



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:49 AM UTC

PDB ID : 7CM4 / pdb_00007cm4
Title : Crystal Structure of COVID-19 virus spike receptor-binding domain complexed with a neutralizing antibody CT-P59
Authors : Kim, Y.G.; Jeong, J.H.; Bae, J.S.; Lee, J.
Deposited on : 2020-07-24
Resolution : 2.71 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

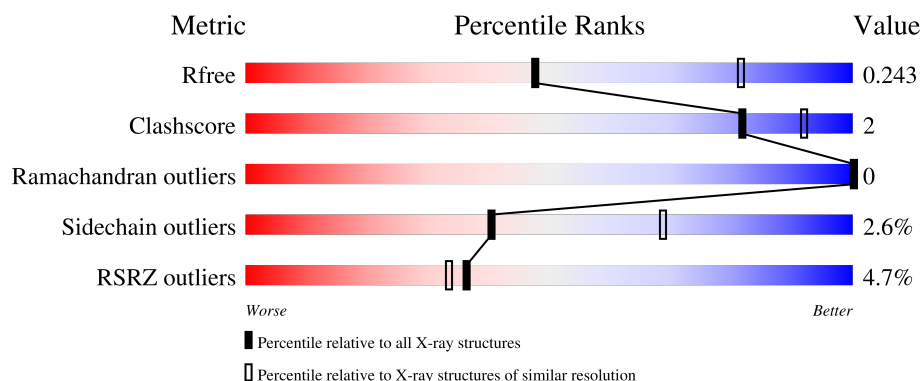
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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	4348 (2.74-2.70)
Clashscore	190562	4665 (2.74-2.70)
Ramachandran outliers	187476	4584 (2.74-2.70)
Sidechain outliers	187428	4585 (2.74-2.70)
RSRZ outliers	180081	4348 (2.74-2.70)

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	226	
2	H	458	
3	L	216	
4	B	5	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4985 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1551	995	258	290	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	HIS	-	expression tag	UNP P0DTC2
A	538	HIS	-	expression tag	UNP P0DTC2
A	539	HIS	-	expression tag	UNP P0DTC2
A	540	HIS	-	expression tag	UNP P0DTC2
A	541	HIS	-	expression tag	UNP P0DTC2
A	542	HIS	-	expression tag	UNP P0DTC2
A	543	HIS	-	expression tag	UNP P0DTC2
A	544	HIS	-	expression tag	UNP P0DTC2

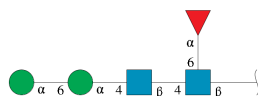
- Molecule 2 is a protein called IgG heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	225	Total	C	N	O	S	0	0	0
			1719	1093	285	333	8			

- Molecule 3 is a protein called IgG light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	214	Total	C	N	O	S	0	0	0
			1580	989	262	325	4			

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-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.

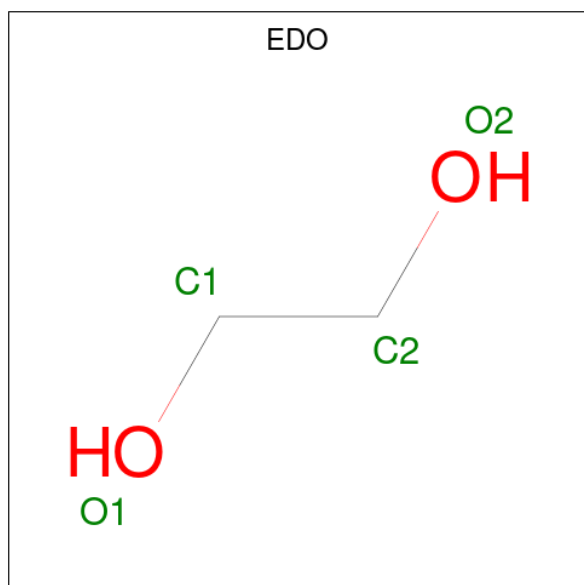


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 5 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Ni	0	0
			1	1		
5	L	1	Total	Ni	0	0
			1	1		

