



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2022 – 12:03 PM EDT

PDB ID : 7TA7
Title : Co-crystal structure of SARS-CoV-2 Mpro C145A with substrate peptide 10/11
Authors : Shaqra, A.M.; Schiffer, C.A.
Deposited on : 2021-12-20
Resolution : 2.28 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 : 2.28.1
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) : 2.28.1

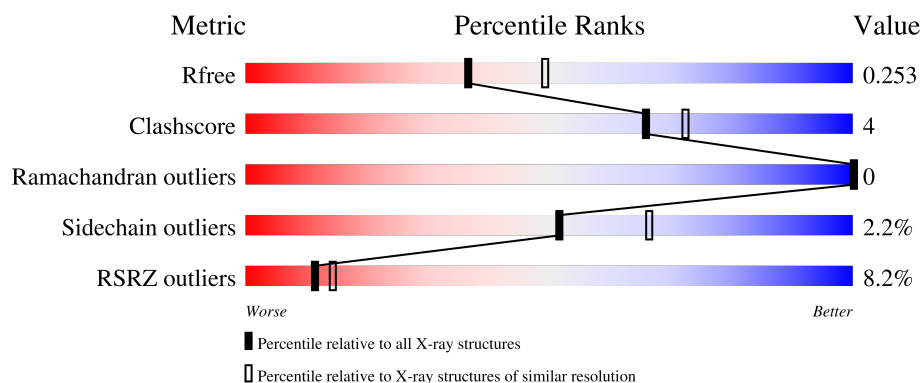
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	
1	B	306	
2	C	11	
2	D	11	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4974 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	305	Total	C	N	O	S	0	0	0
			2304	1455	395	433	21			
1	B	305	Total	C	N	O	S	0	0	0
			2290	1448	387	434	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	145	ALA	CYS	engineered mutation	UNP P0DTD1
B	145	ALA	CYS	engineered mutation	UNP P0DTD1

- Molecule 2 is a protein called Nonstructural protein 10/11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	11	Total	C	N	O	S	0	0	0
			71	43	12	15	1			
2	D	10	Total	C	N	O	S	0	0	0
			63	39	11	12	1			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

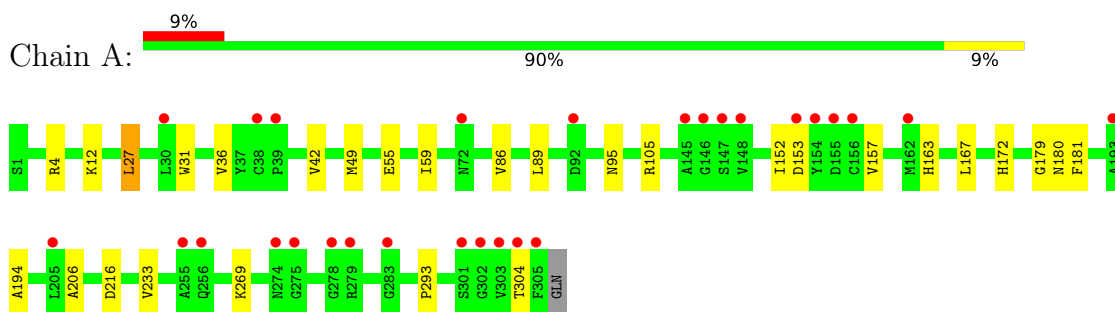
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	123	Total	O	0	0
			123	123		
4	B	104	Total	O	0	0
			104	104		
4	C	5	Total	O	0	0
			5	5		
4	D	2	Total	O	0	0
			2	2		

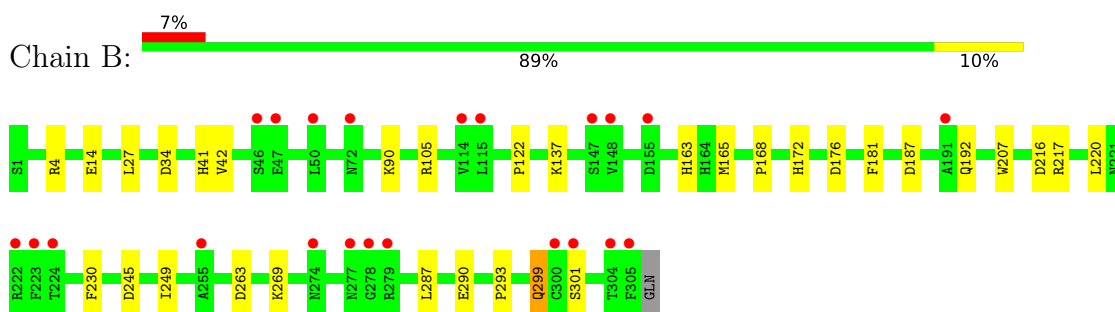
3 Residue-property plots [i](#)

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.

