Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 05:33 AM JST

PDB ID	:	6KYT
Title	:	The structure of the M. tb toxin MazEF-mt1 complex
Authors	:	Xie, W.; Chen, R.; Zhou, J.
Deposited on	:	2019-09-20
Resolution	:	2.00 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:

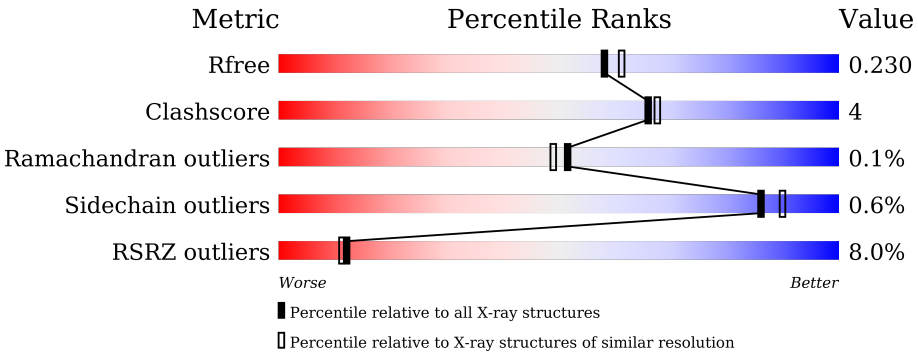
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	122	9% 78% 12% 10%
1	B	122	12% 92% 7% .
1	D	122	9% 93% 5% .
1	E	122	9% 76% 16% 7%
1	G	122	7% 85% 11% .
1	H	122	13% 90% 7% .

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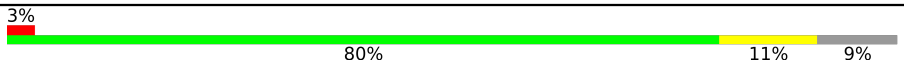
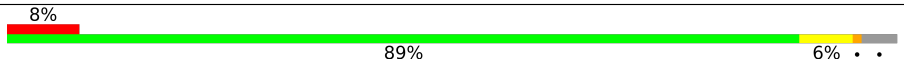
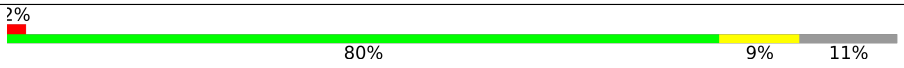
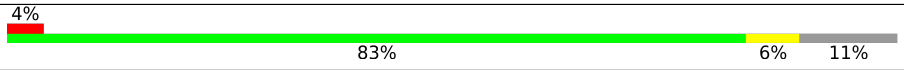
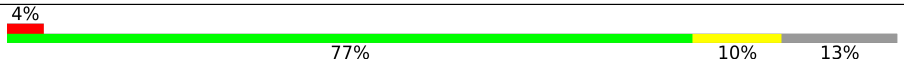
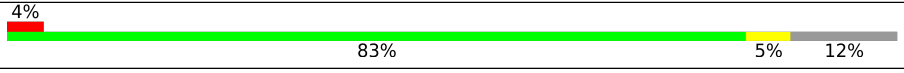
Mol	Chain	Length	Quality of chain
1	J	122	
1	K	122	
2	C	82	
2	F	82	
2	P	82	
2	Q	82	

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 9664 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 Endoribonuclease MazF9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	0	0	0
			827	517	150	158	2			
1	B	120	Total	C	N	O	S	0	0	0
			916	569	172	172	3			
1	D	119	Total	C	N	O	S	0	0	0
			898	559	167	169	3			
1	E	113	Total	C	N	O	S	0	0	0
			856	535	156	162	3			
1	G	118	Total	C	N	O	S	0	0	0
			896	557	166	171	2			
1	H	118	Total	C	N	O	S	0	0	0
			897	559	167	168	3			
1	J	111	Total	C	N	O	S	0	0	0
			845	528	152	162	3			
1	K	117	Total	C	N	O	S	0	0	0
			894	557	166	168	3			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	MET	-	initiating methionine	UNP P71650
A	-2	ALA	-	expression tag	UNP P71650
A	-1	ASP	-	expression tag	UNP P71650
A	0	LEU	-	expression tag	UNP P71650
B	-3	MET	-	initiating methionine	UNP P71650
B	-2	ALA	-	expression tag	UNP P71650
B	-1	ASP	-	expression tag	UNP P71650
B	0	LEU	-	expression tag	UNP P71650
D	-3	MET	-	initiating methionine	UNP P71650
D	-2	ALA	-	expression tag	UNP P71650
D	-1	ASP	-	expression tag	UNP P71650
D	0	LEU	-	expression tag	UNP P71650
E	-3	MET	-	initiating methionine	UNP P71650

