



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:13 PM UTC

PDB ID : 3CGU / pdb_00003cgu
Title : Crystal Structure of unliganded Argos
Authors : Klein, D.E.; Stayrook, S.E.; Lemmon, M.A.
Deposited on : 2008-03-06
Resolution : 2.51 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
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

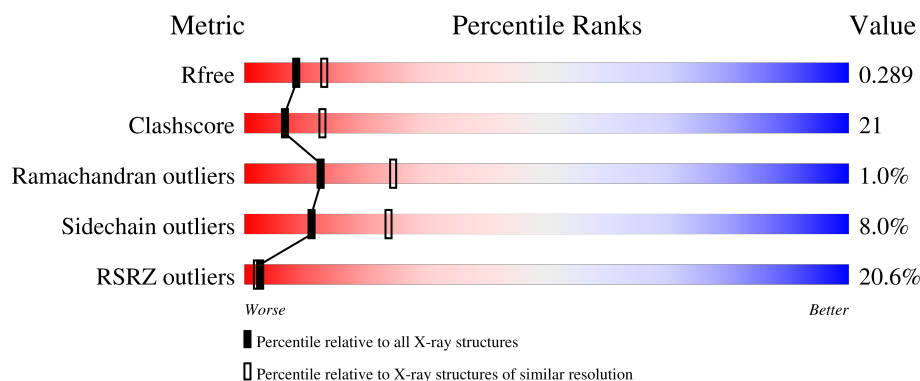
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	223	16% 62% 25% 6% 7%
1	B	223	22% 60% 29% • 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3420 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 giant-lens.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1656	1025	304	309	18			
1	B	205	Total	C	N	O	S	0	0	0
			1637	1015	299	305	18			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ASP	-	linker	UNP Q00805
A	142	GLY	-	linker	UNP Q00805
A	143	ARG	-	linker	UNP Q00805
A	144	THR	-	linker	UNP Q00805
A	420	HIS	-	expression tag	UNP Q00805
A	421	HIS	-	expression tag	UNP Q00805
A	422	HIS	-	expression tag	UNP Q00805
A	423	HIS	-	expression tag	UNP Q00805
A	424	HIS	-	expression tag	UNP Q00805
A	425	HIS	-	expression tag	UNP Q00805
B	141	ASP	-	linker	UNP Q00805
B	142	GLY	-	linker	UNP Q00805
B	143	ARG	-	linker	UNP Q00805
B	144	THR	-	linker	UNP Q00805
B	420	HIS	-	expression tag	UNP Q00805
B	421	HIS	-	expression tag	UNP Q00805
B	422	HIS	-	expression tag	UNP Q00805
B	423	HIS	-	expression tag	UNP Q00805
B	424	HIS	-	expression tag	UNP Q00805
B	425	HIS	-	expression tag	UNP Q00805

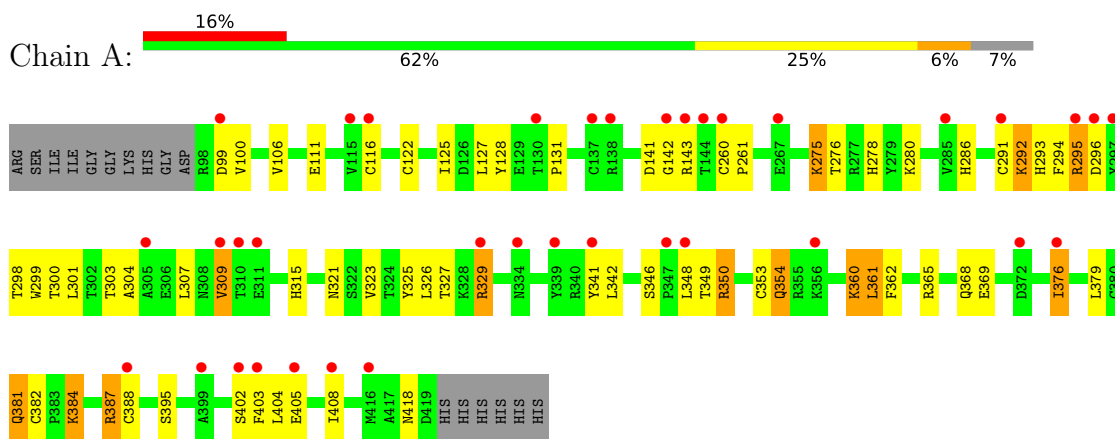
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	81	Total 81	O 81	0	0
2	B	46	Total 46	O 46	0	0

