



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 12:32 PM UTC

PDB ID : 7M6D / pdb_00007m6d
Title : Structure of the SARS-CoV-2 RBD in complex with neutralizing antibodies BG4-25 and CR3022
Authors : Barnes, C.O.; Bjorkman, P.J.
Deposited on : 2021-03-25
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

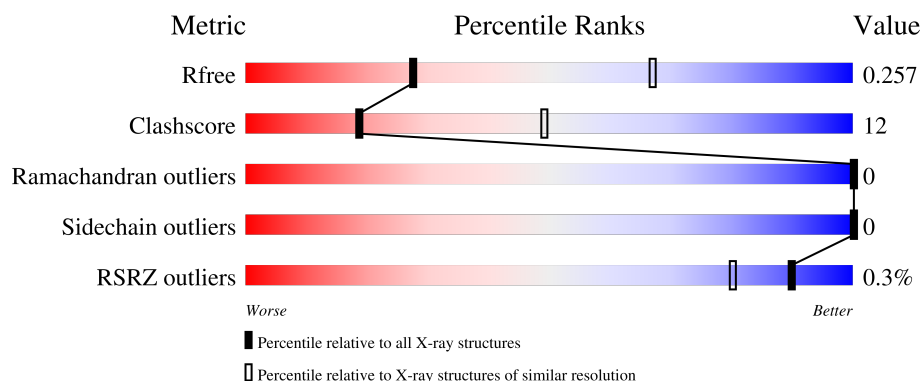
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

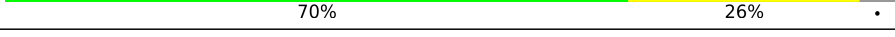
The reported resolution of this entry is 3.10 Å.

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.



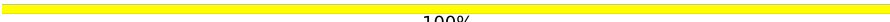
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	225	 75% 24% .
2	B	221	 72% 28%
3	C	212	 75% 17% 8%
4	H	224	 70% 26% .
5	L	215	 82% 18%

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Mol	Chain	Length	Quality of chain
6	D	5	 100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8221 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 CR3022 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1646	1043	268	326	9			

- Molecule 2 is a protein called CR3022 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	221	Total	C	N	O	S	0	0	0
			1716	1076	284	351	5			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	196	Total	C	N	O	S	0	0	0
			1552	995	259	290	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	534	HIS	-	expression tag	UNP P0DTC2
C	535	HIS	-	expression tag	UNP P0DTC2
C	536	HIS	-	expression tag	UNP P0DTC2
C	537	HIS	-	expression tag	UNP P0DTC2
C	538	HIS	-	expression tag	UNP P0DTC2
C	539	HIS	-	expression tag	UNP P0DTC2

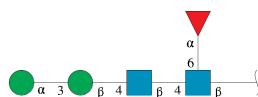
- Molecule 4 is a protein called BG4-25 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	214	Total	C	N	O	S	0	0	0
			1596	1003	270	315	8			

- Molecule 5 is a protein called BG4-25 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	L	215	Total	C	N	O	S	0	0	0
			1651	1034	278	333	6			

- Molecule 6 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acet amido-2-deoxy-beta-D-glucopyranose.

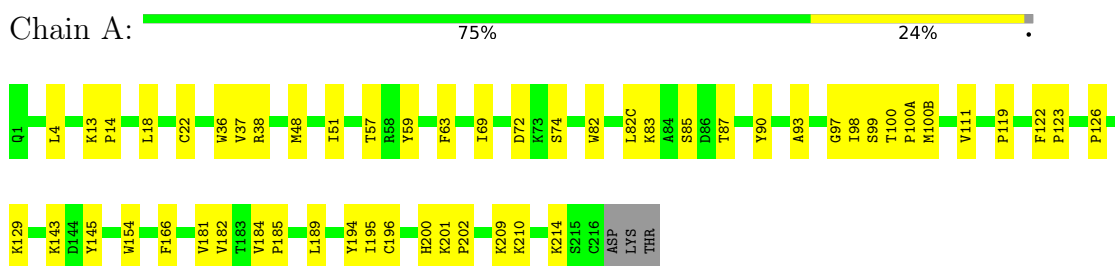


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	D	5	Total	C	N	O	0	0	0
			60	34	2	24			

