



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 12, 2022 – 12:57 PM EDT

PDB ID : 8DRR  
Title : Product structure of SARS-CoV-2 Mpro C145A mutant in complex with nsp4-nsp5 (C4) cut site sequence  
Authors : Lee, J.; Kenward, C.; Worrall, L.J.; Vuckovic, M.; Paetzel, M.; Strynadka, N.C.J.  
Deposited on : 2022-07-21  
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](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)	:	1.13
EDS	:	2.29
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)	:	2.29

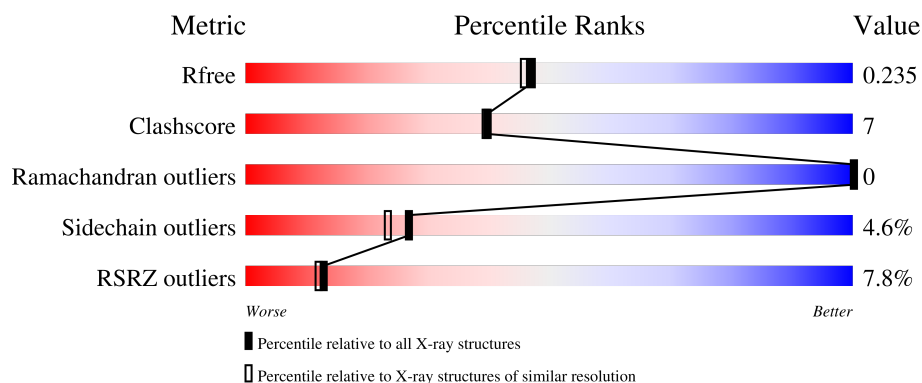
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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  $\geq 3$ , 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	306	<div> <div>5%</div> <div>80%</div> <div>14%</div> <div>...</div> </div>
1	B	306	<div> <div>2%</div> <div>88%</div> <div>11%</div> <div>.</div> </div>
1	C	306	<div> <div>16%</div> <div>70%</div> <div>24%</div> <div>..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7072 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 3C-like proteinase nsp5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total	C	N	O	S	0	1	0
			2273	1442	382	428	21			
1	B	302	Total	C	N	O	S	0	2	0
			2341	1482	397	440	22			
1	C	297	Total	C	N	O	S	0	1	0
			2222	1415	370	417	20			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	145	ALA	CYS	engineered mutation	UNP P0DTD1
A	301	THR	-	expression tag	UNP P0DTD1
A	302	SER	-	expression tag	UNP P0DTD1
A	303	ALA	-	expression tag	UNP P0DTD1
A	304	VAL	-	expression tag	UNP P0DTD1
A	305	LEU	-	expression tag	UNP P0DTD1
A	306	GLN	-	expression tag	UNP P0DTD1
B	145	ALA	CYS	engineered mutation	UNP P0DTD1
B	301	THR	-	expression tag	UNP P0DTD1
B	302	SER	-	expression tag	UNP P0DTD1
B	303	ALA	-	expression tag	UNP P0DTD1
B	304	VAL	-	expression tag	UNP P0DTD1
B	305	LEU	-	expression tag	UNP P0DTD1
B	306	GLN	-	expression tag	UNP P0DTD1
C	145	ALA	CYS	engineered mutation	UNP P0DTD1
C	301	THR	-	expression tag	UNP P0DTD1
C	302	SER	-	expression tag	UNP P0DTD1
C	303	ALA	-	expression tag	UNP P0DTD1
C	304	VAL	-	expression tag	UNP P0DTD1
C	305	LEU	-	expression tag	UNP P0DTD1
C	306	GLN	-	expression tag	UNP P0DTD1

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Na 1	0	0

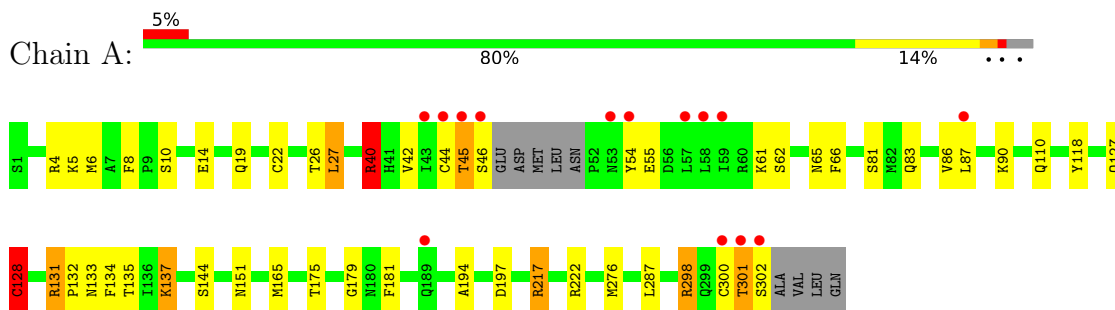
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	112	Total 112	O 112	0	0
3	B	95	Total 95	O 95	0	0
3	C	28	Total 28	O 28	0	0

