



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 05:04 PM UTC

PDB ID : 1Q18 / pdb_00001q18
Title : Crystal structure of E.coli glucokinase (Glk)
Authors : Lunin, V.V.; Li, Y.; Schrag, J.D.; Matte, A.; Cygler, M.; Montreal-Kingston
Bacterial Structural Genomics Initiative (BSGI)
Deposited on : 2003-07-18
Resolution : 2.36 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

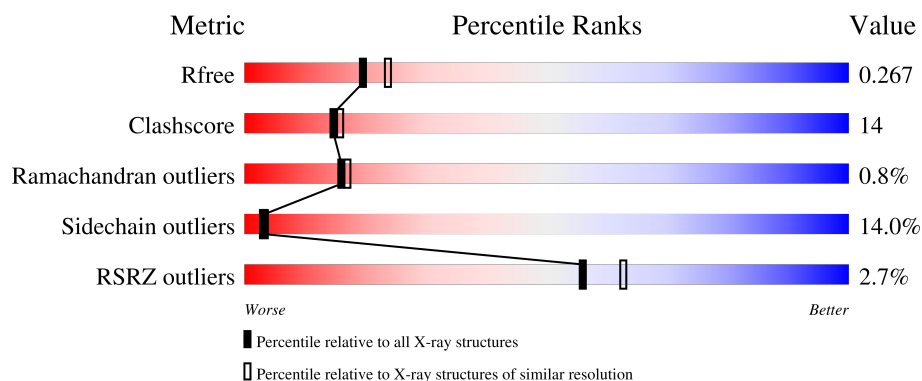
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	332	2% 72% 19% 5% • •
1	B	332	4% 66% 23% 6% • •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5295 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 Glucokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	Se	0	3	0
			2451	1570	423	446	7	5			
1	B	320	Total	C	N	O	S	Se	0	4	0
			2457	1574	426	445	6	6			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MSE	-	modified residue	UNP P0A6V8
A	-9	GLY	-	cloning artifact	UNP P0A6V8
A	-8	SER	-	cloning artifact	UNP P0A6V8
A	-7	SER	-	cloning artifact	UNP P0A6V8
A	-6	HIS	-	expression tag	UNP P0A6V8
A	-5	HIS	-	expression tag	UNP P0A6V8
A	-4	HIS	-	expression tag	UNP P0A6V8
A	-3	HIS	-	expression tag	UNP P0A6V8
A	-2	HIS	-	expression tag	UNP P0A6V8
A	-1	HIS	-	expression tag	UNP P0A6V8
A	11	GLY	-	cloning artifact	UNP P0A6V8
A	1	SER	-	cloning artifact	UNP P0A6V8
A	74	MSE	MET	modified residue	UNP P0A6V8
A	86	MSE	MET	modified residue	UNP P0A6V8
A	106	MSE	MET	modified residue	UNP P0A6V8
A	110	MSE	MET	modified residue	UNP P0A6V8
A	241	MSE	MET	modified residue	UNP P0A6V8
B	-10	MSE	-	modified residue	UNP P0A6V8
B	-9	GLY	-	cloning artifact	UNP P0A6V8
B	-8	SER	-	cloning artifact	UNP P0A6V8
B	-7	SER	-	cloning artifact	UNP P0A6V8
B	-6	HIS	-	expression tag	UNP P0A6V8
B	-5	HIS	-	expression tag	UNP P0A6V8
B	-4	HIS	-	expression tag	UNP P0A6V8
B	-3	HIS	-	expression tag	UNP P0A6V8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP P0A6V8
B	-1	HIS	-	expression tag	UNP P0A6V8
B	11	GLY	-	cloning artifact	UNP P0A6V8
B	1	SER	-	cloning artifact	UNP P0A6V8
B	74	MSE	MET	modified residue	UNP P0A6V8
B	86	MSE	MET	modified residue	UNP P0A6V8
B	106	MSE	MET	modified residue	UNP P0A6V8
B	110	MSE	MET	modified residue	UNP P0A6V8
B	241	MSE	MET	modified residue	UNP P0A6V8

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	243	Total O 243 243	0	0
2	B	144	Total O 144 144	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.47Å 81.47Å 234.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.76 – 2.36 19.76 – 2.36	Depositor EDS
% Data completeness (in resolution range)	95.8 (19.76-2.36) 97.5 (19.76-2.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.206 , 0.267 0.198 , 0.267	Depositor DCC
R_{free} test set	1784 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5295	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% 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

