



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 11:17 am BST

PDB ID : 5XV5
Title : Crystal structure of Rib7 mutant S88E from Methanosarcina mazei
Authors : Yeh, T.M.; Chen, S.C.; Chang, T.H.; Huang, M.F.; Liaw, S.H.
Deposited on : 2017-06-26
Resolution : 2.50 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 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	:	2.11
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)	:	2.11

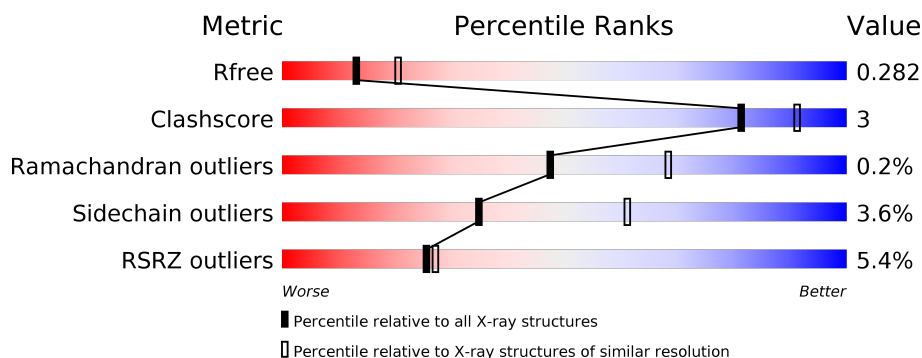
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 on 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	240	<div> <div>90%</div> <div> <div></div> <div></div> <div></div> <div></div> </div> </div>
1	B	240	<div> <div>86%</div> <div>7%</div> <div>7%</div> </div>
1	C	240	<div> <div>6%</div> <div>86%</div> <div>6%</div> <div>8%</div> </div>
1	D	240	<div> <div>23%</div> <div>81%</div> <div>11%</div> <div>6%</div> </div>
1	E	240	<div> <div>87%</div> <div>5%</div> <div>8%</div> </div>
1	F	240	<div> <div>%</div> <div>88%</div> <div>5%</div> <div>5%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10471 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 Conserved protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	1
			1753	1104	303	338	8			
1	B	224	Total	C	N	O	S	0	0	0
			1701	1074	291	328	8			
1	C	222	Total	C	N	O	S	0	0	0
			1685	1065	289	324	7			
1	D	226	Total	C	N	O	S	0	0	0
			1711	1079	293	331	8			
1	E	222	Total	C	N	O	S	0	0	0
			1685	1065	289	324	7			
1	F	227	Total	C	N	O	S	0	0	0
			1723	1088	296	331	8			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP Q8PYN5
A	-10	ARG	-	expression tag	UNP Q8PYN5
A	-9	GLY	-	expression tag	UNP Q8PYN5
A	-8	SER	-	expression tag	UNP Q8PYN5
A	-7	HIS	-	expression tag	UNP Q8PYN5
A	-6	HIS	-	expression tag	UNP Q8PYN5
A	-5	HIS	-	expression tag	UNP Q8PYN5
A	-4	HIS	-	expression tag	UNP Q8PYN5
A	-3	HIS	-	expression tag	UNP Q8PYN5
A	-2	HIS	-	expression tag	UNP Q8PYN5
A	-1	GLY	-	expression tag	UNP Q8PYN5
A	0	SER	-	expression tag	UNP Q8PYN5
A	88	GLU	SER	engineered mutation	UNP Q8PYN5
B	-11	MET	-	expression tag	UNP Q8PYN5
B	-10	ARG	-	expression tag	UNP Q8PYN5
B	-9	GLY	-	expression tag	UNP Q8PYN5
B	-8	SER	-	expression tag	UNP Q8PYN5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-7	HIS	-	expression tag	UNP Q8PYN5
B	-6	HIS	-	expression tag	UNP Q8PYN5
B	-5	HIS	-	expression tag	UNP Q8PYN5
B	-4	HIS	-	expression tag	UNP Q8PYN5
B	-3	HIS	-	expression tag	UNP Q8PYN5
B	-2	HIS	-	expression tag	UNP Q8PYN5