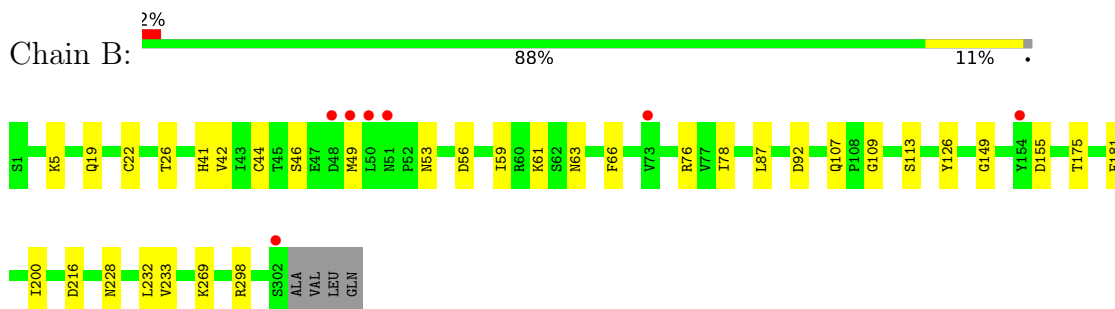
### 3 Residue-property plots [i](#)

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.

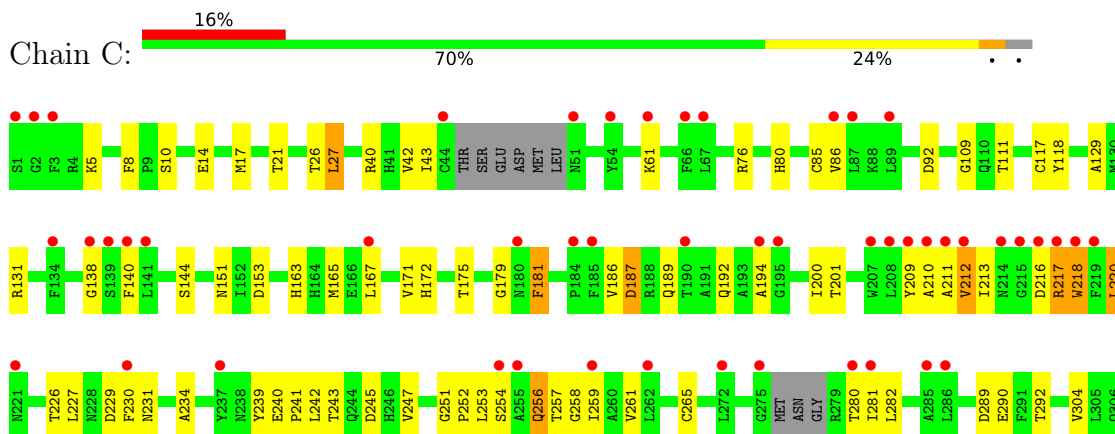
- Molecule 1: 3C-like proteinase nsp5



- Molecule 1: 3C-like proteinase nsp5



- Molecule 1: 3C-like proteinase nsp5



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.25Å 107.42Å 138.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.46 – 2.00 84.78 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (60.46-2.00) 100.0 (84.78-2.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.206 , 0.237 0.204 , 0.235	Depositor DCC
$R_{free}$ test set	3469 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.2	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 58.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7072	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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

### 5.1 Standard geometry

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

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	0.40	0/2324	0.57	2/3161 (0.1%)
1	B	0.32	0/2399	0.51	0/3261
1	C	0.30	0/2275	0.52	0/3102
All	All	0.34	0/6998	0.53	2/9524 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128[A]	CYS	O-C-N	-6.62	112.12	122.70
1	A	128[B]	CYS	O-C-N	-6.62	112.12	122.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	GLN	Mainchain
1	A	128[B]	CYS	Mainchain
1	A	131	ARG	Sidechain
1	A	40	ARG	Sidechain

