



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 12, 2022 – 01:01 PM EDT

PDB ID : 8DRS
Title : Product structure of SARS-CoV-2 Mpro C145A mutant in complex with nsp6-nsp7 (C6) 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 : 1.80 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 types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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

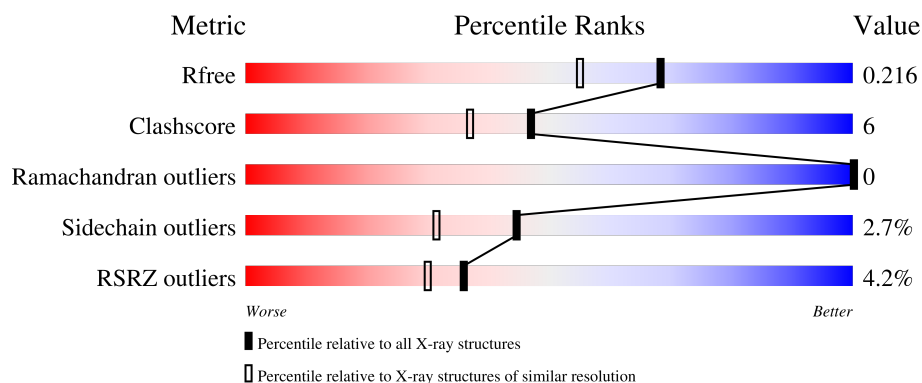
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 ≥ 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>2%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
1	B	306	<div> <div>%</div> <div>87%</div> <div>12%</div> <div>.</div> </div>
1	C	306	<div> <div>10%</div> <div>76%</div> <div>23%</div> <div>.</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7635 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	302	Total	C	N	O	S	0	8	0
			2385	1511	409	441	24			
1	B	302	Total	C	N	O	S	0	4	0
			2362	1497	404	438	23			
1	C	306	Total	C	N	O	S	0	2	0
			2362	1496	402	441	23			

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	LYS	-	expression tag	UNP P0DTD1
A	302	VAL	-	expression tag	UNP P0DTD1
A	303	ALA	-	expression tag	UNP P0DTD1
A	304	THR	-	expression tag	UNP P0DTD1
A	305	VAL	-	expression tag	UNP P0DTD1
A	306	GLN	-	expression tag	UNP P0DTD1
B	145	ALA	CYS	engineered mutation	UNP P0DTD1
B	301	LYS	-	expression tag	UNP P0DTD1
B	302	VAL	-	expression tag	UNP P0DTD1
B	303	ALA	-	expression tag	UNP P0DTD1
B	304	THR	-	expression tag	UNP P0DTD1
B	305	VAL	-	expression tag	UNP P0DTD1
B	306	GLN	-	expression tag	UNP P0DTD1
C	145	ALA	CYS	engineered mutation	UNP P0DTD1
C	301	LYS	-	expression tag	UNP P0DTD1
C	302	VAL	-	expression tag	UNP P0DTD1
C	303	ALA	-	expression tag	UNP P0DTD1
C	304	THR	-	expression tag	UNP P0DTD1
C	305	VAL	-	expression tag	UNP P0DTD1
C	306	GLN	-	expression tag	UNP P0DTD1

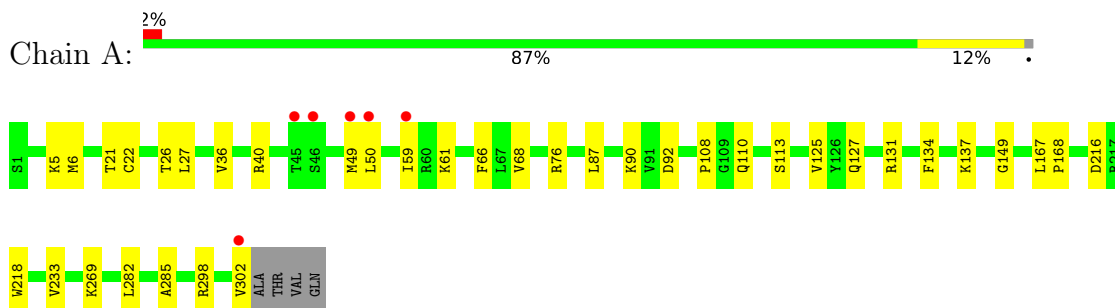
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	231	Total 231	O 231	0	0
2	B	233	Total 233	O 233	0	0
2	C	62	Total 62	O 62	0	0

