



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 01:50 AM UTC

PDB ID : 8BH5 / pdb_00008bh5
Title : SARS-CoV-2 BA.2.12.1 RBD in complex with Beta-27 Fab and C1 nanobody
Authors : Huo, J.; Zhou, D.; Ren, J.; Stuart, D.I.
Deposited on : 2022-10-29
Resolution : 2.38 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

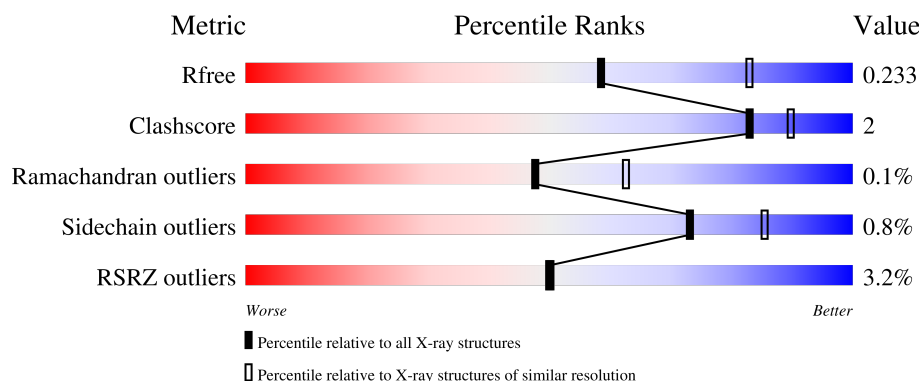
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	H	222	3% 92% 5%
2	L	214	% 93% 7%
3	E	202	5% 87% 6% 7%
4	C	131	3% 85% 10% 5%
5	A	2	100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 5982 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 Beta-27 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	218	Total	C	N	O	S	0	0	0
			1617	1017	274	318	8			

- Molecule 2 is a protein called Beta-27 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	1	0
			1622	1010	275	332	5			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	187	Total	C	N	O	S	0	3	0
			1519	980	256	275	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	327	HIS	-	expression tag	UNP P0DTC2
E	328	HIS	-	expression tag	UNP P0DTC2
E	329	HIS	-	expression tag	UNP P0DTC2
E	330	HIS	-	expression tag	UNP P0DTC2
E	331	HIS	-	expression tag	UNP P0DTC2
E	332	HIS	-	expression tag	UNP P0DTC2
E	339	ASP	GLY	variant	UNP P0DTC2
E	371	PHE	SER	variant	UNP P0DTC2
E	373	PRO	SER	engineered mutation	UNP P0DTC2
E	375	PHE	SER	variant	UNP P0DTC2
E	376	ALA	THR	variant	UNP P0DTC2
E	405	ASN	ASP	variant	UNP P0DTC2
E	408	SER	ARG	variant	UNP P0DTC2
E	417	ASN	LYS	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
E	440	LYS	ASN	variant	UNP P0DTC2
E	452	GLN	LEU	variant	UNP P0DTC2
E	477	ASN	SER	variant	UNP P0DTC2
E	478	LYS	THR	variant	UNP P0DTC2
E	484	ALA	GLU	variant	UNP P0DTC2
E	493	ARG	GLN	variant	UNP P0DTC2
E	498	ARG	GLN	variant	UNP P0DTC2
E	501	TYR	ASN	variant	UNP P0DTC2
E	505	HIS	TYR	variant	UNP P0DTC2
E	527	LYS	PRO	engineered mutation	UNP P0DTC2

- Molecule 4 is a protein called Nanobody C1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	124	Total	C	N	O	S	0	0	0
			965	605	167	189	4			

- Molecule 5 is an oligosaccharide called alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	A	2	Total	C	N	O	0	0	0
			24	14	1	9			

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	H	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	H	1	Total	C	O	0	0
			6	3	3		
6	L	1	Total	C	O	0	0
			6	3	3		
6	L	1	Total	C	O	0	0
			6	3	3		
6	L	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	E	1	Total	C	O	0	0
			6	3	3		
6	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	H	1	Total	O	P	0	0
			5	4	1		

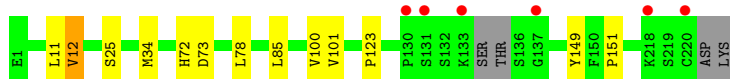
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	H	54	Total	O	0	0
			54	54		
8	L	55	Total	O	0	0
			55	55		
8	E	38	Total	O	0	0
			38	38		
8	C	11	Total	O	0	0
			11	11		

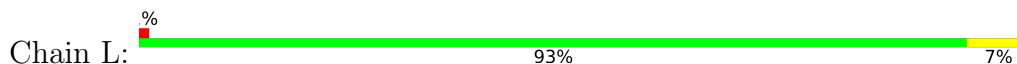
3 Residue-property plots [i](#)

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.