B	-1	GLY	-	expression tag	UNP Q8PYN5
B	0	SER	-	expression tag	UNP Q8PYN5
B	88	GLU	SER	engineered mutation	UNP Q8PYN5
C	-11	MET	-	expression tag	UNP Q8PYN5
C	-10	ARG	-	expression tag	UNP Q8PYN5
C	-9	GLY	-	expression tag	UNP Q8PYN5
C	-8	SER	-	expression tag	UNP Q8PYN5
C	-7	HIS	-	expression tag	UNP Q8PYN5
C	-6	HIS	-	expression tag	UNP Q8PYN5
C	-5	HIS	-	expression tag	UNP Q8PYN5
C	-4	HIS	-	expression tag	UNP Q8PYN5
C	-3	HIS	-	expression tag	UNP Q8PYN5
C	-2	HIS	-	expression tag	UNP Q8PYN5
C	-1	GLY	-	expression tag	UNP Q8PYN5
C	0	SER	-	expression tag	UNP Q8PYN5
C	88	GLU	SER	engineered mutation	UNP Q8PYN5
D	-11	MET	-	expression tag	UNP Q8PYN5
D	-10	ARG	-	expression tag	UNP Q8PYN5
D	-9	GLY	-	expression tag	UNP Q8PYN5
D	-8	SER	-	expression tag	UNP Q8PYN5
D	-7	HIS	-	expression tag	UNP Q8PYN5
D	-6	HIS	-	expression tag	UNP Q8PYN5
D	-5	HIS	-	expression tag	UNP Q8PYN5
D	-4	HIS	-	expression tag	UNP Q8PYN5
D	-3	HIS	-	expression tag	UNP Q8PYN5
D	-2	HIS	-	expression tag	UNP Q8PYN5
D	-1	GLY	-	expression tag	UNP Q8PYN5
D	0	SER	-	expression tag	UNP Q8PYN5
D	88	GLU	SER	engineered mutation	UNP Q8PYN5
E	-11	MET	-	expression tag	UNP Q8PYN5
E	-10	ARG	-	expression tag	UNP Q8PYN5
E	-9	GLY	-	expression tag	UNP Q8PYN5
E	-8	SER	-	expression tag	UNP Q8PYN5
E	-7	HIS	-	expression tag	UNP Q8PYN5
E	-6	HIS	-	expression tag	UNP Q8PYN5
E	-5	HIS	-	expression tag	UNP Q8PYN5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	HIS	-	expression tag	UNP Q8PYN5
E	-3	HIS	-	expression tag	UNP Q8PYN5
E	-2	HIS	-	expression tag	UNP Q8PYN5
E	-1	GLY	-	expression tag	UNP Q8PYN5
E	0	SER	-	expression tag	UNP Q8PYN5
E	88	GLU	SER	engineered mutation	UNP Q8PYN5
F	-11	MET	-	expression tag	UNP Q8PYN5
F	-10	ARG	-	expression tag	UNP Q8PYN5
F	-9	GLY	-	expression tag	UNP Q8PYN5
F	-8	SER	-	expression tag	UNP Q8PYN5
F	-7	HIS	-	expression tag	UNP Q8PYN5
F	-6	HIS	-	expression tag	UNP Q8PYN5
F	-5	HIS	-	expression tag	UNP Q8PYN5
F	-4	HIS	-	expression tag	UNP Q8PYN5
F	-3	HIS	-	expression tag	UNP Q8PYN5
F	-2	HIS	-	expression tag	UNP Q8PYN5
F	-1	GLY	-	expression tag	UNP Q8PYN5
F	0	SER	-	expression tag	UNP Q8PYN5
F	88	GLU	SER	engineered mutation	UNP Q8PYN5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	48	Total O 48 48	0	0
2	B	31	Total O 31 31	0	0
2	C	23	Total O 23 23	0	0
2	D	31	Total O 31 31	0	0
2	E	33	Total O 33 33	0	0
2	F	47	Total O 47 47	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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: Conserved protein

Chain A:  90% . . .




