



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:20 PM UTC

PDB ID : 6M09 / pdb_00006m09
Title : The ligand-free structure of the chloroplast protein At3g03890
Authors : Wang, J.; Liu, L.
Deposited on : 2020-02-20
Resolution : 2.10 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

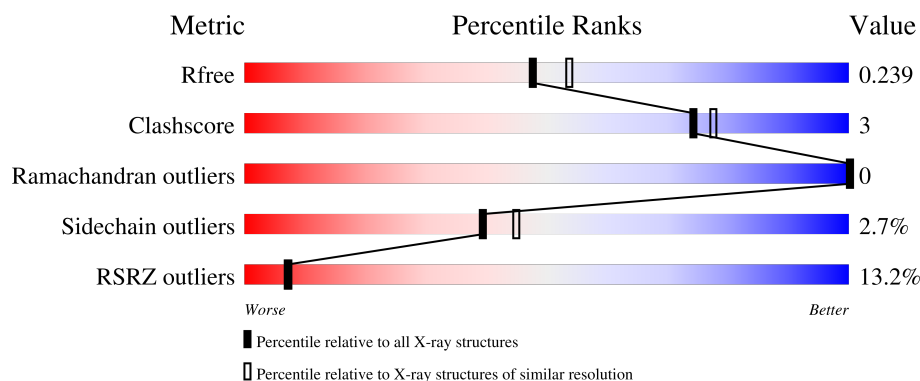
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	292	
1	B	292	
1	C	292	
1	D	292	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8084 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 AT3G03890 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	4	0
			1856	1172	317	356	11			
1	B	252	Total	C	N	O	S	0	4	0
			1901	1205	327	358	11			
1	C	246	Total	C	N	O	S	0	5	0
			1859	1174	317	357	11			
1	D	253	Total	C	N	O	S	0	3	0
			1900	1201	327	361	11			