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	1.10	4/2508 (0.2%)	1.12	6/3389 (0.2%)
1	B	0.97	3/2521 (0.1%)	1.10	5/3403 (0.1%)
All	All	1.04	7/5029 (0.1%)	1.11	11/6792 (0.2%)

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
1	B	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	86	MSE	SE-CE	12.02	2.31	1.95
1	A	86	MSE	SE-CE	-9.48	1.67	1.95
1	A	74	MSE	SE-CE	8.07	2.19	1.95
1	B	172	ILE	CA-CB	5.86	1.61	1.54
1	A	262	GLY	C-O	5.76	1.30	1.24
1	A	110	MSE	SE-CE	5.36	2.11	1.95
1	B	110	MSE	SE-CE	5.27	2.11	1.95

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	254	THR	N-CA-CB	-8.59	99.63	110.45
1	A	90	LEU	N-CA-C	-7.57	100.77	110.53
1	A	90	LEU	CA-C-N	-6.95	107.78	121.41
1	A	90	LEU	C-N-CA	-6.95	107.78	121.41
1	B	132	VAL	CB-CA-C	-6.91	100.40	110.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	289	GLU	N-CA-C	6.15	117.98	111.28
1	B	299	ILE	N-CA-CB	6.02	117.28	110.72
1	B	181	ILE	N-CA-C	-6.00	99.90	109.20
1	A	263	GLY	N-CA-C	-5.28	100.66	113.18
1	A	90	LEU	O-C-N	-5.14	116.32	122.65
1	B	130	ILE	N-CA-C	5.09	116.93	108.99

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	75	THR	Peptide
1	B	91	GLY	Peptide

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	2451	0	2460	72	0
1	B	2457	0	2473	66	0
2	A	243	0	0	23	0
2	B	144	0	0	17	0
All	All	5295	0	4933	137	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 14.