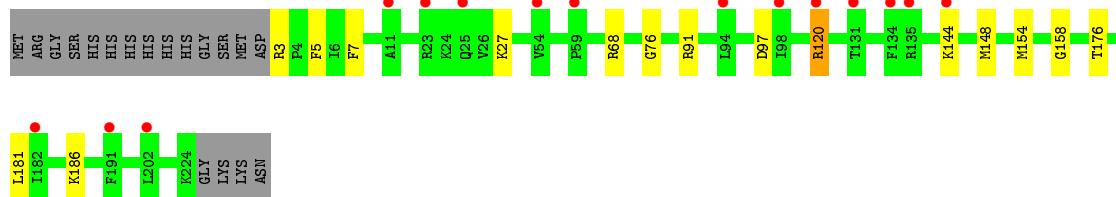
- Molecule 1: Conserved protein

Chain B:  86% 7% 7%




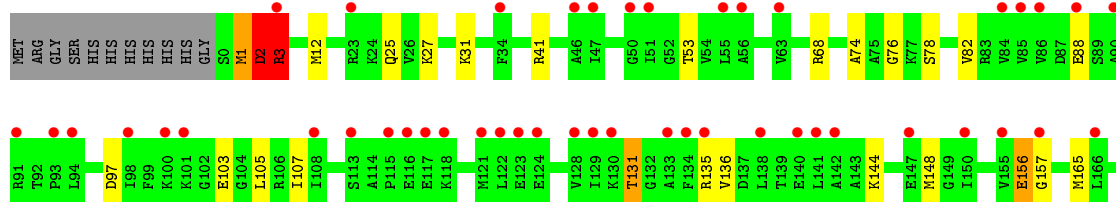
- Molecule 1: Conserved protein

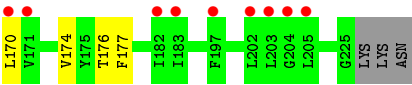
Chain C:  6% 86% 6% 8%



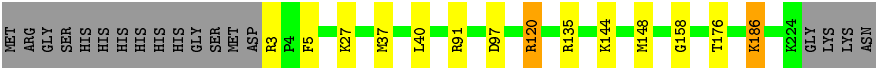
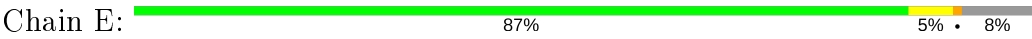
- Molecule 1: Conserved protein

Chain D:  23% 81% 11% 6%

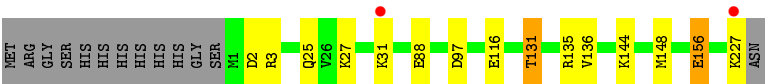
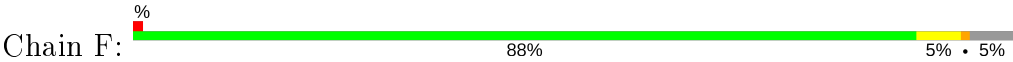




● Molecule 1: Conserved protein



● Molecule 1: Conserved protein



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	116.16Å 116.16Å 380.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.50 27.85 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-2.50) 99.7 (27.85-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.84 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.246 , 0.281 0.249 , 0.282	Depositor DCC
R_{free} test set	3183 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 25.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.480 for -h-k,k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10471	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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	0.71	0/1774	0.89	7/2380 (0.3%)
1	B	0.71	0/1721	0.90	6/2312 (0.3%)
1	C	0.62	0/1705	0.85	5/2291 (0.2%)
1	D	0.64	2/1731 (0.1%)	0.85	5/2325 (0.2%)
1	E	0.70	0/1705	0.87	4/2291 (0.2%)
1	F	0.71	1/1743 (0.1%)	0.84	1/2339 (0.0%)
All	All	0.68	3/10379 (0.0%)	0.87	28/13938 (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	F	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	156	GLU	CD-OE2	-9.07	1.15	1.25
1	D	156	GLU	CD-OE1	-7.10	1.17	1.25
1	F	116	GLU	CD-OE2	5.09	1.31	1.25