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	30	MET	-	expression tag	UNP Q8LDU1
A	31	GLY	-	expression tag	UNP Q8LDU1
A	32	SER	-	expression tag	UNP Q8LDU1
A	33	SER	-	expression tag	UNP Q8LDU1
A	34	HIS	-	expression tag	UNP Q8LDU1
A	35	HIS	-	expression tag	UNP Q8LDU1
A	36	HIS	-	expression tag	UNP Q8LDU1
A	37	HIS	-	expression tag	UNP Q8LDU1
A	38	HIS	-	expression tag	UNP Q8LDU1
A	39	HIS	-	expression tag	UNP Q8LDU1
A	40	SER	-	expression tag	UNP Q8LDU1
A	41	SER	-	expression tag	UNP Q8LDU1
A	42	GLY	-	expression tag	UNP Q8LDU1
A	43	LEU	-	expression tag	UNP Q8LDU1
A	44	VAL	-	expression tag	UNP Q8LDU1
A	45	PRO	-	expression tag	UNP Q8LDU1
A	46	ARG	-	expression tag	UNP Q8LDU1
A	47	GLY	-	expression tag	UNP Q8LDU1
A	48	SER	-	expression tag	UNP Q8LDU1
A	49	HIS	-	expression tag	UNP Q8LDU1
A	50	MET	-	expression tag	UNP Q8LDU1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	51	ALA	-	expression tag	UNP Q8LDU1
A	52	SER	-	expression tag	UNP Q8LDU1
A	53	MET	-	expression tag	UNP Q8LDU1
A	54	THR	-	expression tag	UNP Q8LDU1
A	55	GLY	-	expression tag	UNP Q8LDU1
A	56	GLY	-	expression tag	UNP Q8LDU1
A	57	GLN	-	expression tag	UNP Q8LDU1
A	58	GLN	-	expression tag	UNP Q8LDU1
A	59	MET	-	expression tag	UNP Q8LDU1
A	60	GLY	-	expression tag	UNP Q8LDU1
A	61	ARG	-	expression tag	UNP Q8LDU1
A	62	GLY	-	expression tag	UNP Q8LDU1
B	30	MET	-	expression tag	UNP Q8LDU1
B	31	GLY	-	expression tag	UNP Q8LDU1
B	32	SER	-	expression tag	UNP Q8LDU1
B	33	SER	-	expression tag	UNP Q8LDU1
B	34	HIS	-	expression tag	UNP Q8LDU1
B	35	HIS	-	expression tag	UNP Q8LDU1
B	36	HIS	-	expression tag	UNP Q8LDU1
B	37	HIS	-	expression tag	UNP Q8LDU1
B	38	HIS	-	expression tag	UNP Q8LDU1
B	39	HIS	-	expression tag	UNP Q8LDU1
B	40	SER	-	expression tag	UNP Q8LDU1
B	41	SER	-	expression tag	UNP Q8LDU1
B	42	GLY	-	expression tag	UNP Q8LDU1
B	43	LEU	-	expression tag	UNP Q8LDU1
B	44	VAL	-	expression tag	UNP Q8LDU1
B	45	PRO	-	expression tag	UNP Q8LDU1
B	46	ARG	-	expression tag	UNP Q8LDU1
B	47	GLY	-	expression tag	UNP Q8LDU1
B	48	SER	-	expression tag	UNP Q8LDU1
B	49	HIS	-	expression tag	UNP Q8LDU1
B	50	MET	-	expression tag	UNP Q8LDU1
B	51	ALA	-	expression tag	UNP Q8LDU1
B	52	SER	-	expression tag	UNP Q8LDU1
B	53	MET	-	expression tag	UNP Q8LDU1
B	54	THR	-	expression tag	UNP Q8LDU1
B	55	GLY	-	expression tag	UNP Q8LDU1
B	56	GLY	-	expression tag	UNP Q8LDU1
B	57	GLN	-	expression tag	UNP Q8LDU1
B	58	GLN	-	expression tag	UNP Q8LDU1
B	59	MET	-	expression tag	UNP Q8LDU1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	60	GLY	-	expression tag	UNP Q8LDU1
B	61	ARG	-	expression tag	UNP Q8LDU1
B	62	GLY	-	expression tag	UNP Q8LDU1
C	30	MET	-	expression tag	UNP Q8LDU1
C	31	GLY	-	expression tag	UNP Q8LDU1
C	32	SER	-	expression tag	UNP Q8LDU1
C	33	SER	-	expression tag	UNP Q8LDU1
C	34	HIS	-	expression tag	UNP Q8LDU1
C	35	HIS	-	expression tag	UNP Q8LDU1
C	36	HIS	-	expression tag	UNP Q8LDU1
C	37	HIS	-	expression tag	UNP Q8LDU1
C	38	HIS	-	expression tag	UNP Q8LDU1
C	39	HIS	-	expression tag	UNP Q8LDU1
C	40	SER	-	expression tag	UNP Q8LDU1
C	41	SER	-	expression tag	UNP Q8LDU1
C	42	GLY	-	expression tag	UNP Q8LDU1
C	43	LEU	-	expression tag	UNP Q8LDU1
C	44	VAL	-	expression tag	UNP Q8LDU1
C	45	PRO	-	expression tag	UNP Q8LDU1
C	46	ARG	-	expression tag	UNP Q8LDU1
C	47	GLY	-	expression tag	UNP Q8LDU1
C	48	SER	-	expression tag	UNP Q8LDU1
C	49	HIS	-	expression tag	UNP Q8LDU1
C	50	MET	-	expression tag	UNP Q8LDU1
C	51	ALA	-	expression tag	UNP Q8LDU1
C	52	SER	-	expression tag	UNP Q8LDU1
C	53	MET	-	expression tag	UNP Q8LDU1
C	54	THR	-	expression tag	UNP Q8LDU1
C	55	GLY	-	expression tag	UNP Q8LDU1
C	56	GLY	-	expression tag	UNP Q8LDU1
C	57	GLN	-	expression tag	UNP Q8LDU1
C	58	GLN	-	expression tag	UNP Q8LDU1
C	59	MET	-	expression tag	UNP Q8LDU1
C	60	GLY	-	expression tag	UNP Q8LDU1
C	61	ARG	-	expression tag	UNP Q8LDU1
C	62	GLY	-	expression tag	UNP Q8LDU1
D	30	MET	-	expression tag	UNP Q8LDU1
D	31	GLY	-	expression tag	UNP Q8LDU1
D	32	SER	-	expression tag	UNP Q8LDU1
D	33	SER	-	expression tag	UNP Q8LDU1
D	34	HIS	-	expression tag	UNP Q8LDU1
D	35	HIS	-	expression tag	UNP Q8LDU1

