



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:14 am GMT

PDB ID : 2Y9H
Title : STRUCTURE A OF CRISPR ENDORIBONUCLEASE CSE3 BOUND TO
19 NT RNA
Authors : Sashital, D.G.; Jinek, M.; Doudna, J.A.
Deposited on : 2011-02-14
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

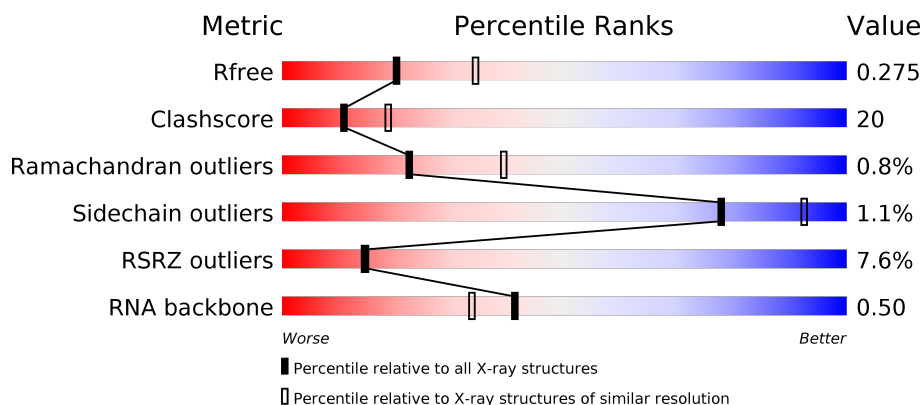
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)
RNA backbone	2435	1019 (2.90-2.10)

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	215	<div> <div>3%</div> <div>61%</div> <div>38%</div> <div>.</div> </div>
1	C	215	<div> <div>3%</div> <div>64%</div> <div>33%</div> <div>..</div> </div>
1	E	215	<div> <div>3%</div> <div>54%</div> <div>44%</div> <div>.</div> </div>
1	G	215	<div> <div>%</div> <div>66%</div> <div>26%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	I	215	
1	K	215	
1	M	215	
1	O	215	
2	B	19	
2	D	19	
2	F	19	
2	H	19	
2	J	19	
2	L	19	
2	N	19	
2	P	19	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15663 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 CSE3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	0	0
			1685	1074	319	290	2			
1	C	211	Total	C	N	O	S	0	0	0
			1676	1069	317	288	2			
1	E	211	Total	C	N	O	S	0	0	0
			1668	1064	316	286	2			
1	G	199	Total	C	N	O	S	0	0	0
			1587	1017	300	268	2			
1	I	195	Total	C	N	O	S	0	0	0
			1545	992	289	262	2			
1	K	191	Total	C	N	O	S	0	0	0
			1519	975	282	260	2			
1	M	193	Total	C	N	O	S	0	0	0
			1528	982	284	260	2			
1	O	177	Total	C	N	O		0	0	0
			908	554	177	177				

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
A	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
A	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
A	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
C	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
C	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
C	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
C	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
E	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
E	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
E	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
E	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
G	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
G	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
G	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
I	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
I	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
I	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
I	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
K	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
K	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
K	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
K	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
M	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
M	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
M	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
M	0	ALA	-	EXPRESSION TAG	UNP Q53WG9
O	-3	GLY	-	EXPRESSION TAG	UNP Q53WG9
O	-2	THR	-	EXPRESSION TAG	UNP Q53WG9
O	-1	GLY	-	EXPRESSION TAG	UNP Q53WG9
O	0	ALA	-	EXPRESSION TAG	UNP Q53WG9

- Molecule 2 is a RNA chain called 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	D	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	F	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	H	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	J	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	L	19	Total	C	N	O	P	0	0	0
			385	171	69	127	18			
2	N	18	Total	C	N	O	P	0	0	0
			381	171	69	124	17			
2	P	18	Total	C	N	O	P	0	0	0
			381	171	69	124	17			