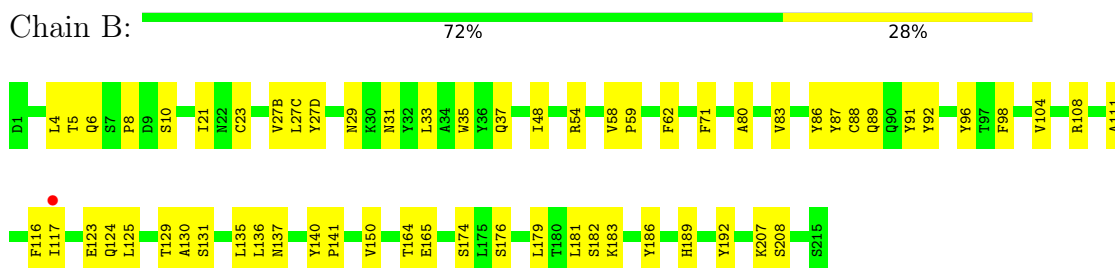
3 Residue-property plots

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.

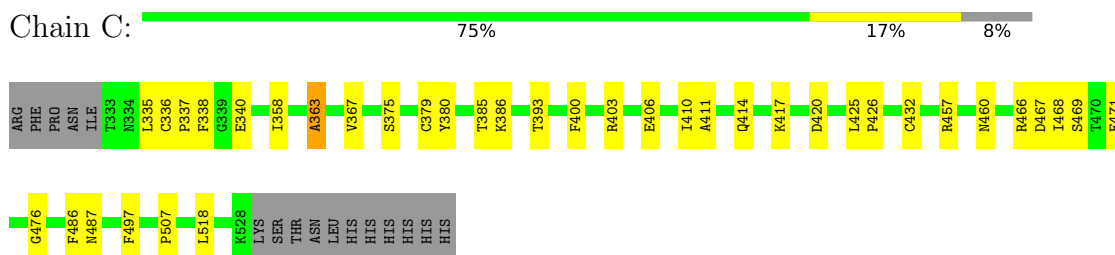
• Molecule 1: CR3022 Fab Heavy Chain



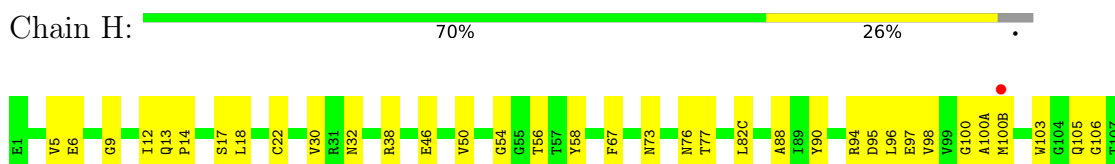
• Molecule 2: CR3022 Fab Light Chain



• Molecule 3: Spike protein S1

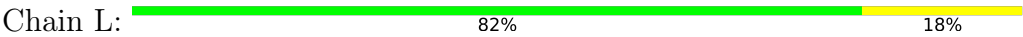


• Molecule 4: BG4-25 Fab Heavy Chain





● Molecule 5: BG4-25 Fab Light Chain



● Molecule 6: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.02Å 104.32Å 268.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.79 – 3.10 38.79 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (38.79-3.10) 98.0 (38.79-3.10)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122	Depositor
R, R_{free}	0.218 , 0.259 0.217 , 0.257	Depositor DCC
R_{free} test set	2000 reflections (6.14%)	wwPDB-VP
Wilson B-factor (Å ²)	74.5	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8221	wwPDB-VP
Average B, all atoms (Å ²)	83.0	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, BMA, MAN, FUC

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	0.46	0/1688	0.84	3/2299 (0.1%)
2	B	0.43	0/1754	0.82	1/2383 (0.0%)
3	C	0.66	0/1596	1.08	3/2172 (0.1%)
4	H	0.60	0/1629	0.92	1/2220 (0.0%)
5	L	0.60	0/1688	1.01	3/2292 (0.1%)
All	All	0.56	0/8355	0.94	11/11366 (0.1%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	L	80	PRO	CA-N-CD	-9.00	99.40	112.00
1	A	214	LYS	CA-C-N	6.96	129.60	120.28
1	A	214	LYS	C-N-CA	6.96	129.60	120.28
4	H	144	ASP	CB-CA-C	6.14	120.09	111.86
5	L	100	GLN	CA-CB-CG	-6.06	101.98	114.10

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	1646	0	1622	47	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1716	0	1658	61	0
3	C	1552	0	1472	33	0
4	H	1596	0	1580	45	0
5	L	1651	0	1604	27	0
6	D	60	0	52	0	0
All	All	8221	0	7988	193	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 12.

