



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:35 AM UTC

PDB ID : 7S2R / pdb_00007s2r
Title : nanobody bound to IL-2Rg
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Deposited on : 2021-09-03
Resolution : 2.49 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

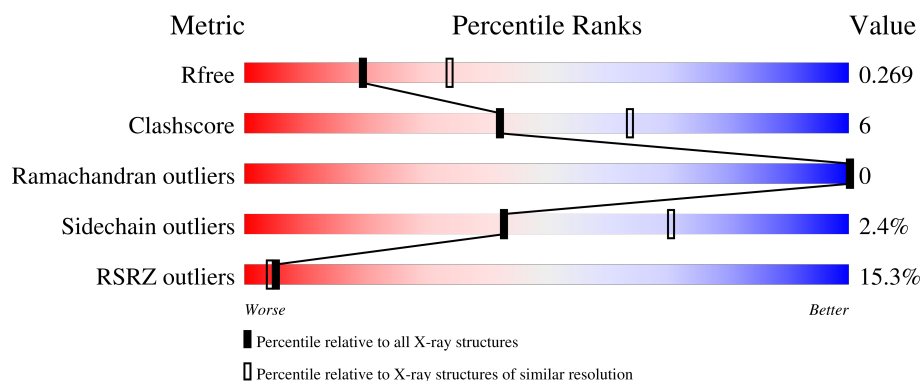
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	209	15% 76% 18% 6%
2	B	159	12% 72% 13% 14%
3	C	2	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SO4	A	311	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 2841 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 Cytokine receptor common subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1641	1042	289	302	8			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	ALA	-	cloning artifact	UNP P31785
A	53	ASP	-	cloning artifact	UNP P31785
A	54	PRO	-	cloning artifact	UNP P31785
A	255	HIS	-	expression tag	UNP P31785
A	256	HIS	-	expression tag	UNP P31785
A	257	HIS	-	expression tag	UNP P31785
A	258	HIS	-	expression tag	UNP P31785
A	259	HIS	-	expression tag	UNP P31785
A	260	HIS	-	expression tag	UNP P31785

- Molecule 2 is a protein called nanobody gamma-nb6.

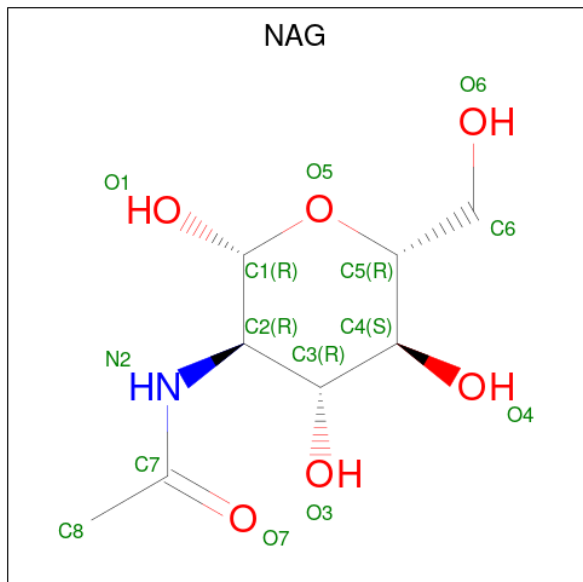
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	136	Total	C	N	O	S	0	0	0
			1042	644	184	209	5			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



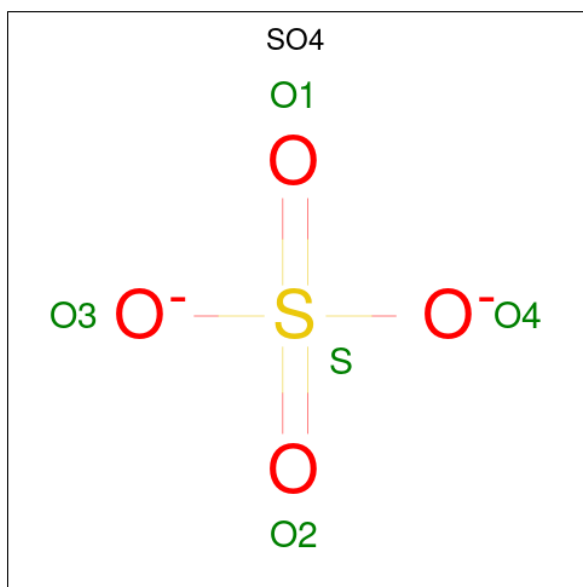
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



