



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 17, 2024 – 06:35 PM EDT

PDB ID : 5U50
Title : Crystal structure of citrus MAF1 in space group C 2 2 21
Authors : Soprano, A.S.; Giuseppe, P.O.; Nascimento, A.F.Z.; Benedetti, C.E.; Murakami, M.T.
Deposited on : 2016-12-06
Resolution : 2.90 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	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

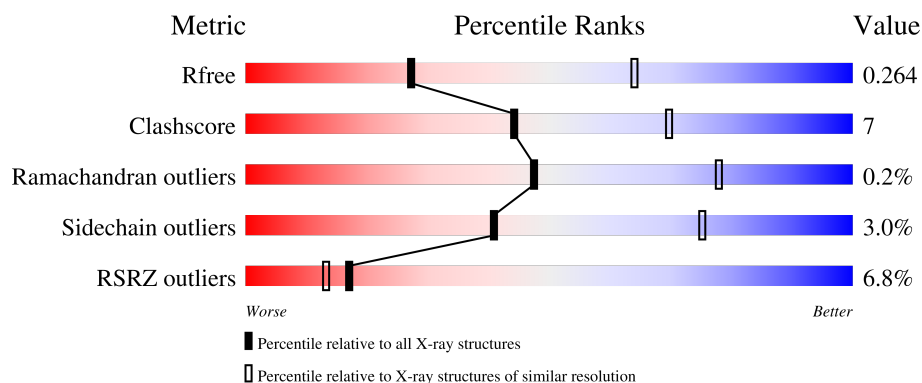
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	
1	B	265	
1	C	265	
1	D	265	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 5690 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 Repressor of RNA polymerase III transcription.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	178	Total	C	N	O	S	0	0	0
			1484	963	236	279	6			
1	B	172	Total	C	N	O	S	0	0	0
			1438	935	230	267	6			
1	C	167	Total	C	N	O	S	0	0	0
			1399	908	224	261	6			
1	D	163	Total	C	N	O	S	0	0	0
			1368	892	215	255	6			

There are 164 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-40	MET	-	initiating methionine	UNP G9I821
A	-39	GLY	-	expression tag	UNP G9I821
A	-38	SER	-	expression tag	UNP G9I821
A	-37	SER	-	expression tag	UNP G9I821
A	-36	HIS	-	expression tag	UNP G9I821
A	-35	HIS	-	expression tag	UNP G9I821
A	-34	HIS	-	expression tag	UNP G9I821
A	-33	HIS	-	expression tag	UNP G9I821
A	-32	HIS	-	expression tag	UNP G9I821
A	-31	HIS	-	expression tag	UNP G9I821
A	-30	SER	-	expression tag	UNP G9I821
A	-29	SER	-	expression tag	UNP G9I821
A	-28	GLY	-	expression tag	UNP G9I821
A	-27	LEU	-	expression tag	UNP G9I821
A	-26	VAL	-	expression tag	UNP G9I821
A	-25	PRO	-	expression tag	UNP G9I821
A	-24	ARG	-	expression tag	UNP G9I821
A	-23	GLY	-	expression tag	UNP G9I821
A	-22	SER	-	expression tag	UNP G9I821
A	-21	HIS	-	expression tag	UNP G9I821
A	-20	MET	-	expression tag	UNP G9I821