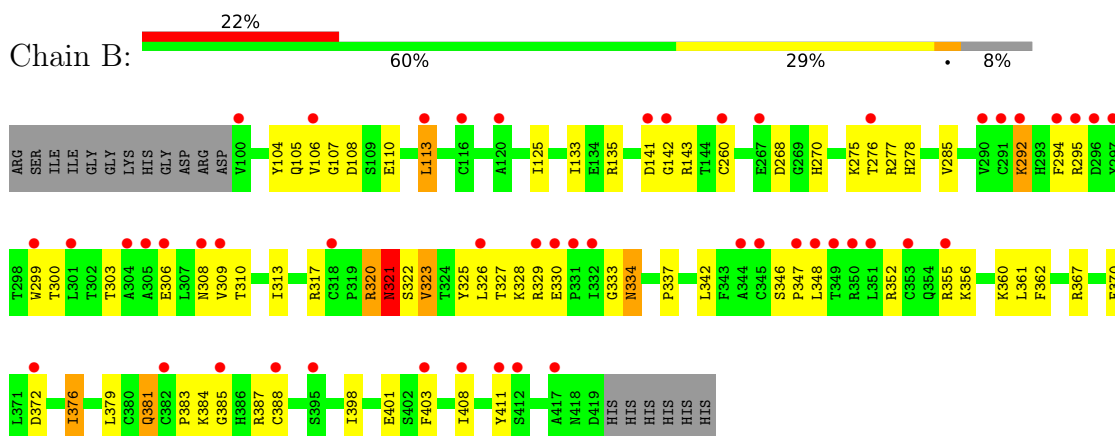
3 Residue-property plots [i](#)

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 giant-lens



• Molecule 1: Protein giant-lens



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	113.58Å 64.25Å 72.53Å 90.00° 101.59° 90.00°	Depositor
Resolution (Å)	35.53 – 2.51 35.53 – 2.51	Depositor EDS
% Data completeness (in resolution range)	93.9 (35.53-2.51) 98.9 (35.53-2.51)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.256 , 0.299 0.283 , 0.289	Depositor DCC
R_{free} test set	900 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.158	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	3420	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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	0.59	0/1695	0.86	3/2299 (0.1%)
1	B	0.56	0/1676	0.81	2/2274 (0.1%)
All	All	0.57	0/3371	0.83	5/4573 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	260	CYS	CA-C-N	6.44	126.46	119.89
1	B	260	CYS	C-N-CA	6.44	126.46	119.89
1	A	382	CYS	CA-C-N	6.08	126.42	119.92
1	A	382	CYS	C-N-CA	6.08	126.42	119.92
1	A	260	CYS	N-CA-C	5.17	116.16	109.65