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3	ARG	NE-CZ-NH2	10.36	125.48	120.30
1	B	3	ARG	NE-CZ-NH1	-9.60	115.50	120.30
1	A	157	GLY	O-C-N	-7.62	110.24	123.20
1	A	157	GLY	C-N-CA	7.60	138.26	122.30
1	A	94	LEU	CB-CG-CD1	7.42	123.62	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3	ARG	CG-CD-NE	7.08	126.67	111.80
1	B	77	LYS	CB-CG-CD	6.61	128.79	111.60
1	E	91	ARG	NE-CZ-NH2	-6.43	117.08	120.30
1	C	91	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	C	91	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	A	120	ARG	NE-CZ-NH1	6.15	123.38	120.30
1	B	3	ARG	CD-NE-CZ	6.12	132.17	123.60
1	E	120	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	D	156	GLU	OE1-CD-OE2	-6.07	116.01	123.30
1	A	157	GLY	CA-C-N	6.07	128.33	116.20
1	E	91	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	E	158	GLY	N-CA-C	-5.63	99.03	113.10
1	C	120	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	D	2	ASP	CB-CG-OD1	5.56	123.30	118.30
1	D	131	THR	N-CA-C	5.47	125.77	111.00
1	B	158	GLY	N-CA-C	-5.47	99.43	113.10
1	A	94	LEU	CB-CG-CD2	-5.37	101.88	111.00
1	D	3	ARG	NE-CZ-NH2	5.34	122.97	120.30
1	F	131	THR	N-CA-C	5.27	125.23	111.00
1	D	68	ARG	NE-CZ-NH1	5.14	122.87	120.30
1	C	68	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	C	158	GLY	N-CA-C	-5.05	100.47	113.10
1	A	131	THR	CB-CA-C	-5.01	98.07	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	157	GLY	Peptide
1	F	156	GLU	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	1753	0	1815	6	0
1	B	1701	0	1767	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1685	0	1751	5	0
1	D	1711	0	1775	24	0
1	E	1685	0	1751	6	0
1	F	1723	0	1796	4	0
2	A	48	0	0	2	0
2	B	31	0	0	1	0
2	C	23	0	0	1	0
2	D	31	0	0	17	0
2	E	33	0	0	2	0
2	F	47	0	0	1	0
All	All	10471	0	10655	55	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 (55) 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:170:LEU:HB2	2:D:325:HOH:O	1.50	1.09
1:D:105:LEU:HG	2:D:310:HOH:O	1.54	1.05
1:D:170:LEU:HD12	2:D:325:HOH:O	1.64	0.98
1:D:107:ILE:HG13	2:D:310:HOH:O	1.66	0.93
1:B:41:ARG:HG2	1:B:154:MET:CE	2.05	0.86
1:E:135:ARG:HD2	2:E:331:HOH:O	1.83	0.78
1:D:170:LEU:CD1	2:D:325:HOH:O	2.23	0.77
1:B:41:ARG:HG2	1:B:154:MET:HE3	1.66	0.76
1:D:76:GLY:HA3	1:E:5:PHE:CD1	2.24	0.72
1:D:170:LEU:HD23	2:D:307:HOH:O	1.89	0.71
