



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 05:24 PM BST

PDB ID : 6O75
Title : Crystal structure of Csm1-Csm4 cassette in complex with pppApA
Authors : Jia, N.; Patel, D.J.
Deposited on : 2019-03-07
Resolution : 2.60 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
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

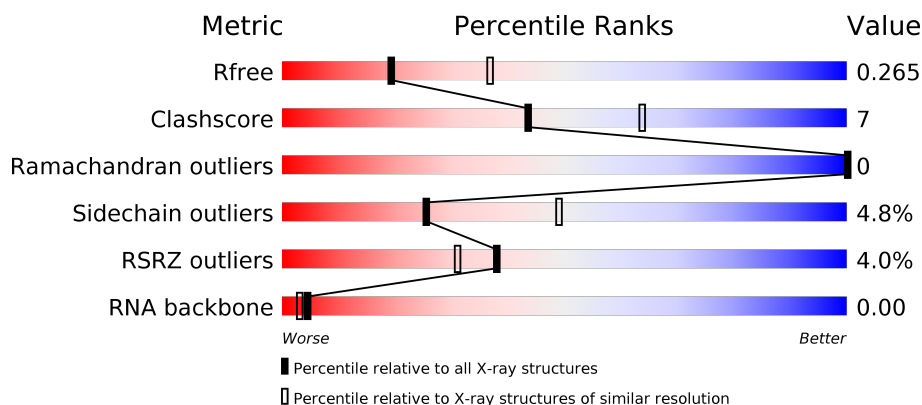
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)
RNA backbone	3102	1040 (2.90-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	791	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>15%</div> <div>• 10%</div> </div> </div>
2	B	289	<div> <div>6%</div> <div> <div></div> <div>73%</div> <div>14%</div> <div>12%</div> </div> </div>
3	C	2	<div> <div>50%</div> <div>50%</div> </div>
3	D	2	<div> <div>50%</div> <div>50%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7831 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 CRISPR system single-strand-specific deoxyribonuclease Cas10/Csm1 (subtype III-A).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	710	Total	C	N	O	S	0	0	0
			5704	3669	983	1036	16			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP B6YWB8
A	-12	GLY	-	expression tag	UNP B6YWB8
A	-11	SER	-	expression tag	UNP B6YWB8
A	-10	SER	-	expression tag	UNP B6YWB8
A	-9	HIS	-	expression tag	UNP B6YWB8
A	-8	HIS	-	expression tag	UNP B6YWB8
A	-7	HIS	-	expression tag	UNP B6YWB8
A	-6	HIS	-	expression tag	UNP B6YWB8
A	-5	HIS	-	expression tag	UNP B6YWB8
A	-4	HIS	-	expression tag	UNP B6YWB8
A	-3	SER	-	expression tag	UNP B6YWB8
A	-2	GLN	-	expression tag	UNP B6YWB8
A	-1	ASP	-	expression tag	UNP B6YWB8
A	0	PRO	-	expression tag	UNP B6YWB8
A	589	ALA	ASP	engineered mutation	UNP B6YWB8

- Molecule 2 is a protein called Csm4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	253	Total	C	N	O	S	0	0	0
			2019	1316	333	366	4			

- Molecule 3 is a RNA chain called RNA (5'-D*(ATP))-R(P*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	P	0	0	0
			53	20	10	19	4			
3	D	2	Total	C	N	O	P	0	0	0
			53	20	10	19	4			