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Chain	Residue	Modelled	Actual	Comment	Reference
D	36	HIS	-	expression tag	UNP Q8LDU1
D	37	HIS	-	expression tag	UNP Q8LDU1
D	38	HIS	-	expression tag	UNP Q8LDU1
D	39	HIS	-	expression tag	UNP Q8LDU1
D	40	SER	-	expression tag	UNP Q8LDU1
D	41	SER	-	expression tag	UNP Q8LDU1
D	42	GLY	-	expression tag	UNP Q8LDU1
D	43	LEU	-	expression tag	UNP Q8LDU1
D	44	VAL	-	expression tag	UNP Q8LDU1
D	45	PRO	-	expression tag	UNP Q8LDU1
D	46	ARG	-	expression tag	UNP Q8LDU1
D	47	GLY	-	expression tag	UNP Q8LDU1
D	48	SER	-	expression tag	UNP Q8LDU1
D	49	HIS	-	expression tag	UNP Q8LDU1
D	50	MET	-	expression tag	UNP Q8LDU1
D	51	ALA	-	expression tag	UNP Q8LDU1
D	52	SER	-	expression tag	UNP Q8LDU1
D	53	MET	-	expression tag	UNP Q8LDU1
D	54	THR	-	expression tag	UNP Q8LDU1
D	55	GLY	-	expression tag	UNP Q8LDU1
D	56	GLY	-	expression tag	UNP Q8LDU1
D	57	GLN	-	expression tag	UNP Q8LDU1
D	58	GLN	-	expression tag	UNP Q8LDU1
D	59	MET	-	expression tag	UNP Q8LDU1
D	60	GLY	-	expression tag	UNP Q8LDU1
D	61	ARG	-	expression tag	UNP Q8LDU1
D	62	GLY	-	expression tag	UNP Q8LDU1

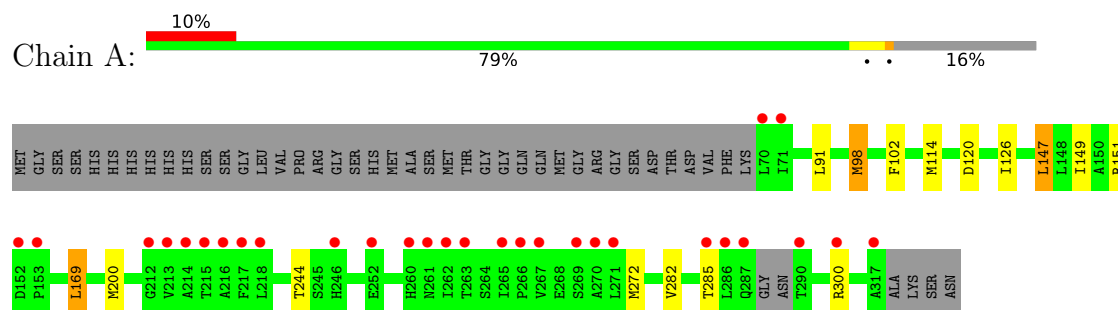
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	151	Total O 151 151	0	0
2	B	128	Total O 128 128	0	0
2	C	131	Total O 131 131	0	0
2	D	158	Total O 158 158	0	0