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	1656	0	1596	66	0
1	B	1637	0	1579	78	0
2	A	81	0	0	12	0
2	B	46	0	0	11	0
All	All	3420	0	3175	139	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 (139) 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:141:ASP:HB3	1:A:142:GLY:HA2	1.26	1.17
1:B:141:ASP:HB3	1:B:142:GLY:HA2	1.35	1.08
1:B:105:GLN:CD	1:B:309:VAL:HG23	1.85	1.00
1:A:106:VAL:HG21	1:A:309:VAL:HG23	1.42	0.98
1:B:348:LEU:HB3	2:B:427:HOH:O	1.63	0.97
1:B:141:ASP:HA	1:B:143:ARG:H	1.33	0.93
1:A:353:CYS:C	1:A:354:GLN:HE21	1.78	0.92
1:A:141:ASP:CB	1:A:142:GLY:HA2	1.99	0.84
1:A:354:GLN:HE21	1:A:354:GLN:N	1.76	0.83
1:B:105:GLN:NE2	1:B:309:VAL:CG2	2.42	0.82
1:A:275:LYS:HD3	1:A:323:VAL:HG11	1.62	0.81
1:A:348:LEU:HD12	1:A:349:THR:N	1.96	0.81
1:B:292:LYS:HB3	1:B:292:LYS:NZ	1.95	0.81
1:B:105:GLN:NE2	1:B:309:VAL:HG23	1.95	0.80
1:A:354:GLN:N	1:A:354:GLN:NE2	2.29	0.80
1:B:141:ASP:CB	1:B:142:GLY:HA2	2.06	0.80
1:A:348:LEU:HD12	1:A:349:THR:H	1.47	0.79
1:A:395:SER:HB2	2:A:468:HOH:O	1.85	0.76
1:A:346:SER:HB2	2:A:459:HOH:O	1.84	0.76
1:B:355:ARG:O	1:B:356:LYS:HB3	1.86	0.75
1:A:275:LYS:HD3	1:A:323:VAL:CG1	2.18	0.73
1:B:360:LYS:NZ	1:B:376:ILE:HD11	2.03	0.73
1:A:294:PHE:HB3	2:A:454:HOH:O	1.89	0.72
1:A:353:CYS:C	1:A:354:GLN:NE2	2.46	0.72
1:B:321:ASN:HD22	1:B:321:ASN:C	1.98	0.71
1:A:376:ILE:HG23	1:B:372:ASP:HB2	1.72	0.71
1:A:365:ARG:HG2	1:A:408:ILE:HG22	1.74	0.70
1:B:294:PHE:HD1	1:B:295:ARG:HE	1.39	0.69
1:B:387:ARG:HD2	2:B:470:HOH:O	1.93	0.68
1:A:106:VAL:CG2	1:A:309:VAL:HG23	2.21	0.68
1:A:141:ASP:HB3	1:A:142:GLY:CA	2.15	0.68
1:A:141:ASP:HA	1:A:143:ARG:H	1.57	0.68
1:A:384:LYS:HE3	1:A:384:LYS:HA	1.74	0.68
1:A:348:LEU:HD12	1:A:349:THR:HG22	1.74	0.68
1:A:361:LEU:HD12	1:A:379:LEU:HD11	1.74	0.67
1:B:141:ASP:HA	1:B:143:ARG:N	2.06	0.67
1:A:278:HIS:HD2	2:A:441:HOH:O	1.78	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ASN:HB2	2:A:473:HOH:O	1.94	0.67
1:B:141:ASP:HB3	1:B:142:GLY:CA	2.21	0.66
1:B:108:ASP:HA	2:B:448:HOH:O	1.97	0.65
1:A:360:LYS:HB2	1:A:388:CYS:SG	2.37	0.64
1:B:321:ASN:HD22	1:B:322:SER:N	1.95	0.64
1:A:360:LYS:CG	1:A:376:ILE:HD11	2.27	0.64
1:B:403:PHE:HB3	1:B:408:ILE:CG1	2.29	0.63
