



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2020 – 09:45 AM BST

PDB ID : 6YUD
Title : Structure of Csx3/Crn3 from *Archaeoglobus fulgidus* in complex with cyclic tetra-adenylate (cA4)
Authors : McQuarrie, S.; Gloster, T.M.; White, M.F.; Graham, S.; Athukoralage, J.S.; Gruschow, S.
Deposited on : 2020-04-27
Resolution : 1.84 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	:	2.13
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)	:	2.13

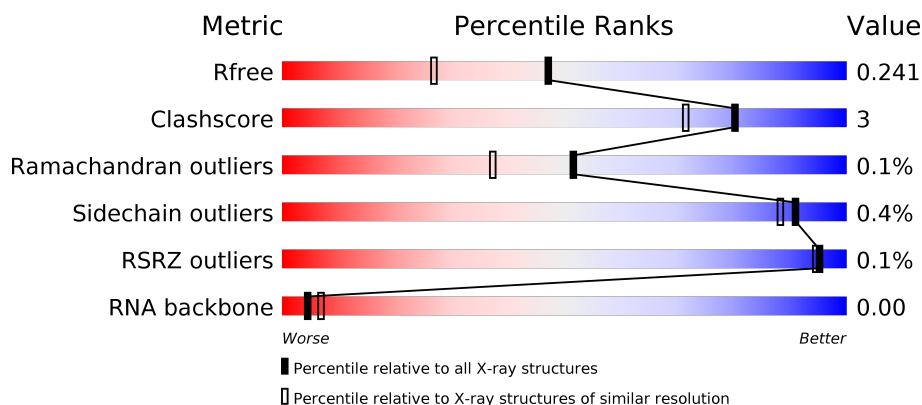
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	4003 (1.86-1.82)
Clashscore	141614	4233 (1.86-1.82)
Ramachandran outliers	138981	4185 (1.86-1.82)
Sidechain outliers	138945	4186 (1.86-1.82)
RSRZ outliers	127900	3957 (1.86-1.82)
RNA backbone	3102	1038 (2.40-1.28)

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	111	<div> <div style="width: 10%; background-color: red;"></div> <div style="width: 85%; background-color: green;"></div> <div style="width: 5%; background-color: yellow;"></div> <div style="width: 10%; background-color: grey;"></div> </div> <div>85% 5% 10%</div>
1	B	111	<div> <div style="width: 88%; background-color: green;"></div> <div style="width: 5%; background-color: yellow;"></div> <div style="width: 6%; background-color: grey;"></div> </div> <div>88% 5% 6%</div>
1	C	111	<div> <div style="width: 83%; background-color: green;"></div> <div style="width: 5%; background-color: yellow;"></div> <div style="width: 12%; background-color: grey;"></div> </div> <div>83% 5% 12%</div>
1	D	111	<div> <div style="width: 83%; background-color: green;"></div> <div style="width: 6%; background-color: yellow;"></div> <div style="width: 11%; background-color: grey;"></div> </div> <div>83% 6% 11%</div>