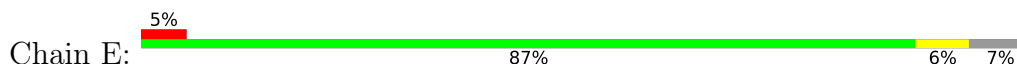
- Molecule 1: Beta-27 heavy chain



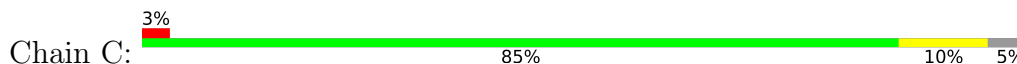
- Molecule 2: Beta-27 light chain



- Molecule 3: Spike protein S1



- Molecule 4: Nanobody C1



- Molecule 5: alpha-L-fucopyranose-(1-6)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	186.85Å 99.99Å 56.49Å 90.00° 104.11° 90.00°	Depositor
Resolution (Å)	54.78 – 2.38 54.78 – 2.38	Depositor EDS
% Data completeness (in resolution range)	91.3 (54.78-2.38) 91.5 (54.78-2.38)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 2.37Å)	Xtriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.186 , 0.233 0.186 , 0.233	Depositor DCC
R_{free} test set	1921 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 49.3	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	0.95	EDS
Total number of atoms	5982	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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: FUC, GOL, PO4, 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	H	0.10	0/1652	0.30	0/2249
2	L	0.08	0/1659	0.28	0/2250
3	E	0.08	0/1572	0.25	0/2134
4	C	0.08	0/990	0.25	0/1347
All	All	0.09	0/5873	0.27	0/7980

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	H	1617	0	1592	7	0
2	L	1622	0	1573	8	0
3	E	1519	0	1446	7	0
4	C	965	0	906	9	0
5	A	24	0	22	0	0
6	C	6	0	8	1	0
6	E	24	0	32	1	0
6	H	24	0	32	2	0
6	L	18	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	H	5	0	0	0	0
8	C	11	0	0	0	0
8	E	38	0	0	1	0
8	H	54	0	0	0	0
8	L	55	0	0	1	0
All	All	5982	0	5635	28	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 2.

All (28) 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)
3:E:457:ARG:HH12	6:E:701:GOL:H12	1.65	0.62
1:H:11:LEU:HD11	1:H:151:PRO:HG3	1.82	0.61
4:C:34:ILE:HG13	4:C:79:VAL:HG21	1.83	0.59
1:H:123:PRO:HB3	1:H:149:TYR:HB3	1.85	0.58
2:L:149:LYS:NZ	2:L:195:GLU:OE1	2.38	0.57
2:L:42:GLY:H	6:L:403:GOL:H2	1.71	0.55
4:C:91:THR:HG23	4:C:121:THR:HA	1.89	0.54
2:L:46:ARG:NH2	8:L:502:HOH:O	2.39	0.54
2:L:185:ASP:HA	2:L:188:LYS:HD3	1.89	0.54
4:C:55:ASP:OD1	4:C:55:ASP:N	2.43	0.51
2:L:108:ARG:NH1	2:L:109:THR:O	2.44	0.50
1:H:12:VAL:HG11	1:H:85:LEU:HD12	1.95	0.49
1:H:101:VAL:HG21	3:E:493:ARG:HD2	1.94	0.48
3:E:396:TYR:HB2	3:E:514[A]:SER:OG	2.14	0.48
3:E:378:LYS:HD3	4:C:105:ASP:HB2	1.96	0.48
2:L:55:ARG:HD2	2:L:60:PRO:O	2.15	0.47
3:E:403:ARG:NH2	8:E:801:HOH:O	2.49	0.46
4:C:107:TRP:CE3	6:C:201:GOL:H31	2.51	0.46
1:H:34:MET:HB3	1:H:78:LEU:HD22	1.97	0.45
1:H:73:ASP:H	6:H:302:GOL:H31	1.83	0.44
1:H:72:HIS:HA	6:H:302:GOL:H2	1.99	0.44
2:L:136:LEU:HB2	2:L:175:LEU:HB3	2.00	0.44
3:E:379:CYS:SG	3:E:384:PRO:HG3	2.58	0.43
4:C:40:ALA:HB3	4:C:43:LYS:HB2	2.01	0.42
4:C:88:PRO:HA	4:C:122:VAL:HB	2.01	0.42
4:C:11:LEU:HD13	4:C:121:THR:HB	2.02	0.42
3:E:401:VAL:HG22	3:E:509:ARG:HG2	2.02	0.41
2:L:27:GLN:HE21	4:C:44:GLU:CD	2.29	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	H	214/222 (96%)	209 (98%)	4 (2%)	1 (0%)	24	34
2	L	212/214 (99%)	207 (98%)	5 (2%)	0	100	100
3	E	186/202 (92%)	179 (96%)	7 (4%)	0	100	100
4	C	122/131 (93%)	118 (97%)	4 (3%)	0	100	100
All	All	734/769 (95%)	713 (97%)	20 (3%)	1 (0%)	48	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	100	VAL

