



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:53 am GMT

PDB ID : 4IWM
Title : Crystal Structure of the Conserved Hypothetical Protein MJ0927 from Methanocaldococcus jannaschii (in P21 form)
Authors : Kuan, S.M.; Chen, S.C.; Yang, C.S.; Chen, Y.R.; Liu, Y.H.; Chen, Y.
Deposited on : 2013-01-24
Resolution : 2.70 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

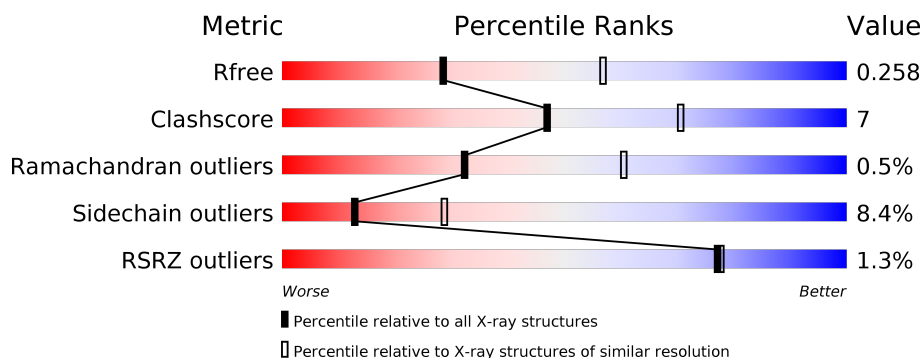
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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. 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	252	<div> <div>79%</div> <div>16%</div> <div>• •</div> </div>
1	B	252	<div> <div>2%</div> <div>71%</div> <div>23%</div> <div>• •</div> </div>
1	C	252	<div> <div>77%</div> <div>17%</div> <div>• •</div> </div>
1	D	252	<div> <div>3%</div> <div>70%</div> <div>24%</div> <div>• •</div> </div>
1	E	252	<div> <div>2%</div> <div>76%</div> <div>19%</div> <div>• •</div> </div>
1	F	252	<div> <div>2%</div> <div>68%</div> <div>25%</div> <div>• •</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11973 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 UPF0135 protein MJ0927.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			
1	B	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			
1	C	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			
1	D	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			
1	E	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			
1	F	244	Total	C	N	O	S	Se	0	0	0
			1932	1255	307	367	1	2			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	250	LEU	-	EXPRESSION TAG	UNP Q58337
A	251	GLU	-	EXPRESSION TAG	UNP Q58337
A	252	HIS	-	EXPRESSION TAG	UNP Q58337
A	253	HIS	-	EXPRESSION TAG	UNP Q58337
A	254	HIS	-	EXPRESSION TAG	UNP Q58337
A	255	HIS	-	EXPRESSION TAG	UNP Q58337
A	256	HIS	-	EXPRESSION TAG	UNP Q58337
A	257	HIS	-	EXPRESSION TAG	UNP Q58337
B	250	LEU	-	EXPRESSION TAG	UNP Q58337
B	251	GLU	-	EXPRESSION TAG	UNP Q58337
B	252	HIS	-	EXPRESSION TAG	UNP Q58337
B	253	HIS	-	EXPRESSION TAG	UNP Q58337
B	254	HIS	-	EXPRESSION TAG	UNP Q58337
B	255	HIS	-	EXPRESSION TAG	UNP Q58337
B	256	HIS	-	EXPRESSION TAG	UNP Q58337
B	257	HIS	-	EXPRESSION TAG	UNP Q58337
C	250	LEU	-	EXPRESSION TAG	UNP Q58337

