Full wwPDB X-ray Structure Validation Report (i)

May 6, 2025 – 12:58 PM JST

PDB ID	:	9IKU / pdb_00009iku
Title	:	Crystal structure of Se-Met CTB10
Authors	:	Fu, K.; Rao, Y.J.
Deposited on	:	2024-06-29
Resolution	:	2.30 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 (i) 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 (1)) were used in the production of this report:

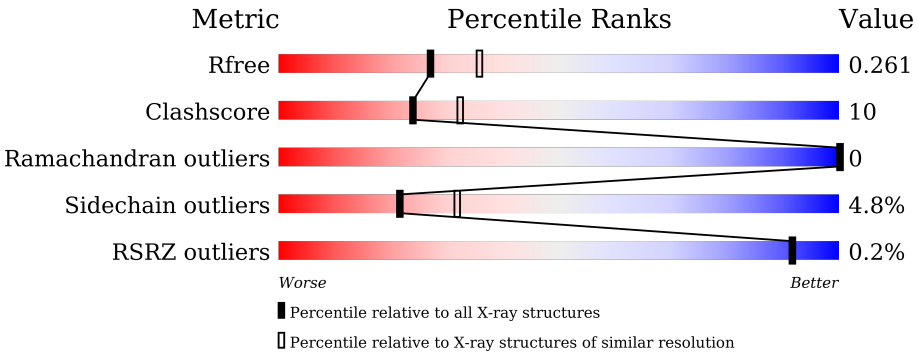
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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 <=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	141	73% 18% •• 8%
1	B	141	65% 18% • 12%
1	C	141	65% 21% • 13%
1	D	141	% 65% 19% • 12%
1	E	141	73% 15% 12%
1	F	141	61% 25% • 11%

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Mol	Chain	Length	Quality of chain
1	G	141	
1	H	141	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 8172 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 CTB10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	130	Total	C	N	O	S	Se	0	0	0
			1063	679	176	201	1	6			
1	B	124	Total	C	N	O	S	Se	0	0	0
			1015	651	166	191	1	6			
1	C	122	Total	C	N	O	S	Se	0	0	0
			995	637	164	187	1	6			
1	D	124	Total	C	N	O	S	Se	0	0	0
			987	632	161	187	1	6			
1	E	124	Total	C	N	O	S	Se	0	0	0
			1007	645	164	191	1	6			
1	F	125	Total	C	N	O	S	Se	0	0	0
			1016	649	171	189	1	6			
1	G	124	Total	C	N	O	S	Se	0	0	0
			1021	654	169	191	1	6			
1	H	124	Total	C	N	O	S	Se	0	0	0
			999	636	165	191	1	6			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	133	ALA	-	expression tag	UNP A0A977K7H6
A	134	LEU	-	expression tag	UNP A0A977K7H6
A	135	GLU	-	expression tag	UNP A0A977K7H6
A	136	HIS	-	expression tag	UNP A0A977K7H6
A	137	HIS	-	expression tag	UNP A0A977K7H6
A	138	HIS	-	expression tag	UNP A0A977K7H6
A	139	HIS	-	expression tag	UNP A0A977K7H6
A	140	HIS	-	expression tag	UNP A0A977K7H6
A	141	HIS	-	expression tag	UNP A0A977K7H6
B	133	ALA	-	expression tag	UNP A0A977K7H6
B	134	LEU	-	expression tag	UNP A0A977K7H6
B	135	GLU	-	expression tag	UNP A0A977K7H6
B	136	HIS	-	expression tag	UNP A0A977K7H6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	137	HIS	-	expression tag	UNP A0A977K7H6
B	138	HIS	-	expression tag	UNP A0A977K7H6
B	139	HIS	-	expression tag	UNP A0A977K7H6
B	140	HIS	-	expression tag	UNP A0A977K7H6
B	141	HIS	-	expression tag	UNP A0A977K7H6
C	133	ALA	-	expression tag	UNP A0A977K7H6
C	134	LEU	-	expression tag	UNP A0A977K7H6
C	135	GLU	-	expression tag	UNP A0A977K7H6
C	136	HIS	-	expression tag	UNP A0A977K7H6
C	137	HIS	-	expression tag	UNP A0A977K7H6
C	138	HIS	-	expression tag	UNP A0A977K7H6
C	139	HIS	-	expression tag	UNP A0A977K7H6
C	140	HIS	-	expression tag	UNP A0A977K7H6
C	141	HIS	-	expression tag	UNP A0A977K7H6
D	133	ALA	-	expression tag	UNP A0A977K7H6
D	134	LEU	-	expression tag	UNP A0A977K7H6
D	135	GLU	-	expression tag	UNP A0A977K7H6
D	136	HIS	-	expression tag	UNP A0A977K7H6
D	137	HIS	-	expression tag	UNP A0A977K7H6
D	138	HIS	-	expression tag	UNP A0A977K7H6
D	139	HIS	-	expression tag	UNP A0A977K7H6
D	140	HIS	-	expression tag	UNP A0A977K7H6
D	141	HIS	-	expression tag	UNP A0A977K7H6
E	133	ALA	-	expression tag	UNP A0A977K7H6
E	134	LEU	-	expression tag	UNP A0A977K7H6
E	135	GLU	-	expression tag	UNP A0A977K7H6
E	136	HIS	-	expression tag	UNP A0A977K7H6
E	137	HIS	-	expression tag	UNP A0A977K7H6
E	138	HIS	-	expression tag	UNP A0A977K7H6
E	139	HIS	-	expression tag	UNP A0A977K7H6
E	140	HIS	-	expression tag	UNP A0A977K7H6
E	141	HIS	-	expression tag	UNP A0A977K7H6
F	133	ALA	-	expression tag	UNP A0A977K7H6
F	134	LEU	-	expression tag	UNP A0A977K7H6
F	135	GLU	-	expression tag	UNP A0A977K7H6
F	136	HIS	-	expression tag	UNP A0A977K7H6
F	137	HIS	-	expression tag	UNP A0A977K7H6
F	138	HIS	-	expression tag	UNP A0A977K7H6
F	139	HIS	-	expression tag	UNP A0A977K7H6
F	140	HIS	-	expression tag	UNP A0A977K7H6
F	141	HIS	-	expression tag	UNP A0A977K7H6
G	133	ALA	-	expression tag	UNP A0A977K7H6