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Mol	Chain	Length	Quality of chain
1	E	111	
1	F	111	
1	G	111	
1	H	111	
1	I	111	
1	J	111	
2	K	4	
2	M	4	
2	O	4	
2	P	4	
2	Q	4	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 8638 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 Csx3/Crn3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	1	0
			778	510	130	136	2			
1	B	104	Total	C	N	O	S	0	0	0
			788	520	137	129	2			
1	C	98	Total	C	N	O	S	0	1	0
			749	494	126	127	2			
1	D	99	Total	C	N	O	S	0	1	0
			773	508	132	131	2			
1	E	99	Total	C	N	O	S	0	1	0
			760	501	130	127	2			
1	F	97	Total	C	N	O	S	0	1	0
			749	496	127	124	2			
1	G	102	Total	C	N	O	S	0	0	0
			776	507	133	134	2			
1	H	103	Total	C	N	O	S	0	0	0
			780	509	134	134	3			
1	I	98	Total	C	N	O	S	0	0	0
			738	488	121	127	2			
1	J	98	Total	C	N	O	S	0	0	0
			730	482	125	121	2			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLY	-	expression tag	UNP A0A101DCB5
A	-5	ALA	-	expression tag	UNP A0A101DCB5
A	-4	ASN	-	expression tag	UNP A0A101DCB5
A	-3	ALA	-	expression tag	UNP A0A101DCB5
A	-2	MET	-	expression tag	UNP A0A101DCB5
A	-1	ALA	-	expression tag	UNP A0A101DCB5
A	0	SER	-	expression tag	UNP A0A101DCB5
A	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
B	-6	GLY	-	expression tag	UNP A0A101DCB5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	ALA	-	expression tag	UNP A0A101DCB5
B	-4	ASN	-	expression tag	UNP A0A101DCB5
B	-3	ALA	-	expression tag	UNP A0A101DCB5
B	-2	MET	-	expression tag	UNP A0A101DCB5
B	-1	ALA	-	expression tag	UNP A0A101DCB5
B	0	SER	-	expression tag	UNP A0A101DCB5
B	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
C	-6	GLY	-	expression tag	UNP A0A101DCB5
C	-5	ALA	-	expression tag	UNP A0A101DCB5
C	-4	ASN	-	expression tag	UNP A0A101DCB5
C	-3	ALA	-	expression tag	UNP A0A101DCB5
C	-2	MET	-	expression tag	UNP A0A101DCB5
C	-1	ALA	-	expression tag	UNP A0A101DCB5
C	0	SER	-	expression tag	UNP A0A101DCB5
C	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
D	-6	GLY	-	expression tag	UNP A0A101DCB5
D	-5	ALA	-	expression tag	UNP A0A101DCB5
D	-4	ASN	-	expression tag	UNP A0A101DCB5
D	-3	ALA	-	expression tag	UNP A0A101DCB5
D	-2	MET	-	expression tag	UNP A0A101DCB5
D	-1	ALA	-	expression tag	UNP A0A101DCB5
D	0	SER	-	expression tag	UNP A0A101DCB5
D	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
E	-6	GLY	-	expression tag	UNP A0A101DCB5
E	-5	ALA	-	expression tag	UNP A0A101DCB5
E	-4	ASN	-	expression tag	UNP A0A101DCB5
E	-3	ALA	-	expression tag	UNP A0A101DCB5
E	-2	MET	-	expression tag	UNP A0A101DCB5
E	-1	ALA	-	expression tag	UNP A0A101DCB5
E	0	SER	-	expression tag	UNP A0A101DCB5
E	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
F	-6	GLY	-	expression tag	UNP A0A101DCB5
F	-5	ALA	-	expression tag	UNP A0A101DCB5
F	-4	ASN	-	expression tag	UNP A0A101DCB5
F	-3	ALA	-	expression tag	UNP A0A101DCB5
F	-2	MET	-	expression tag	UNP A0A101DCB5
F	-1	ALA	-	expression tag	UNP A0A101DCB5
F	0	SER	-	expression tag	UNP A0A101DCB5
F	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
G	-6	GLY	-	expression tag	UNP A0A101DCB5
G	-5	ALA	-	expression tag	UNP A0A101DCB5
G	-4	ASN	-	expression tag	UNP A0A101DCB5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-3	ALA	-	expression tag	UNP A0A101DCB5
G	-2	MET	-	expression tag	UNP A0A101DCB5
G	-1	ALA	-	expression tag	UNP A0A101DCB5
G	0	SER	-	expression tag	UNP A0A101DCB5
G	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
H	-6	GLY	-	expression tag	UNP A0A101DCB5
H	-5	ALA	-	expression tag	UNP A0A101DCB5
H	-4	ASN	-	expression tag	UNP A0A101DCB5
H	-3	ALA	-	expression tag	UNP A0A101DCB5
H	-2	MET	-	expression tag	UNP A0A101DCB5
H	-1	ALA	-	expression tag	UNP A0A101DCB5
H	0	SER	-	expression tag	UNP A0A101DCB5
H	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
I	-6	GLY	-	expression tag	UNP A0A101DCB5
I	-5	ALA	-	expression tag	UNP A0A101DCB5
I	-4	ASN	-	expression tag	UNP A0A101DCB5
I	-3	ALA	-	expression tag	UNP A0A101DCB5
I	-2	MET	-	expression tag	UNP A0A101DCB5
I	-1	ALA	-	expression tag	UNP A0A101DCB5
I	0	SER	-	expression tag	UNP A0A101DCB5
I	60	ALA	HIS	engineered mutation	UNP A0A101DCB5
J	-6	GLY	-	expression tag	UNP A0A101DCB5
J	-5	ALA	-	expression tag	UNP A0A101DCB5
J	-4	ASN	-	expression tag	UNP A0A101DCB5
J	-3	ALA	-	expression tag	UNP A0A101DCB5
J	-2	MET	-	expression tag	UNP A0A101DCB5
J	-1	ALA	-	expression tag	UNP A0A101DCB5
J	0	SER	-	expression tag	UNP A0A101DCB5
J	60	ALA	HIS	engineered mutation	UNP A0A101DCB5