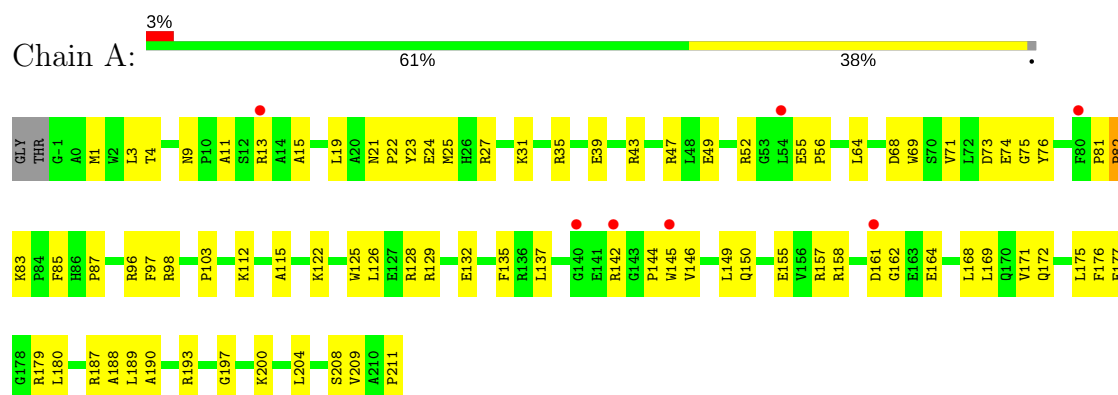
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	35	Total 35	O 35	0	0
3	B	13	Total 13	O 13	0	0
3	C	30	Total 30	O 30	0	0
3	D	19	Total 19	O 19	0	0
3	E	51	Total 51	O 51	0	0
3	F	25	Total 25	O 25	0	0
3	G	30	Total 30	O 30	0	0
3	H	13	Total 13	O 13	0	0
3	I	57	Total 57	O 57	0	0
3	J	24	Total 24	O 24	0	0
3	K	56	Total 56	O 56	0	0
3	L	20	Total 20	O 20	0	0
3	M	44	Total 44	O 44	0	0
3	N	23	Total 23	O 23	0	0
3	O	22	Total 22	O 22	0	0
3	P	13	Total 13	O 13	0	0

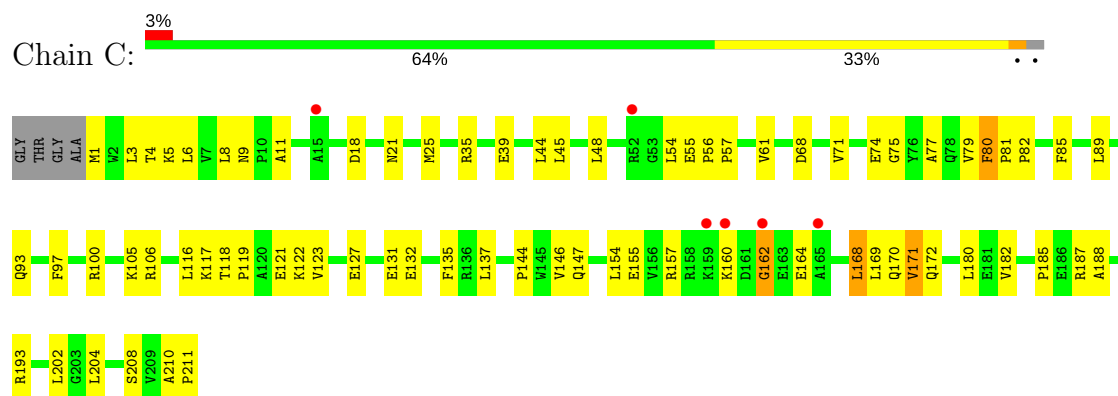
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

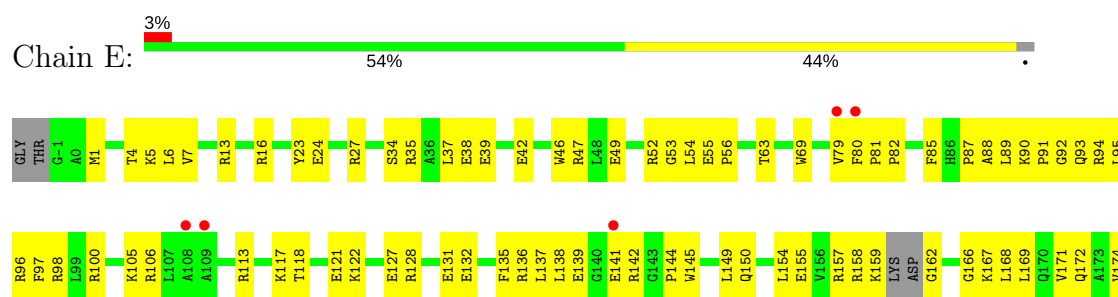
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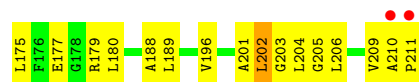