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	ALA	-	expression tag	UNP G9I821
A	-18	SER	-	expression tag	UNP G9I821
A	-17	MET	-	expression tag	UNP G9I821
A	-16	THR	-	expression tag	UNP G9I821
A	-15	GLY	-	expression tag	UNP G9I821
A	-14	GLY	-	expression tag	UNP G9I821
A	-13	GLN	-	expression tag	UNP G9I821
A	-12	GLN	-	expression tag	UNP G9I821
A	-11	MET	-	expression tag	UNP G9I821
A	-10	GLY	-	expression tag	UNP G9I821
A	-9	ARG	-	expression tag	UNP G9I821
A	-8	GLY	-	expression tag	UNP G9I821
A	-7	SER	-	expression tag	UNP G9I821
A	-6	GLU	-	expression tag	UNP G9I821
A	-5	PHE	-	expression tag	UNP G9I821
A	-4	GLU	-	expression tag	UNP G9I821
A	-3	LEU	-	expression tag	UNP G9I821
A	-2	ARG	-	expression tag	UNP G9I821
A	-1	ARG	-	expression tag	UNP G9I821
A	0	PRO	-	expression tag	UNP G9I821
B	-40	MET	-	initiating methionine	UNP G9I821
B	-39	GLY	-	expression tag	UNP G9I821
B	-38	SER	-	expression tag	UNP G9I821
B	-37	SER	-	expression tag	UNP G9I821
B	-36	HIS	-	expression tag	UNP G9I821
B	-35	HIS	-	expression tag	UNP G9I821
B	-34	HIS	-	expression tag	UNP G9I821
B	-33	HIS	-	expression tag	UNP G9I821
B	-32	HIS	-	expression tag	UNP G9I821
B	-31	HIS	-	expression tag	UNP G9I821
B	-30	SER	-	expression tag	UNP G9I821
B	-29	SER	-	expression tag	UNP G9I821
B	-28	GLY	-	expression tag	UNP G9I821
B	-27	LEU	-	expression tag	UNP G9I821
B	-26	VAL	-	expression tag	UNP G9I821
B	-25	PRO	-	expression tag	UNP G9I821
B	-24	ARG	-	expression tag	UNP G9I821
B	-23	GLY	-	expression tag	UNP G9I821
B	-22	SER	-	expression tag	UNP G9I821
B	-21	HIS	-	expression tag	UNP G9I821
B	-20	MET	-	expression tag	UNP G9I821
B	-19	ALA	-	expression tag	UNP G9I821

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	SER	-	expression tag	UNP G9I821
B	-17	MET	-	expression tag	UNP G9I821
B	-16	THR	-	expression tag	UNP G9I821
B	-15	GLY	-	expression tag	UNP G9I821
B	-14	GLY	-	expression tag	UNP G9I821
B	-13	GLN	-	expression tag	UNP G9I821
B	-12	GLN	-	expression tag	UNP G9I821
B	-11	MET	-	expression tag	UNP G9I821
B	-10	GLY	-	expression tag	UNP G9I821
B	-9	ARG	-	expression tag	UNP G9I821
B	-8	GLY	-	expression tag	UNP G9I821
B	-7	SER	-	expression tag	UNP G9I821
B	-6	GLU	-	expression tag	UNP G9I821
B	-5	PHE	-	expression tag	UNP G9I821
B	-4	GLU	-	expression tag	UNP G9I821
B	-3	LEU	-	expression tag	UNP G9I821
B	-2	ARG	-	expression tag	UNP G9I821
B	-1	ARG	-	expression tag	UNP G9I821
B	0	PRO	-	expression tag	UNP G9I821
C	-40	MET	-	initiating methionine	UNP G9I821
C	-39	GLY	-	expression tag	UNP G9I821
C	-38	SER	-	expression tag	UNP G9I821
C	-37	SER	-	expression tag	UNP G9I821
C	-36	HIS	-	expression tag	UNP G9I821
C	-35	HIS	-	expression tag	UNP G9I821
C	-34	HIS	-	expression tag	UNP G9I821
C	-33	HIS	-	expression tag	UNP G9I821
C	-32	HIS	-	expression tag	UNP G9I821
C	-31	HIS	-	expression tag	UNP G9I821
C	-30	SER	-	expression tag	UNP G9I821
C	-29	SER	-	expression tag	UNP G9I821
C	-28	GLY	-	expression tag	UNP G9I821
C	-27	LEU	-	expression tag	UNP G9I821
C	-26	VAL	-	expression tag	UNP G9I821
C	-25	PRO	-	expression tag	UNP G9I821
C	-24	ARG	-	expression tag	UNP G9I821
C	-23	GLY	-	expression tag	UNP G9I821
C	-22	SER	-	expression tag	UNP G9I821
C	-21	HIS	-	expression tag	UNP G9I821
C	-20	MET	-	expression tag	UNP G9I821
C	-19	ALA	-	expression tag	UNP G9I821
C	-18	SER	-	expression tag	UNP G9I821

