



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2025 – 12:39 PM EDT

PDB ID : 9DCF  
Title : Structure of Coxsackievirus B3 cloverleaf RNA in complex with 3Cpro dimer  
Authors : Gottipati, K.; Dias, D.S.A.N.; Choi, K.H.  
Deposited on : 2024-08-26  
Resolution : 2.87 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

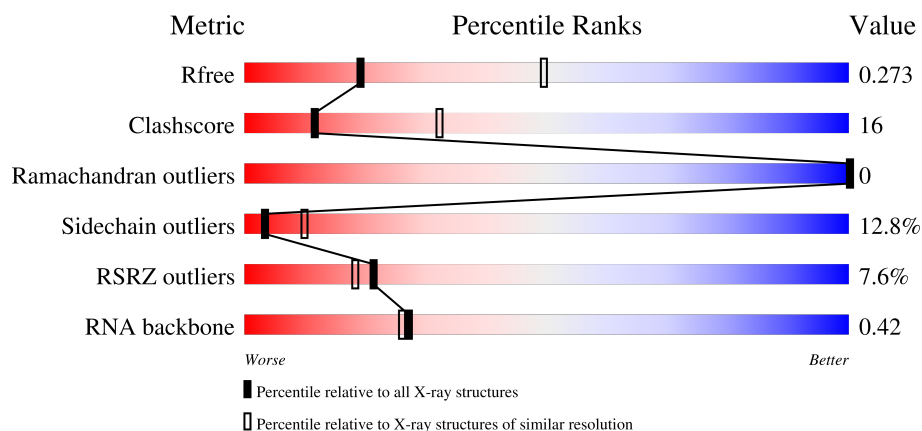
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.87 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))
$R_{free}$	164625	3316 (2.90-2.86)
Clashscore	180529	3609 (2.90-2.86)
Ramachandran outliers	177936	3529 (2.90-2.86)
Sidechain outliers	177891	3532 (2.90-2.86)
RSRZ outliers	164620	3319 (2.90-2.86)
RNA backbone	3690	1088 (3.10-2.66)

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  $\geq 3$ , 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	193	<div> <div>4%</div> <div>57% 31% 5% 7%</div> </div>
1	B	193	<div> <div>6%</div> <div>54% 34% 8%</div> </div>
2	C	90	<div> <div>16%</div> <div>33% 36% 17% 14%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4410 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 Protease 3C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	0	0
			1393	891	241	253	8			
1	B	178	Total	C	N	O	S	0	0	0
			1378	883	236	251	8			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03313
A	0	GLY	-	expression tag	UNP P03313
A	55	ALA	GLY	engineered mutation	UNP P03313
A	58	ALA	ASP	engineered mutation	UNP P03313
A	63	ALA	VAL	engineered mutation	UNP P03313
A	147	ALA	CYS	engineered mutation	UNP P03313
A	184	LEU	-	expression tag	UNP P03313
A	185	GLU	-	expression tag	UNP P03313
A	186	HIS	-	expression tag	UNP P03313
A	187	HIS	-	expression tag	UNP P03313
A	188	HIS	-	expression tag	UNP P03313
A	189	HIS	-	expression tag	UNP P03313
A	190	HIS	-	expression tag	UNP P03313
A	191	HIS	-	expression tag	UNP P03313
B	-1	MET	-	expression tag	UNP P03313
B	0	GLY	-	expression tag	UNP P03313
B	55	ALA	GLY	engineered mutation	UNP P03313
B	58	ALA	ASP	engineered mutation	UNP P03313
B	63	ALA	VAL	engineered mutation	UNP P03313
B	147	ALA	CYS	engineered mutation	UNP P03313
B	184	LEU	-	expression tag	UNP P03313
B	185	GLU	-	expression tag	UNP P03313
B	186	HIS	-	expression tag	UNP P03313
B	187	HIS	-	expression tag	UNP P03313
B	188	HIS	-	expression tag	UNP P03313