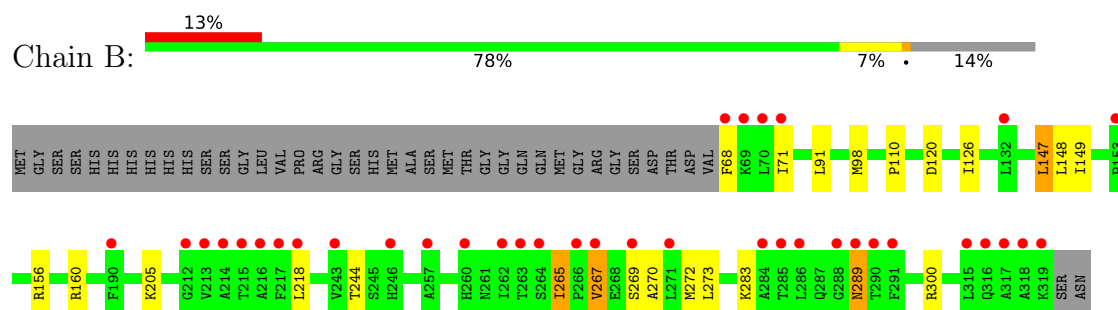
3 Residue-property plots [i](#)

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.

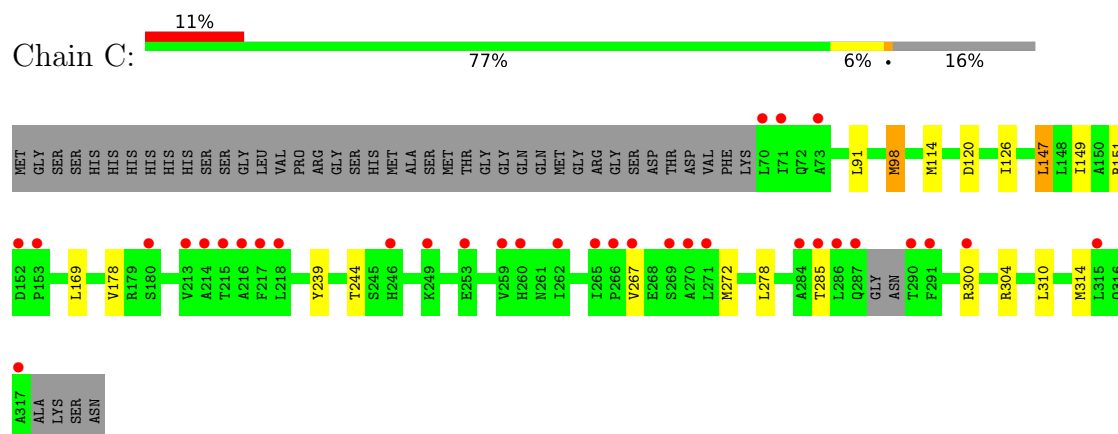
• Molecule 1: AT3G03890 protein



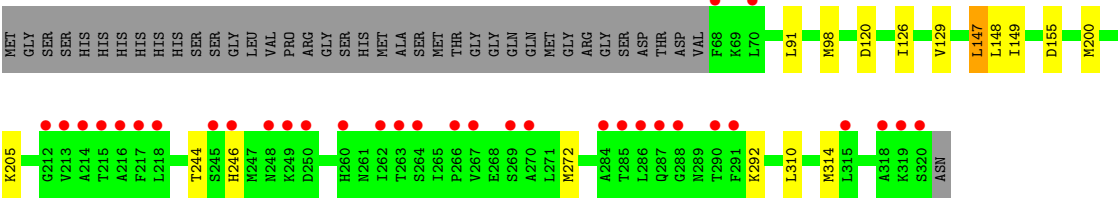
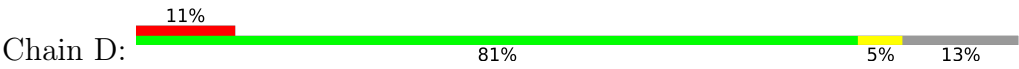
• Molecule 1: AT3G03890 protein