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-17	MET	-	expression tag	UNP G9I821
C	-16	THR	-	expression tag	UNP G9I821
C	-15	GLY	-	expression tag	UNP G9I821
C	-14	GLY	-	expression tag	UNP G9I821
C	-13	GLN	-	expression tag	UNP G9I821
C	-12	GLN	-	expression tag	UNP G9I821
C	-11	MET	-	expression tag	UNP G9I821
C	-10	GLY	-	expression tag	UNP G9I821
C	-9	ARG	-	expression tag	UNP G9I821
C	-8	GLY	-	expression tag	UNP G9I821
C	-7	SER	-	expression tag	UNP G9I821
C	-6	GLU	-	expression tag	UNP G9I821
C	-5	PHE	-	expression tag	UNP G9I821
C	-4	GLU	-	expression tag	UNP G9I821
C	-3	LEU	-	expression tag	UNP G9I821
C	-2	ARG	-	expression tag	UNP G9I821
C	-1	ARG	-	expression tag	UNP G9I821
C	0	PRO	-	expression tag	UNP G9I821
D	-40	MET	-	initiating methionine	UNP G9I821
D	-39	GLY	-	expression tag	UNP G9I821
D	-38	SER	-	expression tag	UNP G9I821
D	-37	SER	-	expression tag	UNP G9I821
D	-36	HIS	-	expression tag	UNP G9I821
D	-35	HIS	-	expression tag	UNP G9I821
D	-34	HIS	-	expression tag	UNP G9I821
D	-33	HIS	-	expression tag	UNP G9I821
D	-32	HIS	-	expression tag	UNP G9I821
D	-31	HIS	-	expression tag	UNP G9I821
D	-30	SER	-	expression tag	UNP G9I821
D	-29	SER	-	expression tag	UNP G9I821
D	-28	GLY	-	expression tag	UNP G9I821
D	-27	LEU	-	expression tag	UNP G9I821
D	-26	VAL	-	expression tag	UNP G9I821
D	-25	PRO	-	expression tag	UNP G9I821
D	-24	ARG	-	expression tag	UNP G9I821
D	-23	GLY	-	expression tag	UNP G9I821
D	-22	SER	-	expression tag	UNP G9I821
D	-21	HIS	-	expression tag	UNP G9I821
D	-20	MET	-	expression tag	UNP G9I821
D	-19	ALA	-	expression tag	UNP G9I821
D	-18	SER	-	expression tag	UNP G9I821
D	-17	MET	-	expression tag	UNP G9I821

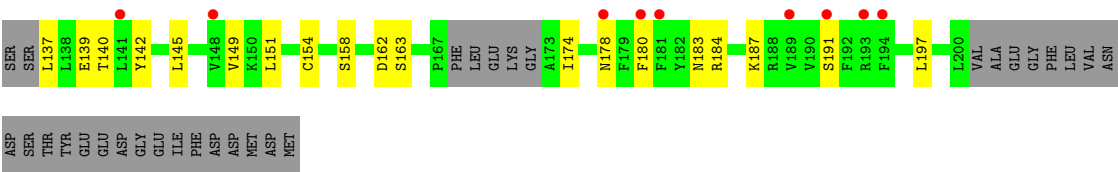
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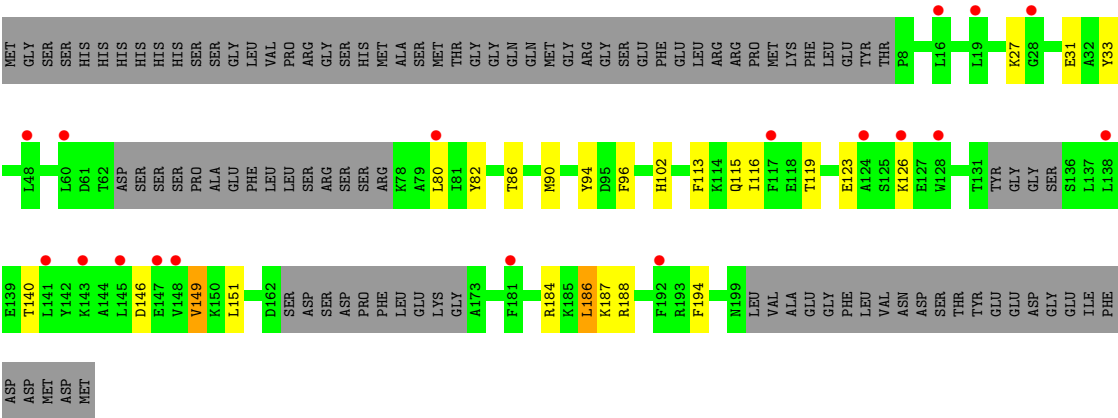
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	THR	-	expression tag	UNP G9I821
D	-15	GLY	-	expression tag	UNP G9I821
D	-14	GLY	-	expression tag	UNP G9I821
D	-13	GLN	-	expression tag	UNP G9I821
D	-12	GLN	-	expression tag	UNP G9I821
D	-11	MET	-	expression tag	UNP G9I821
D	-10	GLY	-	expression tag	UNP G9I821
D	-9	ARG	-	expression tag	UNP G9I821
D	-8	GLY	-	expression tag	UNP G9I821
D	-7	SER	-	expression tag	UNP G9I821
D	-6	GLU	-	expression tag	UNP G9I821
D	-5	PHE	-	expression tag	UNP G9I821
D	-4	GLU	-	expression tag	UNP G9I821
D	-3	LEU	-	expression tag	UNP G9I821
D	-2	ARG	-	expression tag	UNP G9I821
D	-1	ARG	-	expression tag	UNP G9I821
D	0	PRO	-	expression tag	UNP G9I821