## 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	2273	0	2200	27	0
1	B	2341	0	2295	16	0
1	C	2222	0	2109	57	0
2	A	1	0	0	0	0
3	A	112	0	0	1	0
3	B	95	0	0	1	0
3	C	28	0	0	0	0
All	All	7072	0	6604	98	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 (98) 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:C:86:VAL:HG13	1:C:179:GLY:HA2	1.64	0.79
1:C:218:TRP:HE1	1:C:281:ILE:HG13	1.48	0.78
1:A:86:VAL:HG13	1:A:179:GLY:HA2	1.71	0.73
1:C:5:LYS:NZ	1:C:290:GLU:OE1	2.21	0.69
1:C:210:ALA:HA	1:C:213:ILE:HD12	1.74	0.68
1:C:109:GLY:HA2	1:C:200:ILE:HD13	1.75	0.67
1:C:217:ARG:HB3	1:C:220:LEU:HD11	1.77	0.67
1:C:111:THR:HG22	1:C:129:ALA:HB2	1.77	0.66
1:C:201:THR:HG22	1:C:239:TYR:HD2	1.59	0.66
1:A:66:PHE:CZ	1:A:87:LEU:HD21	2.31	0.65
1:A:27:LEU:HD21	1:A:42:VAL:HB	1.80	0.64
1:A:8:PHE:HE2	1:A:151:ASN:HD22	1.47	0.62
1:B:53:ASN:HD22	1:B:56:ASP:H	1.47	0.61
1:B:19:GLN:HE21	1:B:26:THR:HG21	1.66	0.61
1:A:40:ARG:HD2	1:A:54:TYR:CG	2.36	0.61
1:C:256:GLN:O	1:C:256:GLN:HG2	2.01	0.60
1:C:186:VAL:O	1:C:192:GLN:NE2	2.37	0.57
1:A:132:PRO:HD2	1:A:197:ASP:OD1	2.05	0.57
1:C:40:ARG:NE	1:C:187:ASP:OD2	2.38	0.56
1:C:254:SER:O	1:C:258:GLY:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:201:THR:HG22	1:C:239:TYR:CD2	2.41	0.56
1:C:40:ARG:NH2	1:C:187:ASP:OD1	2.27	0.56
1:C:218:TRP:NE1	1:C:281:ILE:HG13	2.17	0.56
1:A:133:ASN:O	1:A:134:PHE:HB2	2.05	0.55
1:B:233:VAL:HG21	1:B:269:LYS:HD2	1.90	0.54
1:A:301:THR:O	1:A:302:SER:C	2.47	0.53
1:C:243:THR:HG22	1:C:245:ASP:H	1.73	0.52
1:C:211:ALA:CB	1:C:282:LEU:HD23	2.41	0.50
1:A:300:CYS:O	1:A:301:THR:C	2.50	0.50
1:C:17:MET:HG3	1:C:117:CYS:SG	2.52	0.50
1:B:109:GLY:HA2	1:B:200:ILE:HD13	1.93	0.49
1:C:27:LEU:HD21	1:C:42:VAL:HB	1.95	0.49
1:C:256:GLN:HG3	1:C:304:VAL:HG22	1.94	0.49
1:A:61:LYS:HZ3	1:A:65:ASN:HB3	1.78	0.49
1:B:76:ARG:NE	1:B:92:ASP:OD2	2.45	0.49
1:C:76:ARG:NH1	1:C:92:ASP:OD2	2.46	0.48
1:C:226:THR:HG23	1:C:229:ASP:H	1.78	0.48
1:C:40:ARG:HD3	1:C:85:CYS:HA	1.94	0.48
1:C:175:THR:HG22	1:C:181:PHE:CD1	2.49	0.48
1:A:83:GLN:O	1:A:86:VAL:HG22	2.14	0.48
1:A:135:THR:HG21	1:A:194:ALA:CB	2.44	0.47
1:C:129:ALA:HB3	1:C:290:GLU:HG2	1.95	0.47
1:C:247:VAL:HG13	1:C:261:VAL:HG11	1.97	0.47
1:A:131:ARG:HB2	1:A:133:ASN:OD1	2.15	0.47
1:C:212:VAL:O	1:C:217:ARG:NH1	2.41	0.47
1:B:41:HIS:O	1:B:44:CYS:HB2	2.16	0.46
1:C:231:ASN:O	1:C:234:ALA:N	2.45	0.46
1:A:45:THR:O	1:A:46:SER:C	2.54	0.46
1:C:192:GLN:H	1:C:192:GLN:HG2	1.53	0.46
1:A:128[A]:CYS:SG	1:A:137:LYS:O	2.73	0.46
1:C:10:SER:O	1:C:14:GLU:HG3	2.15	0.46