All (137) 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:74:MSE:SE	1:A:74:MSE:CE	2.19	1.38
1:B:86:MSE:SE	1:B:86:MSE:CE	2.31	1.28
1:A:293:ASP:HB2	2:A:541:HOH:O	1.24	1.26
1:A:153:SER:HB2	2:A:389:HOH:O	1.46	1.14
1:A:78:THR:HG22	2:A:502:HOH:O	1.62	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65[B]:CYS:SG	1:A:66:PRO:HD2	2.07	0.94
1:A:175:GLU:HG2	1:B:168:GLU:HG3	1.47	0.94
1:A:151:TRP:H	1:A:315:GLN:HE22	1.10	0.89
1:A:42[A]:GLU:HG3	1:A:86:MSE:HE2	1.54	0.87
1:B:43:ALA:C	2:B:397:HOH:O	2.17	0.86
1:A:63:ILE:HG13	1:A:97[A]:ILE:HD12	1.56	0.85
1:A:175:GLU:HG3	2:A:451:HOH:O	1.74	0.85
1:A:282:GLU:OE1	1:A:292:HIS:HD2	1.59	0.83
1:A:75:THR:HA	2:A:532:HOH:O	1.78	0.82
1:B:2:THR:HA	1:B:3:LYS:HB2	1.62	0.82
1:A:292:HIS:HB3	2:A:342:HOH:O	1.78	0.81
1:A:112:LYS:H	1:A:115:HIS:HD2	1.30	0.79
1:B:128[B]:LYS:NZ	2:B:404:HOH:O	2.16	0.77
1:B:117:ILE:HD12	1:B:300:VAL:HG11	1.67	0.76
1:B:112:LYS:H	1:B:115:HIS:HD2	1.35	0.75
1:A:178:ARG:O	1:A:181:ILE:O	2.06	0.74
1:A:231:ARG:CZ	2:A:512:HOH:O	2.35	0.74
1:B:148:ASP:O	1:B:149:LYS:HB2	1.87	0.72
1:B:44:VAL:N	2:B:397:HOH:O	2.22	0.72
1:B:188:ARG:HD3	2:B:350:HOH:O	1.91	0.71
1:A:82:SER:HB3	1:A:85:GLU:HB3	1.73	0.70
1:A:41:LEU:HB3	1:A:86:MSE:HE1	1.72	0.69
1:B:16:ARG:HD3	1:B:32:THR:OG1	1.92	0.68
1:B:190:LEU:HD22	1:B:241[B]:MSE:SE	2.44	0.68
1:A:42[A]:GLU:CG	1:A:86:MSE:HE2	2.23	0.68
1:A:254:THR:CG2	1:A:254:THR:O	2.41	0.68
1:A:234:LEU:HD13	1:A:271:PHE:CD2	2.31	0.66
1:B:43:ALA:CA	2:B:397:HOH:O	2.45	0.65
1:A:112:LYS:H	1:A:115:HIS:CD2	2.11	0.65
1:B:43:ALA:HA	2:B:397:HOH:O	1.97	0.65
1:B:178:ARG:O	1:B:181:ILE:O	2.15	0.64
1:A:282:GLU:OE1	1:A:292:HIS:CD2	2.48	0.64
1:A:65[B]:CYS:SG	1:A:66:PRO:CD	2.83	0.64
1:B:209:LEU:HD12	1:B:210:PRO:HD2	1.79	0.64
1:A:42[A]:GLU:HG3	1:A:86:MSE:HG3	1.81	0.63
1:A:74:MSE:HE3	2:A:504:HOH:O	1.97	0.63
1:A:170:GLU:OE2	1:A:243:ARG:NH2	2.32	0.62
1:B:130:ILE:HD13	1:B:144:LEU:HB3	1.81	0.62
1:B:112:LYS:H	1:B:115:HIS:CD2	2.16	0.61
1:B:130:ILE:HA	1:B:254[A]:THR:HG23	1.82	0.61
1:B:231:ARG:O	1:B:235:SER:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243[A]:ARG:NH1	1:B:283:ASP:OD2	2.34	0.60
1:B:41:LEU:HB3	1:B:86:MSE:HE1	1.85	0.59
1:B:103:ALA:O	1:B:308:GLY:HA3	2.04	0.57
1:B:200:ARG:HD2	2:B:449:HOH:O	2.04	0.57
1:A:99:ASN:HD22	1:A:102:THR:H	1.52	0.57
1:A:231:ARG:NH1	2:A:512:HOH:O	2.37	0.57
1:A:188:ARG:HD3	2:A:333:HOH:O	2.04	0.56
1:B:195:LEU:HD22	1:B:218:ILE:HG21	1.87	0.56
1:A:180:GLU:HG3	2:A:454:HOH:O	2.05	0.55
1:B:2:THR:CA	1:B:3:LYS:HB2	2.36	0.55
1:A:86:MSE:HG2	1:A:90:LEU:HD22	1.89	0.54
1:A:165:PRO:HG3	1:A:174:LEU:HD12	1.90	0.54
1:A:151:TRP:N	1:A:315:GLN:HE22	1.92	0.54
1:A:243:ARG:HD2	2:B:370:HOH:O	2.08	0.54
1:B:128[B]:LYS:HG3	1:B:129:PRO:HD3	1.89	0.54
1:B:76:ASN:HB2	2:B:399:HOH:O	2.07	0.53
1:B:6:LEU:HD13	1:B:61:ILE:HD11	1.90	0.53
1:B:153:SER:HB2	2:B:363:HOH:O	2.07	0.53
1:A:63:ILE:HG13	1:A:97[A]:ILE:CD1	2.34	0.53
1:A:254:THR:O	1:A:254:THR:HG22	2.08	0.52
1:B:206:ASP:CB	1:B:208:ARG:HH21	2.22	0.52
1:B:166:ASN:HD22	1:B:243[A]:ARG:CZ	2.23	0.52
1:A:42[A]:GLU:OE2	1:A:85:GLU:OE1	2.28	0.52
1:B:115:HIS:HB3	1:B:301:HIS:HB2	1.92	0.52