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Chain	Residue	Modelled	Actual	Comment	Reference
B	189	HIS	-	expression tag	UNP P03313
B	190	HIS	-	expression tag	UNP P03313
B	191	HIS	-	expression tag	UNP P03313

- Molecule 2 is a RNA chain called cloverleaf RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	77	Total	C	N	O	P	0	0	0
			1627	727	280	543	77			

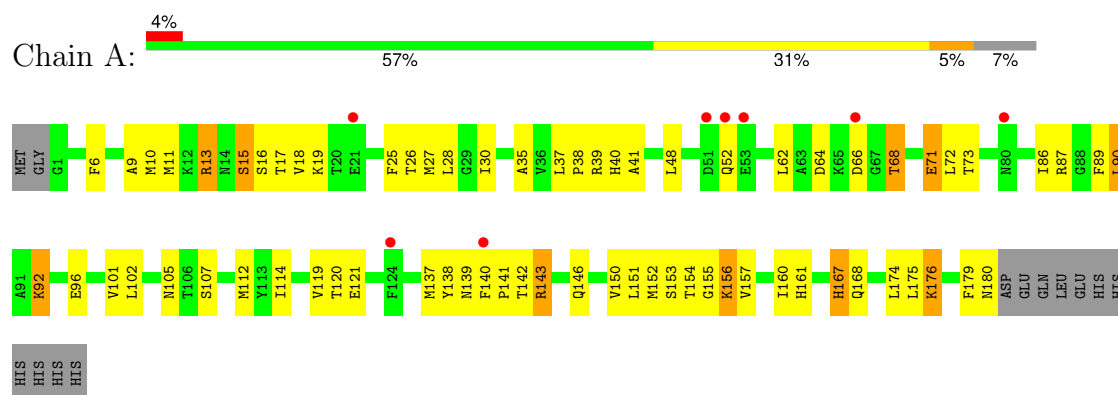
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	O	0	0
			3	3		
3	B	7	Total	O	0	0
			7	7		
3	C	2	Total	O	0	0
			2	2		

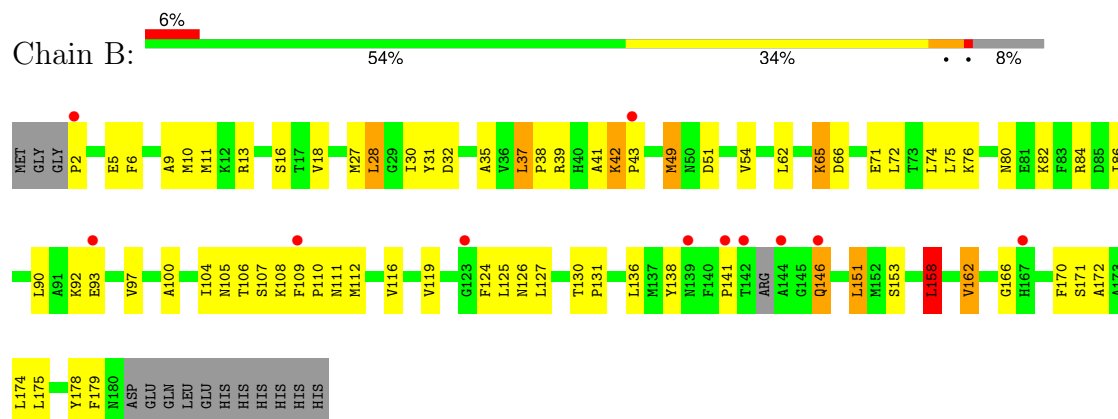
### 3 Residue-property plots [i](#)

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.