1:A:83:GLN:HB3	1:A:86:VAL:HG23	1.97	0.46
1:A:22:CYS:HB2	1:A:42:VAL:HG22	1.97	0.45
1:A:19:GLN:HE21	1:A:26:THR:HG21	1.82	0.45
1:C:140:PHE:HB3	1:C:144:SER:OG	2.17	0.45
1:C:8:PHE:HE2	1:C:151:ASN:HD22	1.64	0.45
1:C:80:HIS:O	1:C:80:HIS:ND1	2.49	0.45
1:C:210:ALA:O	1:C:213:ILE:N	2.49	0.45
1:A:135:THR:HG21	1:A:194:ALA:HB2	1.98	0.45
1:B:56:ASP:O	1:B:59:ILE:HG22	2.17	0.44
1:C:43:ILE:HB	1:C:61:LYS:HE3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:PHE:CD1	1:C:265:CYS:HB3	2.53	0.44
1:A:81:SER:O	1:A:87:LEU:HD12	2.17	0.44
1:C:211:ALA:HB2	1:C:282:LEU:HD23	1.98	0.44
1:A:217:ARG:HD2	1:C:153:ASP:OD2	2.17	0.44
1:B:22:CYS:HB2	1:B:42:VAL:HG22	2.00	0.44
1:B:63:ASN:ND2	1:B:78:ILE:O	2.51	0.44
1:C:240:GLU:HG2	1:C:241:PRO:HD2	2.00	0.44
1:A:276:MET:HE2	1:A:287:LEU:HD23	2.00	0.43
1:A:6:MET:HG3	1:B:126:TYR:HD2	1.83	0.43
1:A:118:TYR:CE1	1:A:144:SER:HB3	2.53	0.43
1:C:131:ARG:NH2	1:C:289:ASP:OD2	2.48	0.43
1:A:175:THR:HG22	1:A:181:PHE:HA	2.00	0.43
1:C:118:TYR:CE2	1:C:144:SER:HB3	2.53	0.43
1:C:21:THR:HG23	1:C:26:THR:HG22	2.01	0.42
1:C:212:VAL:HG12	1:C:213:ILE:N	2.33	0.42
1:C:257:THR:C	1:C:259:ILE:H	2.23	0.42
1:B:113:SER:O	1:B:149:GLY:HA2	2.19	0.42
1:B:228:ASN:O	1:B:232:LEU:HD13	2.19	0.42
1:B:22:CYS:HB3	1:B:61:LYS:HZ3	1.85	0.42
1:C:138:GLY:O	1:C:172:HIS:HE1	2.01	0.42
1:B:107:GLN:NE2	3:B:411:HOH:O	2.52	0.42
1:C:131:ARG:HA	1:C:131:ARG:HD2	1.85	0.42
1:C:165:MET:HE1	1:C:187:ASP:HA	2.02	0.42
1:C:163:HIS:NE2	1:C:172:HIS:HB3	2.34	0.41
1:B:66:PHE:CE2	1:B:87:LEU:HD21	2.55	0.41
1:C:129:ALA:CB	1:C:290:GLU:HG2	2.50	0.41
1:C:167:LEU:HD13	1:C:194:ALA:HB2	2.03	0.41
1:A:10:SER:O	1:A:14:GLU:HG3	2.21	0.41
1:C:253:LEU:O	1:C:257:THR:HG23	2.21	0.41
1:A:298:ARG:HD2	3:A:512:HOH:O	2.20	0.41
1:C:163:HIS:CD2	1:C:172:HIS:HB3	2.56	0.41
1:C:111:THR:HG23	1:C:292:THR:HG23	2.03	0.40
1:C:167:LEU:HD12	1:C:171:VAL:HG23	2.03	0.40
1:C:216:ASP:OD2	1:C:281:ILE:HA	2.22	0.40
1:C:251:GLY:N	1:C:252:PRO:HD2	2.35	0.40
1:C:227:LEU:HD21	1:C:242:LEU:O	2.21	0.40
1:B:175:THR:HG22	1:B:181:PHE:HA	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	294/306 (96%)	286 (97%)	8 (3%)	0	100	100
1	B	302/306 (99%)	298 (99%)	4 (1%)	0	100	100
1	C	292/306 (95%)	281 (96%)	11 (4%)	0	100	100
All	All	888/918 (97%)	865 (97%)	23 (3%)	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	249/262 (95%)	231 (93%)	18 (7%)	14	9
1	B	261/262 (100%)	255 (98%)	6 (2%)	50	53
1	C	235/262 (90%)	224 (95%)	11 (5%)	26	22
All	All	745/786 (95%)	710 (95%)	35 (5%)	27	22