- Molecule 2 is a RNA chain called cyclic tetra-adenylate (cA4).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	4	Total 88	C 40	N 20	O 24	P 4	0	0	0
2	M	4	Total 88	C 40	N 20	O 24	P 4	0	0	0
2	O	4	Total 88	C 40	N 20	O 24	P 4	0	0	0
2	P	4	Total 88	C 40	N 20	O 24	P 4	0	0	0
2	Q	4	Total 88	C 40	N 20	O 24	P 4	0	0	0


- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	61	Total O 61 61	0	0
3	B	77	Total O 78 78	0	1
3	C	58	Total O 58 58	0	0
3	D	66	Total O 66 66	0	0
3	E	51	Total O 51 51	0	0
3	F	48	Total O 48 48	0	0
3	G	42	Total O 42 42	0	0
3	H	56	Total O 56 56	0	0
3	I	37	Total O 37 37	0	0
3	J	41	Total O 42 42	0	1
3	K	7	Total O 7 7	0	0
3	M	7	Total O 7 7	0	0
3	O	10	Total O 10 10	0	0
3	P	6	Total O 6 6	0	0
3	Q	8	Total O 8 8	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: Csx3/Crn3

Chain A: 




- Molecule 1: Csx3/Crn3

Chain B: 




- Molecule 1: Csx3/Crn3

Chain C: 




- Molecule 1: Csx3/Crn3

Chain D: 




- Molecule 1: Csx3/Crn3

Chain E: 

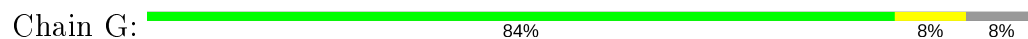


- Molecule 1: Csx3/Crn3

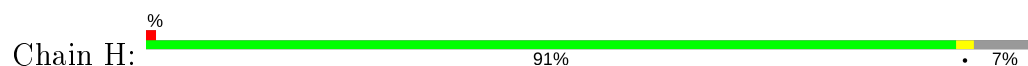
Chain F: 



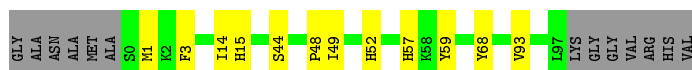
- Molecule 1: Csx3/Crn3



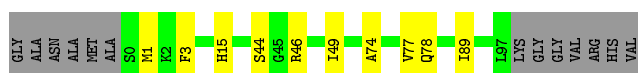
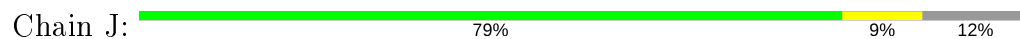
- Molecule 1: Csx3/Crn3