• Molecule 1: CSE3

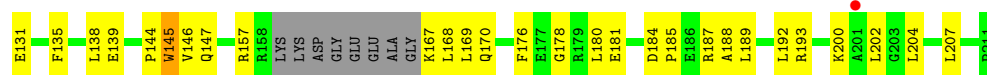
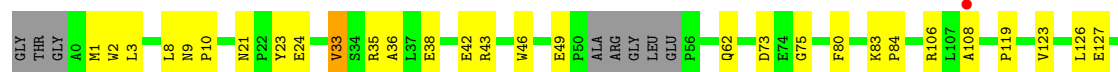


• Molecule 1: CSE3

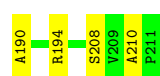
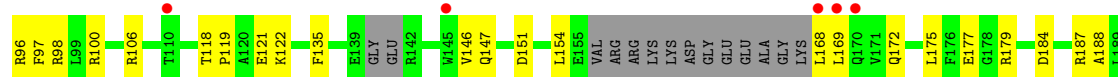
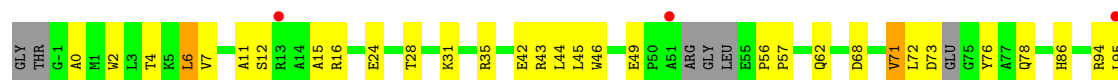




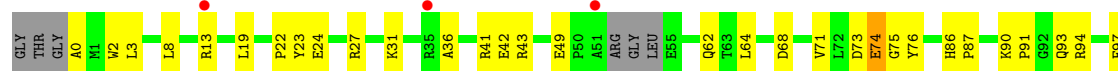
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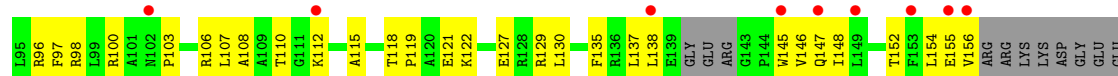
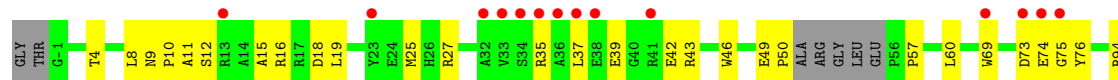
• Molecule 1: CSE3

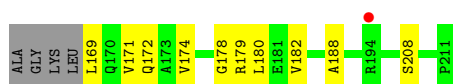


• Molecule 1: CSE3

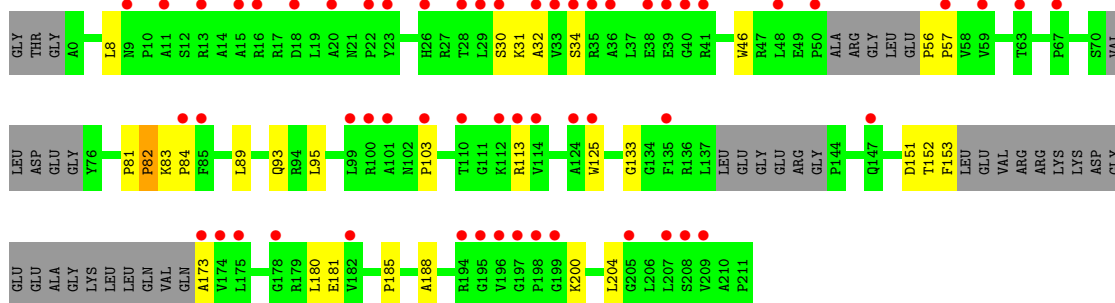


• Molecule 1: CSE3





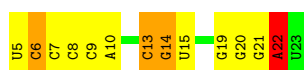
• Molecule 1: CSE3



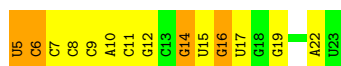
• Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



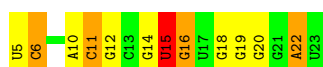
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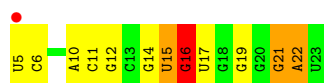
• Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



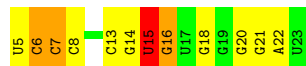
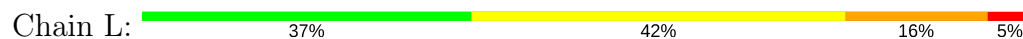
• Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



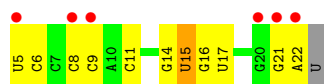
• Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