1:A:350:ARG:HG2	1:B:370:PHE:CZ	2.33	0.63
1:A:362:PHE:CE1	1:A:376:ILE:HD13	2.33	0.63
1:A:295:ARG:NH1	1:A:325:TYR:OH	2.33	0.62
1:B:275:LYS:HG3	1:B:323:VAL:HG21	1.82	0.61
1:B:292:LYS:HB3	1:B:292:LYS:HZ3	1.64	0.61
1:A:261:PRO:HB2	1:A:280:LYS:HE3	1.84	0.60
1:B:360:LYS:HB2	1:B:388:CYS:SG	2.42	0.60
1:B:276:THR:HG23	1:B:277:ARG:HG3	1.83	0.59
1:B:321:ASN:HB3	2:B:468:HOH:O	2.03	0.59
1:B:292:LYS:HB3	1:B:292:LYS:HZ2	1.67	0.58
1:B:303:THR:HG23	1:B:303:THR:O	2.03	0.58
1:A:300:THR:HG23	1:A:315:HIS:NE2	2.19	0.58
1:B:275:LYS:HG3	1:B:323:VAL:CG2	2.34	0.58
1:A:381:GLN:HE21	1:A:381:GLN:HA	1.69	0.57
1:A:111:GLU:OE2	1:A:111:GLU:HA	2.04	0.57
1:A:128:TYR:O	1:B:275:LYS:O	2.23	0.57
1:A:350:ARG:HG2	1:B:370:PHE:HZ	1.68	0.57
1:B:268:ASP:O	1:B:270:HIS:HD2	1.89	0.56
1:B:309:VAL:HG22	1:B:310:THR:N	2.21	0.55
1:A:348:LEU:CD1	1:A:349:THR:HG22	2.37	0.55
1:B:328:LYS:HG2	1:B:329:ARG:N	2.22	0.54
1:B:352:ARG:HH11	1:B:383:PRO:HA	1.72	0.54
1:A:329:ARG:HG3	1:A:341:TYR:CE2	2.43	0.54
1:A:360:LYS:HG3	1:A:376:ILE:CD1	2.38	0.54
1:A:143:ARG:NH2	2:A:436:HOH:O	2.39	0.54
1:B:360:LYS:HZ2	1:B:376:ILE:HD11	1.73	0.54
1:A:111:GLU:OE2	1:A:111:GLU:CA	2.56	0.53
1:B:125:ILE:HG12	1:B:133:ILE:HG12	1.90	0.53
1:B:355:ARG:O	1:B:356:LYS:CB	2.53	0.53
1:A:349:THR:HG23	2:A:493:HOH:O	2.09	0.53
1:B:381:GLN:HG2	2:B:445:HOH:O	2.08	0.53
1:B:141:ASP:CB	1:B:142:GLY:CA	2.84	0.52
1:B:360:LYS:HZ3	1:B:376:ILE:HD11	1.74	0.52
1:A:295:ARG:NH2	2:A:453:HOH:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:403:PHE:HB3	1:B:408:ILE:HG13	1.91	0.52
1:B:292:LYS:NZ	1:B:292:LYS:CB	2.70	0.51
1:A:402:SER:O	1:A:404:LEU:HD12	2.10	0.51
1:A:381:GLN:HE21	1:A:381:GLN:CA	2.24	0.50
1:A:295:ARG:HG3	2:A:467:HOH:O	2.11	0.50
1:B:384:LYS:HD3	1:B:385:GLY:H	1.77	0.49
1:A:294:PHE:N	2:A:454:HOH:O	2.38	0.49
1:B:300:THR:HG22	1:B:342:LEU:HD13	1.92	0.49
1:B:275:LYS:CG	1:B:323:VAL:HG21	2.42	0.49
1:A:360:LYS:CG	1:A:376:ILE:CD1	2.90	0.48
1:A:127:LEU:HD23	1:A:131:PRO:HB3	1.96	0.48
1:B:326:LEU:HD22	1:B:401:GLU:HB2	1.96	0.48
1:A:125:ILE:HB	1:A:278:HIS:HB2	1.94	0.48
1:A:278:HIS:CD2	2:A:441:HOH:O	2.60	0.48
1:B:387:ARG:CG	2:B:470:HOH:O	2.61	0.47