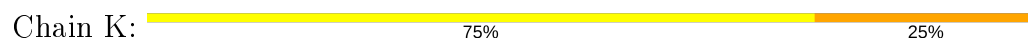
- Molecule 1: Csx3/Crn3



- Molecule 1: Csx3/Crn3



- Molecule 2: cyclic tetra-adenylate (cA4)



- Molecule 2: cyclic tetra-adenylate (cA4)



- Molecule 2: cyclic tetra-adenylate (cA4)




- Molecule 2: cyclic tetra-adenylate (cA4)

Chain P:  25% 50% 25%



- Molecule 2: cyclic tetra-adenylate (cA4)

Chain Q:  50% 25% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	193.97Å 60.36Å 107.08Å 90.00° 116.47° 90.00°	Depositor
Resolution (Å)	53.56 – 1.84 53.56 – 1.84	Depositor EDS
% Data completeness (in resolution range)	96.9 (53.56-1.84) 96.9 (53.56-1.84)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.192 , 0.237 0.199 , 0.241	Depositor DCC
R_{free} test set	4770 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.369	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8638	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.68	0/800	0.85	0/1089
1	B	0.69	0/808	0.85	0/1099
1	C	0.68	0/772	0.82	0/1053
1	D	0.72	0/795	0.82	0/1082
1	E	0.66	0/779	0.84	0/1062
1	F	0.68	0/771	0.84	0/1052
1	G	0.69	0/794	0.81	0/1078
1	H	0.67	0/799	0.81	0/1088
1	I	0.72	0/757	0.83	0/1034
1	J	0.69	0/749	0.77	0/1024
2	K	0.98	0/99	1.46	1/152 (0.7%)
2	M	0.90	0/99	1.41	0/152
2	O	1.05	1/99 (1.0%)	1.39	0/152
2	P	0.85	0/99	1.61	2/152 (1.3%)
2	Q	0.77	0/99	2.10	4/152 (2.6%)
All	All	0.70	1/8319 (0.0%)	0.90	7/11421 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	3	A	N9-C8	-5.19	1.33	1.37

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Q	1	A	O5'-P-OP1	-14.03	93.08	105.70
2	P	2	A	O5'-P-OP1	-9.69	96.98	105.70
2	Q	2	A	P-O3'-C3'	-7.47	110.73	119.70
2	Q	1	A	P-O3'-C3'	-7.37	110.86	119.70
2	K	1	A	O5'-P-OP1	6.14	118.06	110.70
2	P	2	A	OP1-P-OP2	5.97	128.55	119.60
2	Q	1	A	O4'-C1'-N9	5.53	112.62	108.20