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Chain	Residue	Modelled	Actual	Comment	Reference
C	251	GLU	-	EXPRESSION TAG	UNP Q58337
C	252	HIS	-	EXPRESSION TAG	UNP Q58337
C	253	HIS	-	EXPRESSION TAG	UNP Q58337
C	254	HIS	-	EXPRESSION TAG	UNP Q58337
C	255	HIS	-	EXPRESSION TAG	UNP Q58337
C	256	HIS	-	EXPRESSION TAG	UNP Q58337
C	257	HIS	-	EXPRESSION TAG	UNP Q58337
D	250	LEU	-	EXPRESSION TAG	UNP Q58337
D	251	GLU	-	EXPRESSION TAG	UNP Q58337
D	252	HIS	-	EXPRESSION TAG	UNP Q58337
D	253	HIS	-	EXPRESSION TAG	UNP Q58337
D	254	HIS	-	EXPRESSION TAG	UNP Q58337
D	255	HIS	-	EXPRESSION TAG	UNP Q58337
D	256	HIS	-	EXPRESSION TAG	UNP Q58337
D	257	HIS	-	EXPRESSION TAG	UNP Q58337
E	250	LEU	-	EXPRESSION TAG	UNP Q58337
E	251	GLU	-	EXPRESSION TAG	UNP Q58337
E	252	HIS	-	EXPRESSION TAG	UNP Q58337
E	253	HIS	-	EXPRESSION TAG	UNP Q58337
E	254	HIS	-	EXPRESSION TAG	UNP Q58337
E	255	HIS	-	EXPRESSION TAG	UNP Q58337
E	256	HIS	-	EXPRESSION TAG	UNP Q58337
E	257	HIS	-	EXPRESSION TAG	UNP Q58337
F	250	LEU	-	EXPRESSION TAG	UNP Q58337
F	251	GLU	-	EXPRESSION TAG	UNP Q58337
F	252	HIS	-	EXPRESSION TAG	UNP Q58337
F	253	HIS	-	EXPRESSION TAG	UNP Q58337
F	254	HIS	-	EXPRESSION TAG	UNP Q58337
F	255	HIS	-	EXPRESSION TAG	UNP Q58337
F	256	HIS	-	EXPRESSION TAG	UNP Q58337
F	257	HIS	-	EXPRESSION TAG	UNP Q58337

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	80	Total O 80 80	0	0
2	B	87	Total O 87 87	0	0
2	C	79	Total O 79 79	0	0
2	D	50	Total O 50 50	0	0

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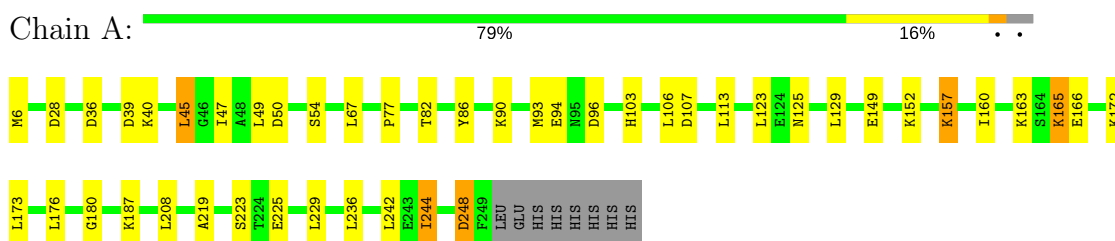
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	49	Total	O	0	0
			49	49		
2	F	36	Total	O	0	0
			36	36		

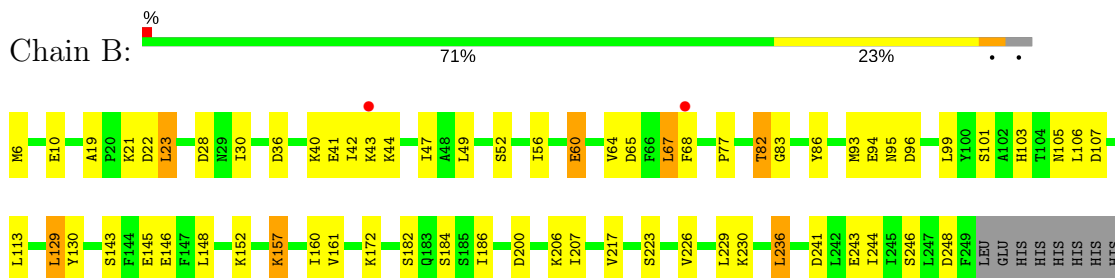
3 Residue-property plots

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.