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	H	182/187 (97%)	180 (99%)	2 (1%)	65	81
2	L	184/184 (100%)	183 (100%)	1 (0%)	81	90
3	E	165/174 (95%)	163 (99%)	2 (1%)	63	79
4	C	103/110 (94%)	103 (100%)	0	100	100
All	All	634/655 (97%)	629 (99%)	5 (1%)	73	85

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	12	VAL
1	H	25	SER
2	L	205	VAL
3	E	392	PHE
3	E	424	LYS

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

Mol	Chain	Res	Type
2	L	160	GLN
2	L	189	HIS
3	E	417	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 ⓘ

2 monosaccharides 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	$\# Z > 2$
5	NAG	A	1	3,5	14,14,15	0.35	0	17,19,21	0.54	0
5	FUC	A	2	5	10,10,11	0.83	0	14,14,16	0.76	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
5	NAG	A	1	3,5	-	2/6/23/26	0/1/1/1
5	FUC	A	2	5	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

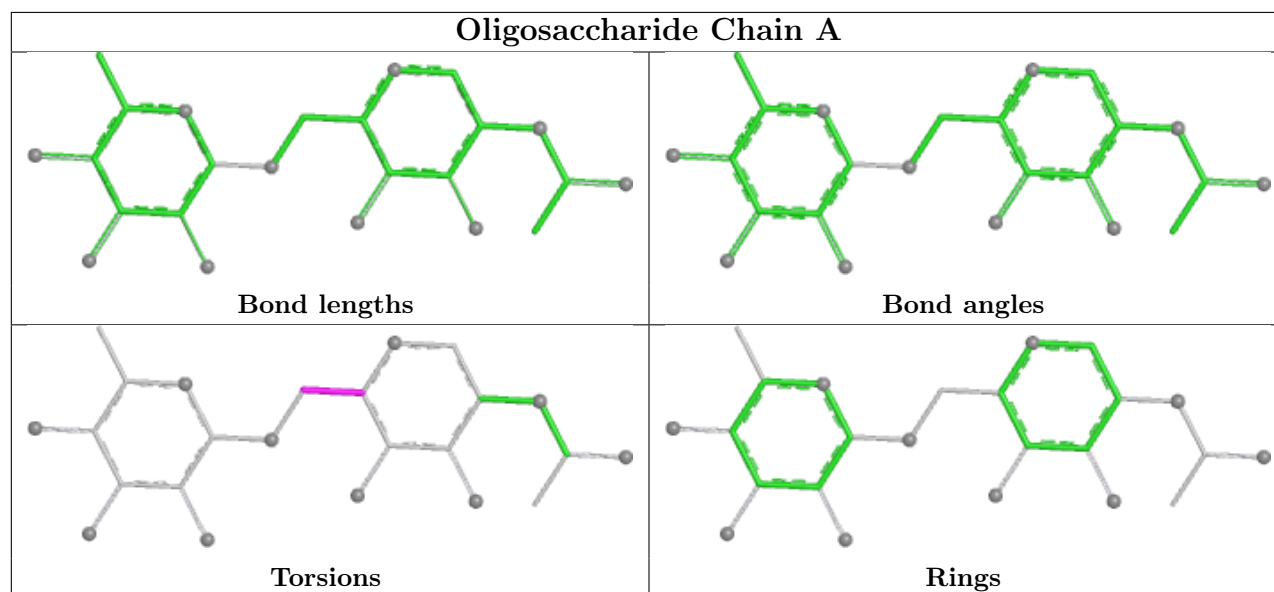
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1	NAG	O5-C5-C6-O6
5	A	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.