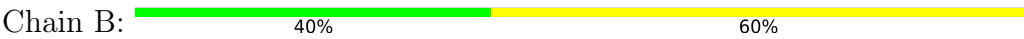
- Molecule 6 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	L	1	Total	C	O	0	0
			4	2	2		
6	L	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	14	Total 14	O 14	0	0
7	H	30	Total 30	O 30	0	0
7	L	21	Total 21	O 21	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	65.55Å 167.60Å 169.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.76 – 2.71 29.76 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.76-2.71) 99.8 (29.76-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.72Å)	Xtriage
Refinement program	Coot 0.8.9.1, PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.217 , 0.242 0.224 , 0.243	Depositor DCC
R_{free} test set	2006 reflections (7.78%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4985	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.67% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MAN, EDO, NI, NAG, 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	0.11	0/1595	0.30	0/2172
2	H	0.13	0/1762	0.37	0/2408
3	L	0.13	0/1618	0.33	0/2210
All	All	0.12	0/4975	0.33	0/6790

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

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	1551	0	1472	8	0
2	H	1719	0	1711	9	0
3	L	1580	0	1537	6	0
4	B	60	0	52	1	0
5	H	1	0	0	0	0
5	L	1	0	0	0	0
6	L	8	0	12	1	0
7	A	14	0	0	0	0
7	H	30	0	0	0	0
7	L	21	0	0	1	0
All	All	4985	0	4784	24	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 (24) 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:357:ARG:HD2	1:A:357:ARG:H	1.56	0.69
2:H:52:LEU:HD12	2:H:100:ILE:HD13	1.79	0.65
3:L:40:LEU:HD23	3:L:85:ALA:HB2	1.81	0.62
2:H:141:PRO:HG3	2:H:153:LEU:HB3	1.84	0.59
2:H:210:ILE:HG12	2:H:225:ARG:HG2	1.87	0.57
2:H:134:PRO:HB3	2:H:160:TYR:HB3	1.87	0.56
3:L:38:GLN:HB2	3:L:48:LEU:HD11	1.87	0.56
3:L:193:ARG:NH2	7:L:401:HOH:O	2.40	0.54
3:L:167:LYS:NZ	6:L:302:EDO:O1	2.41	0.52
2:H:2:ILE:HB	2:H:117:VAL:HG11	1.95	0.49
2:H:141:PRO:HD2	2:H:228:PRO:HA	1.96	0.48
1:A:414:GLN:O	1:A:424:LYS:NZ	2.48	0.47
3:L:136:LEU:HD12	3:L:182:LEU:HD23	1.97	0.47
2:H:229:LYS:H	2:H:229:LYS:HG3	1.46	0.46
2:H:69:LEU:HD21	2:H:84:MET:HE2	1.98	0.46
1:A:439:ASN:O	1:A:443:SER:OG	2.30	0.46
1:A:384:PRO:HA	1:A:387:LEU:HG	1.98	0.46
1:A:357:ARG:HD2	1:A:357:ARG:N	2.28	0.44
4:B:2:NAG:O7	4:B:2:NAG:H3	2.18	0.43
1:A:353:TRP:H	1:A:353:TRP:CD1	2.36	0.42
1:A:360:ASN:H	1:A:523:THR:HG22	1.85	0.42
3:L:26:SER:HA	3:L:30:GLY:HA3	2.03	0.41
1:A:401:VAL:HG22	1:A:509:ARG:HG2	2.01	0.41
2:H:92:THR:HG23	2:H:125:THR:HA	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	194/226 (86%)	185 (95%)	9 (5%)	0	100	100
2	H	221/458 (48%)	214 (97%)	7 (3%)	0	100	100
3	L	212/216 (98%)	208 (98%)	4 (2%)	0	100	100
All	All	627/900 (70%)	607 (97%)	20 (3%)	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	169/199 (85%)	165 (98%)	4 (2%)	43	70
2	H	199/413 (48%)	195 (98%)	4 (2%)	48	74
3	L	177/179 (99%)	171 (97%)	6 (3%)	32	60
All	All	545/791 (69%)	531 (97%)	14 (3%)	40	69