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Chain	Residue	Modelled	Actual	Comment	Reference
G	134	LEU	-	expression tag	UNP A0A977K7H6
G	135	GLU	-	expression tag	UNP A0A977K7H6
G	136	HIS	-	expression tag	UNP A0A977K7H6
G	137	HIS	-	expression tag	UNP A0A977K7H6
G	138	HIS	-	expression tag	UNP A0A977K7H6
G	139	HIS	-	expression tag	UNP A0A977K7H6
G	140	HIS	-	expression tag	UNP A0A977K7H6
G	141	HIS	-	expression tag	UNP A0A977K7H6
H	133	ALA	-	expression tag	UNP A0A977K7H6
H	134	LEU	-	expression tag	UNP A0A977K7H6
H	135	GLU	-	expression tag	UNP A0A977K7H6
H	136	HIS	-	expression tag	UNP A0A977K7H6
H	137	HIS	-	expression tag	UNP A0A977K7H6
H	138	HIS	-	expression tag	UNP A0A977K7H6
H	139	HIS	-	expression tag	UNP A0A977K7H6
H	140	HIS	-	expression tag	UNP A0A977K7H6
H	141	HIS	-	expression tag	UNP A0A977K7H6

- Molecule 2 is water.

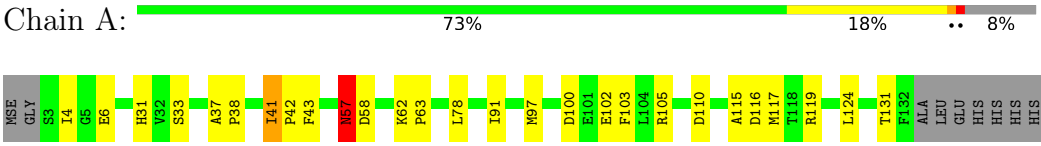
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	10	Total O 10 10	0	0
2	B	11	Total O 11 11	0	0
2	C	10	Total O 10 10	0	0
2	D	5	Total O 5 5	0	0
2	E	6	Total O 6 6	0	0
2	F	12	Total O 12 12	0	0
2	G	11	Total O 11 11	0	0
2	H	4	Total O 4 4	0	0

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.