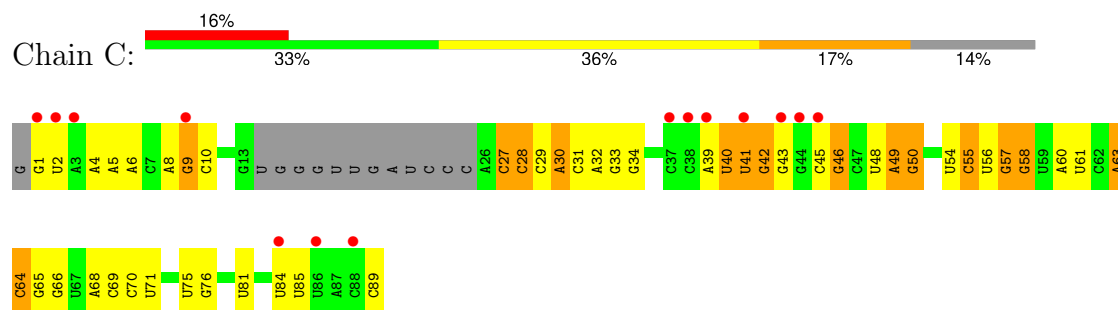
#### • Molecule 1: Protease 3C



#### • Molecule 1: Protease 3C



#### • Molecule 2: cloverleaf RNA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.02Å 200.82Å 71.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.93 – 2.87 48.93 – 2.87	Depositor EDS
% Data completeness (in resolution range)	74.7 (48.93-2.87) 74.6 (48.93-2.87)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.23 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.19_4092: ???)	Depositor
R, $R_{free}$	0.237 , 0.273 0.236 , 0.273	Depositor DCC
$R_{free}$ test set	28471 reflections (6.74%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.5	Xtriage
Anisotropy	1.398	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 40.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	4410	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [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	0.52	0/1422	0.78	0/1919
1	B	0.56	1/1406 (0.1%)	0.80	3/1896 (0.2%)
2	C	0.50	0/1813	1.14	2/2818 (0.1%)
All	All	0.53	1/4641 (0.0%)	0.95	5/6633 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	42	LYS	CD-CE	5.80	1.65	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	41	ALA	C-N-CA	7.47	140.38	121.70
2	C	55	C	C6-N1-C2	-6.01	117.89	120.30
1	B	158	LEU	CA-CB-CG	5.96	129.02	115.30
1	B	151	LEU	CA-CB-CG	5.96	129.00	115.30
2	C	28	C	C5-C6-N1	5.73	123.86	121.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	1393	0	1406	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1378	0	1387	43	0
2	C	1627	0	830	27	0
3	A	3	0	0	1	0
3	B	7	0	0	0	0
3	C	2	0	0	0	0
All	All	4410	0	3623	125	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 16.