1:F:156:GLU:HG2	2:F:444:HOH:O	1.90	0.70
1:B:5:PHE:CD1	1:C:76:GLY:HA3	2.27	0.69
1:D:165:MET:HE3	2:D:325:HOH:O	1.93	0.69
1:B:41:ARG:HG2	1:B:154:MET:HE1	1.75	0.68
1:A:124:GLU:HG2	2:A:347:HOH:O	1.94	0.67
1:D:176:THR:HB	2:D:302:HOH:O	1.95	0.66
1:E:37:MET:SD	2:E:329:HOH:O	2.55	0.65
1:D:1:MET:O	1:D:3:ARG:N	2.28	0.65
1:B:76:GLY:HA3	1:C:5:PHE:CD1	2.34	0.63
1:D:170:LEU:CB	2:D:325:HOH:O	2.24	0.63
1:B:144:LYS:HE3	2:B:330:HOH:O	2.01	0.60
1:D:41:ARG:NH2	1:D:156:GLU:OE2	2.34	0.59
1:A:156:GLU:HG2	2:A:338:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:THR:HA	2:D:326:HOH:O	2.04	0.58
1:D:174:VAL:HB	2:D:305:HOH:O	2.03	0.57
1:A:27:LYS:HG3	1:A:27:LYS:O	2.06	0.55
1:F:144:LYS:O	1:F:148:MET:HG3	2.06	0.55
1:C:144:LYS:O	1:C:148:MET:HG3	2.07	0.55
1:D:177:PHE:C	2:D:302:HOH:O	2.45	0.55
1:F:131:THR:OG1	1:F:131:THR:O	2.25	0.54
1:D:144:LYS:O	1:D:148:MET:HG3	2.07	0.54
1:B:47:ILE:HG12	1:B:154:MET:HE1	1.90	0.53
1:A:144:LYS:O	1:A:148:MET:HG2	2.09	0.53
1:E:144:LYS:O	1:E:148:MET:HG3	2.08	0.53
1:B:144:LYS:O	1:B:148:MET:HG2	2.09	0.53
1:D:88:GLU:HG3	1:D:136:VAL:HG23	1.92	0.51
1:B:98:ILE:HG12	1:B:99:PHE:N	2.25	0.51
1:D:131:THR:OG1	1:D:131:THR:O	2.26	0.51
1:A:88:GLU:HG3	1:A:136:VAL:HG23	1.93	0.51
1:B:154:MET:HE3	1:B:156:GLU:OE1	2.11	0.50
1:D:74:ALA:HB1	1:E:40:LEU:HD21	1.93	0.50
1:F:88:GLU:HG3	1:F:136:VAL:HG23	1.94	0.50
1:A:131:THR:O	1:A:131:THR:OG1	2.29	0.50
1:B:47:ILE:HG23	1:B:154:MET:HE2	1.94	0.49
1:B:47:ILE:HG12	1:B:154:MET:CE	2.43	0.49
1:C:7:PHE:CE1	1:C:154:MET:HG3	2.48	0.49
1:D:82:VAL:HG13	2:D:310:HOH:O	2.13	0.48
1:D:12:MET:HG2	2:D:302:HOH:O	2.14	0.47
1:B:154:MET:CE	1:B:156:GLU:OE1	2.63	0.46
1:D:78:SER:HB2	2:D:314:HOH:O	2.15	0.45
1:C:181:LEU:HB3	2:C:314:HOH:O	2.16	0.45
1:D:103:GLU:HG3	2:D:314:HOH:O	2.20	0.42
1:E:186:LYS:HE2	1:E:186:LYS:HB2	1.81	0.42
1:B:96:ALA:HB1	1:B:98:ILE:HD13	2.03	0.41
1:D:78:SER:CB	2:D:314:HOH:O	2.68	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	230/240 (96%)	226 (98%)	4 (2%)	0	100	100
1	B	222/240 (92%)	218 (98%)	4 (2%)	0	100	100
1	C	220/240 (92%)	215 (98%)	5 (2%)	0	100	100
1	D	224/240 (93%)	216 (96%)	5 (2%)	3 (1%)	12	21
1	E	220/240 (92%)	216 (98%)	4 (2%)	0	100	100
1	F	225/240 (94%)	219 (97%)	6 (3%)	0	100	100
All	All	1341/1440 (93%)	1310 (98%)	28 (2%)	3 (0%)	47	68

