



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 18, 2023 – 12:40 PM EDT

PDB ID : 5D4K
Title : Crystal structure of the human polymeric Ig receptor (pIgR) ectodomain
Authors : Stadtmueller, B.M.; Bjorkman, P.J.
Deposited on : 2015-08-07
Resolution : 2.60 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

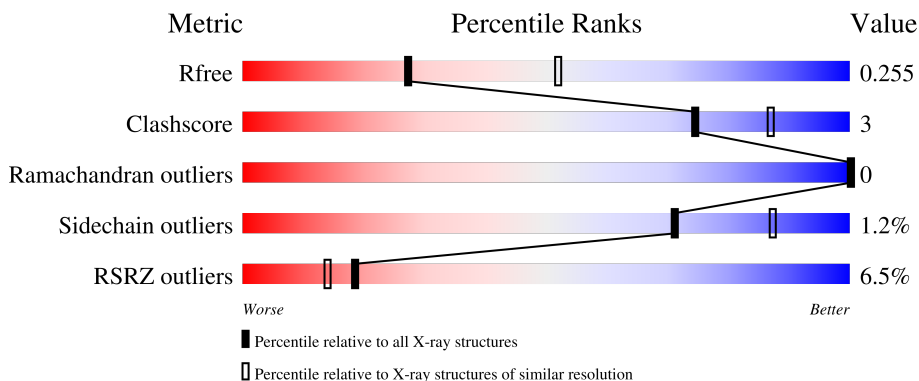
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	557	
1	B	557	
2	C	2	
2	D	2	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 16744 atoms, of which 8214 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 Polymeric immunoglobulin receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	539	8222	2618	4051	726	807	20	0	0	0
1	B	536	8188	2609	4039	723	797	20	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

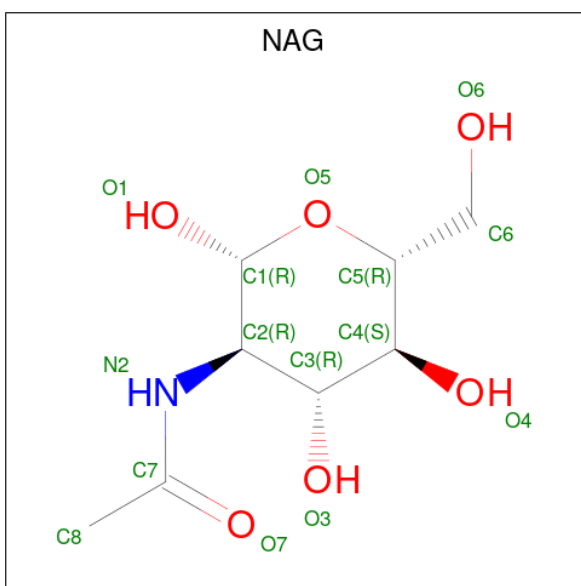
Chain	Residue	Modelled	Actual	Comment	Reference
A	347	SER	GLY	variant	UNP P01833
A	548	GLY	-	expression tag	UNP P01833
A	549	SER	-	expression tag	UNP P01833
A	550	TRP	-	expression tag	UNP P01833
A	551	SER	-	expression tag	UNP P01833
A	552	HIS	-	expression tag	UNP P01833
A	553	PRO	-	expression tag	UNP P01833
A	554	GLN	-	expression tag	UNP P01833
A	555	PHE	-	expression tag	UNP P01833
A	556	GLU	-	expression tag	UNP P01833
A	557	LYS	-	expression tag	UNP P01833
B	347	SER	GLY	variant	UNP P01833
B	548	GLY	-	expression tag	UNP P01833
B	549	SER	-	expression tag	UNP P01833
B	550	TRP	-	expression tag	UNP P01833
B	551	SER	-	expression tag	UNP P01833
B	552	HIS	-	expression tag	UNP P01833
B	553	PRO	-	expression tag	UNP P01833
B	554	GLN	-	expression tag	UNP P01833
B	555	PHE	-	expression tag	UNP P01833
B	556	GLU	-	expression tag	UNP P01833
B	557	LYS	-	expression tag	UNP P01833