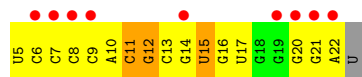
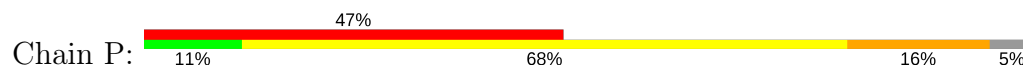
● Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



● Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



● Molecule 2: 5'-R(*UP*CP*CP*CP*CP*AP*CP*GP*CP*GP*UP*GP*UP*GP *GP*GP*DGP*AP*UP)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.86Å 149.81Å 87.26Å 90.00° 94.60° 90.00°	Depositor
Resolution (Å)	58.70 – 2.50 58.70 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (58.70-2.50) 99.9 (58.70-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.40Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.231 , 0.289 0.217 , 0.275	Depositor DCC
R_{free} test set	1764 reflections (2.33%)	DCC
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15663	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 82.85 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.5178e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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	0/1721	0.62	0/2329
1	C	0.47	0/1712	0.63	0/2317
1	E	0.52	0/1703	0.65	0/2304
1	G	0.45	0/1621	0.63	0/2194
1	I	0.50	0/1577	0.67	0/2135
1	K	0.49	0/1552	0.65	0/2103
1	M	0.41	0/1561	0.59	0/2115
1	O	0.32	0/920	0.53	0/1285
2	B	0.99	1/429 (0.2%)	1.10	2/668 (0.3%)
2	D	1.18	6/429 (1.4%)	1.12	0/668
2	F	1.23	7/429 (1.6%)	1.38	9/668 (1.3%)
2	H	1.08	4/429 (0.9%)	1.14	3/668 (0.4%)
2	J	0.72	0/429	1.49	6/668 (0.9%)
2	L	0.62	0/429	1.26	5/668 (0.7%)
2	N	0.50	0/425	0.98	0/661
2	P	0.37	0/425	0.90	0/661
All	All	0.58	18/15791 (0.1%)	0.80	25/22112 (0.1%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	22	A	N7-C5	-9.25	1.33	1.39
2	H	22	A	N7-C5	-8.97	1.33	1.39
2	D	22	A	N3-C4	-8.51	1.29	1.34
2	D	22	A	N7-C5	-7.35	1.34	1.39
2	D	22	A	C6-N1	-7.20	1.30	1.35

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	16	G	C5-N7-C8	-9.87	99.37	104.30
2	J	21	DG	O4'-C1'-N9	9.60	114.72	108.00
2	J	16	G	C4-C5-N7	9.46	114.58	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	22	A	O4'-C1'-C2'	-7.98	97.82	105.80
2	H	15	U	C2-N1-C1'	7.93	127.22	117.70

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	1685	0	1762	98	0
1	C	1676	0	1754	71	1
1	E	1668	0	1744	95	0
1	G	1587	0	1667	48	0
1	I	1545	0	1615	45	0
1	K	1519	0	1582	61	0
1	M	1528	0	1597	65	0
1	O	908	0	513	15	0
2	B	385	0	196	27	0
2	D	385	0	196	23	0
2	F	385	0	196	21	0
2	H	385	0	196	13	0
2	J	385	0	196	18	0
2	L	385	0	196	15	0
2	N	381	0	197	18	0
2	P	381	0	197	19	0
3	A	35	0	0	3	0
3	B	13	0	0	3	0
3	C	30	0	0	1	1
3	D	19	0	0	0	0
3	E	51	0	0	7	2
3	F	25	0	0	3	0
3	G	30	0	0	3	0
3	H	13	0	0	2	0
3	I	57	0	0	5	0
3	J	24	0	0	2	0
3	K	56	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	L	20	0	0	1	0
3	M	44	0	0	2	0
3	N	23	0	0	5	0
3	O	22	0	0	2	0
3	P	13	0	0	0	0
All	All	15663	0	13804	584	2

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 20.