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	ALA	-	expression tag	UNP P71650
E	-1	ASP	-	expression tag	UNP P71650
E	0	LEU	-	expression tag	UNP P71650
G	-3	MET	-	initiating methionine	UNP P71650
G	-2	ALA	-	expression tag	UNP P71650
G	-1	ASP	-	expression tag	UNP P71650
G	0	LEU	-	expression tag	UNP P71650
H	-3	MET	-	initiating methionine	UNP P71650
H	-2	ALA	-	expression tag	UNP P71650
H	-1	ASP	-	expression tag	UNP P71650
H	0	LEU	-	expression tag	UNP P71650
J	-3	MET	-	initiating methionine	UNP P71650
J	-2	ALA	-	expression tag	UNP P71650
J	-1	ASP	-	expression tag	UNP P71650
J	0	LEU	-	expression tag	UNP P71650
K	-3	MET	-	initiating methionine	UNP P71650
K	-2	ALA	-	expression tag	UNP P71650
K	-1	ASP	-	expression tag	UNP P71650
K	0	LEU	-	expression tag	UNP P71650

- Molecule 2 is a protein called Antitoxin MazE9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	71	Total 533	C 334	N 93	O 106	0	0	0
2	F	73	Total 553	C 345	N 95	O 113	0	0	0
2	Q	72	Total 553	C 346	N 95	O 112	0	0	0
2	C	73	Total 549	C 343	N 94	O 112	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-5	GLY	-	expression tag	UNP P0CL61
P	-4	PRO	-	expression tag	UNP P0CL61
P	-3	SER	-	expression tag	UNP P0CL61
P	-2	GLN	-	expression tag	UNP P0CL61
P	-1	ASP	-	expression tag	UNP P0CL61
P	0	PRO	-	expression tag	UNP P0CL61
P	1	VAL	MET	conflict	UNP P0CL61

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	GLY	-	expression tag	UNP P0CL61
F	-4	PRO	-	expression tag	UNP P0CL61
F	-3	SER	-	expression tag	UNP P0CL61
F	-2	GLN	-	expression tag	UNP P0CL61
F	-1	ASP	-	expression tag	UNP P0CL61
F	0	PRO	-	expression tag	UNP P0CL61
F	1	VAL	MET	conflict	UNP P0CL61
Q	-5	GLY	-	expression tag	UNP P0CL61
Q	-4	PRO	-	expression tag	UNP P0CL61
Q	-3	SER	-	expression tag	UNP P0CL61
Q	-2	GLN	-	expression tag	UNP P0CL61
Q	-1	ASP	-	expression tag	UNP P0CL61
Q	0	PRO	-	expression tag	UNP P0CL61
Q	1	VAL	MET	conflict	UNP P0CL61
C	-5	GLY	-	expression tag	UNP P0CL61
C	-4	PRO	-	expression tag	UNP P0CL61
C	-3	SER	-	expression tag	UNP P0CL61
C	-2	GLN	-	expression tag	UNP P0CL61
C	-1	ASP	-	expression tag	UNP P0CL61
C	0	PRO	-	expression tag	UNP P0CL61
C	1	VAL	MET	conflict	UNP P0CL61