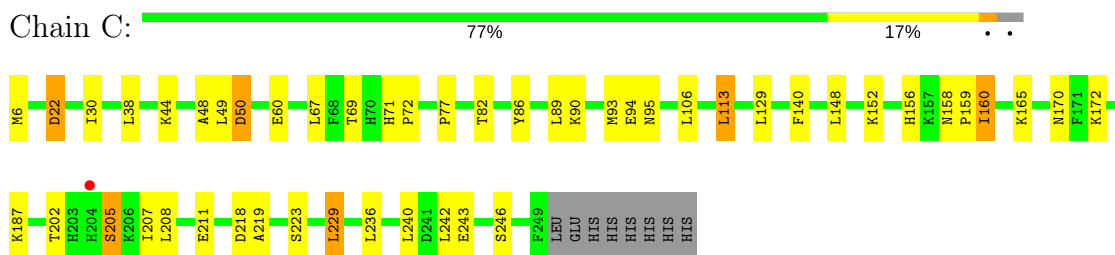
• Molecule 1: UPF0135 protein MJ0927



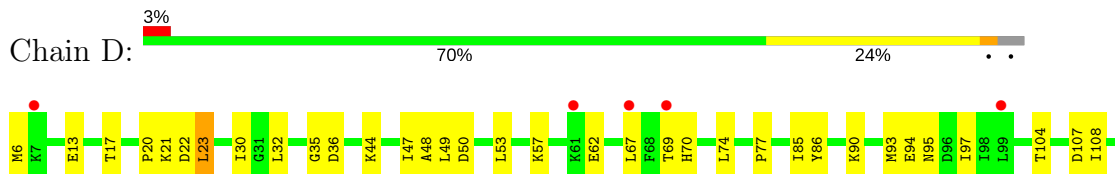
• Molecule 1: UPF0135 protein MJ0927

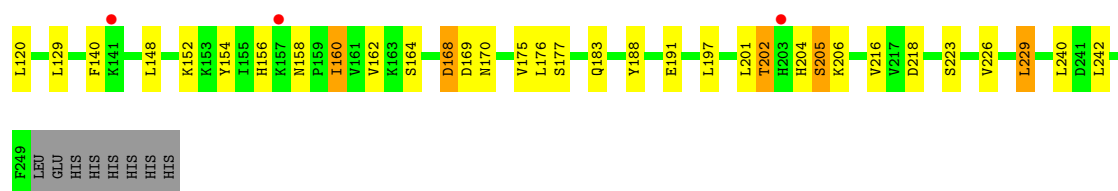


• Molecule 1: UPF0135 protein MJ0927

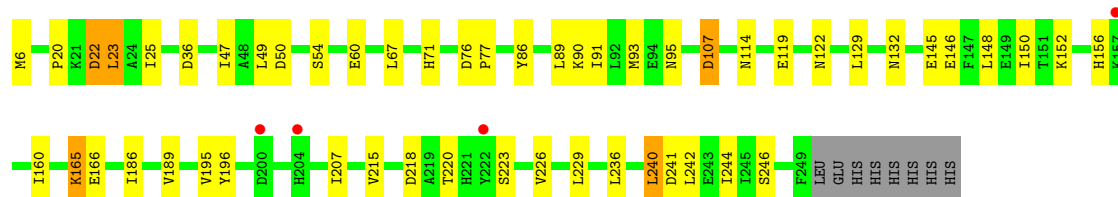
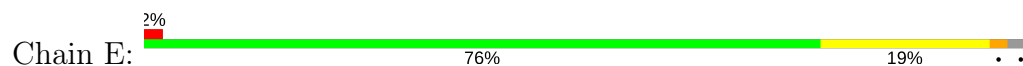