5.6 Ligand geometry [i](#)

13 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	$\# Z > 2$
6	GOL	L	401	-	5,5,5	0.99	0	5,5,5	0.94	0
6	GOL	H	304	-	5,5,5	0.94	0	5,5,5	1.06	0
6	GOL	C	201	-	5,5,5	1.01	0	5,5,5	1.00	0
6	GOL	E	703	-	5,5,5	0.95	0	5,5,5	1.08	0
6	GOL	H	301	-	5,5,5	0.96	0	5,5,5	1.06	0
7	PO4	H	305	-	4,4,4	0.95	0	6,6,6	0.46	0
6	GOL	H	303	-	5,5,5	0.92	0	5,5,5	1.11	0
6	GOL	E	702	-	5,5,5	0.91	0	5,5,5	1.09	0
6	GOL	L	402	-	5,5,5	0.95	0	5,5,5	1.05	0
6	GOL	E	704	-	5,5,5	1.06	0	5,5,5	0.93	0
6	GOL	H	302	-	5,5,5	0.92	0	5,5,5	1.08	0
6	GOL	L	403	-	5,5,5	0.96	0	5,5,5	1.07	0
6	GOL	E	701	-	5,5,5	0.93	0	5,5,5	1.08	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
6	GOL	L	401	-	-	2/4/4/4	-
6	GOL	H	304	-	-	0/4/4/4	-
6	GOL	C	201	-	-	1/4/4/4	-
6	GOL	E	703	-	-	2/4/4/4	-
6	GOL	H	301	-	-	2/4/4/4	-
6	GOL	H	303	-	-	0/4/4/4	-
6	GOL	E	702	-	-	1/4/4/4	-
6	GOL	L	402	-	-	1/4/4/4	-
6	GOL	E	704	-	-	1/4/4/4	-
6	GOL	H	302	-	-	0/4/4/4	-
6	GOL	L	403	-	-	0/4/4/4	-
6	GOL	E	701	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	401	GOL	O1-C1-C2-C3
6	E	701	GOL	C1-C2-C3-O3
6	E	703	GOL	C1-C2-C3-O3
6	E	701	GOL	O2-C2-C3-O3
6	C	201	GOL	O1-C1-C2-C3
6	L	401	GOL	O1-C1-C2-O2
6	E	703	GOL	O2-C2-C3-O3
6	E	702	GOL	O2-C2-C3-O3
6	E	704	GOL	O2-C2-C3-O3
6	E	701	GOL	O1-C1-C2-C3
6	L	402	GOL	C1-C2-C3-O3
6	H	301	GOL	O2-C2-C3-O3
6	H	301	GOL	C1-C2-C3-O3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	201	GOL	1	0
6	H	302	GOL	2	0
6	L	403	GOL	1	0
6	E	701	GOL	1	0

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	H	218/222 (98%)	-0.01	6 (2%)	55 54	38, 46, 75, 127	0
2	L	213/214 (99%)	0.05	3 (1%)	73 72	29, 52, 73, 128	1 (0%)
3	E	187/202 (92%)	0.34	11 (5%)	28 27	26, 51, 115, 142	3 (1%)
4	C	124/131 (94%)	0.49	4 (3%)	50 50	46, 67, 97, 115	0
All	All	742/769 (96%)	0.18	24 (3%)	50 50	26, 52, 102, 142	4 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	1	ASP	3.8
3	E	517	LEU	3.7
3	E	390	LEU	3.4
3	E	333	THR	3.4
4	C	124	SER	3.4
3	E	525	CYS	2.9
1	H	130	PRO	2.9
1	H	133	LYS	2.9
3	E	393	THR	2.9
1	H	131	SER	2.9
2	L	212	GLY	2.8
3	E	392	PHE	2.8
1	H	137	GLY	2.7
1	H	220	CYS	2.6
3	E	335	LEU	2.4
3	E	367	VAL	2.4
3	E	391	CYS	2.3
3	E	387	LEU	2.3
1	H	218	LYS	2.2
4	C	123	SER	2.2
2	L	92	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
3	E	360	ASN	2.1
4	C	1	GLN	2.0
4	C	43	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