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	357	ARG
1	A	385	THR
1	A	517	LEU
1	A	518	LEU
2	H	52	LEU
2	H	109	ARG
2	H	212	ASN
2	H	229	LYS
3	L	18	VAL
3	L	127	GLU
3	L	170	LYS
3	L	194	SER
3	L	213	THR
3	L	214	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	334	ASN
1	A	439	ASN
2	H	1	GLN
2	H	120	GLN
3	L	201	HIS

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	$\# Z > 2$
4	NAG	B	1	1,4	14,14,15	0.60	0	17,19,21	0.47	0
4	NAG	B	2	4	14,14,15	0.31	0	17,19,21	0.62	0
4	MAN	B	3	4	11,11,12	0.72	0	15,15,17	0.92	1 (6%)
4	MAN	B	4	4	11,11,12	0.74	0	15,15,17	0.93	2 (13%)
4	FUC	B	5	4	10,10,11	0.77	0	14,14,16	0.67	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
4	NAG	B	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	B	2	4	-	1/6/23/26	0/1/1/1
4	MAN	B	3	4	-	1/2/19/22	0/1/1/1
4	MAN	B	4	4	-	2/2/19/22	0/1/1/1
4	FUC	B	5	4	-	-	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3	MAN	C1-O5-C5	2.21	115.15	112.19
4	B	4	MAN	O2-C2-C3	-2.11	105.78	110.15
4	B	4	MAN	C1-O5-C5	2.04	114.92	112.19

There are no chirality outliers.

All (5) torsion outliers are listed below:

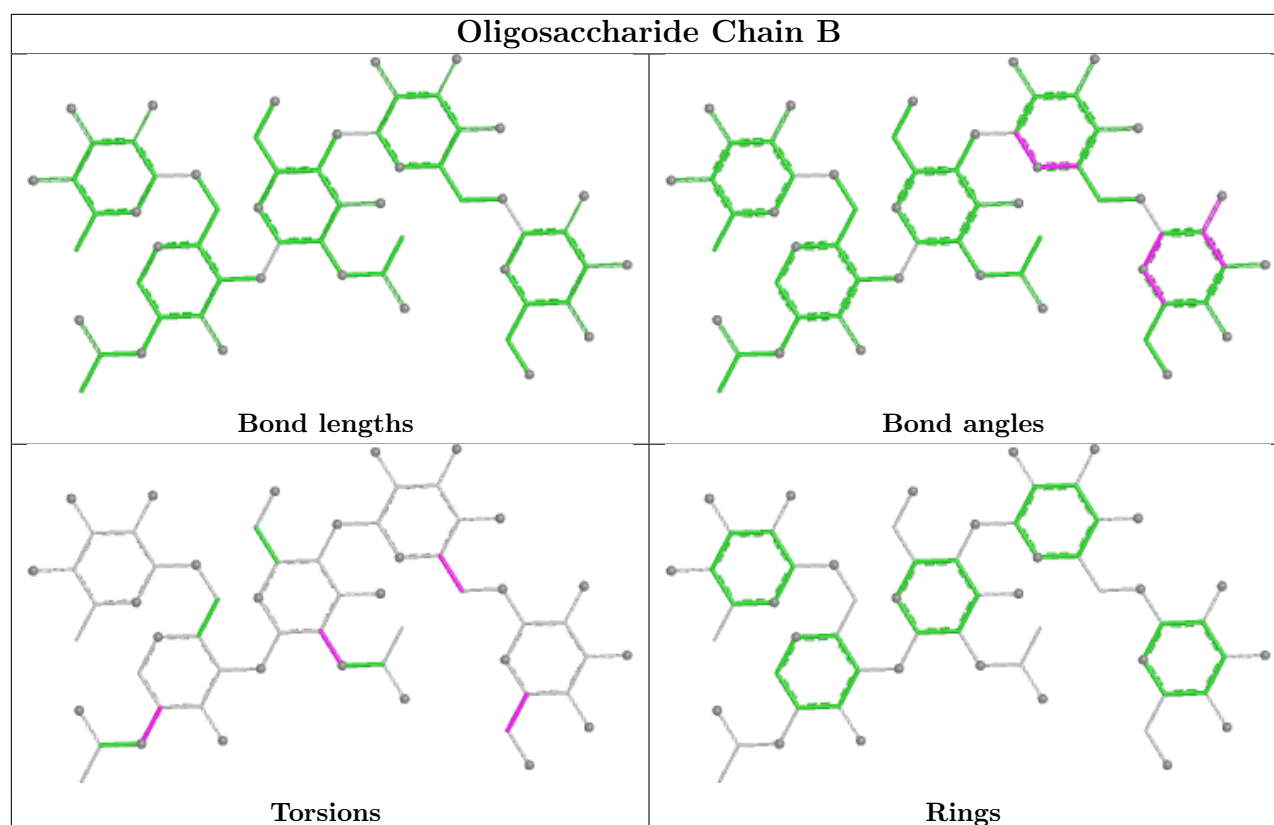
Mol	Chain	Res	Type	Atoms
4	B	3	MAN	O5-C5-C6-O6
4	B	2	NAG	C3-C2-N2-C7
4	B	4	MAN	C4-C5-C6-O6
4	B	4	MAN	O5-C5-C6-O6
4	B	1	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2	NAG	1	0