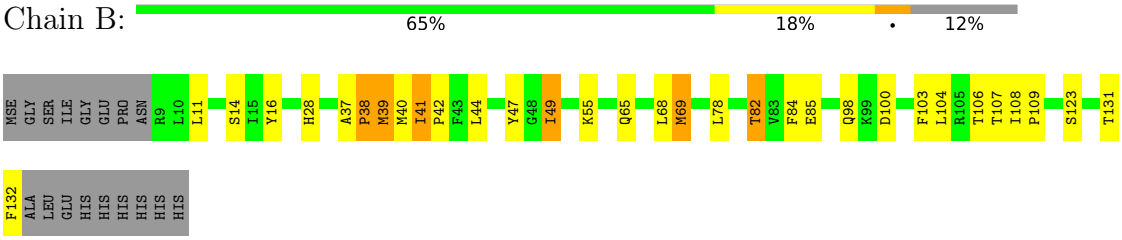
- Molecule 1: CTB10

Chain A:



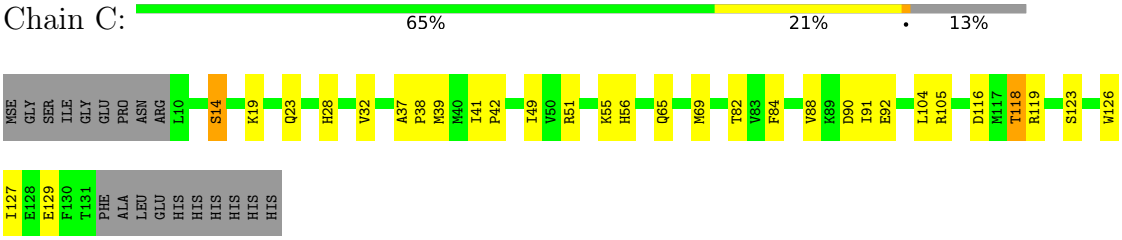
- Molecule 1: CTB10

Chain B:



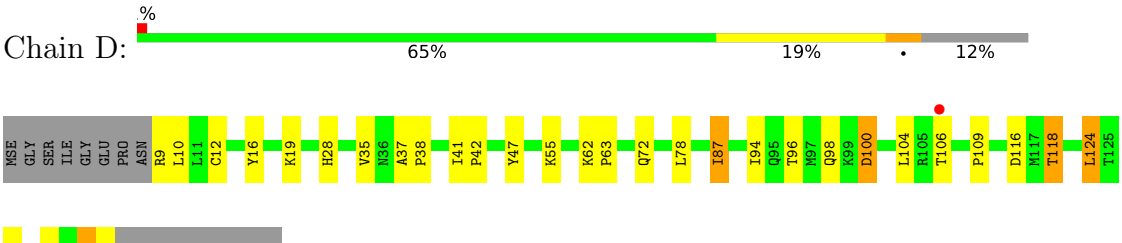
- Molecule 1: CTB10

Chain C:



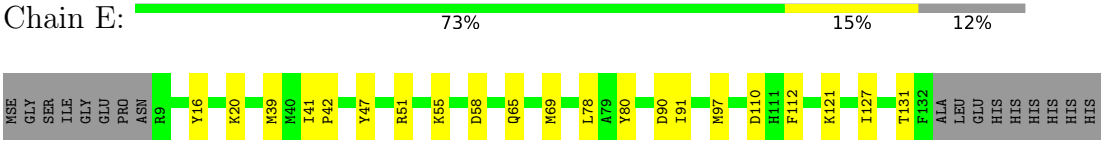
- Molecule 1: CTB10

Chain D:



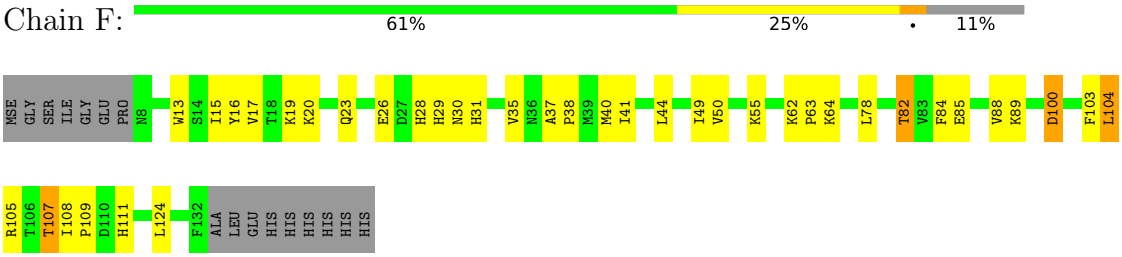
- Molecule 1: CTB10

Chain E:



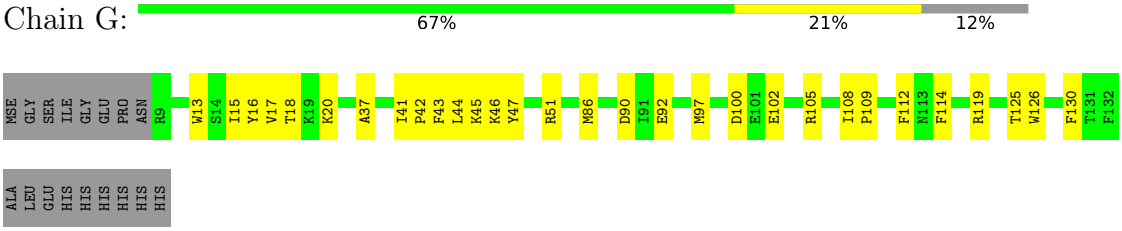
• Molecule 1: CTB10

Chain F:



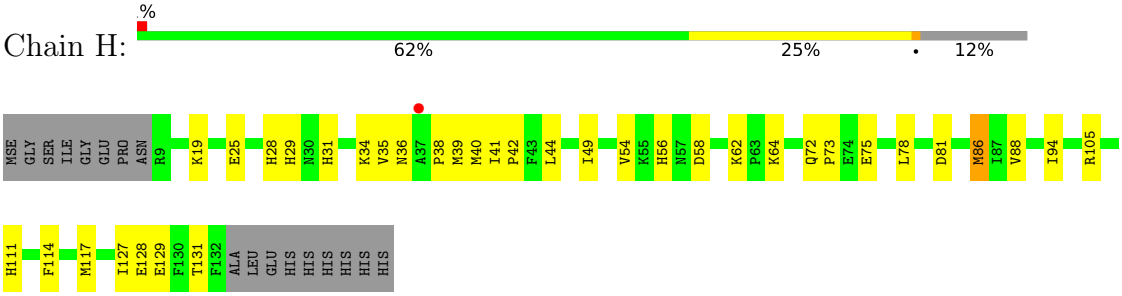
• Molecule 1: CTB10

Chain G:



• Molecule 1: CTB10

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	81.89Å 87.74Å 85.88Å 90.00° 116.81° 90.00°	Depositor
Resolution (Å)	57.72 – 2.30 57.72 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.6 (57.72-2.30) 98.6 (57.72-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.54 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.191 , 0.256 0.195 , 0.261	Depositor DCC
R_{free} test set	2475 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å^2)	50.6	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 38.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8172	wwPDB-VP
Average B, all atoms (Å^2)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.66	0/1084	1.17	1/1456 (0.1%)
1	B	0.68	0/1035	1.19	1/1390 (0.1%)
1	C	0.62	0/1014	1.10	0/1362
1	D	0.58	0/1006	1.10	0/1356
1	E	0.60	0/1027	1.08	1/1382 (0.1%)
1	F	0.67	0/1035	1.24	2/1390 (0.1%)
1	G	0.65	0/1041	1.11	1/1397 (0.1%)
1	H	0.59	0/1019	1.17	0/1373
All	All	0.63	0/8261	1.15	6/11106 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	82	THR	CB-CA-C	5.90	122.51	109.94
1	G	114	PHE	CA-CB-CG	5.72	119.52	113.80
1	F	29	HIS	CA-CB-CG	-5.49	108.31	113.80
1	A	57	ASN	CB-CA-C	5.48	119.81	111.76
1	F	82	THR	CB-CA-C	5.31	121.34	109.56
1	E	131	THR	CA-CB-OG1	-5.14	101.89	109.60

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	1063	0	1037	18	0
1	B	1015	0	988	23	0
1	C	995	0	973	24	0
1	D	987	0	940	25	0
1	E	1007	0	966	14	0
1	F	1016	0	992	32	0
1	G	1021	0	999	26	0
1	H	999	0	937	26	0
2	A	10	0	0	0	0
2	B	11	0	0	0	0
2	C	10	0	0	0	0
2	D	5	0	0	0	0
2	E	6	0	0	0	0
2	F	12	0	0	2	0
2	G	11	0	0	0	0
2	H	4	0	0	0	0
All	All	8172	0	7832	157	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 10.

