02	117.40	110.17
1	A	163	THR	CB-CA-C	5.02	118.62	109.83

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	63	LEU	Mainchain

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	1976	0	2002	39	0
1	B	1881	0	1895	27	0
2	A	1	0	0	0	0
3	A	240	0	0	3	2
3	B	186	0	0	7	1
All	All	4284	0	3897	56	2

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 7.

All (56) 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:55:MSE:SE	1:A:55:MSE:CE	1.32	1.51
1:A:55:MSE:SE	1:A:55:MSE:HE3	1.88	1.13
1:A:55:MSE:SE	1:A:55:MSE:HE1	1.88	1.09
1:A:55:MSE:SE	1:A:55:MSE:HE2	1.88	1.08
1:A:221:MSE:HE1	1:A:249:ALA:HB2	1.44	0.97
1:A:221:MSE:HE3	1:A:229:LEU:HG	1.51	0.92
1:A:55:MSE:CE	1:A:55:MSE:CG	2.52	0.86
1:A:163:THR:HG22	1:A:166:SER:H	1.42	0.84
1:B:192:ASP:HB3	3:B:418:HOH:O	1.79	0.83
1:B:125:THR:H	1:B:130:GLN:HE22	1.30	0.79
1:A:197:GLN:HA	1:A:202:GLN:OE1	1.85	0.75
1:A:20[A]:ARG:HB2	1:A:20[A]:ARG:HH21	1.52	0.74
1:A:158:LEU:HD22	1:A:203:LEU:HD21	1.76	0.67
1:A:124:GLN:HB3	1:B:170:LEU:HD22	1.82	0.61
1:A:125:THR:HB	3:A:456:HOH:O	2.00	0.60
1:B:46:LYS:NZ	3:B:382:HOH:O	2.35	0.59
1:A:1:MSE:HE3	1:B:12:GLN:HG3	1.83	0.59
1:B:221:MSE:HE1	1:B:249:ALA:HB2	1.85	0.59
1:A:13:GLN:HE21	1:B:2:GLN:HE22	1.50	0.59
1:B:125:THR:H	1:B:130:GLN:NE2	2.01	0.59
1:A:1:MSE:CE	1:B:11:LEU:HB3	2.35	0.56
1:A:163:THR:CG2	1:A:166:SER:H	2.14	0.56
1:A:257:ILE:HD12	1:B:257:ILE:HD12	1.89	0.55
1:A:125:THR:HG22	1:A:127:ALA:H	1.74	0.53
1:B:27:HIS:HD2	3:B:401:HOH:O	1.92	0.52
1:B:202:GLN:NE2	3:B:411:HOH:O	2.44	0.50
1:A:1:MSE:HE2	1:B:11:LEU:HB3	1.94	0.50
1:B:153:ASP:OD2	1:B:156:THR:HG23	2.11	0.50
1:A:183:LYS:HB3	1:A:185:PRO:HD2	1.94	0.49
1:A:9:LEU:HD22	1:B:5:ILE:HG12	1.95	0.49
1:A:44:SER:OG	1:A:47:SER:HB3	2.14	0.48
1:A:34:ILE:HD12	1:A:49:TRP:CZ2	2.49	0.48
1:A:163:THR:HG22	1:A:166:SER:CB	2.44	0.48
1:B:194:ALA:HB3	3:B:418:HOH:O	2.13	0.47
1:B:218[A]:GLU:OE1	1:B:232:THR:OG1	2.22	0.47
1:A:106:ASP:CG	1:B:80:ARG:HH12	2.23	0.47
1:A:163:THR:HG22	1:A:166:SER:N	2.21	0.47
1:B:189:ILE:HG23	1:B:247:VAL:HG13	1.96	0.47
1:A:199:ALA:O	1:A:202:GLN:NE2	2.47	0.46
1:A:55:MSE:HE3	1:A:55:MSE:HB2	1.97	0.46
1:A:35:SER:O	1:A:39:LYS:HG3	2.16	0.46
1:B:156:THR:HG22	1:B:224:PRO:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MSE:CE	1:B:12:GLN:HG3	2.46	0.45
1:B:228:THR:HB	3:B:440:HOH:O	2.17	0.44
1:A:6:LEU:HD22	1:A:19:PRO:HG2	2.00	0.44
1:A:125:THR:HG22	1:A:127:ALA:N	2.33	0.44
1:A:1:MSE:HE1	1:B:11:LEU:HB3	2.00	0.43
1:A:26:LYS:NZ	3:A:447:HOH:O	2.51	0.43
1:B:149:VAL:HG11	1:B:180:ILE:HD11	2.00	0.43
1:A:18:ASP:HB2	1:A:19:PRO:CD	2.48	0.43
1:A:210:ILE:HG22	1:A:211:GLU:N	2.33	0.42
1:A:162:ILE:HG12	1:A:166:SER:HB3	2.01	0.42
3:A:434:HOH:O	1:B:61:HIS:HE1	2.03	0.42
1:B:20:ARG:NH2	3:B:290:HOH:O	2.53	0.41
1:B:233:VAL:HA	1:B:234:PRO:HD3	1.93	0.41
1:A:67:ALA:HB2	1:A:77:VAL:HG13	2.02	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:360:HOH:O	3:A:360:HOH:O[2_655]	2.09	0.11
3:A:492:HOH:O	3:B:346:HOH:O[4_456]	2.16	0.04