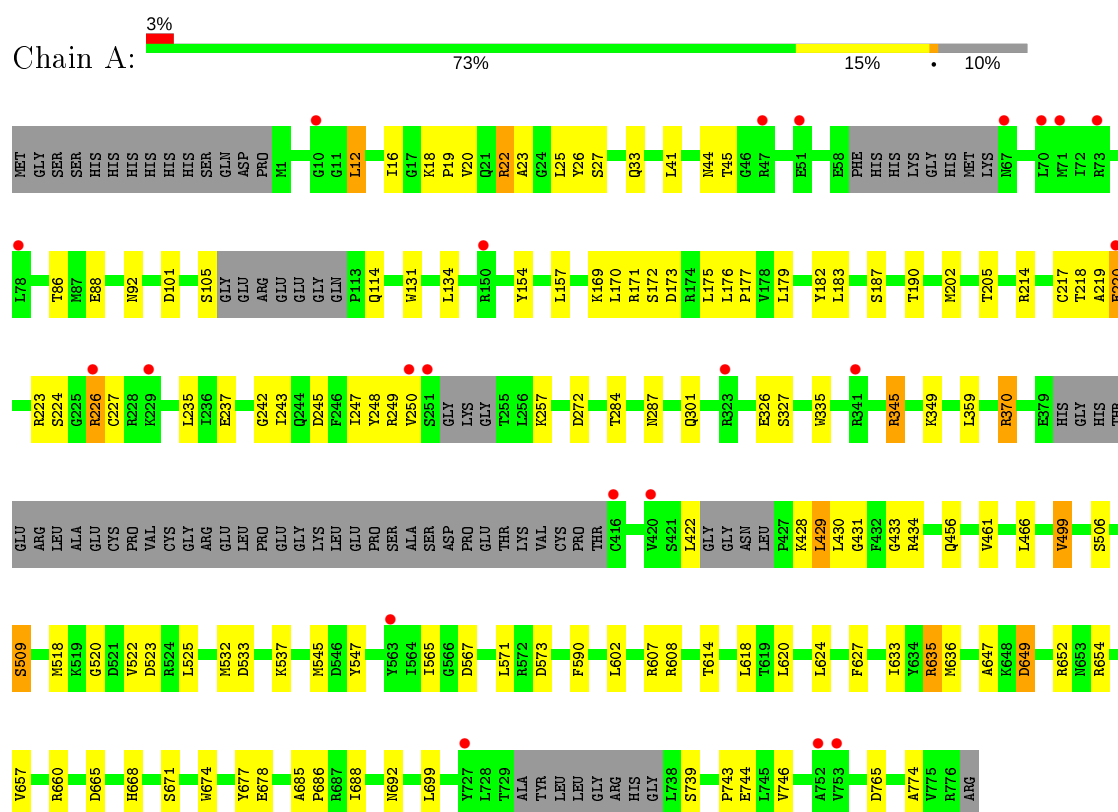
- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mn	0	0
			2	2		

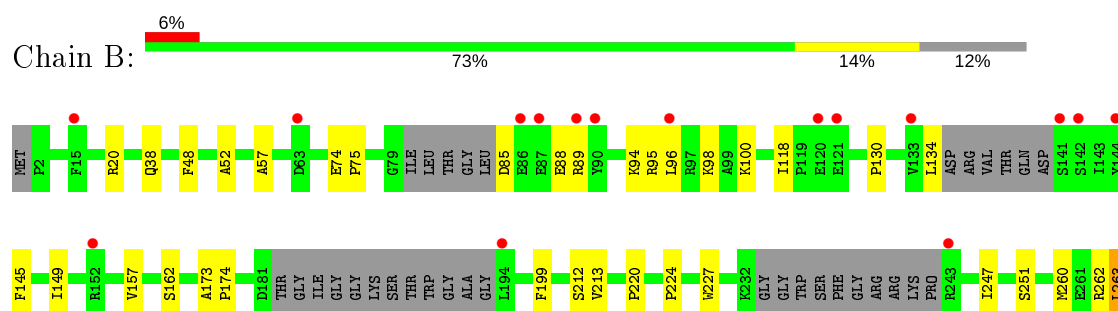
3 Residue-property plots [i](#)

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: CRISPR system single-strand-specific deoxyribonuclease Cas10/Csm1 (subtype III-A)



- Molecule 2: Csm4





- Molecule 3: RNA (5'-D(* (ATP))-R(P*A)-3')



- Molecule 3: RNA (5'-D(* (ATP))-R(P*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	156.44Å 156.44Å 186.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.43 – 2.60 49.38 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.43-2.60) 99.8 (49.38-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.223 , 0.271 0.224 , 0.265	Depositor DCC
R_{free} test set	2104 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	75.5	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7831	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MN, ATP