• Molecule 1: UPF0135 protein MJ0927

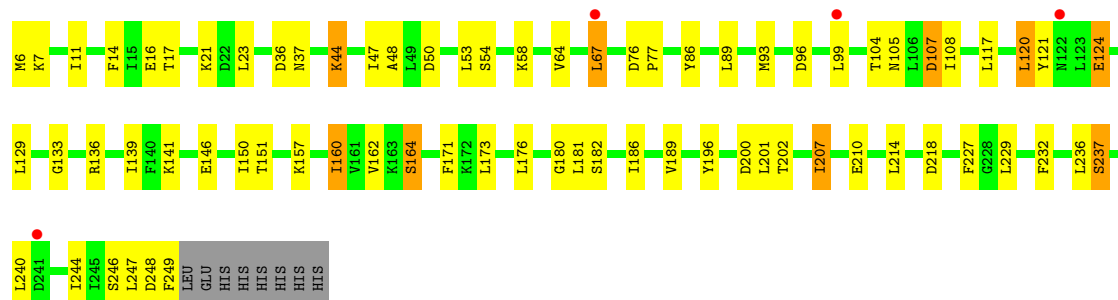




- Molecule 1: UPF0135 protein MJ0927



- Molecule 1: UPF0135 protein MJ0927



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.37Å 77.14Å 131.74Å 90.00° 105.36° 90.00°	Depositor
Resolution (Å)	26.90 – 2.70 26.90 – 2.69	Depositor EDS
% Data completeness (in resolution range)	99.2 (26.90-2.70) 94.5 (26.90-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.72 (at 2.68Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.189 , 0.258 0.189 , 0.258	Depositor DCC
R_{free} test set	2591 reflections (5.10%)	DCC
Wilson B-factor (Å ²)	52.8	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11973	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 3.85% 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	0.46	0/1966	0.61	0/2648
1	B	0.45	0/1966	0.58	0/2648
1	C	0.45	0/1966	0.61	1/2648 (0.0%)
1	D	0.38	0/1966	0.55	0/2648
1	E	0.40	0/1966	0.55	0/2648
1	F	0.35	0/1966	0.54	0/2648
All	All	0.42	0/11796	0.57	1/15888 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	242	LEU	CA-CB-CG	5.39	127.69	115.30