1:B:333:GLY:O	1:B:334:ASN:HB2	2.14	0.47
1:A:294:PHE:CB	2:A:454:HOH:O	2.56	0.47
1:B:320:ARG:O	1:B:321:ASN:ND2	2.47	0.47
1:A:111:GLU:OE2	1:A:111:GLU:O	2.32	0.47
1:B:104:TYR:HE2	1:B:110:GLU:OE2	1.97	0.47
1:B:105:GLN:OE1	1:B:309:VAL:HG23	2.09	0.47
1:B:300:THR:HG22	1:B:342:LEU:CD1	2.44	0.47
1:B:321:ASN:C	1:B:321:ASN:ND2	2.69	0.46
1:A:360:LYS:HG3	1:A:376:ILE:HD12	1.98	0.46
1:B:330:GLU:HG2	1:B:342:LEU:HD21	1.97	0.46
1:B:333:GLY:HA3	2:B:466:HOH:O	2.13	0.46
1:A:292:LYS:HD2	1:A:292:LYS:N	2.30	0.46
1:B:294:PHE:HD1	1:B:295:ARG:NE	2.09	0.46
1:B:362:PHE:HB2	1:B:411:TYR:HB2	1.98	0.46
1:B:381:GLN:HA	1:B:381:GLN:HE21	1.81	0.46
1:B:285:VAL:HB	1:B:317:ARG:HD3	1.98	0.45
1:A:99:ASP:HB3	1:A:100:VAL:H	1.55	0.45
1:B:403:PHE:HB3	1:B:408:ILE:HG12	1.99	0.45
1:A:360:LYS:CD	1:A:376:ILE:HD11	2.46	0.45
1:A:326:LEU:HD23	1:A:327:THR:N	2.32	0.44
1:A:293:HIS:HB2	1:A:296:ASP:OD2	2.18	0.44
1:A:141:ASP:HA	1:A:143:ARG:N	2.27	0.44
1:B:107:GLY:O	2:B:448:HOH:O	2.20	0.44
1:B:306:GLU:HG3	2:B:440:HOH:O	2.17	0.44
1:A:298:THR:HG23	1:A:299:TRP:N	2.32	0.43
1:B:294:PHE:HB2	1:B:295:ARG:NH2	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:ARG:HE	1:A:387:ARG:HB3	1.54	0.43
1:B:325:TYR:CD1	1:B:361:LEU:HD22	2.54	0.43
1:B:141:ASP:OD2	1:B:143:ARG:O	2.38	0.42
1:B:299:TRP:HB2	1:B:313:ILE:O	2.20	0.42
1:B:323:VAL:O	1:B:346:SER:HB3	2.19	0.42
1:B:113:LEU:HD21	1:B:135:ARG:HB3	2.02	0.42
1:B:320:ARG:C	1:B:322:SER:H	2.27	0.42
1:A:376:ILE:CG2	1:B:372:ASP:HB2	2.45	0.42
1:B:125:ILE:HB	1:B:278:HIS:HB2	2.02	0.41
1:B:327:THR:HG23	1:B:328:LYS:N	2.34	0.41
1:B:309:VAL:CG2	1:B:310:THR:N	2.84	0.41
1:B:337:PRO:HA	2:B:431:HOH:O	2.21	0.41
1:A:304:ALA:HB3	1:A:307:LEU:HB2	2.03	0.41
1:A:368:GLN:O	1:A:369:GLU:C	2.64	0.41
1:B:106:VAL:CG1	1:B:308:ASN:O	2.69	0.41
1:B:367:ARG:HD3	1:B:367:ARG:HA	1.90	0.41
1:A:295:ARG:HE	1:A:295:ARG:N	2.19	0.40
1:B:387:ARG:CD	2:B:470:HOH:O	2.61	0.40
1:B:347:PRO:HG2	1:B:379:LEU:HA	2.02	0.40
1:A:261:PRO:HB2	1:A:280:LYS:CE	2.50	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	205/223 (92%)	191 (93%)	12 (6%)	2 (1%)	12	24
1	B	203/223 (91%)	192 (95%)	9 (4%)	2 (1%)	12	24
All	All	408/446 (92%)	383 (94%)	21 (5%)	4 (1%)	12	24