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	5	LYS
1	A	27	LEU
1	A	40	ARG
1	A	44	CYS

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Mol	Chain	Res	Type
1	A	45	THR
1	A	55	GLU
1	A	62	SER
1	A	90	LYS
1	A	110	GLN
1	A	128[A]	CYS
1	A	128[B]	CYS
1	A	137	LYS
1	A	165	MET
1	A	217	ARG
1	A	222	ARG
1	A	298	ARG
1	A	301	THR
1	B	5	LYS
1	B	46	SER
1	B	49	MET
1	B	155	ASP
1	B	216	ASP
1	B	298	ARG
1	C	27	LEU
1	C	181	PHE
1	C	187	ASP
1	C	189	GLN
1	C	209	TYR
1	C	212	VAL
1	C	217	ARG
1	C	218	TRP
1	C	220	LEU
1	C	256	GLN
1	C	280	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	63	ASN
1	A	119	ASN
1	A	151	ASN
1	B	19	GLN
1	B	53	ASN
1	B	72	ASN
1	B	119	ASN

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Mol	Chain	Res	Type
1	B	142	ASN
1	B	164	HIS
1	B	256	GLN
1	C	51	ASN
1	C	172	HIS

### 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](#)

Of 1 ligands modelled in this entry, 1 is 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 [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	297/306 (97%)	0.38	14 (4%) 31 30	31, 49, 102, 154	0
1	B	302/306 (98%)	0.31	7 (2%) 60 59	34, 51, 88, 145	0
1	C	297/306 (97%)	1.02	49 (16%) 1 1	43, 88, 136, 160	0
All	All	896/918 (97%)	0.57	70 (7%) 13 12	31, 59, 122, 160	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	255	ALA	8.4
1	A	54	TYR	7.7
1	C	215	GLY	7.5
1	C	194	ALA	7.3
1	A	58	LEU	6.1
1	C	195	GLY	5.5
1	C	219	PHE	5.2
1	A	45	THR	5.1
1	C	272	LEU	4.8
1	C	1	SER	4.8
1	C	140	PHE	4.4
1	B	50	LEU	4.3
1	C	167	LEU	4.3
1	C	134	PHE	4.3
1	C	67	LEU	4.3
1	A	302	SER	4.2
1	C	190	THR	4.2
1	C	141	LEU	4.0
1	C	230	PHE	4.0
1	C	221	ASN	3.8
1	C	185	PHE	3.5
1	A	301	THR	3.5
1	A	44	CYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	53	ASN	3.3
1	B	48	ASP	3.2
1	C	180	ASN	3.1
1	C	208	LEU	3.1
1	A	59	ILE	3.0
1	C	281	ILE	2.9
1	C	207	TRP	2.9
1	C	2	GLY	2.8
1	C	262	LEU	2.8
1	C	138	GLY	2.7
1	C	259	ILE	2.7
1	C	87	LEU	2.7
1	C	3	PHE	2.7
1	C	211	ALA	2.7
1	B	49	MET	2.6
1	C	61	LYS	2.6
1	A	300	CYS	2.6
1	C	216	ASP	2.6
1	C	280	THR	2.6
1	B	73	VAL	2.5
1	A	46	SER	2.5
1	C	44	CYS	2.5
1	C	184	PRO	2.5
1	B	302	SER	2.5
1	C	285	ALA	2.4
1	C	286	LEU	2.3
1	C	217	ARG	2.3
1	B	51	ASN	2.3
1	A	189	GLN	2.3
1	C	66	PHE	2.3
1	C	237	TYR	2.2
1	C	51	ASN	2.2
1	B	154	TYR	2.2
1	C	212	VAL	2.2
1	C	275	GLY	2.2
1	C	254	SER	2.2
1	A	43	ILE	2.1
1	C	89	LEU	2.1
1	C	139	SER	2.1
1	C	210	ALA	2.1
1	C	54	TYR	2.1
1	C	218	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	87	LEU	2.0
1	C	86	VAL	2.0
1	C	214	ASN	2.0
1	C	209	TYR	2.0
1	A	57	LEU	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	NA	A	401	1/1	0.98	0.07	49,49,49,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.