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	27	Total O 27 27	0	0
3	B	61	Total O 61 61	0	0
3	P	30	Total O 30 30	0	0
3	D	53	Total O 53 53	0	0
3	E	43	Total O 43 43	0	0
3	F	26	Total O 26 26	0	0
3	G	33	Total O 33 33	0	0
3	H	29	Total O 29 29	0	0
3	J	56	Total O 56 56	0	0

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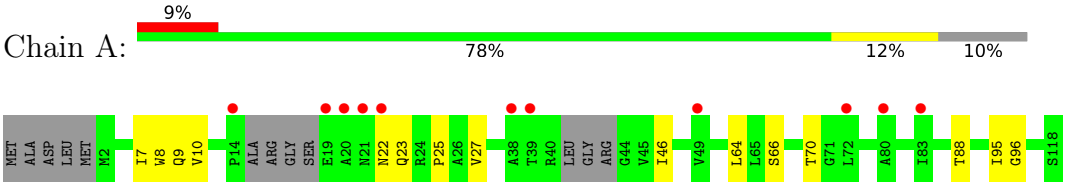
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	K	39	Total O 39 39	0	0
3	Q	30	Total O 30 30	0	0
3	C	20	Total O 20 20	0	0

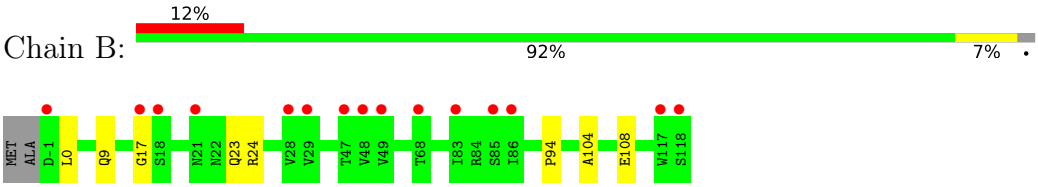
3 Residue-property plots (i)

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.

