



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 12, 2021 – 08:03 PM EST

PDB ID : 7K8M
Title : Structure of the SARS-CoV-2 receptor binding domain in complex with the human neutralizing antibody Fab fragment, C102
Authors : Jette, C.A.; Barnes, C.O.; Bjorkman, P.J.
Deposited on : 2020-09-27
Resolution : 3.20 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 : 2.16
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) : 2.16

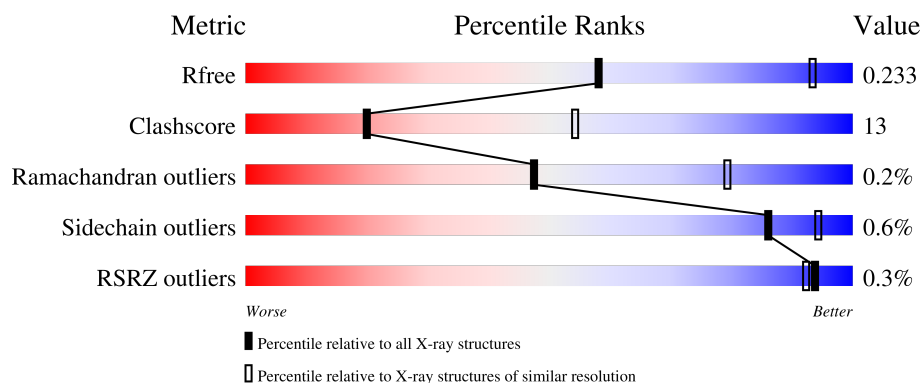
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	229	
2	B	215	
3	E	187	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4753 atoms, of which 8 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 C102 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	1	0
			1606	1018	266	316	6			

- Molecule 2 is a protein called C102 Fab Light Chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	215	Total	C	H	N	O	S	0	1	0
			1657	1028	8	281	334	6			

- Molecule 3 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	184	Total	C	N	O	S	0	1	0
			1476	946	245	278	7			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



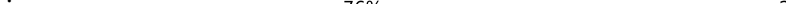
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 1: C102 Fab Heavy Chain

LVS	Q1
SER	V2
THR	Q3
SER	L4
GLY	V5
GLY	E6
T136	
	I12
GL39	Q13
Y145	Q22
E148	S25
P149	G26
V150	F27
	I28
M154	V29
L159	N32
	Y33
L170	M34
L175	S35
Y176	K36
S177	Q39
L178	
	V48
V182	I51
T183	
V184	T57
P185	F58
	Y59
H200	
	V63
S215	
CYS	F67
ASP	T68
LVS	I69
THR	
HIS	K75
HIS	
HIS	L78
HIS	
HIS	A88
	C92
	K93
	R94
	D95
	Y96
	Q97
	P98
	Y99
	K117
	L124
	E126

Chain B:  72% 28%

[illegible]

Chain E:  76% 22%

F497	N334	R346	V350	V362	S371	L387	D398	F400	R403	G416	I418	A419	D420	N422	Y423	K424	G431	Y449	M450	L452	Y453	A475	T478	P479	F486	Y489	S494
Y505	C336			A363	A372	N388	S399			K417	A419	D420	N422	Y423	K424	G431	Y449	M450	L452	Y453	A475	T478	P479	F486	Y489	S494	
Q506				P365		D389				I418	A419	D420	N422	Y423	K424	G431	Y449	M450	L452	Y453	A475	T478	P479	F486	Y489	S494	
P507				V367		L390				A419	D420	N422	Y423	K424	G431	Y449	M450	L452	Y453	A475	T478	P479	F486	Y489	S494		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.60Å 89.25Å 175.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.12 – 3.20 52.12 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (52.12-3.20) 97.0 (52.12-3.20)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.70 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.175 , 0.234 0.175 , 0.233	Depositor DCC
R_{free} test set	1473 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	66.6	Xtriage
Anisotropy	0.610	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 27.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4753	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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](#)

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

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	0.33	0/1648	0.53	0/2245
2	B	0.33	0/1687	0.53	0/2289
3	E	0.35	0/1517	0.48	0/2062
All	All	0.34	0/4852	0.51	0/6596

There are no bond length outliers.