- Molecule 2 is water.

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



● Molecule 1: Repressor of RNA polymerase III transcription



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	140.16Å 228.41Å 85.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.90 49.04 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.98-2.90) 99.4 (49.04-2.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.91Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.222 , 0.260 0.228 , 0.264	Depositor DCC
R_{free} test set	1437 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	82.5	Xtriage
Anisotropy	0.741	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 75.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5690	wwPDB-VP
Average B, all atoms (Å ²)	113.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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	0.31	0/1524	0.47	0/2057
1	B	0.31	0/1475	0.50	0/1989
1	C	0.30	0/1435	0.53	0/1935
1	D	0.27	0/1403	0.47	0/1892
All	All	0.30	0/5837	0.50	0/7873

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	1484	0	1429	17	0
1	B	1438	0	1397	22	0
1	C	1399	0	1348	25	0
1	D	1368	0	1320	13	0
2	A	1	0	0	0	0
All	All	5690	0	5494	74	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 7.

All (74) 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:C:115:GLN:O	1:C:119:THR:OG1	2.06	0.74
1:C:117:PHE:HZ	1:C:137:LEU:HD22	1.54	0.73
1:C:145:LEU:HB3	1:C:151:LEU:HD11	1.73	0.70
1:D:184:ARG:O	1:D:187:LYS:HD2	1.92	0.69
1:B:136:SER:N	1:B:139:GLU:OE2	2.28	0.67
1:B:9:LEU:HD22	1:B:30:LEU:HD13	1.75	0.66
1:D:31:GLU:OE1	1:D:33:TYR:OH	2.11	0.65
1:A:155:GLU:OE1	1:A:184:ARG:NH2	2.28	0.64
1:C:162:ASP:OD1	1:C:163:SER:N	2.29	0.64
1:A:23:GLU:HG2	1:B:116:ILE:HD11	1.82	0.62
1:A:126:LYS:NZ	1:A:130:GLU:OE2	2.32	0.62
1:B:91:TYR:OH	1:B:193:ARG:NH1	2.34	0.61
1:B:136:SER:OG	1:B:137:LEU:N	2.32	0.61
1:C:97:SER:HB3	1:C:100:LYS:HG2	1.82	0.60
1:A:27:LYS:O	1:A:194:PHE:HA	2.03	0.58
1:B:52:ILE:HD13	1:B:80:LEU:HD23	1.87	0.56
1:C:21:LEU:HD21	1:C:123:GLU:CD	2.25	0.56
1:C:118:GLU:O	1:C:122:PHE:HB2	2.07	0.55
1:C:142:TYR:CE1	1:C:151:LEU:HD22	2.43	0.54
1:B:186:LEU:O	1:B:187:LYS:HG2	2.07	0.54
1:C:117:PHE:CZ	1:C:137:LEU:HD22	2.40	0.54
1:A:97:SER:OG	1:A:99:VAL:HG22	2.08	0.53
1:A:78:LYS:HD2	1:A:78:LYS:H	1.75	0.52
1:C:50:HIS:O	1:C:52:ILE:N	2.43	0.52
1:C:184:ARG:O	1:C:187:LYS:HD2	2.10	0.52
1:C:71:LEU:HD23	1:C:103:GLN:HA	1.92	0.50