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	1932	0	1978	22	0
1	B	1932	0	1978	36	0
1	C	1932	0	1978	25	0
1	D	1932	0	1978	37	0
1	E	1932	0	1978	26	0
1	F	1932	0	1978	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	80	0	0	2	0
2	B	87	0	0	4	0
2	C	79	0	0	1	0
2	D	50	0	0	1	0
2	E	49	0	0	2	0
2	F	36	0	0	0	0
All	All	11973	0	11868	166	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 (166) 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:F:160:ILE:HG23	1:F:218:ASP:HB3	1.62	0.82
1:A:47:ILE:HD11	1:A:229:LEU:HD22	1.66	0.77
1:D:160:ILE:HG23	1:D:218:ASP:HB3	1.69	0.73
1:A:40:LYS:NZ	1:A:96:ASP:O	2.24	0.70
1:B:94:GLU:OE1	2:B:365:HOH:O	2.09	0.70
1:E:20:PRO:HD2	1:E:23:LEU:HD22	1.73	0.69
1:E:160:ILE:HG23	1:E:218:ASP:HB3	1.74	0.68
1:F:121:TYR:HH	1:F:151:THR:HG1	1.36	0.67
1:A:93:MSE:SE	1:D:93:MSE:HE1	2.46	0.66
1:E:89:LEU:HD22	1:E:93:MSE:HE3	1.80	0.63
1:A:90:LYS:HA	1:D:93:MSE:HE3	1.81	0.62
1:D:202:THR:HG23	1:D:205:SER:HB2	1.82	0.62
1:F:89:LEU:HB3	1:F:93:MSE:HE3	1.83	0.61
1:F:176:LEU:HD12	1:F:180:GLY:HA3	1.83	0.61
1:B:77:PRO:HB2	1:E:77:PRO:HB2	1.83	0.60
1:C:44:LYS:HG3	1:C:243:GLU:HG3	1.82	0.60
1:B:106:LEU:HG	1:B:113:LEU:HD13	1.84	0.59
1:B:145:GLU:HB2	2:B:316:HOH:O	2.02	0.59
1:C:89:LEU:HD22	1:C:93:MSE:HE3	1.85	0.59
1:A:45:LEU:HB3	1:A:244:ILE:HG23	1.85	0.59
1:A:187:LYS:HE3	1:A:208:LEU:HD11	1.84	0.58
1:C:86:TYR:CE1	1:F:36:ASP:HB2	2.39	0.58
1:A:77:PRO:HB2	1:D:77:PRO:HB2	1.85	0.57
1:F:67:LEU:HD13	1:F:99:LEU:HD13	1.85	0.56
1:F:121:TYR:OH	1:F:151:THR:OG1	2.14	0.56
1:A:165:LYS:HE3	1:A:166:GLU:O	2.05	0.56
1:D:20:PRO:HD2	1:D:23:LEU:HD22	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:181:LEU:HD13	1:F:201:LEU:HD13	1.87	0.56
1:E:6:MSE:SE	1:E:240:LEU:HD21	2.56	0.56
1:D:183:GLN:NE2	1:D:204:HIS:HB3	2.21	0.56
1:D:188:TYR:O	1:D:191:GLU:HG2	2.06	0.55
1:D:176:LEU:HD13	1:D:177:SER:O	2.07	0.55
1:B:206:LYS:NZ	2:B:334:HOH:O	2.36	0.55
1:B:60:GLU:HG3	1:B:95:ASN:ND2	2.21	0.55
1:D:183:GLN:HE21	1:D:204:HIS:HB3	1.70	0.55
1:A:49:LEU:HD21	1:A:225:GLU:HB3	1.88	0.54
1:E:189:VAL:HG11	1:E:196:TYR:CG	2.42	0.54
1:A:176:LEU:HD12	1:A:180:GLY:HA3	1.89	0.54
1:E:25:ILE:HG22	1:E:132:ASN:HB2	1.90	0.54
1:F:58:LYS:HG2	1:F:247:LEU:HD22	1.89	0.53
1:B:47:ILE:HG13	1:B:68:PHE:HD2	1.74	0.52
1:D:44:LYS:NZ	1:D:62:GLU:O	2.28	0.52
1:B:52:SER:O	1:B:56:ILE:HG13	2.09	0.51
1:F:120:LEU:HD13	1:F:227:PHE:HZ	1.74	0.51
1:B:21:LYS:HD2	1:B:30:ILE:HD12	1.92	0.51
1:F:6:MSE:SE	1:F:240:LEU:HD22	2.61	0.51
1:B:49:LEU:HG	1:B:229:LEU:HD12	1.91	0.51
1:F:171:PHE:HE2	1:F:173:LEU:HB2	1.76	0.50
1:B:143:SER:OG	1:B:146:GLU:HG3	2.11	0.50
1:D:70:HIS:NE2	1:D:107:ASP:OD2	2.42	0.50
1:C:6:MSE:HE1	1:C:240:LEU:HB3	1.93	0.49