1:B:22:ILE:CD1	2:B:343:HOH:O	2.57	0.51
1:A:105:SER:O	1:A:144:LEU:HD11	2.11	0.51
1:B:133:TYR:O	1:B:260:ILE:HA	2.10	0.51
1:B:206:ASP:HB3	1:B:208:ARG:HH21	1.75	0.51
1:A:200:ARG:NH2	2:A:454:HOH:O	2.42	0.51
1:A:234:LEU:HD13	1:A:271:PHE:CE2	2.46	0.51
1:A:119:PHE:O	1:A:278:ARG:HD3	2.12	0.50
1:B:299:ILE:HD11	1:B:304:PRO:HG3	1.94	0.50
1:A:72:VAL:HG21	1:A:97[A]:ILE:HD13	1.94	0.50
1:A:83:ILE:HG12	1:A:97[A]:ILE:HG21	1.94	0.50
1:A:88:LYS:HE3	2:A:546:HOH:O	2.11	0.50
1:A:42[A]:GLU:CG	1:A:86:MSE:HG3	2.41	0.49
1:A:293:ASP:CB	2:A:541:HOH:O	2.09	0.49
1:A:16:ARG:HG2	1:A:306:LEU:HD11	1.93	0.49
1:B:130:ILE:HG12	1:B:131:ALA:N	2.25	0.49
1:A:180:GLU:CG	2:A:454:HOH:O	2.60	0.49
1:B:13:THR:HG22	2:B:422:HOH:O	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:ILE:HD11	2:B:343:HOH:O	2.13	0.48
1:A:170:GLU:CD	1:A:243:ARG:HH22	2.22	0.48
1:B:209:LEU:CD1	1:B:210:PRO:HD2	2.43	0.48
1:A:76:ASN:O	1:A:79:TRP:HB2	2.13	0.48
1:A:263:GLY:N	2:A:480:HOH:O	2.25	0.48
1:A:254:THR:O	1:A:254:THR:HG23	2.13	0.47
1:A:188:ARG:CD	2:A:333:HOH:O	2.61	0.47
1:B:105:SER:O	1:B:144:LEU:HD22	2.15	0.47
1:B:42:GLU:H	1:B:86:MSE:HE2	1.80	0.46
1:A:42[A]:GLU:HG3	1:A:86:MSE:CE	2.36	0.46
1:B:148:ASP:O	1:B:149:LYS:CB	2.61	0.46
1:B:243[B]:ARG:HG2	2:B:346:HOH:O	2.15	0.46
1:B:42:GLU:HB2	1:B:86:MSE:HE2	1.98	0.45
1:B:243[B]:ARG:HD2	2:B:329:HOH:O	2.16	0.45
1:A:103:ALA:O	1:A:308:GLY:HA3	2.16	0.45
1:B:43:ALA:O	1:B:44:VAL:HG23	2.17	0.45
1:B:320:ILE:HD12	2:B:459:HOH:O	2.16	0.45
1:B:259:PHE:CD1	1:B:259:PHE:N	2.85	0.45
1:A:60:CYS:HA	1:A:96:GLU:O	2.17	0.45
1:A:175:GLU:CG	2:A:451:HOH:O	2.50	0.45
1:B:153:SER:CB	2:B:363:HOH:O	2.63	0.45
1:A:83:ILE:HG12	1:A:97[B]:ILE:HG13	1.99	0.44
1:A:319:HIS:HE1	2:A:460:HOH:O	2.00	0.44
1:A:36:LEU:HG	2:A:507:HOH:O	2.16	0.44
1:B:128[B]:LYS:HG2	1:B:255:PHE:HB2	2.00	0.44
1:B:60:CYS:HA	1:B:96:GLU:O	2.18	0.43
1:A:262:GLY:HA2	2:A:480:HOH:O	2.19	0.43
1:A:77:HIS:HD2	2:A:550:HOH:O	2.02	0.43
1:B:31:LYS:HE3	1:B:52:HIS:HE2	1.84	0.42
1:A:314:ARG:O	1:A:319:HIS:HB2	2.20	0.42
1:B:241[A]:MSE:HG2	1:B:277:PHE:HE1	1.85	0.42
1:A:302:ASP:HB3	2:A:494:HOH:O	2.20	0.41
1:B:129:PRO:HB3	1:B:145:VAL:HG12	2.02	0.41
1:B:258:VAL:O	1:B:296:VAL:HA	2.21	0.41
1:A:125:VAL:HG12	1:A:128:LYS:HD3	2.03	0.41
1:B:108:ILE:N	1:B:109:PRO:HD2	2.35	0.41
1:B:128[B]:LYS:HG3	1:B:129:PRO:CD	2.50	0.41
1:B:249:ALA:HA	1:B:254[B]:THR:OG1	2.21	0.41
1:B:16:ARG:HG2	1:B:306:LEU:HD11	2.03	0.41
1:B:33:TYR:CD1	1:B:33:TYR:N	2.89	0.41
1:A:110:MSE:HB2	1:A:307:LEU:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:5:ALA:HB2	1:A:22:ILE:HD11	2.04	0.40
1:A:125:VAL:CG1	1:A:128:LYS:HD3	2.52	0.40
1:B:146:HIS:HB2	1:B:151:TRP:CZ3	2.56	0.40
1:A:72:VAL:HG21	1:A:97[A]:ILE:CD1	2.51	0.40
1:A:177:LEU:O	1:A:181:ILE:HD13	2.22	0.40
1:A:151:TRP:H	1:A:315:GLN:NE2	1.94	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	321/332 (97%)	307 (96%)	13 (4%)	1 (0%)	36	43
1	B	322/332 (97%)	300 (93%)	18 (6%)	4 (1%)	10	9
All	All	643/664 (97%)	607 (94%)	31 (5%)	5 (1%)	16	17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	122	ALA
1	A	76	ASN
1	B	3	LYS
1	B	262	GLY
1	B	44	VAL