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	0.63	0/5828	0.75	0/7858
2	B	0.63	0/2070	0.76	0/2800
3	C	4.47	7/24 (29.2%)	6.60	12/35 (34.3%)
3	D	4.22	6/24 (25.0%)	6.17	11/35 (31.4%)
All	All	0.71	13/7946 (0.2%)	0.91	23/10728 (0.2%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	A	N7-C5	-9.50	1.33	1.39
3	D	2	A	N7-C5	-9.31	1.33	1.39
3	C	2	A	C2-N3	8.56	1.41	1.33
3	C	2	A	C5-C6	-7.90	1.33	1.41
3	D	2	A	N1-C2	7.49	1.41	1.34
3	D	2	A	C2-N3	7.45	1.40	1.33
3	C	2	A	N1-C2	7.17	1.40	1.34
3	D	2	A	N9-C4	-6.98	1.33	1.37
3	D	2	A	C5-C6	-6.64	1.35	1.41
3	C	2	A	N9-C4	-6.25	1.34	1.37
3	C	2	A	C5-C4	-5.77	1.34	1.38
3	C	2	A	N9-C8	-5.54	1.33	1.37
3	D	2	A	C5-C4	-5.25	1.35	1.38

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	A	N1-C2-N3	-21.78	118.41	129.30
3	D	2	A	N1-C2-N3	-20.54	119.03	129.30
3	C	2	A	C2-N3-C4	17.95	119.58	110.60
3	D	2	A	C2-N3-C4	16.76	118.98	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	2	A	N7-C8-N9	-11.11	108.25	113.80
3	C	2	A	C5-C6-N6	-10.02	115.68	123.70
3	D	2	A	N7-C8-N9	-9.31	109.15	113.80
3	C	2	A	N3-C4-C5	-9.09	120.44	126.80
3	C	2	A	C5-C6-N1	9.02	122.21	117.70
3	D	2	A	N9-C4-C5	8.80	109.32	105.80
3	D	2	A	C4-C5-C6	8.38	121.19	117.00
3	D	2	A	N3-C4-C5	-8.34	120.96	126.80
3	C	2	A	C5-N7-C8	8.31	108.06	103.90
3	D	2	A	C5-N7-C8	8.21	108.01	103.90
3	C	2	A	C4-C5-C6	7.94	120.97	117.00
3	D	2	A	C4-C5-N7	-7.53	106.94	110.70
3	D	2	A	C5-C6-N6	-6.49	118.50	123.70
3	D	2	A	C5-C6-N1	6.39	120.89	117.70
3	D	2	A	C3'-C2'-C1'	6.34	106.57	101.50
3	C	2	A	C8-N9-C4	6.18	108.27	105.80
3	C	2	A	N3-C4-N9	6.02	132.22	127.40
3	C	2	A	N1-C6-N6	5.85	122.11	118.60
3	C	2	A	C4-C5-N7	-5.24	108.08	110.70