All (157) 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:97:MSE:HE2	1:A:103:PHE:CE1	2.00	0.95
1:D:116:ASP:OD1	1:D:118:THR:HG22	1.66	0.94
1:F:103:PHE:O	1:F:107:THR:HB	1.78	0.83
1:C:49:ILE:HD13	1:C:88:VAL:HG12	1.67	0.77
1:G:43:PHE:C	1:G:97:MSE:HE3	2.10	0.75
1:C:105:ARG:HD2	1:G:112:PHE:CZ	2.26	0.70
1:F:111:HIS:HE1	2:F:211:HOH:O	1.74	0.70
1:D:37:ALA:O	1:D:41:ILE:HG12	1.95	0.67
1:H:58:ASP:O	1:H:62:LYS:HG3	1.96	0.66
1:G:18:THR:HG23	1:G:119:ARG:O	1.95	0.65
1:F:13:TRP:CZ2	1:F:15:ILE:HD11	2.32	0.65
1:C:126:TRP:HE1	1:H:58:ASP:CG	2.04	0.65
1:A:37:ALA:HB3	1:A:38:PRO:HD3	1.78	0.65
1:C:19:LYS:NZ	1:C:23:GLN:O	2.31	0.64
1:C:41:ILE:HB	1:C:42:PRO:HD3	1.79	0.64
1:E:20:LYS:HD2	1:E:112:PHE:O	1.99	0.63
1:B:65:GLN:O	1:B:69:MSE:HG3	1.99	0.63
1:D:116:ASP:CG	1:D:118:THR:HG22	2.24	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:104:LEU:HB3	1:G:108:ILE:HD13	1.82	0.62
1:A:78:LEU:HD22	1:G:16:TYR:CZ	2.36	0.61
1:H:34:LYS:O	1:H:38:PRO:HG2	2.01	0.61
1:B:37:ALA:HB3	1:B:38:PRO:HD3	1.83	0.60
1:C:116:ASP:OD1	1:C:118:THR:HB	2.02	0.59
1:A:97:MSE:CE	1:A:103:PHE:CE1	2.83	0.59
1:D:94:ILE:O	1:D:98:GLN:HB2	2.03	0.59
1:H:36:ASN:ND2	1:H:114:PHE:CZ	2.70	0.59
1:B:85:GLU:OE2	1:F:55:LYS:NZ	2.35	0.58
1:C:91:ILE:HG21	1:H:64:LYS:HB3	1.85	0.58
1:B:39:MSE:SE	1:B:106:THR:HG22	2.53	0.58
1:B:132:PHE:HD2	1:F:49:ILE:O	1.86	0.57
1:F:26:GLU:O	1:F:30:ASN:ND2	2.36	0.57
1:F:100:ASP:O	1:F:104:LEU:HD12	2.05	0.57
1:H:49:ILE:HG12	1:H:86:MSE:HE3	1.87	0.57
1:C:105:ARG:HD2	1:G:112:PHE:CE2	2.40	0.56
1:F:37:ALA:O	1:F:41:ILE:HG12	2.06	0.56
1:G:102:GLU:OE2	1:G:105:ARG:NH1	2.37	0.56
1:C:49:ILE:HD13	1:C:88:VAL:CG1	2.37	0.54
1:D:47:TYR:CE1	1:D:96:THR:HG22	2.43	0.54
1:A:57:ASN:HB2	1:G:125:THR:HG22	1.90	0.53
1:G:41:ILE:HB	1:G:42:PRO:HD3	1.89	0.53
1:A:131:THR:HG22	1:G:51:ARG:HG3	1.90	0.53
1:E:39:MSE:HE1	1:E:110:ASP:CB	2.39	0.53
1:F:37:ALA:HB3	1:F:38:PRO:HD3	1.92	0.52
1:B:40:MSE:HE3	1:B:44:LEU:HD21	1.91	0.52
1:H:40:MSE:O	1:H:44:LEU:HG	2.08	0.52
1:D:100:ASP:OD1	1:D:100:ASP:C	2.52	0.52
1:F:100:ASP:OD1	1:F:100:ASP:C	2.53	0.52
1:H:88:VAL:HG11	1:H:94:ILE:HD11	1.92	0.52
1:B:28:HIS:NE2	1:B:82:THR:CG2	2.73	0.51
1:B:28:HIS:NE2	1:B:82:THR:HG21	2.26	0.51
1:B:55:LYS:NZ	1:F:85:GLU:OE2	2.44	0.51
1:H:35:VAL:O	1:H:38:PRO:HD2	2.10	0.51
1:B:44:LEU:HD22	1:B:49:ILE:HD12	1.93	0.51
1:C:51:ARG:NH2	1:C:129:GLU:OE2	2.44	0.51
1:E:47:TYR:HB2	1:E:97:MSE:HE2	1.93	0.50
1:D:55:LYS:HG2	1:E:127:ILE:HG22	1.92	0.50
1:B:103:PHE:O	1:B:107:THR:HG23	2.12	0.50
1:G:43:PHE:CB	1:G:97:MSE:CE	2.90	0.49