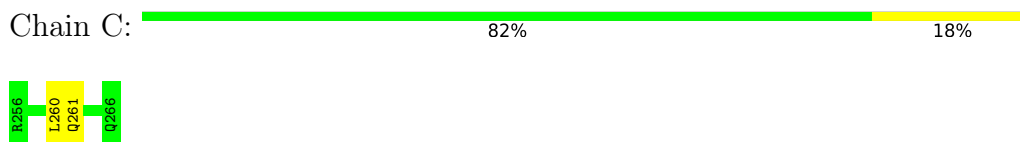
- Molecule 1: 3C-like proteinase



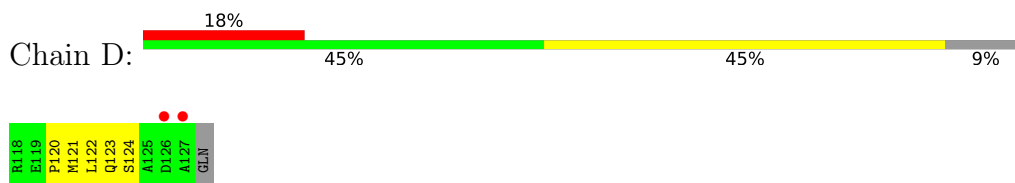
- Molecule 1: 3C-like proteinase



- Molecule 2: Nonstructural protein 10/11



- Molecule 2: Nonstructural protein 10/11



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.66Å 96.40Å 67.40Å 90.00° 103.16° 90.00°	Depositor
Resolution (Å)	23.40 – 2.28 23.40 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.5 (23.40-2.28) 99.5 (23.40-2.28)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.28Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.205 , 0.255 0.205 , 0.253	Depositor DCC
R_{free} test set	1319 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.8	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	4974	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.83% 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: GOL

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	0.25	0/2354	0.46	0/3206
1	B	0.25	0/2340	0.45	0/3189
2	C	0.25	0/71	0.43	0/96
2	D	0.25	0/63	0.44	0/85
All	All	0.25	0/4828	0.45	0/6576

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	2304	0	2209	17	0
1	B	2290	0	2182	22	0
2	C	71	0	59	2	0
2	D	63	0	55	6	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	123	0	0	1	0
4	B	104	0	0	1	0
4	C	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	2	0	0	0	0
All	All	4974	0	4521	37	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 4.

All (37) 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:167:LEU:HD13	1:A:194:ALA:HB2	1.84	0.60
1:A:4:ARG:NH2	1:B:290:GLU:OE1	2.37	0.58
1:B:14:GLU:HG2	1:B:122:PRO:HG2	1.86	0.58
1:A:12:LYS:NZ	4:A:504:HOH:O	2.36	0.57
1:B:217:ARG:HB2	1:B:220:LEU:HD12	1.87	0.57
1:B:163:HIS:NE2	2:D:123:GLN:OE1	2.36	0.56
1:B:4:ARG:O	1:B:299:GLN:NE2	2.35	0.56
1:B:27:LEU:HD12	1:B:42:VAL:HB	1.89	0.55
1:B:41:HIS:HE1	2:D:124:SER:HB3	1.70	0.54
1:A:163:HIS:NE2	2:C:261:GLN:OE1	2.33	0.53
1:A:4:ARG:NH1	1:B:137:LYS:O	2.39	0.53
1:A:86:VAL:HG13	1:A:179:GLY:HA2	1.90	0.52
1:B:34:ASP:OD2	1:B:90:LYS:NZ	2.42	0.52
1:A:49:MET:HG2	2:C:260:LEU:HD12	1.93	0.50
1:B:105:ARG:NH1	1:B:176:ASP:OD2	2.41	0.50
1:B:41:HIS:CE1	2:D:124:SER:HB3	2.47	0.49
1:A:152:ILE:HD13	1:A:157:VAL:HG22	1.94	0.49
1:A:163:HIS:HE1	1:A:172:HIS:HB3	1.77	0.49
1:A:206:ALA:HB2	1:A:293:PRO:HG3	1.97	0.47
1:B:245:ASP:O	1:B:249:ILE:HG12	2.15	0.46
1:B:165:MET:HB3	2:D:122:LEU:HD23	1.97	0.46
1:B:230:PHE:HA	1:B:269:LYS:HD2	1.97	0.46
1:B:269:LYS:NZ	4:B:509:HOH:O	2.48	0.46
1:A:163:HIS:CE1	1:A:172:HIS:HB3	2.51	0.45
1:A:105:ARG:NH2	1:A:180:ASN:O	2.50	0.45
1:A:233:VAL:HG11	1:A:269:LYS:HG3	1.99	0.44
1:B:168:PRO:HD3	2:D:120:PRO:HG3	2.00	0.44
1:B:163:HIS:HE1	1:B:172:HIS:HB3	1.82	0.44
1:B:187:ASP:OD1	1:B:187:ASP:N	2.47	0.43
1:A:31:TRP:CD2	1:A:95:ASN:HB2	2.54	0.42
1:A:27:LEU:HD21	1:A:42:VAL:HB	2.02	0.42
1:A:55:GLU:O	1:A:59:ILE:HG13	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:GLN:HB2	2:D:120:PRO:HG2	2.02	0.41
1:B:207:TRP:CZ3	1:B:287:LEU:HA	2.56	0.41
1:B:27:LEU:HD23	1:B:27:LEU:HA	1.85	0.40
1:B:249:ILE:HG22	1:B:293:PRO:HG2	2.03	0.40
1:A:36:VAL:HB	1:A:89:LEU:HB2	2.03	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	303/306 (99%)	291 (96%)	12 (4%)	0	100	100
1	B	303/306 (99%)	292 (96%)	11 (4%)	0	100	100
2	C	9/11 (82%)	8 (89%)	1 (11%)	0	100	100
2	D	8/11 (73%)	8 (100%)	0	0	100	100
All	All	623/634 (98%)	599 (96%)	24 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	246/262 (94%)	241 (98%)	5 (2%)	55	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	244/262 (93%)	239 (98%)	5 (2%)	55	70
2	C	6/9 (67%)	6 (100%)	0	100	100
2	D	5/9 (56%)	4 (80%)	1 (20%)	1	1
All	All	501/542 (92%)	490 (98%)	11 (2%)	52	66