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	C	2	Total	C	H	N	O	0	0	0
			47	14	23	1	9			
2	D	2	Total	C	H	N	O	0	0	0
			47	14	23	1	9			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	A	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		
3	B	1	Total	C	H	N	O	0	0
			27	8	13	1	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

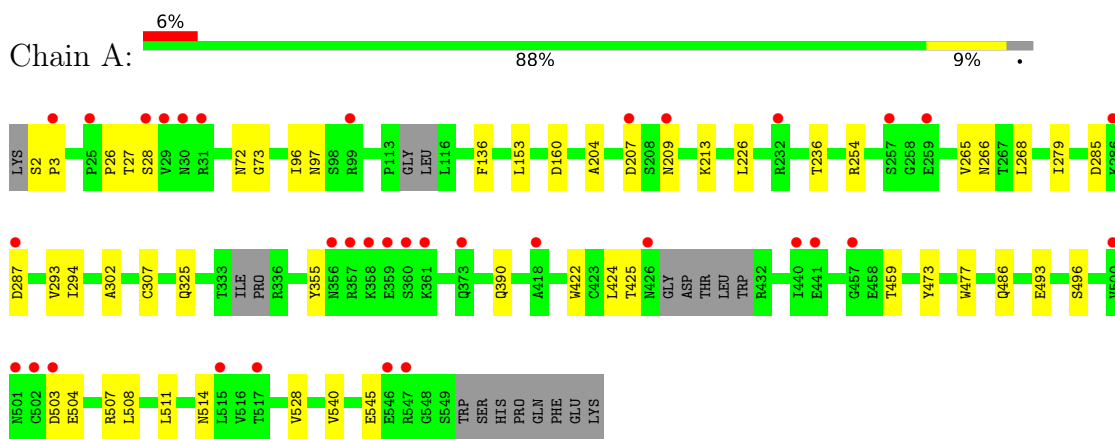
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	27	Total O 27 27	0	0
5	B	31	Total O 31 31	0	0

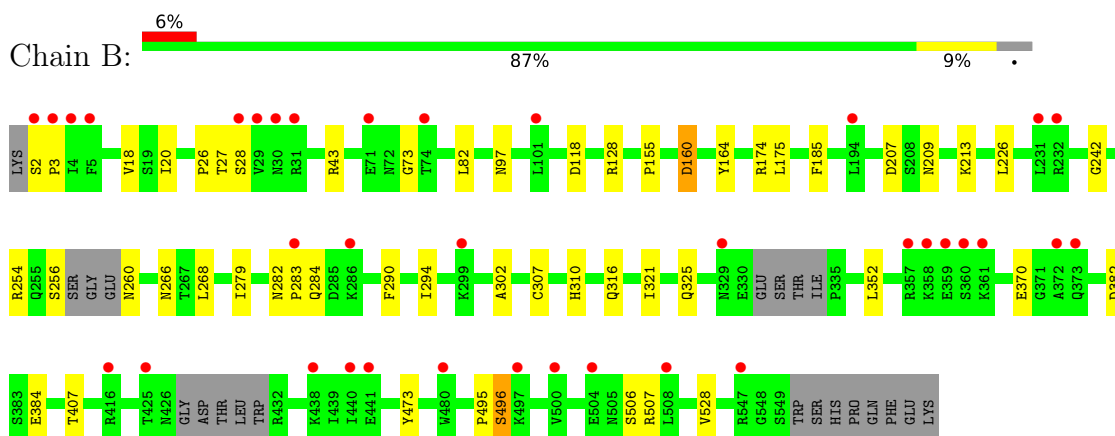
3 Residue-property plots [i](#)

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: Polymeric immunoglobulin receptor



- Molecule 1: Polymeric immunoglobulin receptor



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



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



MAE
FUC2

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.26Å 242.43Å 63.05Å 90.00° 114.89° 90.00°	Depositor
Resolution (Å)	36.98 – 2.60 39.62 – 2.60	Depositor EDS
% Data completeness (in resolution range)	91.0 (36.98-2.60) 91.0 (39.62-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.61Å)	Xtrriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.201 , 0.254 0.204 , 0.255	Depositor DCC
R_{free} test set	1998 reflections (4.30%)	wwPDB-VP
Wilson B-factor (Å ²)	51.5	Xtrriage
Anisotropy	0.446	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 58.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.029 for l,-k,h	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16744	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: SO4, 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	0.49	0/4257	0.64	0/5776
1	B	0.48	0/4236	0.64	0/5748
All	All	0.49	0/8493	0.64	0/11524

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	4171	4051	4050	27	0
1	B	4149	4039	4040	28	0
2	C	24	23	22	1	0
2	D	24	23	22	0	0
3	A	42	39	39	1	0
3	B	42	39	39	0	0
4	A	10	0	0	1	0
4	B	10	0	0	0	0
5	A	27	0	0	0	0
5	B	31	0	0	0	0
All	All	8530	8214	8212	54	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 3.