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	256/265 (97%)	249 (97%)	7 (3%)	0	100	100
1	B	243/265 (92%)	239 (98%)	4 (2%)	0	100	100
All	All	499/530 (94%)	488 (98%)	11 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	212/210 (101%)	188 (89%)	24 (11%)	5	0
1	B	201/210 (96%)	185 (92%)	16 (8%)	11	2
All	All	413/420 (98%)	373 (90%)	40 (10%)	8	1

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	15	LEU
1	A	19	PRO
1	A	20[A]	ARG
1	A	20[B]	ARG
1	A	68	THR
1	A	105	ASP
1	A	107	ASP
1	A	109	LEU
1	A	158	LEU
1	A	163	THR
1	A	173	ASP
1	A	191	GLN
1	A	202	GLN
1	A	212	ARG
1	A	221	MSE
1	A	229	LEU
1	A	235	VAL
1	A	237	GLU
1	A	240	SER
1	A	247	VAL
1	A	248	THR
1	A	258	ILE
1	A	261	LEU
1	B	46	LYS
1	B	63	LEU
1	B	88	LEU

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Mol	Chain	Res	Type
1	B	120	ARG
1	B	145	GLN
1	B	156	THR
1	B	176	LYS
1	B	177	GLU
1	B	182	LEU
1	B	193	GLU
1	B	225	ASP
1	B	228	THR
1	B	229	LEU
1	B	233	VAL
1	B	235	VAL
1	B	247	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	198	ASN
1	B	2	GLN
1	B	96	GLN
1	B	112	ASN
1	B	130	GLN
1	B	243	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is 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

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	255/265 (96%)	0.66	30 (11%) 9 10	22, 35, 64, 87	2 (0%)
1	B	244/265 (92%)	0.79	24 (9%) 13 15	26, 39, 61, 81	2 (0%)
All	All	499/530 (94%)	0.72	54 (10%) 11 12	22, 37, 62, 87	4 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	137	ALA	6.7
1	A	-1	HIS	5.6
1	A	241	LEU	4.8
1	A	244	GLY	4.5
1	B	66	ARG	3.8
1	B	226	GLY	3.8
1	A	214	ALA	3.6
1	A	205	GLY	3.6
1	B	-1	HIS	3.6
1	B	227	GLN	3.5
1	A	239	THR	3.5
1	A	163	THR	3.4
1	B	239	THR	3.4
1	B	145	GLN	3.4
1	A	206	ILE	3.4
1	A	186	TRP	3.3
1	B	192	ASP	3.3
1	A	210	ILE	3.3
1	B	225	ASP	3.3
1	A	198	ASN	3.2
1	A	68	THR	3.1
1	A	106	ASP	3.1
1	A	235	VAL	3.0
1	B	95	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	223	LEU	3.0
1	B	210	ILE	2.8
1	B	224	PRO	2.8
1	B	236	ASN	2.8
1	A	236	ASN	2.7
1	B	121	PHE	2.7
1	A	74	GLY	2.7
1	A	238	ALA	2.6
1	A	245	GLN	2.6
1	B	157	ARG	2.6
1	B	168	ALA	2.5
1	B	156	THR	2.5
1	A	237	GLU	2.4
1	A	243	GLN	2.3
1	A	67	ALA	2.3
1	A	173	ASP	2.3
1	B	118	ILE	2.3
1	A	204	PRO	2.2
1	B	214	ALA	2.2
1	A	240	SER	2.2
1	B	2	GLN	2.1
1	A	158	LEU	2.1
1	A	247	VAL	2.1
1	A	207	ILE	2.1
1	A	196	ALA	2.1
1	A	165	GLN	2.1
1	A	242	GLN	2.1
1	B	228	THR	2.1
1	B	154	GLY	2.0
1	B	155	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	NI	A	263	1/1	0.98	0.07	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.