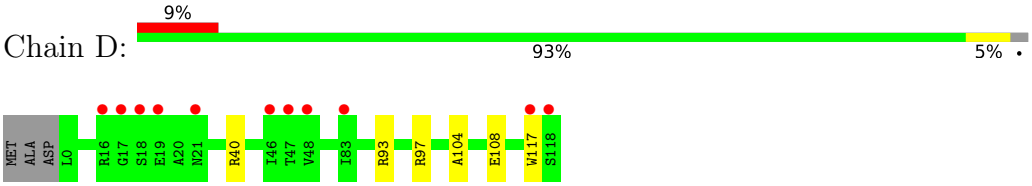
• Molecule 1: Endoribonuclease MazF9



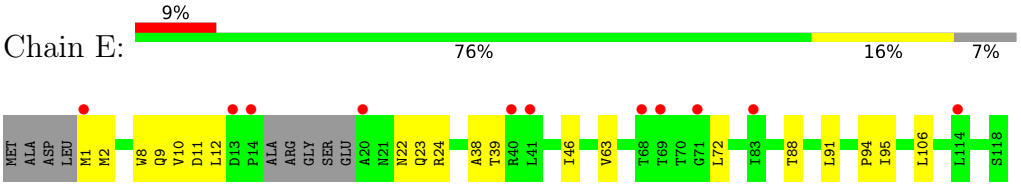
• Molecule 1: Endoribonuclease MazF9



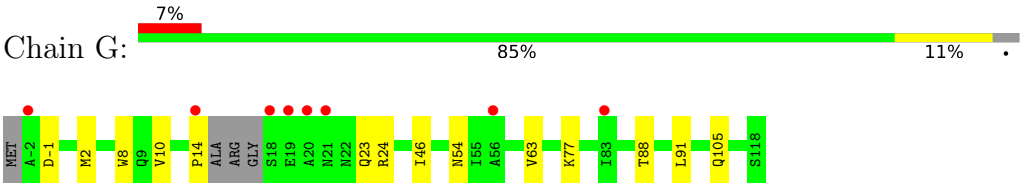
• Molecule 1: Endoribonuclease MazF9



• Molecule 1: Endoribonuclease MazF9

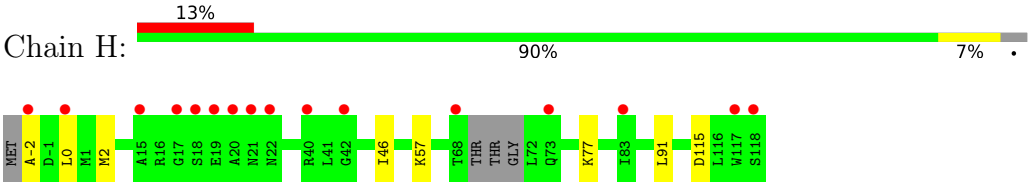


• Molecule 1: Endoribonuclease MazF9



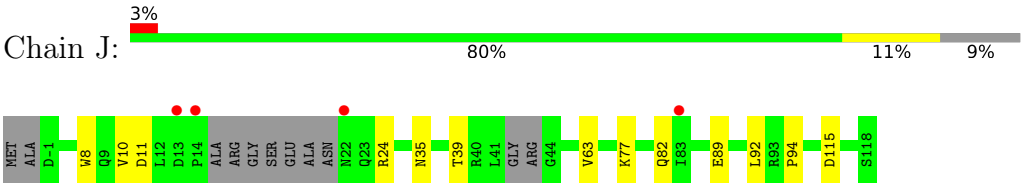
• Molecule 1: Endoribonuclease MazF9

Chain H:



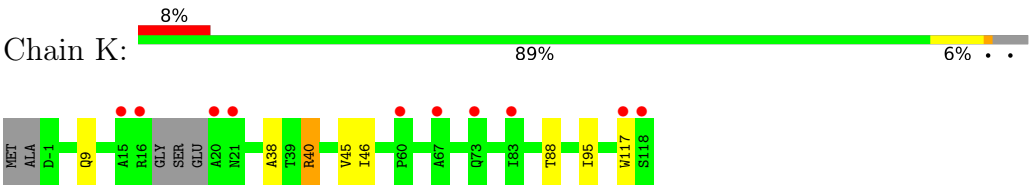
• Molecule 1: Endoribonuclease MazF9

Chain J:



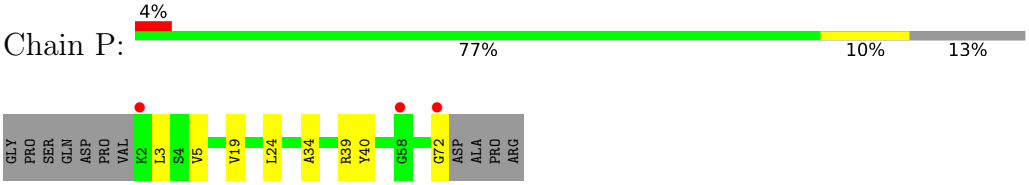
• Molecule 1: Endoribonuclease MazF9

Chain K:



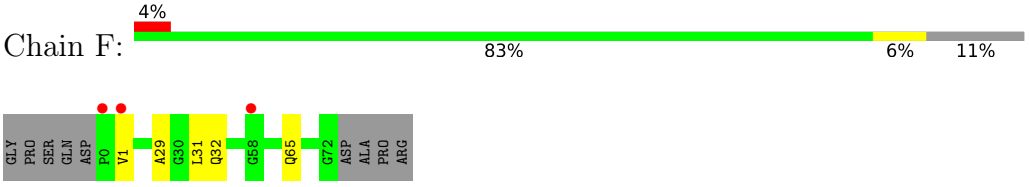
• Molecule 2: Antitoxin MazE9

Chain P:



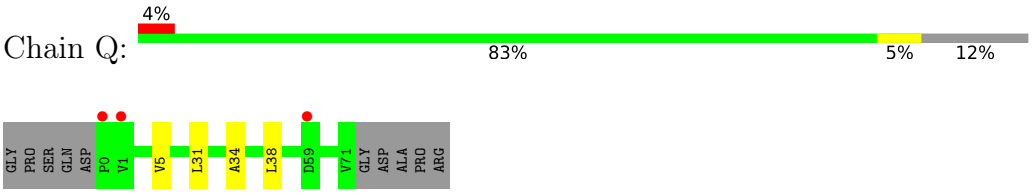
• Molecule 2: Antitoxin MazE9

Chain F:



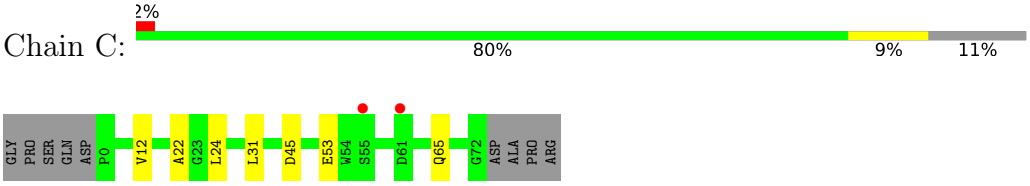
• Molecule 2: Antitoxin MazE9

Chain Q:



• Molecule 2: Antitoxin MazE9

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	51.70Å 161.14Å 78.85Å 90.00° 99.63° 90.00°	Depositor
Resolution (Å)	28.68 – 2.00 28.68 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.68-2.00) 99.7 (28.68-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155, PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.195 , 0.230 0.194 , 0.230	Depositor DCC
R_{free} test set	4231 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	38.0	Xtriage
Anisotropy	0.207	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	9664	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.52% 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	0.25	0/836	0.46	0/1139
1	B	0.24	0/927	0.47	0/1260
1	D	0.27	0/909	0.50	0/1238
1	E	0.28	0/866	0.53	0/1178
1	G	0.25	0/906	0.46	0/1233
1	H	0.24	0/907	0.45	0/1232
1	J	0.25	0/854	0.45	0/1162
1	K	0.24	0/904	0.44	0/1228
2	C	0.26	0/561	0.43	0/768
2	F	0.24	0/565	0.42	0/773
2	P	0.25	0/544	0.43	0/743
2	Q	0.24	0/565	0.39	0/772
All	All	0.25	0/9344	0.46	0/12726

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

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	827	0	831	8	0
1	B	916	0	942	6	0
1	D	898	0	916	7	0
1	E	856	0	874	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	896	0	912	9	1
1	H	897	0	918	4	0
1	J	845	0	857	7	0
1	K	894	0	918	6	0
2	C	549	0	513	6	0
2	F	553	0	519	4	0
2	P	533	0	501	11	1
2	Q	553	0	527	6	0
3	A	27	0	0	1	0
3	B	61	0	0	3	0
3	C	20	0	0	0	0
3	D	53	0	0	4	0
3	E	43	0	0	1	0
3	F	26	0	0	0	0
3	G	33	0	0	1	0
3	H	29	0	0	0	0
3	J	56	0	0	0	0
3	K	39	0	0	1	0
3	P	30	0	0	0	0
3	Q	30	0	0	0	0
All	All	9664	0	9228	73	1

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 4.