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	153	ASP
1	A	181	PHE
1	A	216	ASP
1	A	304	THR
1	B	181	PHE
1	B	216	ASP
1	B	263	ASP
1	B	299	GLN
1	B	301	SER
2	D	121	MET

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

Mol	Chain	Res	Type
1	A	64	HIS
1	B	41	HIS
1	B	274	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 ligands are 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	$\# Z > 2$
3	GOL	B	401	-	5,5,5	0.89	0	5,5,5	1.00	0
3	GOL	A	401	-	5,5,5	0.89	0	5,5,5	1.01	0

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
3	GOL	B	401	-	-	2/4/4/4	-
3	GOL	A	401	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	GOL	O1-C1-C2-O2
3	B	401	GOL	O1-C1-C2-C3

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	305/306 (99%)	0.50	28 (9%) 9 11	20, 31, 46, 66	0
1	B	305/306 (99%)	0.46	22 (7%) 15 19	21, 31, 51, 64	0
2	C	11/11 (100%)	0.93	0 100 100	25, 33, 46, 46	0
2	D	10/11 (90%)	1.59	2 (20%) 1 1	31, 42, 49, 54	0
All	All	631/634 (99%)	0.51	52 (8%) 11 14	20, 31, 50, 66	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	305	PHE	6.8
1	A	304	THR	6.3
1	A	303	VAL	5.8
2	D	127	ALA	5.6
1	A	301	SER	5.3
1	B	50	LEU	4.4
1	A	274	ASN	4.3
1	A	302	GLY	4.3
1	B	277	ASN	4.0
1	B	278	GLY	3.7
1	B	223	PHE	3.7
1	A	155	ASP	3.7
1	B	47	GLU	3.6
2	D	126	ASP	3.6
1	B	274	ASN	3.4
1	B	301	SER	3.3
1	B	222	ARG	3.3
1	A	279	ARG	3.2
1	B	300	CYS	3.2
1	B	304	THR	3.1
1	A	72	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	38	CYS	3.0
1	B	305	PHE	2.9
1	B	46	SER	2.9
1	A	153	ASP	2.8
1	B	191	ALA	2.8
1	A	278	GLY	2.6
1	A	147	SER	2.6
1	A	156	CYS	2.6
1	A	162	MET	2.5
1	B	155	ASP	2.5
1	A	205	LEU	2.5
1	A	193	ALA	2.4
1	A	30	LEU	2.4
1	A	154	TYR	2.4
1	A	39	PRO	2.4
1	A	148	VAL	2.4
1	B	279	ARG	2.3
1	A	283	GLY	2.3
1	A	145	ALA	2.3
1	A	255	ALA	2.3
1	A	275	GLY	2.3
1	B	224	THR	2.3
1	B	147	SER	2.2
1	B	114	VAL	2.2
1	A	146	GLY	2.2
1	B	255	ALA	2.1
1	B	115	LEU	2.1
1	B	148	VAL	2.1
1	B	72	ASN	2.1
1	A	92	ASP	2.0
1	A	256	GLN	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(\AA^2)	Q<0.9
3	GOL	B	401	6/6	0.79	0.25	41,44,47,51	0
3	GOL	A	401	6/6	0.89	0.21	37,40,42,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.