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	778	0	777	4	0
1	B	788	0	797	4	0
1	C	749	0	744	4	0
1	D	773	0	782	5	0
1	E	760	0	760	7	0
1	F	749	0	751	3	0
1	G	776	0	768	7	0
1	H	780	0	776	2	0
1	I	738	0	719	8	0
1	J	730	0	717	6	0
2	K	88	0	44	1	0
2	M	88	0	44	0	0
2	O	88	0	44	0	0
2	P	88	0	44	1	0
2	Q	88	0	44	3	0
3	A	61	0	0	1	0
3	B	78	0	0	0	0
3	C	58	0	0	1	0
3	D	66	0	0	2	0
3	E	51	0	0	0	0
3	F	48	0	0	0	0
3	G	42	0	0	1	0
3	H	56	0	0	1	0
3	I	37	0	0	1	0
3	J	42	0	0	0	0
3	K	7	0	0	0	0
3	M	7	0	0	0	0
3	O	10	0	0	0	0
3	P	6	0	0	0	0
3	Q	8	0	0	0	0
All	All	8638	0	7811	43	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 (43) 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:G:79:SER:OG	1:G:82:GLU:O	1.70	1.06
1:C:79:SER:OG	1:C:82:GLU:O	1.94	0.84
1:D:85[B]:GLU:OE1	3:D:202:HOH:O	2.09	0.70
1:A:7:ASP:HB3	3:A:247:HOH:O	1.99	0.62
1:G:79:SER:OG	1:G:83:LEU:O	2.23	0.56
1:E:79:SER:OG	1:E:82:GLU:O	2.13	0.55
1:B:77:VAL:HG23	1:B:78:GLN:HG3	1.91	0.52
1:J:46:ARG:HD3	2:Q:2:A:OP2	2.11	0.50
1:A:46:ARG:HH22	1:E:61:HIS:CE1	2.30	0.49
1:E:49:ILE:HG12	1:F:49:ILE:HG12	1.94	0.48
1:J:74:ALA:HB3	1:J:89:ILE:HB	1.94	0.48
1:G:40:GLY:HA3	1:G:64:PHE:CE2	2.49	0.48
1:G:49:ILE:HG12	1:H:49:ILE:HG12	1.95	0.47
1:I:14:ILE:CD1	1:I:59:TYR:CZ	2.99	0.46
1:C:79:SER:OG	1:C:83:LEU:O	2.35	0.44
1:C:78:GLN:HG2	1:D:57:HIS:CG	2.53	0.44
1:E:46:ARG:HD3	2:P:2:A:OP2	2.18	0.44
1:J:77:VAL:HG23	1:J:78:GLN:HG3	1.98	0.44
1:G:68:TYR:CE1	1:G:93:VAL:HG23	2.52	0.44
1:G:68:TYR:CD1	1:G:93:VAL:HG23	2.53	0.44
1:I:68:TYR:CE1	1:I:93:VAL:HG23	2.53	0.43
1:D:8:ARG:NH2	3:D:206:HOH:O	2.46	0.43
1:B:21:PRO:HB3	1:E:81:SER:HA	2.00	0.43
1:D:1:MET:CE	1:D:3:PHE:CZ	3.02	0.43
1:C:8:ARG:NH2	3:C:203:HOH:O	2.42	0.43
1:I:57:HIS:HB3	3:I:218:HOH:O	2.18	0.43
1:I:48:PRO:HA	2:Q:3:A:OP2	2.19	0.43
1:B:1:MET:HE2	1:B:16:PHE:HB2	2.00	0.42
1:E:14:ILE:CD1	1:E:59:TYR:CZ	3.02	0.42
3:G:212:HOH:O	1:H:57:HIS:HB3	2.19	0.42
1:I:52:HIS:CG	1:J:49:ILE:HG21	2.55	0.42
1:D:77:VAL:HG23	1:D:78:GLN:HG3	2.01	0.42
1:G:57:HIS:HB3	3:H:212:HOH:O	2.20	0.42
1:F:1:MET:CE	1:F:3:PHE:CZ	3.03	0.41
1:B:71:ARG:NH2	1:F:61:HIS:HA	2.35	0.41
1:I:1:MET:CE	1:I:3:PHE:CZ	3.03	0.41
1:J:1:MET:CE	1:J:3:PHE:CZ	3.03	0.41
1:J:15:HIS:HA	1:J:44:SER:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:49:ILE:HD12	2:Q:2:A:H1'	2.03	0.40
1:A:54:PHE:CZ	1:A:58:LYS:HE2	2.57	0.40
1:E:5:VAL:HG21	1:E:33:PRO:HB3	2.03	0.40
1:I:15:HIS:HA	1:I:44:SER:O	2.22	0.40
1:A:49:ILE:HD12	2:K:4:A:H1'	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	99/111 (89%)	95 (96%)	4 (4%)	0	100	100
1	B	102/111 (92%)	101 (99%)	1 (1%)	0	100	100
1	C	97/111 (87%)	91 (94%)	5 (5%)	1 (1%)	15	5
1	D	98/111 (88%)	95 (97%)	3 (3%)	0	100	100
1	E	98/111 (88%)	93 (95%)	5 (5%)	0	100	100
1	F	96/111 (86%)	94 (98%)	2 (2%)	0	100	100
1	G	98/111 (88%)	91 (93%)	7 (7%)	0	100	100
1	H	101/111 (91%)	99 (98%)	2 (2%)	0	100	100
1	I	96/111 (86%)	89 (93%)	7 (7%)	0	100	100
1	J	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
All	All	981/1110 (88%)	939 (96%)	41 (4%)	1 (0%)	51	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	83	LEU