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	5704	0	5719	78	0
2	B	2019	0	2021	29	0
3	C	53	0	23	3	0
3	D	53	0	23	3	0
4	A	2	0	0	0	0
All	All	7831	0	7786	105	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 (105) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:VAL:HG21	1:A:545:MET:HE1	1.49	0.90
2:B:224:PRO:HG3	2:B:247:ILE:HD11	1.56	0.87
2:B:264:GLU:N	2:B:264:GLU:OE1	2.10	0.85
1:A:26:TYR:H	1:A:33:GLN:NE2	1.78	0.81
2:B:262:ARG:HD3	2:B:270:GLU:HG3	1.67	0.76
2:B:267:LEU:HD23	2:B:267:LEU:N	2.03	0.73
1:A:92:ASN:OD1	1:A:219:ALA:N	2.20	0.72
2:B:269:HIS:CD2	2:B:269:HIS:H	2.06	0.71
1:A:18:LYS:O	1:A:22:ARG:HG3	1.91	0.71
2:B:224:PRO:HG2	2:B:227:TRP:CE3	2.26	0.71
1:A:522:VAL:HG21	1:A:545:MET:CE	2.20	0.70
2:B:263:LEU:HD13	2:B:265:LEU:HD21	1.76	0.67
1:A:565:ILE:O	1:A:608:ARG:HD2	1.96	0.66
1:A:247:ILE:HD13	3:D:2:A:C2	2.32	0.65
1:A:327:SER:O	1:A:370:ARG:NH2	2.31	0.63
1:A:218:THR:HG23	1:A:220:GLU:HG3	1.80	0.62
1:A:649:ASP:OD2	2:B:95:ARG:NH2	2.29	0.61
2:B:98:LYS:HE2	3:C:2:A:H61	1.68	0.59
1:A:506:SER:O	1:A:509:SER:OG	2.20	0.59
1:A:22:ARG:NH2	1:A:187:SER:O	2.37	0.57
1:A:660:ARG:HD2	1:A:765:ASP:OD2	2.04	0.57
2:B:57:ALA:HB1	2:B:157:VAL:HG13	1.86	0.57
1:A:183:LEU:HD12	1:A:202:MET:HE1	1.86	0.56
1:A:647:ALA:HA	1:A:671:SER:OG	2.05	0.56
2:B:173:ALA:HB3	2:B:174:PRO:HD3	1.86	0.56
1:A:284:THR:H	1:A:287:ASN:HD22	1.53	0.55
2:B:269:HIS:N	2:B:269:HIS:CD2	2.73	0.55
1:A:430:LEU:HD11	1:A:456:GLN:HA	1.89	0.55
2:B:247:ILE:HG23	2:B:251:SER:CB	2.37	0.55
2:B:38:GLN:NE2	2:B:269:HIS:HB3	2.21	0.54
1:A:532:MET:HE3	1:A:537:LYS:HB3	1.89	0.54
2:B:96:LEU:HD22	2:B:118:ILE:CG1	2.38	0.53
1:A:18:LYS:HB2	1:A:19:PRO:HD3	1.90	0.52
1:A:176:LEU:HB2	1:A:177:PRO:HD3	1.91	0.52
1:A:518:MET:HE1	1:A:602:LEU:HD23	1.91	0.52
1:A:243:ILE:N	3:D:1:ATP:O2A	2.42	0.51
1:A:573:ASP:H	1:A:692:ASN:HD21	1.58	0.51
1:A:522:VAL:HG11	1:A:545:MET:CE	2.41	0.50
1:A:345:ARG:NH1	1:A:533:ASP:OD1	2.45	0.50
2:B:263:LEU:HD12	2:B:271:VAL:CG1	2.41	0.50
1:A:235:LEU:O	1:A:335:TRP:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ASP:HA	1:A:205:THR:HG22	1.92	0.49
1:A:635:ARG:HD2	2:B:145:PHE:CZ	2.48	0.49
1:A:242:GLY:N	3:D:1:ATP:O2A	2.42	0.49
1:A:571:LEU:HD22	1:A:774:ALA:HB2	1.95	0.48
1:A:525:LEU:HD13	1:A:545:MET:HE2	1.95	0.48
1:A:41:LEU:O	1:A:44:ASN:O	2.31	0.48
1:A:224:SER:CB	1:A:226:ARG:HE	2.27	0.48
1:A:607:ARG:HG3	1:A:674:TRP:CD2	2.49	0.47
1:A:157:LEU:CD1	1:A:182:TYR:HB3	2.44	0.47
1:A:134:LEU:C	1:A:134:LEU:HD23	2.33	0.47
1:A:665:ASP:OD1	1:A:668:HIS:HD2	1.97	0.47
1:A:171:ARG:HB3	1:A:173:ASP:OD1	2.15	0.47
2:B:85:ASP:HB3	2:B:88:GLU:HB2	1.96	0.47