1:D:148:LEU:HD21	1:D:152:LYS:HE3	1.94	0.49
1:A:36:ASP:HB3	2:A:322:HOH:O	2.11	0.49
1:A:125:ASN:HB2	2:A:328:HOH:O	2.11	0.49
1:B:86:TYR:CE1	1:E:36:ASP:HB2	2.47	0.49
1:B:6:MSE:N	1:B:41:GLU:OE2	2.45	0.49
1:C:77:PRO:HB2	1:F:77:PRO:HB2	1.93	0.49
1:F:164:SER:OG	1:F:214:LEU:O	2.23	0.49
1:E:22:ASP:N	1:E:22:ASP:OD2	2.37	0.49
1:D:95:ASN:HB2	1:D:97:ILE:HG13	1.94	0.49
1:E:195:VAL:HG22	1:E:215:VAL:HB	1.94	0.48
1:B:19:ALA:O	1:B:105:ASN:ND2	2.41	0.48
1:D:201:LEU:HD13	1:D:216:VAL:HG11	1.95	0.48
1:F:105:ASN:OD1	1:F:105:ASN:N	2.45	0.48
1:C:93:MSE:HG2	1:F:86:TYR:CE2	2.49	0.48
1:B:93:MSE:HG2	1:E:86:TYR:CE2	2.49	0.48
1:E:71:HIS:HB3	2:E:344:HOH:O	2.13	0.47
1:E:236:LEU:HB3	1:E:244:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:146:GLU:O	1:F:150:ILE:HG13	2.14	0.47
1:B:129:LEU:HD13	1:B:130:TYR:CE2	2.50	0.47
1:B:93:MSE:HE1	1:E:93:MSE:SE	2.64	0.47
1:A:152:LYS:HG2	1:A:157:LYS:O	2.14	0.47
1:D:6:MSE:SE	1:D:240:LEU:HD22	2.65	0.47
1:A:28:ASP:OD2	1:A:103:HIS:HB3	2.14	0.47
1:C:158:ASN:ND2	2:C:307:HOH:O	2.48	0.47
1:C:219:ALA:O	1:C:223:SER:HB2	2.14	0.47
1:F:14:PHE:O	1:F:17:THR:HB	2.15	0.47
1:A:219:ALA:O	1:A:223:SER:HB2	2.15	0.47
1:B:236:LEU:HB3	1:B:244:ILE:HD13	1.97	0.47
1:B:30:ILE:HG22	1:B:103:HIS:H	1.79	0.47
1:C:140:PHE:O	1:C:170:ASN:HA	2.15	0.47
1:C:50:ASP:OD1	1:C:71:HIS:ND1	2.47	0.46
1:B:44:LYS:HE3	1:B:243:GLU:CD	2.35	0.46
1:B:93:MSE:HE3	1:E:90:LYS:HA	1.96	0.46
1:C:60:GLU:HG3	1:C:95:ASN:OD1	2.15	0.46
1:D:21:LYS:HB3	1:D:30:ILE:HD12	1.98	0.46
1:C:160:ILE:HG23	1:C:218:ASP:HB3	1.98	0.46
1:B:40:LYS:NZ	1:B:65:ASP:HB2	2.30	0.45
1:D:152:LYS:HA	1:D:156:HIS:O	2.16	0.45
1:B:44:LYS:HB3	1:B:64:VAL:HA	1.98	0.45
1:B:182:SER:O	1:B:186:ILE:HG12	2.16	0.45
1:E:152:LYS:HA	1:E:156:HIS:O	2.17	0.45
1:A:49:LEU:HB2	1:A:248:ASP:OD2	2.17	0.45
1:C:148:LEU:HA	1:C:148:LEU:HD23	1.67	0.45
1:D:48:ALA:O	1:D:69:THR:HA	2.16	0.45
1:A:86:TYR:CE2	1:D:93:MSE:HG2	2.52	0.45
1:F:48:ALA:HB1	1:F:248:ASP:HB2	1.98	0.45
1:C:48:ALA:O	1:C:69:THR:HA	2.17	0.45
1:D:175:VAL:HG12	1:D:197:LEU:HB3	1.99	0.45
1:F:7:LYS:O	1:F:11:ILE:HG13	2.17	0.44
1:B:42:ILE:O	2:B:321:HOH:O	2.21	0.44
1:F:171:PHE:CE2	1:F:173:LEU:HB2	2.52	0.44
1:C:90:LYS:O	1:C:94:GLU:HB2	2.18	0.44
1:B:152:LYS:HG2	1:B:157:LYS:O	2.18	0.44
1:D:168:ASP:HB3	1:D:169:ASP:H	1.59	0.44
1:D:93:MSE:HB2	1:D:93:MSE:HE2	1.89	0.44
1:E:107:ASP:HB3	1:E:114:ASN:ND2	2.33	0.44
1:E:146:GLU:O	1:E:150:ILE:HG13	2.17	0.44
1:D:13:GLU:O	1:D:17:THR:OG1	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:76:ASP:HA	1:E:77:PRO:HD3	1.83	0.44
1:F:47:ILE:HD11	1:F:249:PHE:HZ	1.83	0.44
1:F:58:LYS:HB2	1:F:58:LYS:HE3	1.70	0.44
1:C:90:LYS:NZ	1:F:93:MSE:O	2.50	0.43