All (73) 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:E:9:GLN:HG2	1:E:95:ILE:HD11	1.36	1.08
2:P:3:LEU:HD13	2:P:5:VAL:HG13	1.52	0.90
1:E:12:LEU:O	2:F:65:GLN:NE2	2.12	0.82
2:P:5:VAL:HG11	2:Q:31:LEU:HD12	1.69	0.72
1:D:40:ARG:NH1	3:D:201:HOH:O	2.22	0.72
2:P:3:LEU:CD1	2:P:5:VAL:HG13	2.20	0.71
1:E:72:LEU:HD21	1:E:95:ILE:HG22	1.75	0.69
1:E:1:MET:HA	1:E:39:THR:HG21	1.80	0.62
1:K:46:ILE:HG12	1:K:88:THR:HG22	1.82	0.61
1:G:105:GLN:NE2	3:G:201:HOH:O	2.33	0.60
1:A:46:ILE:HG12	1:A:88:THR:HG22	1.83	0.60
1:A:70:THR:O	1:A:96:GLY:HA3	2.03	0.59
1:D:104:ALA:O	1:D:108:GLU:HG2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:ARG:NH1	3:B:202:HOH:O	2.25	0.58
1:E:38:ALA:HB1	1:E:88:THR:HG21	1.86	0.56
1:D:117:TRP:HB2	3:D:204:HOH:O	2.06	0.54
1:E:72:LEU:HD21	1:E:95:ILE:CG2	2.37	0.54
1:E:46:ILE:HG12	1:E:88:THR:HG22	1.90	0.54
1:B:9:GLN:NE2	3:B:201:HOH:O	2.22	0.53
1:H:0:LEU:H	1:H:0:LEU:HD12	1.74	0.52
1:J:11:ASP:HB2	1:J:92:LEU:HD11	1.91	0.52
2:P:3:LEU:HD11	2:Q:5:VAL:HG22	1.92	0.52
1:K:40:ARG:NH2	3:K:203:HOH:O	2.41	0.51
1:G:54:ASN:ND2	2:C:53:GLU:OE1	2.44	0.51
1:A:70:THR:HG21	3:A:201:HOH:O	2.10	0.51
1:H:-2:ALA:HB1	1:K:117:TRP:CE2	2.47	0.50
1:A:66:SER:O	1:A:70:THR:HG23	2.12	0.50
1:A:8:TRP:O	1:A:25:PRO:HA	2.11	0.50
1:B:104:ALA:O	1:B:108:GLU:HG2	2.12	0.50
1:H:46:ILE:HD11	1:H:91:LEU:HD21	1.94	0.49
1:G:14:PRO:HA	2:C:65:GLN:HG2	1.94	0.49
1:G:46:ILE:HG12	1:G:88:THR:HG22	1.94	0.49
1:D:97:ARG:NH1	3:D:206:HOH:O	2.42	0.48
1:G:2:MET:HG2	1:G:8:TRP:CZ2	2.49	0.48
1:J:89:GLU:H	1:J:89:GLU:CD	2.17	0.47
1:E:2:MET:SD	1:E:91:LEU:HD22	2.55	0.47
1:E:22:ASN:N	3:E:205:HOH:O	2.40	0.47
2:P:39:ARG:HG2	2:P:40:TYR:CE2	2.50	0.46
2:C:22:ALA:HB3	2:C:24:LEU:HG	1.96	0.46
1:A:10:VAL:O	1:A:23:GLN:HA	2.16	0.46
2:P:34:ALA:HB2	2:Q:38:LEU:HG	1.98	0.46
1:A:7:ILE:HG13	1:A:27:VAL:HG22	1.97	0.45
2:P:3:LEU:CD1	2:Q:5:VAL:HG22	2.47	0.45
1:A:9:GLN:HB2	1:A:95:ILE:HD11	1.98	0.45
2:P:19:VAL:HG13	2:P:24:LEU:HB2	1.99	0.45
2:P:34:ALA:HB1	2:Q:34:ALA:HB1	1.98	0.45
1:E:12:LEU:HB2	1:E:22:ASN:O	2.18	0.44
1:D:93:ARG:NH2	3:D:203:HOH:O	2.29	0.44
1:E:10:VAL:HG22	1:E:24:ARG:O	2.18	0.43
1:B:0:LEU:HD13	1:B:94:PRO:HB2	2.01	0.43
2:F:31:LEU:HD22	2:C:31:LEU:HD22	2.00	0.43
1:G:10:VAL:O	1:G:23:GLN:HA	2.19	0.43
1:J:8:TRP:CZ2	1:J:94:PRO:HG3	2.54	0.43
1:B:24:ARG:NH2	2:P:72:GLY:H	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:11:ASP:HA	1:E:23:GLN:HG2	2.01	0.42
1:J:82:GLN:HE22	1:K:45:VAL:HG21	1.84	0.42
1:J:10:VAL:HG22	1:J:24:ARG:O	2.20	0.42
1:D:40:ARG:NH1	2:C:45:ASP:OD1	2.52	0.42
2:P:5:VAL:HG11	2:Q:31:LEU:CD1	2.46	0.41
2:F:1:VAL:HG11	2:C:12:VAL:HG21	2.01	0.41
1:E:8:TRP:CZ2	1:E:94:PRO:HG3	2.55	0.41
1:J:35:ASN:O	1:J:39:THR:HG23	2.21	0.41
1:G:10:VAL:HG22	1:G:24:ARG:O	2.20	0.41
1:H:57:LYS:O	1:H:77:LYS:NZ	2.42	0.41
1:J:63:VAL:O	1:J:77:LYS:HA	2.20	0.41
1:E:63:VAL:HG21	1:E:106:LEU:HA	2.03	0.41
1:K:38:ALA:HB1	1:K:88:THR:HG21	2.02	0.41
1:B:23:GLN:HG2	3:B:201:HOH:O	2.21	0.40
1:K:9:GLN:HB2	1:K:95:ILE:HD11	2.04	0.40
1:D:108:GLU:OE2	1:D:117:TRP:HH2	2.03	0.40
2:F:29:ALA:HA	2:F:32:GLN:HE21	1.86	0.40
1:G:2:MET:SD	1:G:91:LEU:HD22	2.61	0.40
1:G:63:VAL:O	1:G:77:LYS:HA	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:39:ARG:NH2	1:G:-1:ASP:O[1_554]	2.14	0.06