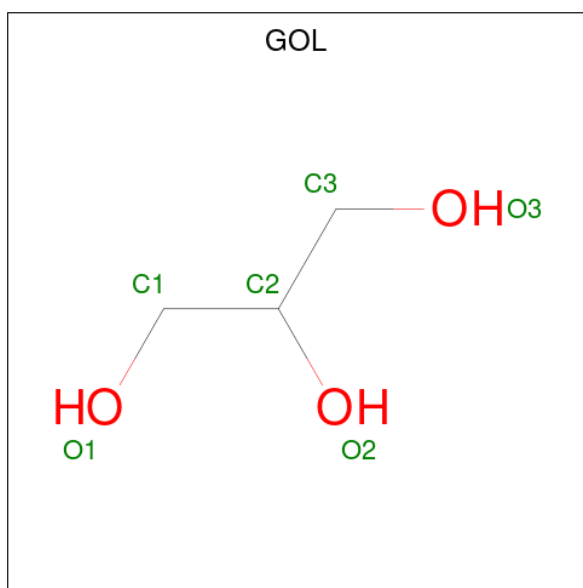
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	15	Total	O	0	0
			15	15		
7	B	11	Total	O	0	0
			11	11		

4 Data and refinement statistics

Property	Value	Source
Space group	I 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	120.08Å 120.08Å 237.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.64 – 2.49 48.64 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.1 (48.64-2.49) 99.1 (48.64-2.49)	Depositor EDS
R_{merge}	0.32	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
R, R_{free}	0.246 , 0.271 0.242 , 0.269	Depositor DCC
R_{free} test set	2319 reflections (7.53%)	wwPDB-VP
Wilson B-factor (Å ²)	75.9	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 66.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2841	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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: NAG, GOL, SO4

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	0.14	0/1697	0.33	0/2320
2	B	0.12	0/1065	0.26	0/1444
All	All	0.13	0/2762	0.31	0/3764

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	1641	0	1503	20	0
2	B	1042	0	971	14	0
3	C	28	0	25	0	0
4	A	28	0	26	0	0
5	A	30	0	0	4	0
5	B	10	0	0	0	0
6	A	24	0	32	1	0
6	B	12	0	16	1	0
7	A	15	0	0	0	0
7	B	11	0	0	0	0
All	All	2841	0	2573	34	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 6.