All (125) 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:B:93:GLU:HA	1:B:175:LEU:HD12	1.57	0.85
1:B:92:LYS:HG3	1:B:93:GLU:OE1	1.77	0.84
1:A:96:GLU:HG2	1:A:120:THR:HA	1.60	0.81
1:A:143:ARG:H	1:A:146:GLN:HE22	1.34	0.75
1:B:39:ARG:O	1:B:42:LYS:HG2	1.86	0.75
1:A:11:MET:HA	1:A:15:SER:HB3	1.70	0.74
1:A:40:HIS:O	1:A:40:HIS:ND1	2.21	0.73
1:A:142:THR:HG21	1:A:161:HIS:HE1	1.53	0.73
1:A:9:ALA:O	1:A:13:ARG:HG3	1.93	0.69
2:C:5:A:H2'	2:C:6:A:H8	1.61	0.66
1:A:18:VAL:HG21	1:A:27:MET:SD	2.36	0.66
1:B:93:GLU:HA	1:B:175:LEU:CD1	2.27	0.64
1:A:30:ILE:HA	1:A:86:ILE:HD11	1.81	0.63
2:C:30:A:H2'	2:C:31:C:C6	2.33	0.63
2:C:54:U:H2'	2:C:55:C:C6	2.34	0.63
1:A:96:GLU:CG	1:A:120:THR:HA	2.29	0.62
1:A:121:GLU:OE1	3:A:201:HOH:O	2.16	0.61
1:B:74:LEU:HD21	1:B:179:PHE:CE1	2.35	0.60
2:C:31:C:H2'	2:C:32:A:C8	2.37	0.60
1:A:143:ARG:H	1:A:146:GLN:NE2	1.99	0.60
1:A:102:LEU:O	1:A:114:ILE:HG22	2.03	0.59
1:B:92:LYS:O	1:B:93:GLU:HG3	2.03	0.59
1:A:90:LEU:O	1:A:176:LYS:NZ	2.36	0.59
1:B:90:LEU:HD22	1:B:174:LEU:HB3	1.85	0.58
1:B:10:MET:HA	1:B:84:ARG:NH2	2.17	0.58
2:C:68:A:H2'	2:C:69:C:C6	2.39	0.58
1:A:64:ASP:OD1	1:A:68:THR:N	2.37	0.57
1:A:119:VAL:HG21	1:A:151:LEU:HD21	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:ASP:HA	1:B:82:LYS:HB3	1.86	0.57
1:B:27:MET:HG3	1:B:37:LEU:HG	1.84	0.57
1:B:49:MET:HE3	1:B:54:VAL:HG21	1.85	0.57
1:B:43:PRO:HG2	1:B:75:LEU:HD23	1.88	0.56
2:C:5:A:H2'	2:C:6:A:C8	2.41	0.56
1:B:138:TYR:OH	1:B:171:SER:OG	2.24	0.56
2:C:49:A:H4'	2:C:50:G:OP1	2.06	0.55
2:C:31:C:H2'	2:C:32:A:H8	1.71	0.55
1:B:9:ALA:O	1:B:13:ARG:HG3	2.07	0.55
2:C:63:A:H4'	2:C:64:C:OP2	2.07	0.55
1:B:38:PRO:HB3	1:B:162:VAL:HG13	1.88	0.55
1:A:39:ARG:HA	1:A:73:THR:OG1	2.07	0.54
1:A:154:THR:HG21	2:C:65:G:C8	2.41	0.54
2:C:8:A:O2'	2:C:9:G:H5'	2.06	0.54
1:A:102:LEU:HB3	1:A:114:ILE:CG2	2.38	0.54
2:C:9:G:N2	2:C:46:G:H1'	2.24	0.53
1:A:143:ARG:N	1:A:146:GLN:HE22	2.04	0.53
2:C:27:C:H2'	2:C:28:C:C6	2.44	0.53
1:A:153:SER:HB3	1:A:156:LYS:CG	2.38	0.53
1:B:39:ARG:HB2	1:B:71:GLU:C	2.28	0.53
1:A:10:MET:HE2	1:A:28:LEU:HD11	1.92	0.52
1:B:151:LEU:CD1	1:B:158:LEU:HD12	2.39	0.52
1:A:142:THR:HG21	1:A:161:HIS:CE1	2.40	0.52
1:B:104:ILE:HD13	1:B:146:GLN:HB3	1.93	0.51
1:A:138:TYR:OH	1:A:161:HIS:ND1	2.34	0.51
1:A:153:SER:HB3	1:A:156:LYS:HG3	1.92	0.51
1:A:96:GLU:HG2	1:A:119:VAL:O	2.11	0.50
1:A:87:ARG:HA	1:A:90:LEU:CD2	2.42	0.50
1:A:25:PHE:CE2	1:A:41:ALA:HA	2.46	0.50
1:B:141:PRO:HA	1:B:166:GLY:O	2.13	0.49
1:A:17:THR:OG1	1:A:105:ASN:O	2.30	0.49
1:B:175:LEU:HD23	1:B:178:TYR:CZ	2.48	0.49
1:A:10:MET:CE	1:A:86:ILE:HD13	2.43	0.48
1:A:28:LEU:HD13	1:A:150:VAL:HG21	1.95	0.48
1:A:155:GLY:HA3	2:C:65:G:O2'	2.14	0.48
1:B:125:LEU:HD23	1:B:126:ASN:N	2.29	0.48
1:A:156:LYS:HB3	1:A:156:LYS:HE3	1.48	0.48
1:B:30:ILE:HD12	1:B:35:ALA:HA	1.96	0.48
1:B:136:LEU:O	1:B:170:PHE:HA	2.14	0.48