The worst 5 of 193 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:C:466:ARG:NH1	3:C:468:ILE:HD11	1.71	1.05
1:A:87:THR:HG22	1:A:111:VAL:H	1.27	0.99
4:H:9:GLY:HA2	4:H:18:LEU:HD21	1.45	0.95
2:B:54:ARG:HD2	2:B:58:VAL:HG23	1.48	0.94
2:B:181:LEU:HD11	2:B:186:TYR:HB2	1.52	0.91

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	220/225 (98%)	216 (98%)	4 (2%)	0	100	100
2	B	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
3	C	194/212 (92%)	187 (96%)	7 (4%)	0	100	100
4	H	210/224 (94%)	190 (90%)	20 (10%)	0	100	100
5	L	213/215 (99%)	203 (95%)	10 (5%)	0	100	100
All	All	1056/1097 (96%)	1002 (95%)	54 (5%)	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	187/190 (98%)	187 (100%)	0	100	100
2	B	196/196 (100%)	196 (100%)	0	100	100
3	C	169/185 (91%)	169 (100%)	0	100	100
4	H	180/188 (96%)	180 (100%)	0	100	100
5	L	186/186 (100%)	186 (100%)	0	100	100
All	All	918/945 (97%)	918 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	354	ASN
3	C	474	GLN
4	H	82(A)	ASN
3	C	493	GLN
2	B	160	GLN

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 ⓘ

5 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$
6	NAG	D	1	3,6	14,14,15	0.55	0	17,19,21	0.86	1 (5%)
6	NAG	D	2	6	14,14,15	0.75	1 (7%)	17,19,21	0.64	0
6	BMA	D	3	6	11,11,12	2.18	4 (36%)	15,15,17	1.25	2 (13%)
6	MAN	D	4	6	11,11,12	1.54	3 (27%)	15,15,17	1.53	3 (20%)
6	FUC	D	5	6	10,10,11	1.58	1 (10%)	14,14,16	1.40	2 (14%)

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	NAG	D	1	3,6	-	2/6/23/26	0/1/1/1
6	NAG	D	2	6	-	0/6/23/26	0/1/1/1
6	BMA	D	3	6	-	1/2/19/22	0/1/1/1
6	MAN	D	4	6	-	1/2/19/22	0/1/1/1
6	FUC	D	5	6	-	-	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	3	BMA	O3-C3	4.47	1.54	1.43
6	D	5	FUC	C1-C2	3.74	1.61	1.52
6	D	3	BMA	C2-C3	3.46	1.57	1.52
6	D	3	BMA	C1-C2	3.04	1.59	1.52
6	D	4	MAN	C2-C3	2.94	1.57	1.52

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	4	MAN	C1-O5-C5	4.27	117.91	112.19
6	D	5	FUC	C1-C2-C3	3.39	114.58	109.64
6	D	1	NAG	C1-O5-C5	2.98	116.17	112.19
6	D	3	BMA	O3-C3-C2	2.90	115.97	110.05
6	D	3	BMA	O3-C3-C4	2.78	116.92	110.38

There are no chirality outliers.