There are no bond angle outliers.

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	1606	0	1562	44	0
2	B	1649	8	1604	49	0
3	E	1476	0	1392	34	0
4	E	14	0	13	0	0
All	All	4745	8	4571	117	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 13.

All (117) 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:99:TYR:HH	3:E:453:TYR:HH	1.08	0.99
1:A:29:VAL:HG13	1:A:34:MET:HG3	1.45	0.94
3:E:452:LEU:HD23	3:E:494:SER:HA	1.66	0.77
2:B:33:LEU:HD22	2:B:71:PHE:CG	2.20	0.76
1:A:170:LEU:HD13	1:A:176:TYR:CE1	2.25	0.72
1:A:170:LEU:HD13	1:A:176:TYR:CZ	2.26	0.71
2:B:142:ARG:HB2	2:B:173:TYR:CE1	2.30	0.66
1:A:6:GLU:N	1:A:6:GLU:OE1	2.28	0.66
2:B:136:LEU:HD21	2:B:196:VAL:HG13	1.80	0.63
2:B:201:LEU:HD13	2:B:205:VAL:HG23	1.81	0.63
1:A:178:LEU:C	1:A:178:LEU:HD23	2.20	0.62
1:A:2:VAL:HG21	3:E:486:PHE:CZ	2.35	0.62
2:B:185:ASP:HA	2:B:188:LYS:HE2	1.82	0.61
1:A:75:LYS:HB2	1:A:75:LYS:NZ	2.16	0.61
1:A:139:GLY:HA2	1:A:154:TRP:CH2	2.36	0.60
2:B:12:SER:O	2:B:13:LEU:HD23	2.01	0.60
2:B:81:GLU:OE1	2:B:81:GLU:N	2.34	0.60
2:B:193:ALA:HB2	2:B:208:SER:HB3	1.83	0.59
1:A:145:TYR:CE2	1:A:150:VAL:HG13	2.37	0.59
2:B:47:LEU:C	2:B:48:ILE:HD12	2.22	0.59
3:E:346:ARG:HH12	3:E:450:ASN:HB3	1.68	0.58
2:B:175:LEU:HD23	2:B:176:SER:N	2.19	0.57
2:B:100:GLN:N	2:B:100:GLN:OE1	2.32	0.57
3:E:346:ARG:HH12	3:E:450:ASN:CB	2.18	0.56
2:B:105:GLU:HG2	2:B:106:ILE:H	1.71	0.56
3:E:336:CYS:SG	3:E:363:ALA:HB2	2.46	0.56
1:A:117:LYS:HD3	1:A:175:LEU:HD13	1.87	0.56
3:E:497:PHE:HB3	3:E:507:PRO:HD3	1.89	0.55
1:A:150:VAL:HG12	1:A:200:HIS:CD2	2.41	0.55
1:A:2:VAL:HG21	3:E:486:PHE:HZ	1.72	0.55
3:E:334:ASN:O	3:E:362:VAL:HG12	2.08	0.54
1:A:150:VAL:HG12	1:A:200:HIS:HD2	1.73	0.53
1:A:94:ARG:HH21	3:E:489:TYR:HE2	1.55	0.53
2:B:125:LEU:O	2:B:183:LYS:HD2	2.08	0.53
1:A:12:ILE:HD12	1:A:13:GLN:H	1.73	0.53
1:A:159:LEU:HD21	1:A:182:VAL:HG21	1.90	0.52
2:B:10:THR:HG22	2:B:103:LYS:HB3	1.92	0.52
2:B:55:ALA:HB3	2:B:58:ILE:HG13	1.91	0.52
3:E:517:LEU:N	3:E:517:LEU:HD12	2.25	0.51
1:A:28:ILE:O	1:A:32:ASN:ND2	2.44	0.51
2:B:181:LEU:HD23	2:B:185:ASP:OD2	2.11	0.51
2:B:49:TYR:O	2:B:53:SER:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:478:THR:HG22	3:E:479:PRO:O	2.10	0.51
1:A:96:TYR:O	1:A:99:TYR:HB2	2.10	0.50
2:B:75:ILE:HG21	2:B:78:LEU:HD12	1.93	0.50
3:E:449:TYR:HB3	3:E:494:SER:OG	2.11	0.50
1:A:51:ILE:O	1:A:51:ILE:HG23	2.11	0.50
2:B:124:GLN:HG2	2:B:129:THR:O	2.11	0.50
2:B:33:LEU:HD22	2:B:71:PHE:CB	2.41	0.50
2:B:136:LEU:HD21	2:B:196:VAL:CG1	2.41	0.49
3:E:362:VAL:O	3:E:362:VAL:HG13	2.11	0.49
2:B:193:ALA:CB	2:B:208:SER:HB3	2.42	0.49
2:B:179:LEU:HG	2:B:181:LEU:HD11	1.93	0.49
3:E:418:ILE:HA	3:E:422:ASN:HD22	1.77	0.49
2:B:33:LEU:HD22	2:B:71:PHE:CD2	2.47	0.49
1:A:22:CYS:HB3	1:A:78:LEU:HB3	1.94	0.49
1:A:94:ARG:NH2	3:E:489:TYR:OH	2.46	0.49
2:B:6:GLN:N	2:B:100:GLN:HE22	2.11	0.49