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	81/95 (85%)	79 (98%)	2 (2%)	47	31
1	B	80/95 (84%)	80 (100%)	0	100	100
1	C	78/95 (82%)	77 (99%)	1 (1%)	69	58
1	D	81/95 (85%)	81 (100%)	0	100	100
1	E	77/95 (81%)	76 (99%)	1 (1%)	69	58
1	F	76/95 (80%)	76 (100%)	0	100	100
1	G	80/95 (84%)	80 (100%)	0	100	100
1	H	81/95 (85%)	81 (100%)	0	100	100
1	I	73/95 (77%)	73 (100%)	0	100	100
1	J	72/95 (76%)	72 (100%)	0	100	100
All	All	779/950 (82%)	775 (100%)	4 (0%)	91	85

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25[A]	GLU
1	A	25[B]	GLU
1	C	1	MET
1	E	7	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	GLN
1	H	57	HIS
1	I	80	HIS
1	J	57	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	K	3/4 (75%)	3 (100%)	0
2	M	3/4 (75%)	3 (100%)	0
2	O	3/4 (75%)	3 (100%)	0
2	P	3/4 (75%)	3 (100%)	0
2	Q	3/4 (75%)	3 (100%)	0
All	All	15/20 (75%)	15 (100%)	0

All (15) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	K	2	A
2	K	3	A
2	K	4	A
2	M	2	A
2	M	3	A
2	M	4	A
2	O	2	A
2	O	3	A
2	O	4	A
2	P	2	A
2	P	3	A
2	P	4	A
2	Q	2	A
2	Q	3	A
2	Q	4	A

There are no RNA pucker outliers to report.

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, 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	100/111 (90%)	-0.41	0 100 100	19, 28, 55, 63	0
1	B	104/111 (93%)	-0.42	0 100 100	20, 27, 47, 59	0
1	C	98/111 (88%)	-0.47	0 100 100	23, 33, 55, 64	0
1	D	99/111 (89%)	-0.51	0 100 100	20, 29, 49, 73	0
1	E	99/111 (89%)	-0.39	0 100 100	23, 36, 60, 93	0
1	F	97/111 (87%)	-0.37	0 100 100	24, 37, 58, 66	0
1	G	102/111 (91%)	-0.15	0 100 100	26, 41, 67, 77	0
1	H	103/111 (92%)	-0.38	1 (0%) 82 82	26, 36, 56, 68	0
1	I	98/111 (88%)	-0.30	0 100 100	30, 41, 62, 72	0
1	J	98/111 (88%)	-0.20	0 100 100	28, 42, 63, 73	0
2	K	4/4 (100%)	-0.90	0 100 100	35, 35, 36, 37	0
2	M	4/4 (100%)	-0.74	0 100 100	31, 34, 37, 40	0
2	O	4/4 (100%)	-0.92	0 100 100	28, 30, 31, 33	0
2	P	4/4 (100%)	-0.88	0 100 100	33, 35, 35, 38	0
2	Q	4/4 (100%)	-0.64	0 100 100	39, 39, 44, 47	0
All	All	1018/1130 (90%)	-0.37	1 (0%) 95 94	19, 35, 60, 93	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	-1	ALA	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 [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.