The worst 5 of 584 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:K:74:GLU:HA	1:K:76:TYR:H	1.08	1.17
1:K:74:GLU:HG3	1:K:75:GLY:HA2	1.25	1.14
2:J:21:DG:C2'	2:J:22:A:H5'	1.92	0.99
1:A:83:LYS:HE2	2:F:9:C:OP1	1.63	0.97
1:A:145:TRP:CD1	1:A:179:ARG:HB2	2.00	0.95

All (2) 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)
3:C:2021:HOH:O	3:E:2020:HOH:O[2_445]	2.01	0.19
1:C:155:GLU:OE2	3:E:2026:HOH:O[2_445]	2.16	0.04

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	211/215 (98%)	198 (94%)	12 (6%)	1 (0%)	32 53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	209/215 (97%)	194 (93%)	14 (7%)	1 (0%)	32	53
1	E	207/215 (96%)	196 (95%)	10 (5%)	1 (0%)	32	53
1	G	193/215 (90%)	185 (96%)	5 (3%)	3 (2%)	11	19
1	I	185/215 (86%)	175 (95%)	10 (5%)	0	100	100
1	K	183/215 (85%)	174 (95%)	7 (4%)	2 (1%)	17	29
1	M	185/215 (86%)	174 (94%)	11 (6%)	0	100	100
1	O	167/215 (78%)	139 (83%)	24 (14%)	4 (2%)	7	11
All	All	1540/1720 (90%)	1435 (93%)	93 (6%)	12 (1%)	22	39

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	33	VAL
1	K	145	TRP
1	O	8	LEU
1	O	31	LYS
1	O	34	SER

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	172/173 (99%)	172 (100%)	0	100	100
1	C	172/173 (99%)	167 (97%)	5 (3%)	48	75
1	E	170/173 (98%)	168 (99%)	2 (1%)	75	91
1	G	164/173 (95%)	162 (99%)	2 (1%)	75	91
1	I	159/173 (92%)	155 (98%)	4 (2%)	53	79
1	K	157/173 (91%)	157 (100%)	0	100	100
1	M	158/173 (91%)	158 (100%)	0	100	100
1	O	17/173 (10%)	17 (100%)	0	100	100
All	All	1169/1384 (84%)	1156 (99%)	13 (1%)	78	92

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	46	TRP
1	E	202	LEU
1	I	71	VAL
1	C	187	ARG
1	I	6	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	93	GLN
1	G	147	GLN
1	I	86	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	16/19 (84%)	5 (31%)	0
2	D	16/19 (84%)	4 (25%)	0
2	F	16/19 (84%)	6 (37%)	0
2	H	16/19 (84%)	6 (37%)	0
2	J	16/19 (84%)	3 (18%)	0
2	L	16/19 (84%)	6 (37%)	0
2	N	16/19 (84%)	3 (18%)	0
2	P	16/19 (84%)	6 (37%)	0
All	All	128/152 (84%)	39 (30%)	0

5 of 39 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	6	C
2	B	11	C
2	B	13	C
2	B	15	U
2	B	16	G

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 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	213/215 (99%)	0.18	7 (3%) 47 50	23, 41, 78, 118	0
1	C	211/215 (98%)	0.15	6 (2%) 53 56	21, 41, 82, 115	0
1	E	211/215 (98%)	0.17	7 (3%) 47 50	18, 41, 75, 112	0
1	G	199/215 (92%)	0.08	2 (1%) 82 83	21, 41, 64, 95	0
1	I	195/215 (90%)	0.05	8 (4%) 38 40	12, 32, 64, 98	0
1	K	191/215 (88%)	0.10	5 (2%) 56 59	15, 35, 63, 99	0
1	M	193/215 (89%)	0.70	24 (12%) 4 4	27, 47, 78, 109	0
1	O	177/215 (82%)	1.62	57 (32%) 0 0	63, 85, 116, 132	0
2	B	19/19 (100%)	-0.03	0 100 100	43, 57, 104, 110	0
2	D	19/19 (100%)	0.19	0 100 100	36, 52, 68, 69	0
2	F	19/19 (100%)	-0.04	0 100 100	34, 42, 58, 74	0
2	H	19/19 (100%)	-0.00	0 100 100	41, 55, 72, 84	0
2	J	19/19 (100%)	0.28	1 (5%) 27 28	25, 37, 104, 118	0
2	L	19/19 (100%)	0.14	0 100 100	28, 46, 88, 148	0
2	N	18/19 (94%)	1.01	6 (33%) 0 0	41, 57, 87, 99	0
2	P	18/19 (94%)	2.57	9 (50%) 0 0	116, 128, 162, 176	0
All	All	1740/1872 (92%)	0.37	132 (7%) 15 14	12, 43, 95, 176	0

The worst 5 of 132 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	O	101	ALA	8.0
1	A	142	ARG	7.8
2	P	22	A	6.9
2	J	5	U	6.7
2	P	21	DG	6.4

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.