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	EDO	L	301	-	3,3,3	0.46	0	2,2,2	0.27	0
6	EDO	L	302	-	3,3,3	0.48	0	2,2,2	0.30	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	EDO	L	301	-	-	0/1/1/1	-
6	EDO	L	302	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	302	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	L	302	EDO	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	A	196/226 (86%)	0.61	19 (9%)	13 11	37, 68, 121, 164	0
2	H	225/458 (49%)	0.13	7 (3%)	51 48	33, 56, 88, 127	0
3	L	214/216 (99%)	0.17	4 (1%)	66 63	32, 60, 89, 121	0
All	All	635/900 (70%)	0.29	30 (4%)	36 33	32, 61, 104, 164	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	517	LEU	5.1
1	A	332	ILE	4.7
1	A	520	ALA	3.8
1	A	519	HIS	3.5
3	L	213	THR	3.4
1	A	518	LEU	3.2
2	H	143	SER	3.1
3	L	1	GLU	3.0
1	A	523	THR	3.0
1	A	521	PRO	2.7
2	H	1	GLN	2.7
2	H	142	SER	2.7
1	A	335	LEU	2.6
1	A	524	VAL	2.6
1	A	333	THR	2.6
3	L	161	ALA	2.6
1	A	392	PHE	2.5
1	A	334	ASN	2.3
1	A	527	PRO	2.3
2	H	155	CYS	2.3
2	H	204	LEU	2.3
1	A	385	THR	2.2
1	A	393	THR	2.2

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Mol	Chain	Res	Type	RSRZ
2	H	211	CYS	2.2
1	A	365	TYR	2.2
2	H	54	ASP	2.2
1	A	337	PRO	2.1
1	A	432	CYS	2.1
3	L	197	CYS	2.1
1	A	394	ASN	2.0