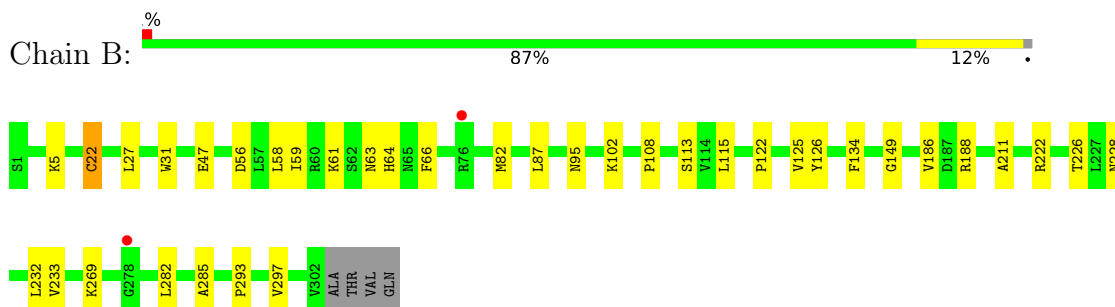
3 Residue-property plots [i](#)

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.

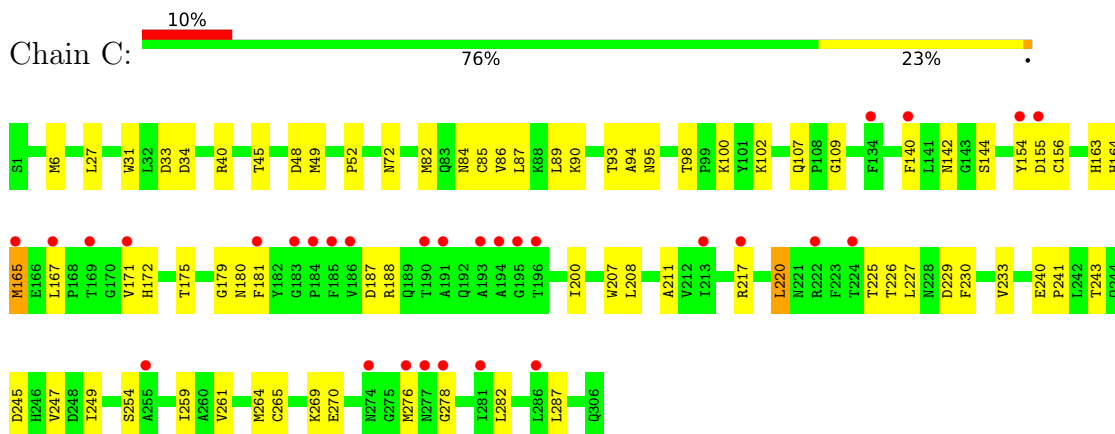
- Molecule 1: 3C-like proteinase nsp5



- Molecule 1: 3C-like proteinase nsp5



- Molecule 1: 3C-like proteinase nsp5



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	67.09Å 108.53Å 137.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.32 – 1.80 60.32 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (60.32-1.80) 100.0 (60.32-1.80)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.180 , 0.218 0.178 , 0.216	Depositor DCC
R_{free} test set	4638 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	26.6	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7635	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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	0.83	0/2456	0.82	0/3336
1	B	0.77	0/2424	0.85	0/3293
1	C	0.61	0/2417	0.73	0/3285
All	All	0.74	0/7297	0.80	0/9914

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	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	63	ASN	Mainchain

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	2385	0	2354	21	0
1	B	2362	0	2324	23	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2362	0	2310	48	0
2	A	231	0	0	2	0
2	B	233	0	0	0	0
2	C	62	0	0	1	0
All	All	7635	0	6988	87	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 6.