1:F:111:HIS:CE1	2:F:211:HOH:O	2.55	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:GLN:O	1:E:69:MSE:HG3	2.12	0.49
1:F:28:HIS:NE2	1:F:82:THR:HG22	2.28	0.49
1:F:17:VAL:HG21	1:F:84:PHE:HE1	1.78	0.49
1:B:78:LEU:HD22	1:F:16:TYR:CE1	2.48	0.49
1:C:19:LYS:CE	1:C:23:GLN:O	2.60	0.49
1:D:19:LYS:CB	1:D:28:HIS:ND1	2.76	0.49
1:D:12:CYS:SG	1:E:55:LYS:HE3	2.53	0.49
1:B:11:LEU:HD11	1:F:64:LYS:HE2	1.94	0.48
1:D:41:ILE:N	1:D:42:PRO:CD	2.76	0.48
1:F:108:ILE:N	1:F:109:PRO:CD	2.76	0.48
1:B:65:GLN:HB2	1:F:124:LEU:HB3	1.95	0.48
1:G:43:PHE:CB	1:G:97:MSE:HE3	2.43	0.48
1:G:44:LEU:HD23	1:G:97:MSE:HE1	1.95	0.48
1:C:55:LYS:HG2	1:H:127:ILE:HG22	1.95	0.48
1:D:62:LYS:N	1:D:63:PRO:CD	2.77	0.48
1:H:19:LYS:CB	1:H:28:HIS:ND1	2.77	0.47
1:D:37:ALA:N	1:D:38:PRO:CD	2.77	0.47
1:C:118:THR:HG22	1:C:119:ARG:HG3	1.96	0.47
1:B:98:GLN:O	1:B:104:LEU:HD11	2.14	0.47
1:G:90:ASP:OD2	1:G:92:GLU:HB3	2.15	0.47
1:C:37:ALA:HB3	1:C:38:PRO:HD3	1.96	0.47
1:C:90:ASP:HB2	1:C:92:GLU:OE1	2.15	0.47
1:H:41:ILE:N	1:H:42:PRO:HD2	2.30	0.47
1:A:115:ALA:O	1:A:117:MSE:HE2	2.16	0.46
1:B:108:ILE:N	1:B:109:PRO:HD2	2.30	0.46
1:F:28:HIS:NE2	1:F:82:THR:CG2	2.78	0.46
1:D:87:ILE:N	1:D:87:ILE:HD12	2.31	0.46
1:F:55:LYS:O	1:F:82:THR:HA	2.16	0.46
1:E:90:ASP:CG	1:E:91:ILE:N	2.73	0.46
1:C:65:GLN:O	1:C:69:MSE:HG3	2.16	0.46
1:F:40:MSE:CE	1:F:44:LEU:HD21	2.46	0.46
1:G:43:PHE:HB3	1:G:97:MSE:CE	2.46	0.46
1:A:116:ASP:OD2	1:A:119:ARG:HD3	2.16	0.45
1:C:56:HIS:NE2	1:H:128:GLU:OE2	2.49	0.45
1:B:16:TYR:CZ	1:F:78:LEU:HD22	2.51	0.45
1:D:129:GLU:CD	1:E:51:ARG:HD2	2.41	0.45
1:B:41:ILE:HB	1:B:42:PRO:HD3	1.97	0.45
1:G:13:TRP:CD1	1:G:86:MSE:HE3	2.51	0.45
1:F:17:VAL:HB	1:F:82:THR:HG23	1.99	0.45
1:F:107:THR:HG22	1:F:108:ILE:HD12	1.98	0.45
1:G:44:LEU:CD2	1:G:97:MSE:HE1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:41:ILE:HG22	1:G:45:LYS:HD3	1.99	0.45
1:H:35:VAL:C	1:H:38:PRO:HD2	2.42	0.45
1:B:47:TYR:OH	1:B:100:ASP:HB2	2.17	0.44
1:A:41:ILE:HG22	1:A:42:PRO:HD3	1.99	0.44
1:C:91:ILE:HD13	1:H:64:LYS:HB3	2.00	0.44
1:F:104:LEU:HA	1:F:108:ILE:HD13	1.98	0.44
1:G:43:PHE:O	1:G:47:TYR:HD2	2.00	0.44
1:C:127:ILE:HA	1:H:54:VAL:O	2.18	0.44
1:D:116:ASP:OD1	1:D:118:THR:CG2	2.52	0.44
1:H:73:PRO:HB2	1:H:75:GLU:HG2	1.98	0.44
1:F:49:ILE:HG13	1:F:88:VAL:CG1	2.49	0.43
1:H:25:GLU:O	1:H:29:HIS:HD2	2.02	0.43
1:C:123:SER:HB2	1:H:78:LEU:HB3	2.00	0.43
1:D:131:THR:HG22	1:E:51:ARG:HG3	1.99	0.43
1:G:108:ILE:HB	1:G:109:PRO:HD3	1.99	0.43
1:D:87:ILE:N	1:D:87:ILE:CD1	2.81	0.43
1:H:19:LYS:HB3	1:H:28:HIS:ND1	2.33	0.43
1:A:37:ALA:O	1:A:41:ILE:HD13	2.19	0.43