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	403	PHE
1	B	321	ASN
1	B	334	ASN
1	A	275	LYS

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	189/202 (94%)	167 (88%)	22 (12%)	5	11
1	B	187/202 (93%)	179 (96%)	8 (4%)	26	51
All	All	376/404 (93%)	346 (92%)	30 (8%)	11	24

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	CYS
1	A	122	CYS
1	A	276	THR
1	A	286	HIS
1	A	291	CYS
1	A	292	LYS
1	A	295	ARG
1	A	301	LEU
1	A	303	THR
1	A	309	VAL
1	A	321	ASN
1	A	329	ARG
1	A	342	LEU
1	A	350	ARG
1	A	354	GLN
1	A	360	LYS
1	A	361	LEU
1	A	376	ILE
1	A	381	GLN
1	A	384	LYS

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Mol	Chain	Res	Type
1	A	387	ARG
1	A	405	GLU
1	B	113	LEU
1	B	292	LYS
1	B	320	ARG
1	B	321	ASN
1	B	323	VAL
1	B	376	ILE
1	B	381	GLN
1	B	398	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	GLN
1	A	312	GLN
1	A	321	ASN
1	A	354	GLN
1	A	381	GLN
1	A	391	HIS
1	A	407	ASN
1	B	270	HIS
1	B	312	GLN
1	B	321	ASN
1	B	334	ASN
1	B	354	GLN
1	B	377	ASN
1	B	381	GLN
1	B	391	HIS
1	B	407	ASN

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 [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	207/223 (92%)	1.31	36 (17%) 4 3	24, 42, 53, 59	0
1	B	205/223 (91%)	1.45	49 (23%) 2 1	26, 45, 59, 63	0
All	All	412/446 (92%)	1.38	85 (20%) 2 2	24, 43, 57, 63	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	142	GLY	5.4
1	B	348	LEU	4.6
1	A	295	ARG	4.4
1	B	297	TYR	4.1
1	A	116	CYS	3.8
1	B	294	PHE	3.8
1	B	306	GLU	3.7
1	B	260	CYS	3.6
1	B	295	ARG	3.6
1	B	305	ALA	3.5
1	B	344	ALA	3.5
1	A	144	THR	3.4
1	B	395	SER	3.3
1	A	296	ASP	3.3
1	B	291	CYS	3.2
1	A	334	ASN	3.2
1	B	292	LYS	3.1
1	A	291	CYS	3.1
1	B	388	CYS	3.0
1	A	142	GLY	3.0
1	A	130	THR	3.0
1	B	296	ASP	3.0
1	B	417	ALA	3.0
1	A	405	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	276	THR	2.9
1	A	309	VAL	2.9
1	B	349	THR	2.9
1	A	260	CYS	2.9
1	B	372	ASP	2.8
1	A	99	ASP	2.7
1	B	351	LEU	2.7
1	B	318	CYS	2.7
1	A	402	SER	2.6
1	B	412	SER	2.6
1	A	329	ARG	2.6
1	A	372	ASP	2.6
1	B	100	VAL	2.6
1	A	339	TYR	2.6
1	B	116	CYS	2.5
1	B	290	VAL	2.5
1	A	285	VAL	2.5
1	B	141	ASP	2.5
1	B	301	LEU	2.5
1	A	403	PHE	2.5
1	B	326	LEU	2.4
1	A	347	PRO	2.4
1	B	330	GLU	2.4
1	A	388	CYS	2.4
1	B	332	ILE	2.4
1	B	120	ALA	2.4
1	A	137	CYS	2.4
1	B	106	VAL	2.4
1	B	309	VAL	2.3
1	B	347	PRO	2.3
1	B	353	CYS	2.3
1	A	341	TYR	2.3
1	A	376	ILE	2.3
1	B	113	LEU	2.3
1	B	299	TRP	2.3
1	A	408	ILE	2.2
1	A	348	LEU	2.2
1	A	311	GLU	2.2
1	B	267	GLU	2.2
1	A	138	ARG	2.2
1	B	331	PRO	2.2
1	A	143	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	403	PHE	2.2
1	A	356	LYS	2.2
1	A	416	MET	2.2
1	B	382	CYS	2.2
1	A	305	ALA	2.1
1	B	304	ALA	2.1
1	B	385	GLY	2.1
1	B	345	CYS	2.1
1	B	355	ARG	2.1
1	A	115	VAL	2.1
1	A	399	ALA	2.1
1	B	408	ILE	2.1
1	A	297	TYR	2.1
1	B	350	ARG	2.1
1	A	310	THR	2.1
1	B	329	ARG	2.0
1	A	267	GLU	2.0
1	B	308	ASN	2.0
1	B	411	TYR	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.