1:A:51:GLU:OE1	1:A:98:ALA:N	2.42	0.49
1:A:49:GLU:HA	1:A:52:ILE:HG22	1.95	0.49
1:A:184:ARG:O	1:A:187:LYS:HD2	2.13	0.49
1:D:27:LYS:O	1:D:194:PHE:HA	2.13	0.48
1:D:94:TYR:HB3	1:D:96:PHE:CE2	2.48	0.48
1:A:24:ARG:NH2	1:B:176:SER:O	2.44	0.48
1:C:151:LEU:HA	1:C:154:CYS:SG	2.54	0.48
1:B:71:LEU:N	1:B:106:THR:HG22	2.29	0.47
1:B:139:GLU:OE1	1:B:139:GLU:N	2.44	0.47
1:B:142:TYR:CD2	1:B:151:LEU:HD23	2.51	0.46
1:C:142:TYR:HE1	1:C:151:LEU:HD22	1.79	0.46
1:B:108:GLU:HB3	1:B:112:THR:OG1	2.16	0.46
1:A:168:PHE:HB3	1:A:178:ASN:ND2	2.31	0.46
1:B:86:THR:O	1:B:90:MET:HG3	2.16	0.46
1:B:186:LEU:HD22	1:B:188:ARG:HE	1.80	0.46
1:D:113:PHE:O	1:D:116:ILE:HG22	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:155:GLU:OE2	1:B:184:ARG:NH2	2.46	0.45
1:C:139:GLU:HG2	1:C:140:THR:N	2.32	0.45
1:A:82:TYR:O	1:A:86:THR:HG23	2.17	0.45
1:C:11:ARG:HD2	1:C:132:TYR:OH	2.17	0.44
1:A:86:THR:HG21	1:A:189:VAL:HG11	1.99	0.44
1:D:82:TYR:O	1:D:86:THR:HG23	2.17	0.44
1:C:44:LEU:O	1:C:48:LEU:HD13	2.17	0.44
1:C:178:ASN:ND2	1:C:180:PHE:CZ	2.85	0.44
1:B:36:LYS:HB2	1:B:36:LYS:HE3	1.81	0.44
1:D:123:GLU:O	1:D:126:LYS:HB3	2.18	0.44
1:D:80:LEU:HD22	1:D:102:HIS:HB2	1.98	0.44
1:A:114:LYS:O	1:A:118:GLU:HG3	2.17	0.43
1:C:149:VAL:CG1	1:C:183:ASN:HB2	2.48	0.43
1:C:45:SER:OG	1:C:85:LEU:HD11	2.17	0.43
1:A:142:TYR:CD1	1:A:151:LEU:HD23	2.54	0.43
1:D:146:ASP:HA	1:D:149:VAL:O	2.18	0.43
1:C:78:LYS:HE3	1:C:78:LYS:HB2	1.82	0.43
1:C:106:THR:OG1	1:C:158:SER:OG	2.33	0.42
1:D:115:GLN:O	1:D:119:THR:OG1	2.29	0.42
1:B:77:ARG:O	1:B:80:LEU:HB3	2.19	0.42
1:C:174:ILE:HG21	1:D:119:THR:HG21	2.02	0.42
1:C:24:ARG:HB2	1:C:197:LEU:O	2.20	0.42
1:B:128:TRP:CD1	1:B:137:LEU:HB2	2.55	0.41
1:B:48:LEU:O	1:B:52:ILE:HG13	2.20	0.41
1:D:186:LEU:HD13	1:D:188:ARG:HH21	1.85	0.41
1:A:83:LEU:HB3	1:A:105:PHE:CZ	2.56	0.41
1:A:28:GLY:HA2	1:A:193:ARG:O	2.21	0.41
1:C:139:GLU:HG2	1:C:140:THR:H	1.84	0.41
1:D:86:THR:O	1:D:90:MET:HG3	2.21	0.41
1:B:142:TYR:O	1:B:146:ASP:HB2	2.21	0.41
1:B:111:ASN:O	1:B:115:GLN:HG3	2.21	0.40
1:B:151:LEU:HA	1:B:151:LEU:HD12	1.88	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	174/265 (66%)	170 (98%)	4 (2%)	0	100	100
1	B	166/265 (63%)	162 (98%)	4 (2%)	0	100	100
1	C	159/265 (60%)	155 (98%)	3 (2%)	1 (1%)	25	58
1	D	155/265 (58%)	152 (98%)	3 (2%)	0	100	100
All	All	654/1060 (62%)	639 (98%)	14 (2%)	1 (0%)	47	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	51	GLU