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

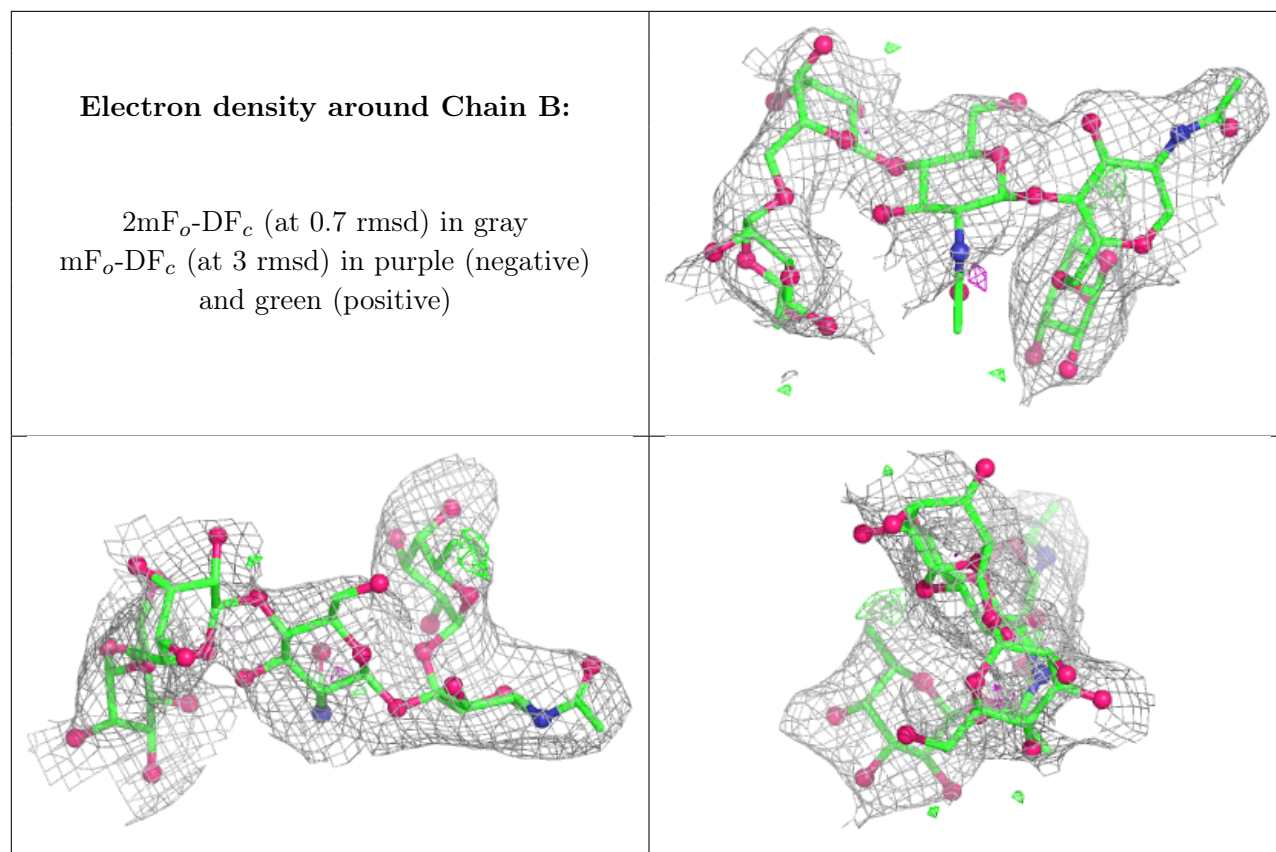
There are no non-standard protein/DNA/RNA residues in this entry.

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
4	NAG	B	1	14/15	-	-	71,98,111,112	0
4	NAG	B	2	14/15	-	-	122,127,135,140	0
4	MAN	B	3	11/12	-	-	140,145,147,148	0
4	MAN	B	4	11/12	-	-	123,141,148,151	0
4	FUC	B	5	10/11	-	-	116,116,116,116	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($\text{\AA}^2$)	Q<0.9
6	EDO	L	302	4/4	0.41	0.34	82,82,82,82	0
5	NI	L	303	1/1	0.83	0.15	119,119,119,119	0
6	EDO	L	301	4/4	0.92	0.12	61,61,61,61	0
5	NI	H	501	1/1	0.97	0.17	100,100,100,100	0

6.5 Other polymers [i](#)

There are no such residues in this entry.