All (87) 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	1.43	0.99
1:B:226:THR:HG22	1:B:228:ASN:H	1.28	0.95
1:B:226:THR:HG22	1:B:228:ASN:N	1.92	0.85
1:B:228:ASN:O	1:B:232:LEU:HD23	1.88	0.72
1:C:276:MET:HG3	1:C:278:GLY:H	1.54	0.72
1:C:225:THR:OG1	1:C:269:LYS:NZ	2.22	0.72
1:A:131:ARG:HD3	1:A:137:LYS:HE3	1.71	0.71
1:C:52:PRO:HD2	1:C:188:ARG:HG2	1.71	0.71
1:C:245:ASP:O	1:C:249:ILE:HD12	1.90	0.70
1:C:226:THR:HG23	1:C:229:ASP:H	1.57	0.69
1:C:87:LEU:HD21	1:C:89:LEU:HD21	1.75	0.68
1:B:82:MET:HE2	1:B:87:LEU:HD21	1.76	0.67
1:C:40:ARG:HD3	1:C:85:CYS:HA	1.76	0.66
1:C:100:LYS:HD3	1:C:156:CYS:HB2	1.78	0.64
1:A:76:ARG:HB3	1:A:92:ASP:OD2	1.98	0.64
1:C:188:ARG:HG3	1:C:188:ARG:HH11	1.64	0.60
1:C:163:HIS:NE2	1:C:172:HIS:HB3	2.18	0.59
1:C:220:LEU:HD21	1:C:259:ILE:HD13	1.84	0.59
1:C:243:THR:O	1:C:247:VAL:HG23	2.04	0.58
1:B:47:GLU:HA	1:C:217:ARG:NH2	2.20	0.57
1:C:211:ALA:HA	1:C:282:LEU:HD11	1.84	0.57
1:B:22[A]:CYS:SG	1:B:61:LYS:HD2	2.45	0.56
1:A:110:GLN:HG3	2:A:532:HOH:O	2.06	0.56
1:B:58:LEU:HD22	1:B:82:MET:HE3	1.88	0.56
1:A:131:ARG:HD3	1:A:137:LYS:CE	2.36	0.56
1:C:225:THR:HG22	1:C:226:THR:O	2.07	0.55
1:C:165:MET:CE	1:C:187:ASP:HA	2.39	0.53
1:C:208:LEU:HB3	1:C:264:MET:HE1	1.91	0.53
1:C:167:LEU:HD12	1:C:171:VAL:HG23	1.89	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:VAL:HG11	1:B:269:LYS:HG3	1.91	0.52
1:A:218:TRP:O	1:C:100:LYS:NZ	2.43	0.51
1:B:56:ASP:O	1:B:59:ILE:HG22	2.11	0.51
1:C:249:ILE:HD12	1:C:249:ILE:H	1.75	0.51
1:C:207:TRP:CZ3	1:C:287:LEU:HA	2.46	0.50
1:A:40:ARG:HA	1:A:87:LEU:HG	1.94	0.50
1:A:6:MET:HG3	1:B:126:TYR:HD2	1.77	0.49
1:C:154:TYR:O	1:C:155:ASP:HB2	2.12	0.49
1:A:22[A]:CYS:SG	1:A:61:LYS:HD2	2.53	0.48
1:C:45:THR:HG22	1:C:48:ASP:CG	2.34	0.48
1:C:208:LEU:HB3	1:C:264:MET:CE	2.43	0.48
1:C:40:ARG:HH11	1:C:82:MET:CE	2.26	0.48
1:C:188:ARG:HG3	1:C:188:ARG:NH1	2.26	0.48
1:C:164:HIS:CE1	1:C:175:THR:HG23	2.49	0.48
1:C:230:PHE:CD1	1:C:265:CYS:HB3	2.49	0.48
1:A:285:ALA:HB3	1:B:285:ALA:HB3	1.96	0.47
1:C:33:ASP:O	1:C:95:ASN:N	2.43	0.47
1:A:125:VAL:HG11	1:B:125:VAL:HG11	1.97	0.47
1:B:226:THR:CG2	1:B:228:ASN:H	2.15	0.47
1:B:22[B]:CYS:SG	1:B:66:PHE:CD2	3.08	0.47
1:B:115:LEU:HD11	1:B:122:PRO:HB3	1.96	0.47
1:C:72:ASN:OD1	1:C:72:ASN:N	2.46	0.46
1:A:167:LEU:HB3	1:A:168:PRO:HD2	1.97	0.46
1:B:293:PRO:O	1:B:297:VAL:HG13	2.16	0.46
1:A:108:PRO:HG3	1:A:134:PHE:CE1	2.51	0.46
1:C:247:VAL:HG13	1:C:261:VAL:HG11	1.98	0.45
1:C:48:ASP:O	1:C:52:PRO:HB3	2.16	0.45
1:B:186:VAL:HG23	1:B:188:ARG:HG2	1.99	0.45
1:A:113:SER:O	1:A:149:GLY:HA2	2.17	0.45
1:C:180:ASN:ND2	2:C:402:HOH:O	2.28	0.45
1:B:108:PRO:HG3	1:B:134:PHE:CE1	2.52	0.44
1:C:240:GLU:HG2	1:C:241:PRO:HD2	1.99	0.44
1:B:282:LEU:HD23	1:B:282:LEU:HA	1.92	0.44
1:C:226:THR:CG2	1:C:229:ASP:H	2.27	0.44
1:C:233:VAL:HG11	1:C:269:LYS:HG3	1.99	0.43
1:B:31:TRP:CD2	1:B:95:ASN:HB2	2.54	0.43
1:C:165:MET:SD	1:C:165:MET:N	2.92	0.43
1:C:33:ASP:O	1:C:94:ALA:HA	2.19	0.43
1:A:22[B]:CYS:SG	1:A:66:PHE:CD1	3.12	0.43
1:C:84:ASN:HB3	1:C:179:GLY:O	2.18	0.42
1:A:50:LEU:HD12	1:A:50:LEU:HA	1.80	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:ARG:HH11	1:B:222:ARG:HG2	1.84	0.42
1:C:140:PHE:HB3	1:C:144:SER:OG	2.19	0.42
1:B:113:SER:O	1:B:149:GLY:HA2	2.20	0.42
1:A:5:LYS:HG3	1:A:127:GLN:HB3	2.01	0.42
1:A:21:THR:OG1	1:A:26[B]:THR:HG22	2.19	0.41
1:A:36:VAL:HG21	1:A:68:VAL:HG11	2.03	0.41
1:A:59:ILE:HG13	2:A:449:HOH:O	2.21	0.41
1:A:282:LEU:HD23	1:A:282:LEU:HA	1.92	0.41
1:C:34:ASP:OD2	1:C:90:LYS:NZ	2.52	0.41
1:C:109:GLY:HA2	1:C:200:ILE:HD13	2.03	0.41
1:C:270:GLU:OE1	1:C:270:GLU:HA	2.21	0.41
1:A:233:VAL:HG21	1:A:269:LYS:HD2	2.03	0.41
1:C:95:ASN:HB3	1:C:98:THR:OG1	2.21	0.40
1:C:31:TRP:HZ2	1:C:93:THR:HG22	1.86	0.40
1:B:211:ALA:HA	1:B:282:LEU:HG	2.03	0.40
1:C:6:MET:HE3	1:C:6:MET:HB2	1.77	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	308/306 (101%)	302 (98%)	6 (2%)	0	100	100
1	B	304/306 (99%)	298 (98%)	6 (2%)	0	100	100
1	C	306/306 (100%)	295 (96%)	11 (4%)	0	100	100
All	All	918/918 (100%)	895 (98%)	23 (2%)	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	267/262 (102%)	260 (97%)	7 (3%)	46	32
1	B	263/262 (100%)	256 (97%)	7 (3%)	44	31
1	C	260/262 (99%)	250 (96%)	10 (4%)	33	18
All	All	790/786 (100%)	766 (97%)	24 (3%)	44	27