All (34) 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)
5:A:311:SO4:O4	2:B:54:ARG:NH1	2.25	0.70
1:A:70:MET:HE1	1:A:148:LEU:HD22	1.82	0.61
1:A:162:LEU:HD13	1:A:246:TRP:HB2	1.82	0.61
2:B:114:GLY:H	6:B:203:GOL:H32	1.67	0.60
1:A:94:SER:OG	5:A:311:SO4:O4	2.20	0.59
1:A:221:PHE:HB2	1:A:244:ILE:HG22	1.84	0.59
2:B:102:ASP:OD2	2:B:109:ARG:NH2	2.34	0.58
1:A:222:ARG:HH12	6:A:310:GOL:H2	1.69	0.58
1:A:62:CYS:HB3	1:A:70:MET:HE2	1.90	0.52
1:A:133:GLN:HG3	1:A:141:GLN:HB3	1.91	0.52
2:B:94:THR:HG23	2:B:130:THR:HA	1.93	0.50
5:A:311:SO4:S	2:B:54:ARG:NH1	2.85	0.50
2:B:70:ARG:NH2	2:B:93:ASP:OD2	2.44	0.50
2:B:36:TRP:NE1	2:B:84:LEU:HB2	2.27	0.50
1:A:65:PHE:HE2	1:A:71:ASN:HB2	1.77	0.49
1:A:186:LEU:HD11	1:A:199:GLU:HB2	1.95	0.48
1:A:83:THR:HG21	1:A:136:ARG:HH11	1.79	0.48
1:A:187:VAL:HG22	1:A:223:VAL:HG22	1.96	0.48
1:A:91:TYR:CE1	1:A:123:HIS:HB2	2.49	0.48
2:B:86:MET:HB3	2:B:89:LEU:HD21	1.96	0.47
2:B:102:ASP:HB2	2:B:120:TYR:HA	1.96	0.46
1:A:79:GLU:OE1	1:A:140:ARG:NH2	2.47	0.46
2:B:45:ARG:NH2	2:B:117:GLU:OE2	2.40	0.46
1:A:174:TRP:CD1	1:A:176:ASN:HD21	2.35	0.45
2:B:34:MET:HE2	2:B:82:LEU:HD22	1.98	0.44
2:B:110:VAL:HG12	2:B:112:LEU:H	1.81	0.44
2:B:66:SER:O	2:B:70:ARG:NH1	2.51	0.43
1:A:245:HIS:N	5:A:303:SO4:O4	2.51	0.43
1:A:190:ARG:HG2	1:A:197:TRP:CZ3	2.54	0.43
1:A:122:ILE:HG22	1:A:124:LEU:HD12	2.00	0.42
1:A:60:VAL:HG12	1:A:74:TRP:HB3	2.01	0.42
1:A:79:GLU:CD	1:A:140:ARG:HH22	2.27	0.41
1:A:66:ASN:O	1:A:68:GLU:HG3	2.19	0.41
2:B:90:LYS:HE2	2:B:90:LYS:HB3	1.84	0.41

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	195/209 (93%)	189 (97%)	6 (3%)	0	100	100
2	B	134/159 (84%)	134 (100%)	0	0	100	100
All	All	329/368 (89%)	323 (98%)	6 (2%)	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	183/201 (91%)	177 (97%)	6 (3%)	33	61
2	B	106/129 (82%)	105 (99%)	1 (1%)	70	87
All	All	289/330 (88%)	282 (98%)	7 (2%)	43	70

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASP
1	A	176	ASN
1	A	177	ARG
1	A	205	ARG
1	A	206	HIS
1	A	207	LYS
2	B	90	LYS

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	200	GLN
1	A	236	HIS
2	B	118	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	$\# Z > 2$
3	NAG	C	1	3,1	14,14,15	0.48	0	17,19,21	0.49	0
3	NAG	C	2	3	14,14,15	0.30	0	17,19,21	0.47	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	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