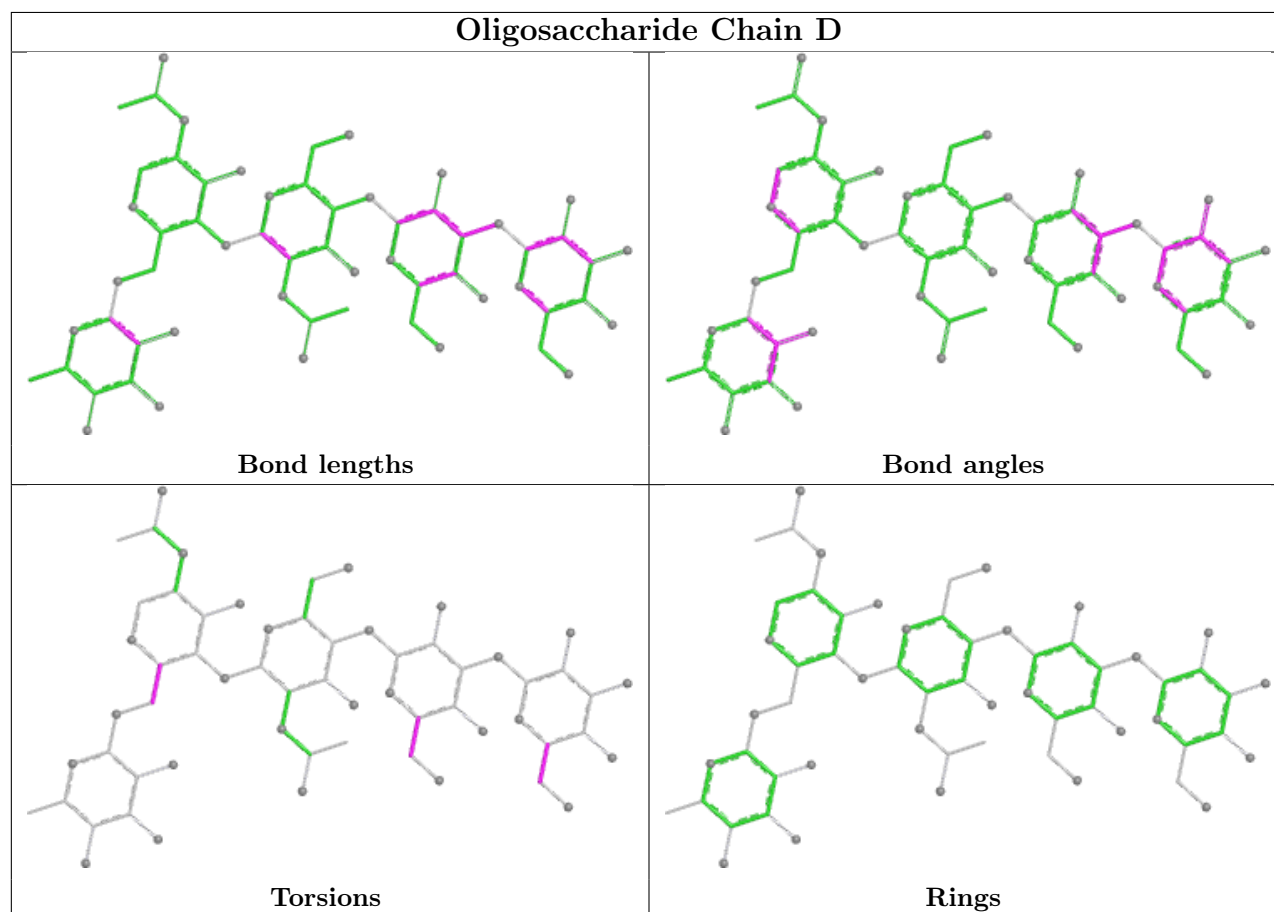
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	1	NAG	O5-C5-C6-O6
6	D	1	NAG	C4-C5-C6-O6
6	D	4	MAN	O5-C5-C6-O6
6	D	3	BMA	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

There are no ligands in this entry.

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 [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	222/225 (98%)	0.01	0 100 100	58, 87, 168, 193	0
2	B	221/221 (100%)	0.12	1 (0%) 87 73	75, 123, 159, 190	0
3	C	196/212 (92%)	-0.07	0 100 100	44, 60, 105, 131	0
4	H	214/224 (95%)	-0.27	1 (0%) 87 73	42, 61, 92, 107	0
5	L	215/215 (100%)	-0.19	1 (0%) 87 73	44, 64, 82, 120	0
All	All	1068/1097 (97%)	-0.08	3 (0%) 90 80	42, 73, 149, 193	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	117	ILE	2.6
5	L	98	PHE	2.3
4	H	100(B)	MET	2.2

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.