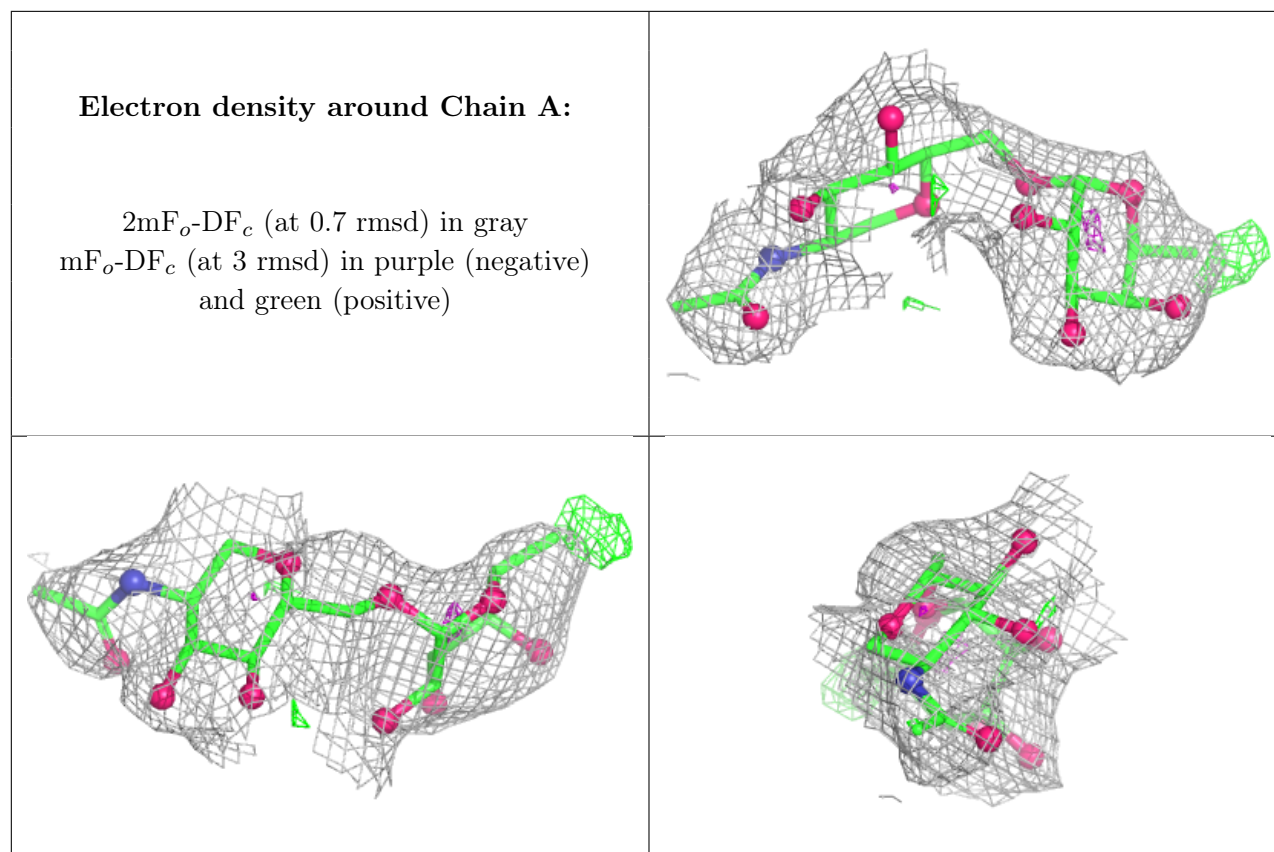
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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
5	NAG	A	1	14/15	-	-	82,95,102,103	0
5	FUC	A	2	10/11	-	-	84,99,103,103	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



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
6	GOL	E	704	6/6	0.69	0.20	60,65,70,70	0
6	GOL	H	302	6/6	0.78	0.15	68,73,75,78	0
6	GOL	E	703	6/6	0.80	0.19	52,65,72,73	0
7	PO4	H	305	5/5	0.82	0.11	74,76,90,97	0
6	GOL	L	401	6/6	0.83	0.14	63,73,76,78	0
6	GOL	E	701	6/6	0.87	0.13	55,63,64,68	0
6	GOL	H	303	6/6	0.87	0.15	52,62,65,67	0
6	GOL	H	304	6/6	0.88	0.14	54,59,62,62	0
6	GOL	C	201	6/6	0.88	0.17	51,58,68,73	0
6	GOL	L	403	6/6	0.88	0.14	56,63,66,67	0
6	GOL	L	402	6/6	0.90	0.14	53,57,61,63	0
6	GOL	E	702	6/6	0.91	0.15	71,75,82,90	0
6	GOL	H	301	6/6	0.95	0.10	46,53,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.