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	256/257 (100%)	227 (89%)	29 (11%)	5	5
1	B	257/257 (100%)	212 (82%)	45 (18%)	2	1
All	All	513/514 (100%)	439 (86%)	74 (14%)	3	3

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	6	LEU
1	A	13	THR
1	A	16	ARG
1	A	41	LEU
1	A	54	VAL
1	A	57	LYS
1	A	63	ILE
1	A	85	GLU
1	A	88	LYS
1	A	90	LEU
1	A	95	LEU
1	A	97[A]	ILE
1	A	97[B]	ILE
1	A	116	LEU
1	A	148	ASP
1	A	149	LYS
1	A	174	LEU
1	A	181	ILE
1	A	189	VAL
1	A	209	LEU
1	A	214	LYS
1	A	232	ARG
1	A	234	LEU
1	A	252	LEU
1	A	254	THR
1	A	267	ARG
1	A	289	GLU
1	A	307	LEU
1	B	6	LEU
1	B	13	THR
1	B	16	ARG
1	B	26	GLU

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Mol	Chain	Res	Type
1	B	41	LEU
1	B	51	GLU
1	B	54	VAL
1	B	56	VAL
1	B	61	ILE
1	B	85	GLU
1	B	88	LYS
1	B	95	LEU
1	B	110	MSE
1	B	112	LYS
1	B	114	GLU
1	B	128[A]	LYS
1	B	128[B]	LYS
1	B	130	ILE
1	B	132	VAL
1	B	133	TYR
1	B	141	VAL
1	B	153	SER
1	B	181	ILE
1	B	188	ARG
1	B	189	VAL
1	B	195	LEU
1	B	204	LYS
1	B	209	LEU
1	B	211	GLU
1	B	216	LYS
1	B	218	ILE
1	B	220	GLU
1	B	231	ARG
1	B	232	ARG
1	B	234	LEU
1	B	235	SER
1	B	236	LEU
1	B	254[A]	THR
1	B	254[B]	THR
1	B	269	LEU
1	B	270	GLU
1	B	286	ARG
1	B	288	LYS
1	B	299	ILE
1	B	307	LEU

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	29	GLN
1	A	77	HIS
1	A	99	ASN
1	A	115	HIS
1	A	292	HIS
1	A	315	GLN
1	B	14	ASN
1	B	77	HIS
1	B	89	ASN
1	B	99	ASN
1	B	115	HIS
1	B	247	ASN
1	B	292	HIS
1	B	312	HIS

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 oligosaccharides 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 ⓘ

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	315/332 (94%)	-0.20	5 (1%) 70 76	11, 29, 42, 58	3 (0%)
1	B	315/332 (94%)	0.27	12 (3%) 44 50	18, 40, 66, 75	3 (0%)
All	All	630/664 (94%)	0.04	17 (2%) 56 63	11, 34, 60, 75	6 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	43	ALA	5.3
1	A	77	HIS	3.9
1	B	2	THR	3.9
1	A	75	THR	3.7
1	A	76	ASN	3.6
1	B	224	ALA	3.3
1	A	262	GLY	3.0
1	B	91	GLY	2.6
1	B	114	GLU	2.6
1	A	180	GLU	2.4
1	B	209	LEU	2.3
1	B	223	LEU	2.2
1	B	148	ASP	2.2
1	B	55	GLU	2.2
1	B	84	ALA	2.2
1	B	205	ALA	2.1
1	B	51	GLU	2.1

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 [i](#)

There are no oligosaccharides 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.