2:B:47:LEU:HD23	2:B:58:ILE:HD12	1.95	0.48
1:A:150:VAL:O	1:A:150:VAL:HG23	2.13	0.48
1:A:33:TYR:CD2	1:A:97:GLY:HA2	2.49	0.48
1:A:178:LEU:O	1:A:178:LEU:HD23	2.13	0.48
2:B:142:ARG:HG2	2:B:142:ARG:O	2.13	0.48
3:E:403:ARG:CZ	3:E:505:TYR:CD1	2.97	0.48
1:A:27:PHE:O	1:A:28:ILE:HD13	2.14	0.47
3:E:371:SER:O	3:E:372:ALA:HB3	2.13	0.47
2:B:113:PRO:HB3	2:B:139:PHE:HB3	1.97	0.47
1:A:51:ILE:HG13	1:A:57:THR:HG22	1.96	0.47
1:A:33:TYR:CE2	1:A:97:GLY:HA2	2.50	0.47
2:B:201:LEU:HD13	2:B:205:VAL:CG2	2.44	0.46
1:A:99:TYR:OH	3:E:453:TYR:OH	2.00	0.46
3:E:403:ARG:CZ	3:E:505:TYR:HD1	2.28	0.46
3:E:403:ARG:NH1	3:E:505:TYR:HE1	2.14	0.46
2:B:186:TYR:HA	2:B:192:TYR:OH	2.16	0.46
2:B:175:LEU:HD23	2:B:175:LEU:C	2.37	0.46
3:E:398:ASP:O	3:E:511:VAL:HA	2.16	0.46
2:B:181:LEU:HD12	2:B:181:LEU:N	2.32	0.45
1:A:3:GLN:O	1:A:4:LEU:HD23	2.17	0.45
1:A:39:GLN:C	1:A:88:ALA:HB1	2.37	0.45
1:A:184:VAL:HB	1:A:185:PRO:HD2	1.98	0.45
2:B:142:ARG:HB2	2:B:173:TYR:CD1	2.52	0.45
1:A:148:GLU:HB3	1:A:149:PRO:HA	1.99	0.44
2:B:80:PRO:HA	2:B:83:PHE:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:36:TRP:CZ3	1:A:92:CYS:HB3	2.53	0.44
2:B:154:LEU:N	2:B:154:LEU:HD12	2.33	0.44
3:E:452:LEU:CD2	3:E:494:SER:HA	2.42	0.44
1:A:48:VAL:HG13	1:A:63:VAL:HG21	1.99	0.44
2:B:167:ASP:HB3	2:B:170:ASP:OD1	2.18	0.44
3:E:366:SER:OG	3:E:388:ASN:ND2	2.50	0.44
2:B:163:VAL:HG22	2:B:175:LEU:HD12	1.99	0.43
1:A:124:LEU:HB3	2:B:118:PHE:CD1	2.54	0.43
1:A:99:TYR:CE1	3:E:417:LYS:NZ	2.87	0.43
2:B:21:LEU:HG	2:B:102:THR:HG21	1.99	0.43
2:B:47:LEU:O	2:B:48:ILE:HD12	2.19	0.43
2:B:61:ARG:CZ	2:B:79:GLU:HG3	2.49	0.43
2:B:75:ILE:HG21	2:B:78:LEU:CD1	2.49	0.42
3:E:350:VAL:HA	3:E:400:PHE:HB2	2.01	0.42
2:B:35:TRP:CZ3	2:B:88:CYS:HB3	2.54	0.42
2:B:11:LEU:N	2:B:103:LYS:O	2.49	0.42
1:A:2:VAL:HG21	3:E:486:PHE:CE2	2.55	0.42
2:B:85:VAL:HA	2:B:102:THR:O	2.20	0.42
1:A:32:ASN:OD1	3:E:475:ALA:HB1	2.20	0.42
1:A:63:VAL:HG11	1:A:67:PHE:CE2	2.55	0.41
2:B:6:GLN:H	2:B:100:GLN:HE22	1.67	0.41
3:E:419:ALA:O	3:E:424:LYS:HD3	2.20	0.41
1:A:36:TRP:HD1	1:A:69:ILE:HD12	1.86	0.41
1:A:59:TYR:CE1	1:A:69:ILE:HG22	2.55	0.41
3:E:431:GLY:HA3	3:E:513:LEU:O	2.21	0.41
2:B:89:GLN:HG2	2:B:90:GLN:N	2.36	0.41
2:B:23:CYS:HB2	2:B:35:TRP:CH2	2.56	0.41
2:B:179:LEU:HG	2:B:181:LEU:CD1	2.50	0.41
3:E:390:LEU:HD22	3:E:390:LEU:N	2.36	0.41
1:A:2:VAL:HA	1:A:25:SER:O	2.21	0.40
3:E:364:ASP:OD1	3:E:367:VAL:HG13	2.20	0.40
1:A:139:GLY:HA2	1:A:154:TRP:CZ2	2.57	0.40
3:E:335:LEU:HD12	3:E:335:LEU:N	2.36	0.40
3:E:416:GLY:O	3:E:420:ASP: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	210/229 (92%)	198 (94%)	12 (6%)	0	100	100
2	B	214/215 (100%)	201 (94%)	12 (6%)	1 (0%)	29	67
3	E	183/187 (98%)	169 (92%)	14 (8%)	0	100	100
All	All	607/631 (96%)	568 (94%)	38 (6%)	1 (0%)	47	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	138	ASN