• Molecule 1: AT3G03890 protein



• Molecule 1: AT3G03890 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	59.93Å 79.96Å 80.15Å 99.63° 109.80° 104.48°	Depositor
Resolution (Å)	37.76 – 2.10 37.76 – 2.10	Depositor EDS
% Data completeness (in resolution range)	87.0 (37.76-2.10) 87.0 (37.76-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 2.10Å)	Xtriage
Refinement program	PHENIX v1.12	Depositor
R, R_{free}	0.200 , 0.239 0.200 , 0.239	Depositor DCC
R_{free} test set	3358 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8084	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.12% 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 [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	0.18	0/1904	0.36	0/2586
1	B	0.16	0/1947	0.35	0/2643
1	C	0.16	0/1910	0.36	0/2594
1	D	0.17	0/1945	0.36	0/2640
All	All	0.17	0/7706	0.36	0/10463

There are no bond length outliers.

There are no bond angle outliers.

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	1856	0	1782	11	0
1	B	1901	0	1856	17	0
1	C	1859	0	1787	11	0
1	D	1900	0	1857	12	0
2	A	151	0	0	2	0
2	B	128	0	0	5	0
2	C	131	0	0	1	0
2	D	158	0	0	2	0
All	All	8084	0	7282	46	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 3.

All (46) 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:D:129:VAL:HG21	1:D:200:MET:HE2	1.51	0.90
1:A:147:LEU:HD13	1:A:149:ILE:HD11	1.61	0.83
1:D:147:LEU:HD13	1:D:149[A]:ILE:HD11	1.61	0.82
1:C:98[A]:MET:HB3	1:D:98[A]:MET:HE2	1.74	0.70
1:A:151:ARG:NH2	2:A:404:HOH:O	2.29	0.63
1:C:151:ARG:NH1	2:C:403:HOH:O	2.32	0.62
1:B:147:LEU:HD13	1:B:149[A]:ILE:HD11	1.80	0.62
1:D:246:HIS:NE2	2:D:405:HOH:O	2.31	0.61
1:B:265:ILE:HG22	1:B:267:VAL:HG12	1.86	0.58
1:B:244:THR:HG22	1:B:272:MET:HE2	1.85	0.57
1:B:68:PHE:N	2:B:405:HOH:O	2.38	0.56
1:D:244:THR:HG22	1:D:272:MET:HE2	1.87	0.56
1:C:120:ASP:HB3	1:C:126:ILE:HD11	1.87	0.55
1:A:98[A]:MET:HB3	1:B:98[A]:MET:HE2	1.90	0.54
1:D:205:LYS:NZ	2:D:409:HOH:O	2.36	0.54
1:A:98[A]:MET:HG3	1:A:114:MET:SD	2.48	0.53
1:B:273:LEU:HD21	1:B:283:LYS:HE3	1.91	0.53
1:B:205:LYS:NZ	2:B:408:HOH:O	2.43	0.52
1:B:289:ASN:N	1:B:289:ASN:OD1	2.43	0.51
1:C:98[A]:MET:HG3	1:C:114:MET:SD	2.50	0.51
1:B:300:ARG:NE	2:B:409:HOH:O	2.44	0.50
1:B:120:ASP:HB3	1:B:126:ILE:HD11	1.94	0.50
1:D:120:ASP:HB3	1:D:126:ILE:HD11	1.93	0.50
1:C:244:THR:HG22	1:C:272:MET:HG2	1.95	0.49
1:C:98[B]:MET:HE2	1:D:98[B]:MET:HB3	1.94	0.49
1:A:120:ASP:HB3	1:A:126:ILE:HD11	1.95	0.48
1:B:156:ARG:NH2	2:B:410:HOH:O	2.47	0.48
1:C:239:TYR:CD1	1:C:304:ARG:HD3	2.49	0.47
1:B:244:THR:HG22	1:B:272:MET:HB3	1.95	0.47
1:B:160:ARG:NH2	2:B:411:HOH:O	2.47	0.47
1:A:102:PHE:HE2	1:B:110:PRO:HD3	1.80	0.47
1:C:147:LEU:HD13	1:C:149:ILE:HD11	1.96	0.46
1:A:114:MET:SD	1:B:98[B]:MET:HE3	2.55	0.46
1:D:244:THR:HG22	1:D:272:MET:HB3	1.97	0.45
1:B:98[B]:MET:HG3	1:B:148:LEU:HD23	1.98	0.45
1:C:126:ILE:HG21	1:C:178:VAL:HG13	1.99	0.45
1:C:278:LEU:HD21	1:C:300:ARG:NH1	2.32	0.44
1:D:310:LEU:O	1:D:314:MET:HG3	2.18	0.44
1:B:267:VAL:HG21	1:B:270:ALA:HB2	1.99	0.43
1:A:169:LEU:HD13	1:A:200:MET:HE2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:310:LEU:O	1:C:314:MET:HG3	2.18	0.43
1:A:300:ARG:NH1	2:A:407:HOH:O	2.43	0.42
1:A:244:THR:HG22	1:A:272:MET:HG2	2.02	0.42
1:A:272:MET:HA	1:A:282:VAL:HG12	2.01	0.42
1:D:148:LEU:O	1:D:149[B]:ILE:HD13	2.20	0.41
1:D:155:ASP:OD2	1:D:292:LYS:NZ	2.49	0.41