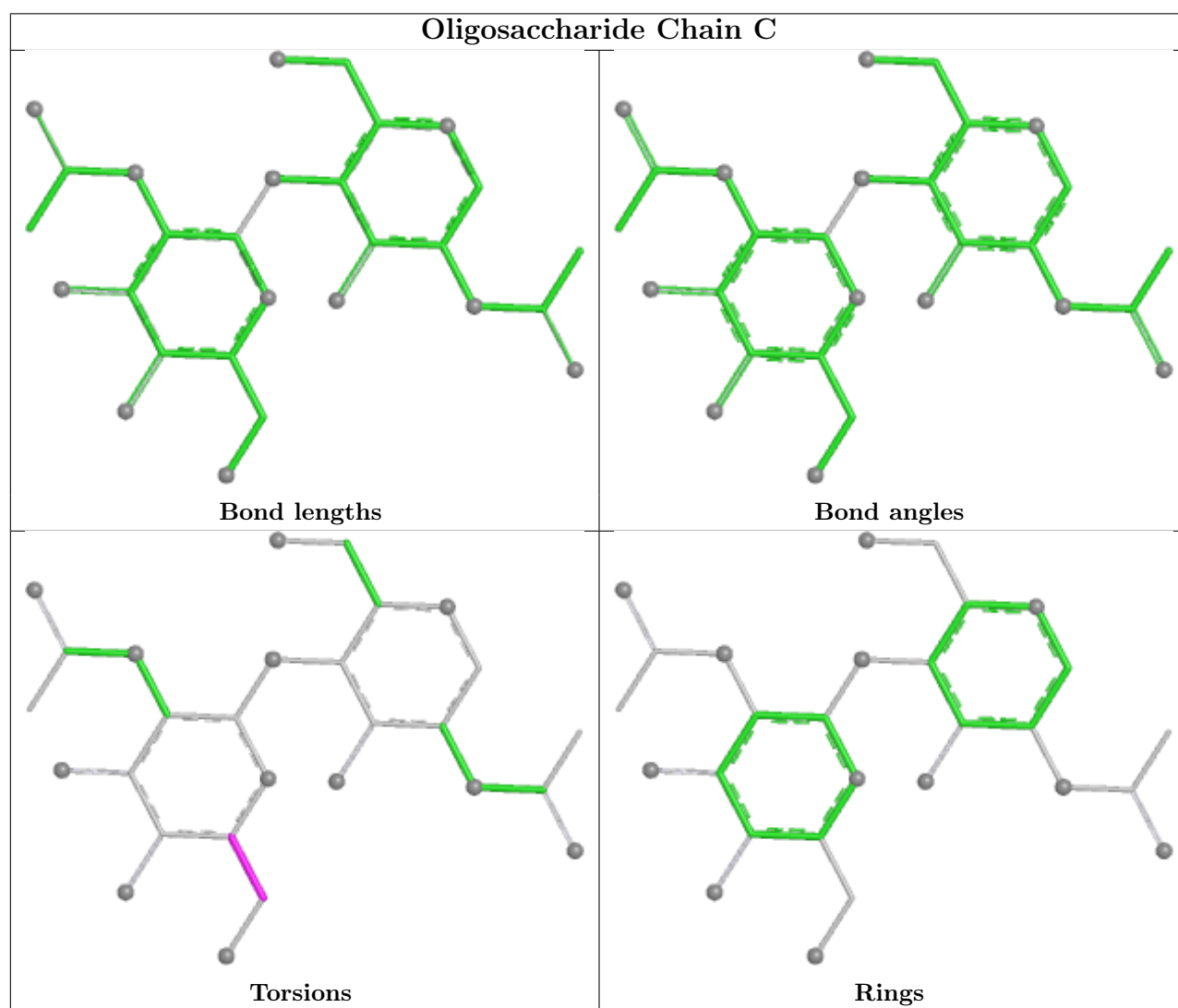
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	O5-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](#)