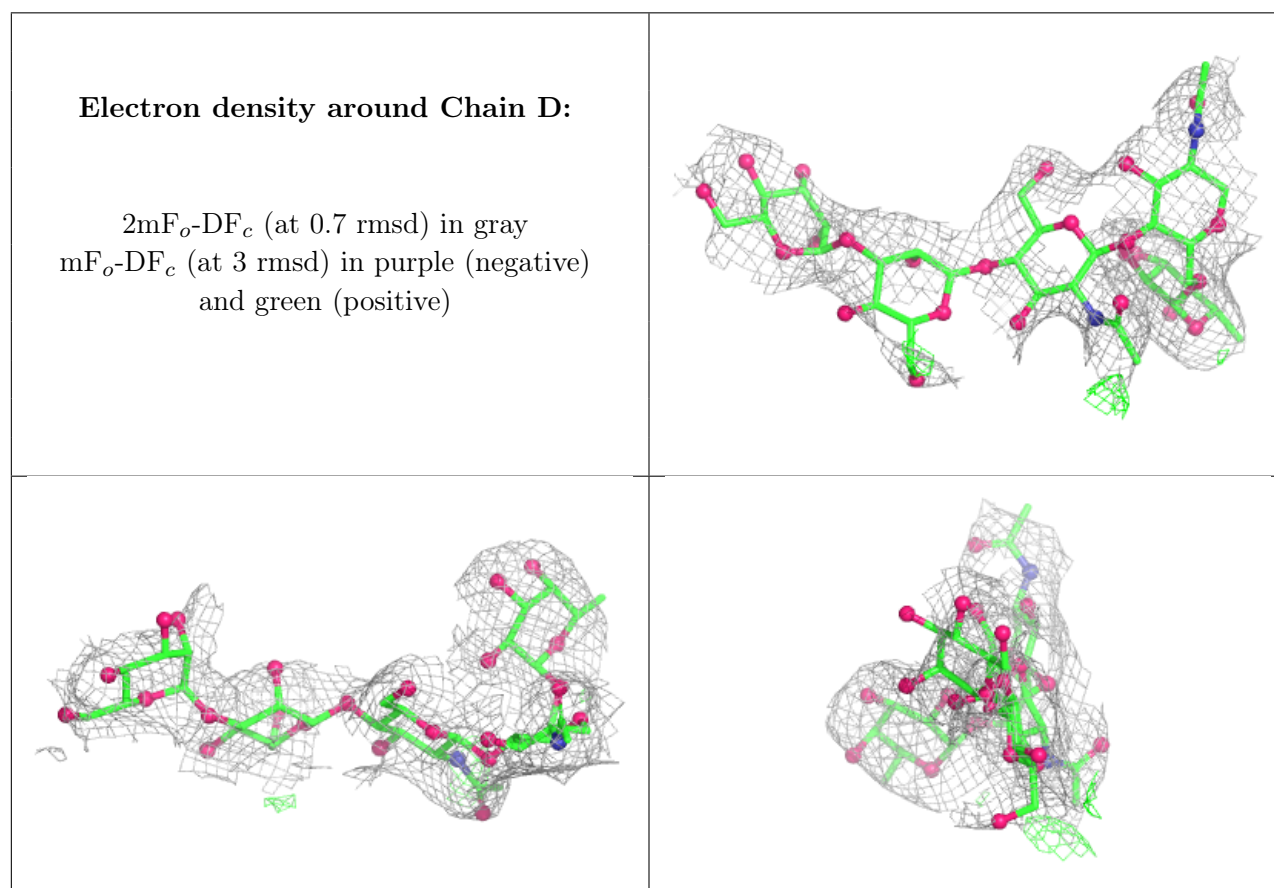
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	NAG	D	1	14/15	-	-	72,84,95,101	0
6	NAG	D	2	14/15	-	-	88,100,114,130	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	BMA	D	3	11/12	-	-	130,138,143,146	0
6	MAN	D	4	11/12	-	-	131,145,148,152	0
6	FUC	D	5	10/11	-	-	81,94,100,101	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.