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	104/122 (85%)	101 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	118/122 (97%)	112 (95%)	5 (4%)	1 (1%)	19 13
1	D	117/122 (96%)	113 (97%)	4 (3%)	0	100 100
1	E	109/122 (89%)	104 (95%)	5 (5%)	0	100 100
1	G	114/122 (93%)	111 (97%)	3 (3%)	0	100 100
1	H	114/122 (93%)	110 (96%)	4 (4%)	0	100 100
1	J	105/122 (86%)	104 (99%)	1 (1%)	0	100 100
1	K	113/122 (93%)	111 (98%)	2 (2%)	0	100 100
2	C	71/82 (87%)	70 (99%)	1 (1%)	0	100 100
2	F	71/82 (87%)	70 (99%)	1 (1%)	0	100 100
2	P	69/82 (84%)	69 (100%)	0	0	100 100
2	Q	70/82 (85%)	70 (100%)	0	0	100 100
All	All	1175/1304 (90%)	1145 (97%)	29 (2%)	1 (0%)	51 49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	17	GLY

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	87/100 (87%)	85 (98%)	2 (2%)	50 53
1	B	97/100 (97%)	97 (100%)	0	100 100
1	D	94/100 (94%)	94 (100%)	0	100 100
1	E	91/100 (91%)	91 (100%)	0	100 100
1	G	95/100 (95%)	95 (100%)	0	100 100
1	H	94/100 (94%)	92 (98%)	2 (2%)	53 57
1	J	91/100 (91%)	90 (99%)	1 (1%)	73 78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	K	95/100 (95%)	94 (99%)	1 (1%)	73 78
2	C	55/64 (86%)	55 (100%)	0	100 100
2	F	56/64 (88%)	56 (100%)	0	100 100
2	P	52/64 (81%)	52 (100%)	0	100 100
2	Q	57/64 (89%)	57 (100%)	0	100 100
All	All	964/1056 (91%)	958 (99%)	6 (1%)	86 90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	64	LEU
1	H	2	MET
1	H	115	ASP
1	J	115	ASP
1	K	40	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	23	GLN
1	E	73	GLN
2	F	32	GLN
2	F	65	GLN
1	G	54	ASN
1	J	23	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 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 (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, 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	110/122 (90%)	0.50	11 (10%) 7 6	24, 41, 67, 95	0
1	B	120/122 (98%)	0.36	15 (12%) 3 3	21, 31, 61, 84	0
1	D	119/122 (97%)	0.27	11 (9%) 9 8	22, 32, 64, 81	0
1	E	113/122 (92%)	0.53	11 (9%) 7 7	25, 42, 71, 80	0
1	G	118/122 (96%)	0.30	8 (6%) 17 16	27, 44, 75, 82	0
1	H	118/122 (96%)	0.47	16 (13%) 3 2	28, 43, 77, 87	0