1:G:46:LYS:HD3	1:G:47:TYR:CE2	2.54	0.43
1:H:29:HIS:ND1	1:H:56:HIS:HB3	2.34	0.43
1:A:62:LYS:N	1:A:63:PRO:CD	2.81	0.43
1:G:100:ASP:OD1	1:G:100:ASP:C	2.62	0.43
1:H:31:HIS:HD1	1:H:31:HIS:C	2.26	0.43
1:A:78:LEU:HD22	1:G:16:TYR:CE1	2.54	0.42
1:D:124:LEU:C	1:D:124:LEU:HD13	2.43	0.42
1:B:78:LEU:HD22	1:F:16:TYR:CZ	2.54	0.42
1:C:28:HIS:O	1:C:32:VAL:HG23	2.20	0.42
1:C:51:ARG:HD3	1:H:129:GLU:OE1	2.20	0.42
1:D:35:VAL:C	1:D:38:PRO:HD2	2.44	0.42
1:F:31:HIS:CE1	1:F:35:VAL:HG11	2.54	0.42
1:H:29:HIS:HE1	1:H:81:ASP:O	2.02	0.42
1:D:78:LEU:HD22	1:E:16:TYR:CE2	2.54	0.42
1:D:126:TRP:HE1	1:E:58:ASP:CG	2.26	0.42
1:F:62:LYS:N	1:F:63:PRO:CD	2.83	0.42
1:G:37:ALA:O	1:G:41:ILE:HG12	2.20	0.42
1:B:68:LEU:HD12	1:B:68:LEU:HA	1.92	0.41
1:E:41:ILE:N	1:E:42:PRO:HD2	2.35	0.41
1:F:103:PHE:CZ	1:F:107:THR:HG21	2.55	0.41
1:A:31:HIS:HE2	1:A:110:ASP:CG	2.28	0.41
1:F:19:LYS:HE2	1:F:23:GLN:O	2.20	0.41
1:D:19:LYS:HB3	1:D:28:HIS:ND1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:ASP:OD1	1:B:100:ASP:C	2.63	0.41
1:A:100:ASP:OD1	1:A:102:GLU:N	2.52	0.41
1:E:80:TYR:OH	1:E:121:LYS:HD2	2.20	0.41
1:D:106:THR:O	1:D:109:PRO:HD2	2.20	0.41
1:A:43:PHE:HB2	1:A:97:MSE:HE3	2.03	0.41
1:C:14:SER:HA	1:C:84:PHE:O	2.20	0.41
1:A:58:ASP:CG	1:G:126:TRP:HE1	2.27	0.41
1:A:91:ILE:HD12	1:A:91:ILE:HA	1.93	0.41
1:D:16:TYR:CZ	1:E:78:LEU:HD22	2.55	0.41
1:A:124:LEU:C	1:A:124:LEU:HD13	2.46	0.40
1:F:124:LEU:HD13	1:F:124:LEU:C	2.46	0.40
1:B:14:SER:HA	1:B:84:PHE:O	2.21	0.40
1:H:111:HIS:ND1	1:H:117:MSE:HE2	2.37	0.40
1:H:40:MSE:HE3	1:H:40:MSE:HB3	2.00	0.40
1:D:35:VAL:O	1:D:38:PRO:HD2	2.22	0.40
1:G:43:PHE:HB3	1:G:97:MSE:HE3	2.03	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	128/141 (91%)	123 (96%)	5 (4%)	0	100	100
1	B	122/141 (86%)	120 (98%)	2 (2%)	0	100	100
1	C	120/141 (85%)	118 (98%)	2 (2%)	0	100	100
1	D	122/141 (86%)	116 (95%)	6 (5%)	0	100	100
1	E	122/141 (86%)	118 (97%)	4 (3%)	0	100	100
1	F	123/141 (87%)	120 (98%)	3 (2%)	0	100	100
1	G	122/141 (86%)	118 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	H	122/141 (86%)	116 (95%)	6 (5%)	0	100 100
All	All	981/1128 (87%)	949 (97%)	32 (3%)	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	119/121 (98%)	113 (95%)	6 (5%)	20 30
1	B	113/121 (93%)	106 (94%)	7 (6%)	15 22
1	C	111/121 (92%)	107 (96%)	4 (4%)	30 44
1	D	107/121 (88%)	97 (91%)	10 (9%)	7 9
1	E	111/121 (92%)	111 (100%)	0	100 100
1	F	112/121 (93%)	105 (94%)	7 (6%)	15 21
1	G	114/121 (94%)	110 (96%)	4 (4%)	31 46
1	H	108/121 (89%)	103 (95%)	5 (5%)	23 33
All	All	895/968 (92%)	852 (95%)	43 (5%)	21 32