5.3.2 Protein sidechains [i](#)

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	180/194 (93%)	180 (100%)	0	100	100
2	B	187/186 (100%)	186 (100%)	1 (0%)	88	95
3	E	161/163 (99%)	159 (99%)	2 (1%)	71	88
All	All	528/543 (97%)	525 (99%)	3 (1%)	86	94

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	74	THR
3	E	346	ARG

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Mol	Chain	Res	Type
3	E	387	LEU

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

Mol	Chain	Res	Type
3	E	388	ASN

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	E	601	3	14,14,15	0.45	0	17,19,21	0.62	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '–' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	601	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	601	NAG	C1-O5-C5	2.07	114.99	112.19

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 [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	213/229 (93%)	-0.14	0 100 100	46, 67, 96, 118	0
2	B	215/215 (100%)	-0.20	1 (0%) 91 86	46, 68, 97, 139	0
3	E	184/187 (98%)	0.04	1 (0%) 91 86	46, 73, 140, 165	0
All	All	612/631 (96%)	-0.11	2 (0%) 94 92	46, 69, 116, 165	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	214	CYS	9.0
3	E	334	ASN	3.5

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	NAG	E	601	14/15	0.83	0.13	73,117,126,127	0

6.5 Other polymers [i](#)

There are no such residues in this entry.