1	J	111/122 (90%)	0.20	4 (3%) 42 42	29, 40, 64, 80	0
1	K	117/122 (95%)	0.45	10 (8%) 10 10	30, 44, 69, 89	0
2	C	73/82 (89%)	-0.09	2 (2%) 54 53	31, 48, 69, 76	0
2	F	73/82 (89%)	0.06	3 (4%) 37 36	29, 46, 67, 74	0
2	P	71/82 (86%)	0.09	3 (4%) 36 35	25, 46, 66, 73	0
2	Q	72/82 (87%)	-0.07	3 (4%) 36 35	32, 47, 68, 74	0
All	All	1215/1304 (93%)	0.29	97 (7%) 12 11	21, 42, 70, 95	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	ASN	5.6
1	D	17	GLY	5.4
1	H	18	SER	5.4
1	K	20	ALA	4.8
1	E	68	THR	4.7
1	A	20	ALA	4.7
1	E	83	ILE	4.6
2	F	1	VAL	4.5
1	H	118	SER	4.5
1	K	15	ALA	4.3
1	K	118	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	D	117	TRP	4.2
1	H	21	ASN	4.2
1	J	14	PRO	4.1
1	H	17	GLY	4.1
1	E	20	ALA	4.0
1	G	-2	ALA	4.0
1	K	117	TRP	3.8
1	A	83	ILE	3.8
2	P	72	GLY	3.7
1	K	21	ASN	3.7
1	H	0	LEU	3.6
1	H	117	TRP	3.5
1	G	14	PRO	3.5
1	H	-2	ALA	3.5
1	B	83	ILE	3.4
2	F	0	PRO	3.4
1	A	39	THR	3.3
1	E	14	PRO	3.3
1	H	20	ALA	3.3
1	E	69	THR	3.3
2	P	58	GLY	3.2
1	B	18	SER	3.2
1	G	18	SER	3.2
1	H	19	GLU	3.2
1	D	18	SER	3.1
1	J	83	ILE	3.1
1	A	19	GLU	3.1
1	H	15	ALA	3.0
2	Q	59	ASP	3.0
1	E	71	GLY	3.0
1	D	118	SER	3.0
1	B	17	GLY	2.9
2	Q	1	VAL	2.9
1	A	22	ASN	2.9
1	B	29	VAL	2.9
1	G	19	GLU	2.9
1	H	22	ASN	2.9
1	E	114	LEU	2.8
1	D	83	ILE	2.8
1	J	22	ASN	2.7
1	B	-1	ASP	2.7
1	H	73	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	47	THR	2.7
1	B	48	VAL	2.7
1	H	40	ARG	2.6
1	K	83	ILE	2.6
1	B	118	SER	2.6
1	B	47	THR	2.6
1	E	41	LEU	2.6
1	G	56	ALA	2.6
1	D	21	ASN	2.5
2	P	2	LYS	2.5
1	B	68	THR	2.5
1	B	117	TRP	2.4
1	G	21	ASN	2.4
1	B	85	SER	2.4
2	F	58	GLY	2.4
1	G	83	ILE	2.4
1	K	67	ALA	2.3
1	K	60	PRO	2.3
1	E	13	ASP	2.3
1	K	73	GLN	2.3
1	B	21	ASN	2.3
1	A	49	VAL	2.3
1	A	80	ALA	2.3
1	E	1	MET	2.3
1	H	68	THR	2.3
1	D	19	GLU	2.3
1	K	16	ARG	2.2
1	B	49	VAL	2.2
2	C	55	SER	2.2
2	Q	0	PRO	2.2
1	B	28	VAL	2.2
1	D	48	VAL	2.2
1	A	38	ALA	2.2
1	G	20	ALA	2.2
1	A	72	LEU	2.1
1	E	40	ARG	2.1
1	A	14	PRO	2.1
1	H	42	GLY	2.1
2	C	61	ASP	2.1
1	J	13	ASP	2.1
1	D	16	ARG	2.0
1	D	46	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	H	83	ILE	2.0
1	B	86	ILE	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.