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	246/292 (84%)	244 (99%)	2 (1%)	0	100	100
1	B	254/292 (87%)	251 (99%)	3 (1%)	0	100	100
1	C	247/292 (85%)	244 (99%)	3 (1%)	0	100	100
1	D	254/292 (87%)	251 (99%)	3 (1%)	0	100	100
All	All	1001/1168 (86%)	990 (99%)	11 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	193/244 (79%)	187 (97%)	6 (3%)	35	39
1	B	197/244 (81%)	189 (96%)	8 (4%)	27	29
1	C	194/244 (80%)	187 (96%)	7 (4%)	31	34
1	D	198/244 (81%)	196 (99%)	2 (1%)	68	76
All	All	782/976 (80%)	759 (97%)	23 (3%)	39	42

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	LEU
1	A	98[A]	MET
1	A	98[B]	MET
1	A	147	LEU
1	A	169	LEU
1	A	285	THR
1	B	71	ILE
1	B	91	LEU
1	B	147	LEU
1	B	218	LEU
1	B	265	ILE
1	B	267	VAL
1	B	269	SER
1	B	289	ASN
1	C	91	LEU
1	C	98[A]	MET
1	C	98[B]	MET
1	C	147	LEU
1	C	169	LEU
1	C	267	VAL
1	C	285	THR
1	D	91	LEU
1	D	147	LEU

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

Mol	Chain	Res	Type
1	A	135	HIS
1	B	261	ASN
1	B	281	ASN
1	C	281	ASN

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	246/292 (84%)	0.50	29 (11%)	9 9	11, 29, 66, 73	6 (2%)
1	B	252/292 (86%)	0.65	37 (14%)	6 6	11, 31, 65, 76	6 (2%)
1	C	246/292 (84%)	0.64	33 (13%)	7 7	11, 31, 65, 76	8 (3%)
1	D	253/292 (86%)	0.52	33 (13%)	7 7	10, 29, 64, 80	8 (3%)
All	All	997/1168 (85%)	0.58	132 (13%)	7 7	10, 30, 65, 80	28 (2%)