1:A:743:PRO:O	1:A:746:VAL:HG22	2.15	0.47
1:A:627:PHE:CD2	1:A:636:MET:HG2	2.50	0.46
2:B:74:GLU:HB2	2:B:75:PRO:HD3	1.97	0.46
1:A:608:ARG:NH1	1:A:678:GLU:OE1	2.49	0.46
1:A:627:PHE:HB2	1:A:636:MET:HE2	1.98	0.46
1:A:214:ARG:HB2	1:A:301:GLN:HB3	1.98	0.46
1:A:134:LEU:HD11	1:A:547:TYR:CE2	2.50	0.45
2:B:130:PRO:HB3	2:B:145:PHE:CE1	2.51	0.45
1:A:607:ARG:HG3	1:A:674:TRP:CE2	2.51	0.45
1:A:26:TYR:HB2	1:A:33:GLN:HG3	1.98	0.45
2:B:96:LEU:HD23	2:B:96:LEU:N	2.32	0.45
2:B:38:GLN:HE22	2:B:269:HIS:HB3	1.81	0.45
1:A:183:LEU:HD12	1:A:202:MET:CE	2.48	0.44
2:B:260:MET:HE1	2:B:272:TYR:HB3	1.99	0.44
1:A:433:GLY:HA3	1:A:461:VAL:O	2.18	0.44
1:A:627:PHE:HB2	1:A:636:MET:CE	2.47	0.44
1:A:237:GLU:HB2	1:A:359:LEU:HD21	1.98	0.44
1:A:248:TYR:O	1:A:249:ARG:HB2	2.17	0.44
1:A:250:VAL:HB	1:A:633:ILE:HD11	2.00	0.44
1:A:257:LYS:HG2	1:A:499:VAL:HG13	2.00	0.44
1:A:685:ALA:HB3	1:A:686:PRO:HD3	2.00	0.44
2:B:220:PRO:HB3	2:B:247:ILE:HD12	1.99	0.44
1:A:86:THR:HG22	1:A:88:GLU:H	1.83	0.44
1:A:224:SER:OG	1:A:226:ARG:NE	2.47	0.44
1:A:614:THR:HG21	1:A:618:LEU:HB2	1.99	0.44
1:A:12:LEU:HD23	1:A:175:LEU:HD23	2.00	0.43
1:A:520:GLY:HA3	1:A:590:PHE:CZ	2.53	0.43
1:A:431:GLY:HA3	1:A:466:LEU:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:ASP:CG	1:A:652:ARG:HB3	2.39	0.42
1:A:272:ASP:OD1	1:A:434:ARG:NH1	2.51	0.42
1:A:20:VAL:HG23	1:A:33:GLN:HG2	2.01	0.42
2:B:96:LEU:HD22	2:B:118:ILE:HG13	2.02	0.42
1:A:12:LEU:HD12	1:A:12:LEU:HA	1.84	0.42
1:A:131:TRP:CH2	1:A:157:LEU:HD13	2.55	0.42
1:A:525:LEU:N	3:C:1:ATP:O2B	2.53	0.42
1:A:16:ILE:O	1:A:19:PRO:HD2	2.20	0.41
1:A:218:THR:HG1	1:A:219:ALA:H	1.68	0.41
1:A:522:VAL:HG22	1:A:620:LEU:HD23	2.01	0.41
2:B:48:PHE:HD1	2:B:52:ALA:HB3	1.85	0.41
2:B:98:LYS:HE2	3:C:2:A:N6	2.35	0.41
1:A:114:GLN:O	1:A:190:THR:HB	2.21	0.41
1:A:157:LEU:HD12	1:A:182:TYR:HB3	2.02	0.41
1:A:179:LEU:HB3	1:A:202:MET:HE1	2.01	0.41
1:A:23:ALA:HB2	1:A:154:TYR:HB3	2.03	0.41
1:A:429:LEU:HD23	1:A:429:LEU:O	2.21	0.41
1:A:688:ILE:HA	1:A:699:LEU:CD1	2.50	0.41
2:B:262:ARG:HD3	2:B:270:GLU:CG	2.45	0.41
1:A:657:VAL:HG21	1:A:677:TYR:CD1	2.56	0.41
2:B:247:ILE:HG23	2:B:251:SER:OG	2.21	0.40
1:A:518:MET:HB3	1:A:624:LEU:HD23	2.03	0.40
1:A:169:LYS:O	1:A:170:LEU:HB2	2.22	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	696/791 (88%)	660 (95%)	36 (5%)	0	100	100
2	B	243/289 (84%)	236 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	939/1080 (87%)	896 (95%)	43 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	599/664 (90%)	571 (95%)	28 (5%)	26	50
2	B	214/240 (89%)	203 (95%)	11 (5%)	24	46
All	All	813/904 (90%)	774 (95%)	39 (5%)	25	49