16 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	A	310	-	5,5,5	0.92	0	5,5,5	1.09	0
5	SO4	A	306	-	4,4,4	0.25	0	6,6,6	0.14	0
5	SO4	B	202	-	4,4,4	0.24	0	6,6,6	0.10	0
6	GOL	A	308	-	5,5,5	0.98	0	5,5,5	0.98	0
5	SO4	A	312	-	4,4,4	0.23	0	6,6,6	0.08	0
6	GOL	A	307	-	5,5,5	1.01	0	5,5,5	1.03	0
6	GOL	B	203	-	5,5,5	0.93	0	5,5,5	1.11	0
6	GOL	B	204	-	5,5,5	0.98	0	5,5,5	1.06	0
5	SO4	A	305	-	4,4,4	0.24	0	6,6,6	0.06	0
5	SO4	A	303	-	4,4,4	0.24	0	6,6,6	0.09	0
4	NAG	A	302	1	14,14,15	0.25	0	17,19,21	0.40	0
5	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	B	201	-	4,4,4	0.26	0	6,6,6	0.12	0
5	SO4	A	311	-	4,4,4	0.24	0	6,6,6	0.09	0
4	NAG	A	301	1	14,14,15	0.26	0	17,19,21	0.48	0
6	GOL	A	309	-	5,5,5	0.89	0	5,5,5	1.18	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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	A	310	-	-	1/4/4/4	-
6	GOL	A	308	-	-	0/4/4/4	-
6	GOL	B	203	-	-	0/4/4/4	-
6	GOL	A	307	-	-	0/4/4/4	-
6	GOL	B	204	-	-	0/4/4/4	-
4	NAG	A	302	1	-	0/6/23/26	0/1/1/1
4	NAG	A	301	1	-	2/6/23/26	0/1/1/1
6	GOL	A	309	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	301	NAG	C4-C5-C6-O6
4	A	301	NAG	O5-C5-C6-O6
6	A	310	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	310	GOL	1	0
6	B	203	GOL	1	0
5	A	303	SO4	1	0
5	A	311	SO4	3	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	197/209 (94%)	1.23	32 (16%) 4 3	62, 92, 145, 183	0
2	B	136/159 (85%)	0.86	19 (13%) 6 5	65, 87, 130, 163	0
All	All	333/368 (90%)	1.08	51 (15%) 5 4	62, 89, 142, 183	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	204	TYR	6.1
1	A	212	SER	5.0
1	A	81	GLN	4.9
1	A	76	SER	4.5
2	B	59	GLY	4.3
1	A	93	ASN	3.9
1	A	206	HIS	3.9
1	A	203	ASP	3.8
1	A	207	LYS	3.8
1	A	175	ASN	3.8
2	B	55	GLY	3.7
1	A	78	SER	3.7
1	A	176	ASN	3.7
1	A	195	HIS	3.6
2	B	30	ARG	3.5
1	A	52	ALA	3.5
2	B	53	THR	3.5
1	A	210	LEU	3.3
2	B	135	ALA	3.2
1	A	248	SER	3.2
1	A	205	ARG	3.1
2	B	27	TYR	3.0
1	A	80	PRO	3.0
1	A	215	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
2	B	58	GLU	2.9
1	A	82	PRO	2.9
1	A	193	TRP	2.8
2	B	1	GLN	2.8
2	B	112	LEU	2.7
1	A	177	ARG	2.7
1	A	213	VAL	2.6
1	A	211	PRO	2.6
2	B	136	PRO	2.5
2	B	29	TYR	2.5
1	A	189	TYR	2.4
2	B	32	TYR	2.4
1	A	164	LYS	2.4
2	B	79	LYS	2.4
1	A	106	LEU	2.3
2	B	12	VAL	2.2
1	A	182	CYS	2.2
2	B	56	SER	2.2
1	A	246	TRP	2.2
2	B	134	GLY	2.1
1	A	163	HIS	2.1
1	A	170	LEU	2.1
2	B	52	TYR	2.1
2	B	133	SER	2.1
1	A	181	HIS	2.1
1	A	79	GLU	2.0
2	B	106	TRP	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.