1:C:106:LEU:HG	1:C:113:LEU:HD13	1.99	0.43
1:F:182:SER:O	1:F:186:ILE:HG12	2.18	0.43
1:F:164:SER:HB3	1:F:210:GLU:HA	2.00	0.43
1:A:106:LEU:HG	1:A:113:LEU:HD13	2.00	0.43
1:B:28:ASP:OD2	1:B:103:HIS:HB3	2.17	0.43
1:D:47:ILE:HD11	1:D:229:LEU:HD22	2.01	0.43
1:D:74:LEU:HD21	1:D:85:ILE:HD13	2.01	0.43
1:C:187:LYS:HE3	1:C:208:LEU:HD21	2.00	0.43
1:F:108:ILE:O	1:F:136:ARG:NH2	2.52	0.43
1:D:90:LYS:NZ	1:D:94:GLU:OE2	2.51	0.43
1:F:237:SER:HA	1:F:244:ILE:HD12	2.00	0.42
1:A:94:GLU:HG2	1:D:94:GLU:HG2	2.01	0.42
1:B:157:LYS:HB3	1:B:157:LYS:HE2	1.89	0.42
1:B:107:ASP:HA	1:B:113:LEU:HB2	2.01	0.42
1:B:67:LEU:HD13	1:B:99:LEU:HD13	2.02	0.42
1:F:124:GLU:OE1	1:F:141:LYS:HE2	2.19	0.42
1:B:82:THR:OG1	1:B:83:GLY:N	2.52	0.42
1:E:223:SER:HA	1:E:226:VAL:HG12	2.02	0.42
1:D:36:ASP:HB3	2:D:316:HOH:O	2.19	0.42
1:E:165:LYS:HE3	1:E:166:GLU:O	2.20	0.42
1:F:108:ILE:HG12	1:F:133:GLY:O	2.19	0.42
1:F:124:GLU:HB3	1:F:139:ILE:HB	2.02	0.42
1:A:123:LEU:HD21	1:A:173:LEU:HD23	2.01	0.42
1:A:107:ASP:HA	1:A:113:LEU:HB2	2.01	0.42
1:D:140:PHE:O	1:D:170:ASN:HA	2.19	0.42
1:B:161:VAL:HG22	1:B:217:VAL:HG22	2.02	0.42
1:D:53:LEU:HG	1:D:57:LYS:HE3	2.01	0.42
1:B:23:LEU:HD21	1:C:211:GLU:HG3	2.01	0.42
1:F:207:ILE:HA	1:F:207:ILE:HD13	1.77	0.41
1:B:226:VAL:HG22	1:B:230:LYS:HE3	2.00	0.41
1:F:44:LYS:HB3	1:F:64:VAL:HA	2.02	0.41
1:C:202:THR:OG1	1:C:205:SER:HB2	2.20	0.41
1:D:32:LEU:HD11	1:D:35:GLY:HA3	2.03	0.41
1:E:189:VAL:HG21	1:E:196:TYR:CZ	2.55	0.41
1:C:22:ASP:OD2	1:C:22:ASP:N	2.45	0.41
1:F:16:GLU:HG2	1:F:21:LYS:HG3	2.02	0.41
1:D:120:LEU:HD11	1:D:154:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:189:VAL:HG11	1:F:196:TYR:CG	2.54	0.41
1:C:229:LEU:HD23	1:C:229:LEU:HA	1.79	0.41
1:A:36:ASP:HB2	1:D:86:TYR:CD1	2.56	0.41
1:F:232:PHE:O	1:F:236:LEU:HB2	2.20	0.41
1:C:71:HIS:HA	1:C:72:PRO:HD3	1.93	0.41
1:F:104:THR:HA	1:F:107:ASP:HB2	2.03	0.41
1:E:91:ILE:O	1:E:95:ASN:ND2	2.49	0.41
1:B:207:ILE:HA	1:B:207:ILE:HD13	1.94	0.40
1:C:158:ASN:HA	1:C:159:PRO:HD3	1.88	0.40
1:E:145:GLU:HB2	2:E:317:HOH:O	2.22	0.40
1:B:36:ASP:HB3	1:E:86:TYR:CD1	2.56	0.40
1:E:89:LEU:HA	1:E:89:LEU:HD23	1.74	0.40
1:C:152:LYS:HA	1:C:156:HIS:O	2.21	0.40
1:D:104:THR:O	1:D:108:ILE:HG13	2.21	0.40
1:D:223:SER:HA	1:D:226:VAL:HG12	2.03	0.40
1:D:162:VAL:HG21	1:D:206:LYS:HG3	2.03	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	242/252 (96%)	231 (96%)	11 (4%)	0	100	100
1	B	242/252 (96%)	230 (95%)	11 (4%)	1 (0%)	38	66
1	C	242/252 (96%)	229 (95%)	13 (5%)	0	100	100
1	D	242/252 (96%)	229 (95%)	12 (5%)	1 (0%)	38	66
1	E	242/252 (96%)	224 (93%)	15 (6%)	3 (1%)	15	37
1	F	242/252 (96%)	223 (92%)	17 (7%)	2 (1%)	22	49
All	All	1452/1512 (96%)	1366 (94%)	79 (5%)	7 (0%)	32	60