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	2	ASP
1	D	1	MET
1	D	157	GLY

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	187/195 (96%)	180 (96%)	7 (4%)	34	60
1	B	182/195 (93%)	177 (97%)	5 (3%)	44	71
1	C	180/195 (92%)	174 (97%)	6 (3%)	38	64
1	D	183/195 (94%)	176 (96%)	7 (4%)	33	58
1	E	180/195 (92%)	174 (97%)	6 (3%)	38	64
1	F	184/195 (94%)	176 (96%)	8 (4%)	29	53
All	All	1096/1170 (94%)	1057 (96%)	39 (4%)	35	61

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	3	ARG
1	A	27	LYS
1	A	94	LEU
1	A	97	ASP
1	A	120	ARG
1	A	135	ARG
1	B	23	ARG
1	B	27	LYS
1	B	97	ASP
1	B	98	ILE
1	B	176	THR
1	C	3	ARG
1	C	27	LYS
1	C	97	ASP
1	C	120	ARG
1	C	176	THR
1	C	186	LYS
1	D	2	ASP
1	D	3	ARG
1	D	25	GLN
1	D	27	LYS
1	D	31	LYS
1	D	97	ASP
1	D	135	ARG
1	E	3	ARG
1	E	27	LYS
1	E	97	ASP
1	E	120	ARG
1	E	176	THR
1	E	186	LYS
1	F	2	ASP
1	F	3	ARG
1	F	25	GLN
1	F	27	LYS
1	F	31	LYS
1	F	97	ASP
1	F	135	ARG
1	F	227	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	200	ASN
1	B	9	ASN
1	B	80	ASN
1	B	200	ASN
1	C	9	ASN
1	C	80	ASN
1	D	9	ASN
1	D	80	ASN
1	E	9	ASN
1	E	80	ASN
1	F	9	ASN
1	F	80	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 carbohydrates 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	232/240 (96%)	0.10	1 (0%) 92 93	31, 43, 75, 120	0
1	B	224/240 (93%)	0.11	0 100 100	32, 51, 78, 123	0
1	C	222/240 (92%)	0.76	15 (6%) 17 17	54, 81, 111, 135	0
1	D	226/240 (94%)	1.49	55 (24%) 0 0	50, 102, 153, 185	0
1	E	222/240 (92%)	0.11	0 100 100	33, 50, 75, 93	0
1	F	227/240 (94%)	0.10	2 (0%) 84 86	29, 43, 71, 97	0
All	All	1353/1440 (93%)	0.44	73 (5%) 25 27	29, 57, 122, 185	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	94	LEU	7.2
1	D	157	GLY	7.0
1	D	122	LEU	6.6
1	D	138	LEU	6.6
1	D	115	PRO	6.1
1	D	129	ILE	6.1
1	D	98	ILE	4.9
1	D	116	GLU	4.9
1	D	121	MET	4.6
1	D	197	PHE	4.5
1	D	134	PHE	4.2
1	D	142	ALA	3.9
1	D	130	LYS	3.8
1	D	46	ALA	3.7
1	C	11	ALA	3.5
1	C	135	ARG	3.4
1	F	227	LYS	3.4
1	D	147	GLU	3.4
1	D	118	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	86	VAL	3.3
1	D	141	LEU	3.2
1	D	85	VAL	3.2
1	C	23	ARG	3.1
1	D	182	ILE	3.0
1	D	203	LEU	3.0
1	D	101	LYS	2.9
1	D	135	ARG	2.9
1	D	88	GLU	2.9
1	D	91	ARG	2.9
1	D	123	GLU	2.9
1	C	144	LYS	2.8
1	A	228	ASN	2.7
1	D	51	ILE	2.7
1	D	55	LEU	2.7
1	D	170	LEU	2.7
1	D	3	ARG	2.7
1	D	23	ARG	2.7
1	D	150	ILE	2.6
1	D	93	PRO	2.6
1	D	56	ALA	2.6
1	C	131	THR	2.6
1	D	133	ALA	2.5
1	D	128	VAL	2.5
1	D	34	PHE	2.5
1	D	202	LEU	2.5
1	D	183	ILE	2.5
1	D	205	LEU	2.4
1	D	84	VAL	2.4
1	C	182	ILE	2.4
1	D	47	ILE	2.4
1	C	98	ILE	2.4
1	D	63	VAL	2.3
1	D	108	ILE	2.3
1	D	204	GLY	2.3
1	C	54	VAL	2.3
1	C	202	LEU	2.3
1	D	171	VAL	2.3
1	C	94	LEU	2.2
1	C	25	GLN	2.2
1	C	120	ARG	2.2
1	D	140	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	124	GLU	2.1
1	D	113	SER	2.1
1	D	100	LYS	2.1
1	D	155	VAL	2.1
1	C	59	PRO	2.1
1	D	117	GLU	2.1
1	D	90	ALA	2.1
1	C	134	PHE	2.1
1	D	50	GLY	2.1
1	C	191	PHE	2.0
1	D	166	LEU	2.0
1	F	31	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 carbohydrates 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.