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ILE
1	A	6	GLU
1	A	33	SER
1	A	41	ILE
1	A	57	ASN
1	A	105	ARG
1	B	38	PRO
1	B	39	MSE
1	B	41	ILE
1	B	49	ILE

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Mol	Chain	Res	Type
1	B	69	MSE
1	B	123	SER
1	B	131	THR
1	C	14	SER
1	C	39	MSE
1	C	82	THR
1	C	118	THR
1	D	9	ARG
1	D	10	LEU
1	D	72	GLN
1	D	87	ILE
1	D	100	ASP
1	D	104	LEU
1	D	118	THR
1	D	124	LEU
1	D	131	THR
1	D	132	PHE
1	F	20	LYS
1	F	50	VAL
1	F	89	LYS
1	F	100	ASP
1	F	104	LEU
1	F	105	ARG
1	F	107	THR
1	G	15	ILE
1	G	17	VAL
1	G	20	LYS
1	G	130	PHE
1	H	39	MSE
1	H	72	GLN
1	H	86	MSE
1	H	105	ARG
1	H	131	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	B	23	GLN
1	B	57	ASN
1	D	113	ASN
1	E	95	GLN

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Mol	Chain	Res	Type
1	E	111	HIS
1	F	30	ASN
1	G	23	GLN
1	G	57	ASN
1	H	57	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

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

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, 95^{th} 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	124/141 (87%)	-0.05	0 100 100	36, 55, 77, 90	0
1	B	118/141 (83%)	-0.24	0 100 100	32, 48, 71, 78	0
1	C	116/141 (82%)	-0.11	0 100 100	40, 54, 78, 85	0
1	D	118/141 (83%)	0.17	1 (0%) 82 83	41, 64, 90, 104	0
1	E	118/141 (83%)	0.05	0 100 100	36, 63, 85, 93	0
1	F	119/141 (84%)	-0.15	0 100 100	32, 52, 73, 88	0
1	G	118/141 (83%)	-0.21	0 100 100	36, 49, 73, 81	0
1	H	118/141 (83%)	0.20	1 (0%) 82 83	42, 66, 91, 112	0
All	All	949/1128 (84%)	-0.04	2 (0%) 92 92	32, 56, 82, 112	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	37	ALA	2.1
1	D	106	THR	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

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.