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	165/239 (69%)	164 (99%)	1 (1%)	86	96
1	B	161/239 (67%)	154 (96%)	7 (4%)	29	62
1	C	156/239 (65%)	149 (96%)	7 (4%)	27	61
1	D	152/239 (64%)	148 (97%)	4 (3%)	46	77
All	All	634/956 (66%)	615 (97%)	19 (3%)	41	75

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	LYS
1	B	109	SER
1	B	158	SER
1	B	184	ARG
1	B	186	LEU

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Mol	Chain	Res	Type
1	B	187	LYS
1	B	200	LEU
1	B	201	VAL
1	C	21	LEU
1	C	24	ARG
1	C	52	ILE
1	C	99	VAL
1	C	116	ILE
1	C	119	THR
1	C	191	SER
1	D	140	THR
1	D	149	VAL
1	D	151	LEU
1	D	186	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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 ⓘ

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	178/265 (67%)	0.38	2 (1%) 80 80	61, 87, 126, 161	0
1	B	172/265 (64%)	0.53	9 (5%) 27 23	77, 108, 162, 190	0
1	C	167/265 (63%)	0.68	17 (10%) 6 5	87, 127, 170, 186	0
1	D	163/265 (61%)	0.73	18 (11%) 5 4	76, 121, 167, 185	0
All	All	680/1060 (64%)	0.57	46 (6%) 17 13	61, 108, 165, 190	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	145	LEU	4.6
1	D	141	LEU	4.2
1	D	147	GLU	4.2
1	B	141	LEU	3.8
1	D	143	LYS	3.3
1	C	141	LEU	3.1
1	B	15	PHE	3.1
1	B	12	ILE	3.1
1	A	48	LEU	3.0
1	C	178	ASN	2.9
1	D	80	LEU	2.9
1	C	189	VAL	2.9
1	C	113	PHE	2.9
1	D	16	LEU	2.8
1	D	148	VAL	2.8
1	C	94	TYR	2.8
1	D	124	ALA	2.8
1	C	148	VAL	2.8
1	B	33	TYR	2.8
1	C	12	ILE	2.7
1	D	28	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	180	PHE	2.7
1	C	33	TYR	2.6
1	D	181	PHE	2.6
1	C	191	SER	2.6
1	B	19	LEU	2.5
1	D	126	LYS	2.4
1	D	192	PHE	2.4
1	A	126	LYS	2.3
1	B	26	ILE	2.3
1	B	122	PHE	2.3
1	D	128	TRP	2.2
1	C	81	ILE	2.2
1	B	53	LEU	2.2
1	C	78	LYS	2.2
1	D	19	LEU	2.2
1	C	193	ARG	2.2
1	C	194	PHE	2.2
1	D	60	LEU	2.2
1	C	181	PHE	2.2
1	B	11	ARG	2.1
1	D	48	LEU	2.1
1	D	138	LEU	2.1
1	C	122	PHE	2.1
1	D	117	PHE	2.1
1	C	30	LEU	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 monosaccharides 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.