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	49	MET
1	A	90	LYS
1	A	216	ASP
1	A	298[A]	ARG
1	A	298[B]	ARG
1	A	302	VAL
1	B	5	LYS
1	B	22[A]	CYS
1	B	22[B]	CYS
1	B	27	LEU
1	B	64[A]	HIS
1	B	64[B]	HIS
1	B	102	LYS
1	C	27	LEU
1	C	49	MET
1	C	102	LYS
1	C	107	GLN
1	C	142	ASN
1	C	165	MET
1	C	181	PHE
1	C	220	LEU
1	C	227	LEU
1	C	254	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	110	GLN
1	C	41	HIS
1	C	256	GLN

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](#)

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	302/306 (98%)	-0.15	6 (1%) 65 61	19, 33, 63, 119	0
1	B	302/306 (98%)	-0.09	2 (0%) 87 86	18, 33, 66, 107	0
1	C	306/306 (100%)	0.54	30 (9%) 7 5	28, 71, 117, 148	0
All	All	910/918 (99%)	0.10	38 (4%) 36 30	18, 41, 101, 148	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	195	GLY	6.9
1	C	167	LEU	5.7
1	C	194	ALA	5.5
1	C	191	ALA	4.7
1	C	184	PRO	4.7
1	C	171	VAL	4.3
1	A	45	THR	3.8
1	C	186	VAL	3.8
1	C	277	ASN	3.6
1	C	181	PHE	3.1
1	C	155	ASP	3.1
1	C	183	GLY	3.1
1	A	49	MET	3.0
1	B	278	GLY	2.9
1	C	224	THR	2.9
1	C	165	MET	2.9
1	C	190	THR	2.8
1	C	278	GLY	2.8
1	A	59	ILE	2.8
1	C	217	ARG	2.8
1	C	276	MET	2.8
1	C	140	PHE	2.6
1	C	134	PHE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	196	THR	2.4
1	A	46	SER	2.3
1	A	50	LEU	2.3
1	C	193	ALA	2.2
1	C	222	ARG	2.2
1	C	281	ILE	2.2
1	C	255	ALA	2.1
1	C	169	THR	2.1
1	C	274	ASN	2.1
1	A	302	VAL	2.1
1	C	213	ILE	2.1
1	B	76	ARG	2.0
1	C	154	TYR	2.0
1	C	185	PHE	2.0
1	C	286	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.