1:A:6:PHE:HE1	1:A:152:MET:HG2	1.79	0.47
1:A:139:ASN:OD1	1:A:139:ASN:N	2.46	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:MET:HE1	1:A:168:GLN:HG2	1.97	0.47
1:B:109:PHE:HB3	1:B:112:MET:SD	2.56	0.46
1:B:106:THR:CG2	1:B:109:PHE:H	2.28	0.46
1:A:102:LEU:HB3	1:A:114:ILE:HG22	1.96	0.46
2:C:57:G:H5'	2:C:58:G:OP2	2.15	0.46
1:B:2:PRO:HB2	1:B:5:GLU:HB3	1.98	0.46
1:B:28:LEU:HD21	1:B:86:ILE:HD11	1.97	0.46
1:B:108:LYS:HD3	1:B:109:PHE:CE2	2.51	0.45
2:C:60:A:H2'	2:C:61:U:C6	2.51	0.45
2:C:75:U:H2'	2:C:76:G:C8	2.51	0.45
1:B:49:MET:CE	1:B:54:VAL:HG21	2.46	0.45
1:B:124:PHE:CZ	1:B:131:PRO:HB3	2.51	0.45
2:C:10:C:H5'	2:C:45:C:O2'	2.17	0.45
1:B:65:LYS:HE3	1:B:65:LYS:HB2	1.74	0.44
1:A:167:HIS:C	1:A:168:GLN:HG3	2.38	0.44
2:C:40:U:H1'	2:C:42:G:C6	2.53	0.44
1:A:25:PHE:HE2	1:A:41:ALA:HA	1.82	0.44
1:B:30:ILE:HD12	1:B:30:ILE:N	2.33	0.44
1:A:39:ARG:HB2	1:A:71:GLU:C	2.38	0.44
1:A:92:LYS:O	1:A:175:LEU:HD12	2.18	0.44
2:C:40:U:O2'	2:C:41:U:OP1	2.36	0.44
1:A:30:ILE:HG13	1:A:179:PHE:CZ	2.53	0.44
1:A:37:LEU:HD23	1:A:38:PRO:HD2	1.99	0.44
1:A:90:LEU:HD23	1:A:90:LEU:H	1.81	0.44
1:A:89:PHE:O	1:A:156:LYS:HA	2.18	0.43
1:B:62:LEU:HD12	1:B:72:LEU:HB2	2.00	0.43
1:A:27:MET:HE3	1:A:35:ALA:HB3	2.00	0.43
1:A:10:MET:HG2	1:A:152:MET:SD	2.58	0.43
1:B:10:MET:HA	1:B:84:ARG:HH21	1.82	0.43
1:B:108:LYS:O	1:B:110:PRO:HD3	2.18	0.42
1:B:11:MET:CE	1:B:105:ASN:HB2	2.49	0.42
1:B:162:VAL:HG23	1:B:172:ALA:H	1.84	0.42
1:A:62:LEU:HB2	1:A:72:LEU:O	2.20	0.42
1:A:140:PHE:CD1	1:A:141:PRO:HD2	2.54	0.42
2:C:70:C:H2'	2:C:71:U:O4'	2.19	0.42
2:C:1:G:C2	2:C:89:C:C2	3.07	0.42
1:B:18:VAL:HG21	1:B:27:MET:SD	2.59	0.42
1:A:10:MET:CE	1:A:28:LEU:HD11	2.50	0.42
1:A:37:LEU:CD2	1:A:38:PRO:HD2	2.50	0.42
1:A:160:ILE:CD1	1:A:174:LEU:HD11	2.50	0.42
2:C:84:U:H2'	2:C:85:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:LYS:HB3	1:A:48:LEU:HD12	2.02	0.41
1:B:62:LEU:HA	1:B:62:LEU:HD23	1.78	0.41
1:A:27:MET:CE	1:A:35:ALA:HB3	2.50	0.41
1:A:137:MET:CE	1:A:168:GLN:HG2	2.51	0.41
2:C:68:A:H2'	2:C:69:C:H6	1.85	0.41
1:B:80:ASN:OD1	2:C:60:A:O2'	2.17	0.41
1:B:97:VAL:CG1	1:B:100:ALA:HB2	2.51	0.41
1:A:102:LEU:HD12	1:A:150:VAL:O	2.21	0.41
1:A:160:ILE:HD12	1:A:174:LEU:HD11	2.02	0.41
2:C:1:G:H2'	2:C:2:U:C6	2.56	0.41
2:C:33:G:H2'	2:C:34:G:H8	1.84	0.41
1:A:11:MET:CA	1:A:15:SER:HB3	2.46	0.41
1:B:97:VAL:HG12	1:B:119:VAL:HB	2.03	0.40
1:B:124:PHE:CE2	1:B:131:PRO:HB3	2.55	0.40
1:A:26:THR:HG23	1:A:105:ASN:HB3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	178/193 (92%)	166 (93%)	12 (7%)	0	100	100
1	B	174/193 (90%)	162 (93%)	12 (7%)	0	100	100
All	All	352/386 (91%)	328 (93%)	24 (7%)	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	145/157 (92%)	127 (88%)	18 (12%)	4	10
1	B	144/157 (92%)	125 (87%)	19 (13%)	3	9
All	All	289/314 (92%)	252 (87%)	37 (13%)	3	10