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LEU
1	A	22	ARG
1	A	25	LEU
1	A	27	SER
1	A	45	THR
1	A	105	SER
1	A	172	SER
1	A	217	CYS
1	A	220	GLU
1	A	223	ARG
1	A	226	ARG
1	A	227	CYS
1	A	245	ASP
1	A	326	GLU
1	A	345	ARG
1	A	349	LYS
1	A	370	ARG
1	A	422	LEU
1	A	428	LYS
1	A	429	LEU

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Mol	Chain	Res	Type
1	A	499	VAL
1	A	509	SER
1	A	567	ASP
1	A	635	ARG
1	A	649	ASP
1	A	654	ARG
1	A	739	SER
1	A	744	GLU
2	B	20	ARG
2	B	89	ARG
2	B	94	LYS
2	B	100	LYS
2	B	134	LEU
2	B	149	ILE
2	B	162	SER
2	B	199	PHE
2	B	212	SER
2	B	213	VAL
2	B	263	LEU

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

Mol	Chain	Res	Type
1	A	21	GLN
1	A	33	GLN
1	A	287	ASN
1	A	472	ASN
1	A	668	HIS
1	A	675	ASN
1	A	692	ASN
2	B	38	GLN
2	B	200	HIS
2	B	269	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	0/2	-	-
3	D	0/2	-	-
All	All	0/4	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	710/791 (89%)	0.14	22 (3%)	49	42	50, 80, 131, 179	0
2	B	253/289 (87%)	0.11	17 (6%)	17	13	55, 78, 127, 162	0
3	C	1/2 (50%)	-0.18	0	100	100	129, 129, 129, 129	0
3	D	1/2 (50%)	-0.27	0	100	100	81, 81, 81, 81	0
All	All	965/1084 (89%)	0.13	39 (4%)	38	31	50, 79, 131, 179	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	90	TYR	5.8
1	A	250	VAL	5.7
1	A	323	ARG	4.7
2	B	141	SER	4.5
2	B	142	SER	4.1
1	A	229	LYS	4.1
2	B	86	GLU	3.8
2	B	63	ASP	3.7
2	B	243	ARG	3.6
2	B	89	ARG	3.5
1	A	70	LEU	3.4
2	B	120	GLU	3.3
1	A	226	ARG	3.3
2	B	87	GLU	3.1
1	A	753	VAL	3.1
1	A	341	ARG	2.8
1	A	727	TYR	2.8
1	A	220	GLU	2.8
2	B	194	LEU	2.8
1	A	150	ARG	2.7
1	A	416	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	78	LEU	2.6
2	B	96	LEU	2.6
1	A	420	VAL	2.6
2	B	15	PHE	2.6
1	A	251	SER	2.5
1	A	73	ARG	2.4
2	B	152	ARG	2.4
1	A	10	GLY	2.4
2	B	144	TYR	2.3
1	A	752	ALA	2.3
2	B	270	GLU	2.3
1	A	51	GLU	2.2
2	B	121	GLU	2.1
1	A	47	ARG	2.1
1	A	71	MET	2.1
1	A	563	TYR	2.1
2	B	133	VAL	2.0
1	A	67	ASN	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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MN	A	801	1/1	0.96	0.15	92,92,92,92	0
4	MN	A	802	1/1	0.99	0.16	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.