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	168	ASP
1	E	241	ASP
1	E	242	LEU
1	B	200	ASP
1	F	96	ASP
1	F	200	ASP
1	E	220	THR

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	215/221 (97%)	197 (92%)	18 (8%)	13	29
1	B	215/221 (97%)	195 (91%)	20 (9%)	10	24
1	C	215/221 (97%)	198 (92%)	17 (8%)	14	33
1	D	215/221 (97%)	202 (94%)	13 (6%)	22	48
1	E	215/221 (97%)	196 (91%)	19 (9%)	12	27
1	F	215/221 (97%)	193 (90%)	22 (10%)	8	20
All	All	1290/1326 (97%)	1181 (92%)	109 (8%)	13	29

All (109) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	MSE
1	A	39	ASP
1	A	45	LEU
1	A	50	ASP
1	A	54	SER
1	A	67	LEU
1	A	82	THR
1	A	129	LEU
1	A	149	GLU
1	A	157	LYS

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Mol	Chain	Res	Type
1	A	160	ILE
1	A	163	LYS
1	A	165	LYS
1	A	172	LYS
1	A	236	LEU
1	A	242	LEU
1	A	244	ILE
1	A	248	ASP
1	B	10	GLU
1	B	22	ASP
1	B	23	LEU
1	B	43	LYS
1	B	60	GLU
1	B	67	LEU
1	B	82	THR
1	B	96	ASP
1	B	101	SER
1	B	129	LEU
1	B	148	LEU
1	B	157	LYS
1	B	160	ILE
1	B	172	LYS
1	B	184	SER
1	B	223	SER
1	B	236	LEU
1	B	241	ASP
1	B	246	SER
1	B	248	ASP
1	C	22	ASP
1	C	30	ILE
1	C	38	LEU
1	C	49	LEU
1	C	50	ASP
1	C	67	LEU
1	C	82	THR
1	C	113	LEU
1	C	129	LEU
1	C	160	ILE
1	C	165	LYS
1	C	172	LYS
1	C	205	SER
1	C	207	ILE

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Mol	Chain	Res	Type
1	C	229	LEU
1	C	236	LEU
1	C	246	SER
1	D	22	ASP
1	D	23	LEU
1	D	49	LEU
1	D	50	ASP
1	D	67	LEU
1	D	129	LEU
1	D	158	ASN
1	D	160	ILE
1	D	164	SER
1	D	202	THR
1	D	205	SER
1	D	229	LEU
1	D	242	LEU
1	E	22	ASP
1	E	23	LEU
1	E	47	ILE
1	E	49	LEU
1	E	50	ASP
1	E	54	SER
1	E	60	GLU
1	E	67	LEU
1	E	107	ASP
1	E	119	GLU
1	E	122	ASN
1	E	129	LEU
1	E	148	LEU
1	E	165	LYS
1	E	186	ILE
1	E	207	ILE
1	E	229	LEU
1	E	240	LEU
1	E	246	SER
1	F	23	LEU
1	F	37	ASN
1	F	44	LYS
1	F	50	ASP
1	F	53	LEU
1	F	54	SER
1	F	67	LEU

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Mol	Chain	Res	Type
1	F	76	ASP
1	F	107	ASP
1	F	117	LEU
1	F	120	LEU
1	F	124	GLU
1	F	129	LEU
1	F	157	LYS
1	F	160	ILE
1	F	162	VAL
1	F	164	SER
1	F	202	THR
1	F	207	ILE
1	F	229	LEU
1	F	237	SER
1	F	246	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	95	ASN
1	D	183	GLN

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	242/252 (96%)	-0.34	0 100 100	33, 45, 63, 75	0
1	B	242/252 (96%)	-0.29	2 (0%) 86 86	34, 49, 65, 73	0
1	C	242/252 (96%)	-0.28	1 (0%) 92 93	33, 51, 66, 76	0
1	D	242/252 (96%)	0.05	8 (3%) 47 46	47, 62, 80, 88	0
1	E	242/252 (96%)	-0.16	4 (1%) 70 72	41, 61, 74, 89	0
1	F	242/252 (96%)	0.08	4 (1%) 70 72	47, 73, 93, 109	0
All	All	1452/1512 (96%)	-0.16	19 (1%) 77 78	33, 56, 84, 109	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	204	HIS	3.3
1	D	99	LEU	2.9
1	D	67	LEU	2.7
1	D	157	LYS	2.6
1	D	141	LYS	2.5
1	D	69	THR	2.4
1	F	241	ASP	2.3
1	D	203	HIS	2.3
1	F	99	LEU	2.3
1	E	157	LYS	2.2
1	E	204	HIS	2.2
1	E	200	ASP	2.1
1	B	68	PHE	2.1
1	F	122	ASN	2.1
1	F	67	LEU	2.1
1	B	43	LYS	2.1
1	D	61	LYS	2.1
1	D	7	LYS	2.0
1	E	222	TYR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no 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.