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	214	ALA	9.3
1	A	214	ALA	6.0
1	D	217	PHE	5.5
1	B	214	ALA	5.4
1	A	213	VAL	5.4
1	B	68	PHE	5.4
1	B	217	PHE	5.3
1	D	213	VAL	5.2
1	B	70	LEU	5.1
1	C	70	LEU	5.1
1	A	70	LEU	5.0
1	C	290	THR	4.8
1	D	214	ALA	4.6
1	A	290	THR	4.4
1	D	68	PHE	4.4
1	B	318	ALA	4.4
1	C	215	THR	4.3
1	B	216	ALA	4.2
1	A	246	HIS	4.2
1	B	262	ILE	4.2
1	C	213	VAL	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	270	ALA	4.2
1	A	285	THR	3.9
1	C	287	GLN	3.8
1	C	216	ALA	3.8
1	B	190[A]	PHE	3.7
1	A	286	LEU	3.7
1	B	218	LEU	3.7
1	D	284	ALA	3.7
1	D	266	PRO	3.7
1	C	286	LEU	3.6
1	D	285	THR	3.6
1	A	317	ALA	3.6
1	C	266	PRO	3.6
1	C	217	PHE	3.6
1	C	284	ALA	3.5
1	D	318	ALA	3.5
1	B	267	VAL	3.5
1	C	267	VAL	3.5
1	D	70	LEU	3.4
1	C	246	HIS	3.4
1	C	285	THR	3.4
1	D	260	HIS	3.3
1	A	218	LEU	3.3
1	C	317	ALA	3.3
1	A	217	PHE	3.3
1	B	271	LEU	3.2
1	C	315	LEU	3.2
1	B	71	ILE	3.2
1	D	269	SER	3.2
1	A	271	LEU	3.2
1	C	265	ILE	3.1
1	B	264	SER	3.1
1	C	152	ASP	3.1
1	C	218	LEU	3.1
1	C	269	SER	3.1
1	C	291	PHE	3.1
1	D	315	LEU	3.1
1	D	287	GLN	3.1
1	A	262	ILE	3.1
1	D	288	GLY	3.0
1	B	263	THR	3.0
1	D	216	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	260	HIS	3.0
1	B	319	LYS	3.0
1	C	153	PRO	3.0
1	D	270	ALA	2.9
1	D	319	LYS	2.9
1	D	264	SER	2.9
1	C	271	LEU	2.9
1	D	291	PHE	2.9
1	A	260	HIS	2.9
1	B	288	GLY	2.9
1	B	315	LEU	2.8
1	B	153	PRO	2.8
1	C	71	ILE	2.8
1	B	316	GLN	2.7
1	D	250	ASP	2.7
1	B	291	PHE	2.7
1	A	263	THR	2.7
1	A	152	ASP	2.7
1	C	270	ALA	2.7
1	C	262	ILE	2.7
1	A	216	ALA	2.6
1	B	257	ALA	2.6
1	A	269	SER	2.6
1	B	215	THR	2.6
1	B	132	LEU	2.6
1	D	218	LEU	2.6
1	D	215	THR	2.6
1	D	262	ILE	2.5
1	D	246	HIS	2.5
1	B	69	LYS	2.5
1	A	287	GLN	2.5
1	C	180	SER	2.5
1	B	286	LEU	2.5
1	B	212	GLY	2.5
1	A	267	VAL	2.4
1	B	243	VAL	2.4
1	A	266	PRO	2.4
1	A	261	ASN	2.4
1	A	153	PRO	2.4
1	C	253	GLU	2.4
1	B	285	THR	2.4
1	B	246	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	266	PRO	2.3
1	B	289	ASN	2.3
1	C	260	HIS	2.3
1	B	213	VAL	2.3
1	D	249	LYS	2.3
1	A	265	ILE	2.3
1	B	290	THR	2.3
1	D	245	SER	2.2
1	A	252	GLU	2.2
1	B	269	SER	2.2
1	C	259	VAL	2.2
1	D	267	VAL	2.2
1	D	320	SER	2.2
1	C	300	ARG	2.2
1	D	263	THR	2.1
1	D	290	THR	2.1
1	D	212	GLY	2.1
1	D	248	ASN	2.1
1	A	71	ILE	2.1
1	A	212	GLY	2.1
1	D	286	LEU	2.1
1	A	300	ARG	2.1
1	B	284	ALA	2.1
1	B	317	ALA	2.1
1	C	73	ALA	2.1
1	A	215	THR	2.0
1	C	249	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.