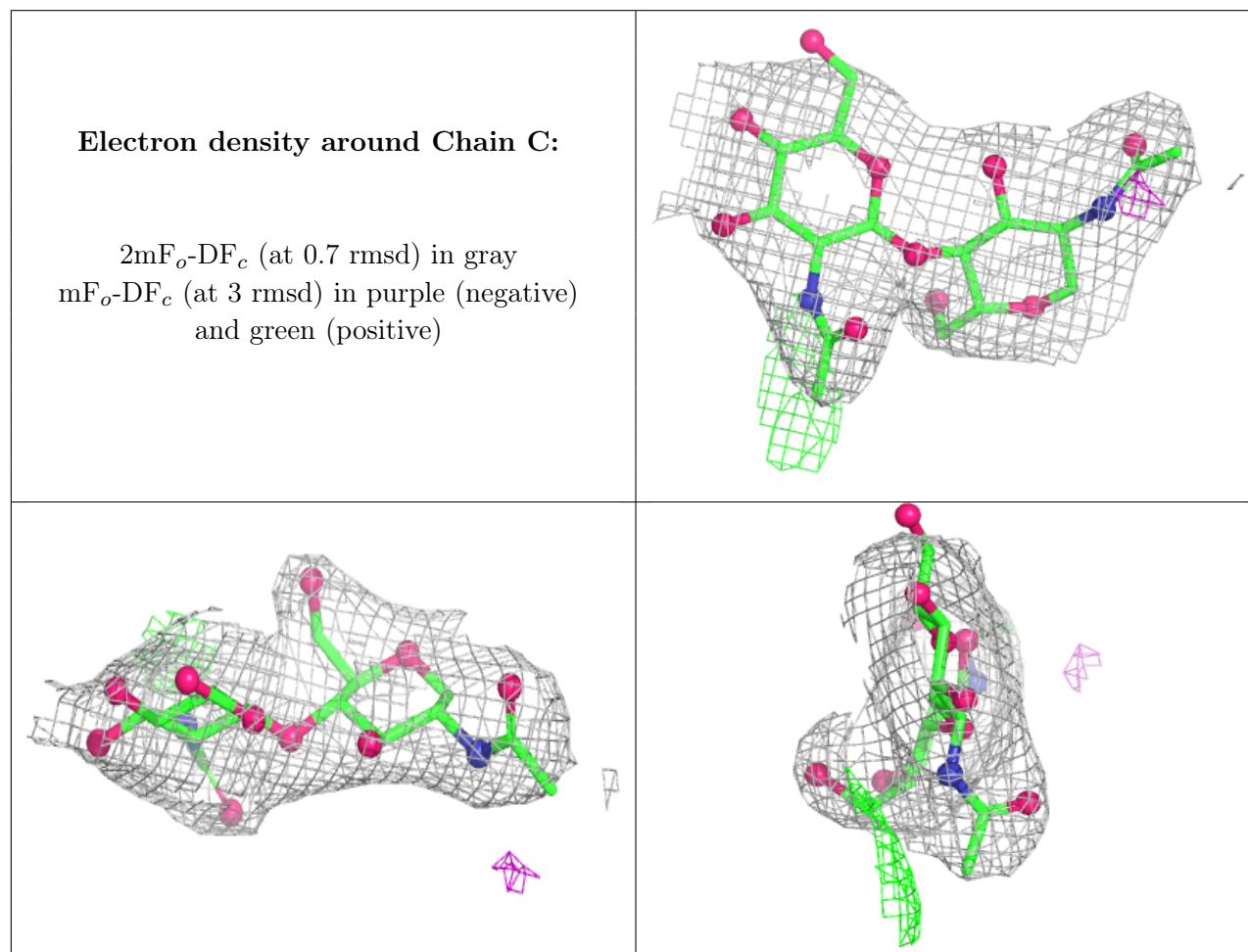
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	C	2	14/15	0.75	0.13	105,116,128,132	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	C	1	14/15	0.92	0.11	75,91,104,107	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 ⓘ

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
5	SO4	A	303	5/5	0.61	0.12	122,135,153,155	0
5	SO4	A	311	5/5	0.62	0.21	143,153,174,175	0
5	SO4	A	312	5/5	0.66	0.18	145,147,157,174	5
6	GOL	B	203	6/6	0.68	0.27	85,92,104,115	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	GOL	A	309	6/6	0.72	0.29	89,100,113,114	0
6	GOL	A	310	6/6	0.74	0.20	84,102,107,110	0
5	SO4	A	304	5/5	0.76	0.11	133,136,149,163	0
6	GOL	A	308	6/6	0.79	0.24	88,94,100,100	0
5	SO4	B	201	5/5	0.81	0.18	101,112,129,143	0
4	NAG	A	301	14/15	0.82	0.16	94,118,139,148	0
5	SO4	A	305	5/5	0.83	0.07	145,150,168,171	0
5	SO4	B	202	5/5	0.83	0.09	94,112,128,135	0
4	NAG	A	302	14/15	0.84	0.15	119,139,150,156	0
6	GOL	B	204	6/6	0.85	0.17	96,105,107,107	0
5	SO4	A	306	5/5	0.87	0.12	89,92,122,130	0
6	GOL	A	307	6/6	0.89	0.20	94,105,112,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.