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	15	SER
1	A	16	SER
1	A	52	GLN
1	A	66	ASP
1	A	68	THR
1	A	71	GLU
1	A	90	LEU
1	A	92	LYS
1	A	101	VAL
1	A	107	SER
1	A	112	MET
1	A	143	ARG
1	A	156	LYS
1	A	157	VAL
1	A	167	HIS
1	A	176	LYS
1	A	180	ASN
1	B	6	PHE
1	B	16	SER
1	B	28	LEU
1	B	31	TYR
1	B	37	LEU
1	B	49	MET
1	B	51	ASP
1	B	65	LYS
1	B	66	ASP
1	B	76	LYS
1	B	107	SER
1	B	111	ASN
1	B	116	VAL

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Mol	Chain	Res	Type
1	B	127	LEU
1	B	130	THR
1	B	146	GLN
1	B	153	SER
1	B	158	LEU
1	B	162	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	75/90 (83%)	20 (26%)	3 (4%)

All (20) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	4	A
2	C	9	G
2	C	27	C
2	C	29	C
2	C	30	A
2	C	39	A
2	C	40	U
2	C	41	U
2	C	42	G
2	C	43	G
2	C	46	G
2	C	49	A
2	C	50	G
2	C	56	U
2	C	57	G
2	C	58	G
2	C	63	A
2	C	64	C
2	C	66	G
2	C	81	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	C	40	U
2	C	48	U
2	C	63	A

#### 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 oligosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	180/193 (93%)	0.32	8 (4%) 39 34	39, 52, 86, 131	0
1	B	178/193 (92%)	0.38	11 (6%) 28 24	37, 53, 89, 164	0
2	C	77/90 (85%)	0.87	14 (18%) 4 4	50, 136, 207, 231	0
All	All	435/476 (91%)	0.44	33 (7%) 21 18	37, 55, 174, 231	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	21	GLU	7.8
1	B	2	PRO	6.4
1	B	144	ALA	5.4
2	C	2	U	4.6
1	B	93	GLU	4.5
1	A	53	GLU	3.9
1	B	167	HIS	3.5
1	A	140	PHE	3.3
2	C	1	G	3.3
1	B	146	GLN	3.2
1	B	109	PHE	3.0
2	C	86	U	3.0
1	B	141	PRO	2.9
2	C	38	C	2.9
2	C	44	G	2.8
2	C	3	A	2.8
2	C	45	C	2.8
1	B	139	ASN	2.7
2	C	84	U	2.7
1	A	80	ASN	2.7
1	A	66	ASP	2.6
2	C	39	A	2.5
1	A	51	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	52	GLN	2.5
1	A	124	PHE	2.5
2	C	88	C	2.2
1	B	142	THR	2.2
1	B	123	GLY	2.2
2	C	41	U	2.2
2	C	9	G	2.2
2	C	43	G	2.1
2	C	37	C	2.1
1	B	43	PRO	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.