All (54) 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:72:ASN:ND2	2:C:1:NAG:O7	2.30	0.64
1:B:43:ARG:NH2	1:B:321:ILE:O	2.32	0.62
1:A:266:ASN:HB3	1:A:268:LEU:H	1.73	0.54
1:A:279:ILE:HD12	1:A:294:ILE:HG12	1.90	0.53
1:A:153:LEU:HD21	1:B:155:PRO:HB3	1.91	0.52
1:B:279:ILE:HD12	1:B:294:ILE:HG12	1.91	0.52
1:B:266:ASN:HB3	1:B:268:LEU:H	1.75	0.51
1:B:118:ASP:OD1	1:B:213:LYS:HG3	2.12	0.50
1:B:226:LEU:HD22	1:B:325:GLN:HB3	1.91	0.50
1:A:503:ASP:OD1	1:A:504:GLU:N	2.44	0.49
1:A:459:THR:HG23	1:A:514:ASN:HA	1.95	0.48
1:B:2:SER:N	1:B:3:PRO:CD	2.78	0.47
1:A:254:ARG:NH2	1:A:302:ALA:O	2.47	0.47
1:B:473:TYR:HB3	1:B:528:VAL:CG1	2.44	0.47
1:B:352:LEU:HD23	1:B:407:THR:HG22	1.97	0.47
1:B:175:LEU:HD21	1:B:185:PHE:CD2	2.51	0.46
1:A:96:ILE:CD1	1:A:390:GLN:HG3	2.45	0.45
1:B:310:HIS:CE1	1:B:316:GLN:HG3	2.51	0.45
1:B:254:ARG:NH2	1:B:302:ALA:O	2.49	0.45
1:A:285:ASP:HB3	1:A:287:ASP:H	1.82	0.45
1:A:226:LEU:HD22	1:A:325:GLN:HB3	1.99	0.45
1:A:473:TYR:HD2	1:A:528:VAL:CG1	2.30	0.45
1:A:422:TRP:HB3	1:A:424:LEU:HD13	1.98	0.44
1:B:207:ASP:HB2	1:B:209:ASN:H	1.82	0.44
1:B:282:ASN:HB3	1:B:283:PRO:HD2	1.98	0.44
1:B:382:ASP:OD1	1:B:384:GLU:N	2.37	0.44
1:B:370:GLU:OE1	1:B:370:GLU:N	2.51	0.44
1:A:26:PRO:HG3	1:A:73:GLY:HA3	2.00	0.44
1:B:495:PRO:HA	1:B:507:ARG:HA	1.98	0.44
1:A:486:GLN:NE2	3:A:605:NAG:O7	2.49	0.43
1:A:493:GLU:O	1:A:507:ARG:NH1	2.46	0.43
1:B:26:PRO:HG3	1:B:73:GLY:HA3	2.01	0.43
1:A:2:SER:HB2	1:A:3:PRO:HD3	2.01	0.43
1:A:236:THR:HG22	1:A:293:VAL:HG22	2.00	0.43
1:A:136:PHE:HB3	1:A:204:ALA:CB	2.49	0.43
1:B:160:ASP:HB2	1:B:164:TYR:HB3	2.00	0.43
1:B:496:SER:O	1:B:506:SER:OG	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:VAL:CG2	1:B:82:LEU:HD11	2.49	0.42
1:B:473:TYR:HD2	1:B:528:VAL:CG1	2.33	0.42
1:A:355:TYR:HB2	1:A:425:THR:HG21	2.00	0.42
1:B:2:SER:HB2	1:B:3:PRO:HD3	2.02	0.42
1:A:207:ASP:HB2	1:A:209:ASN:H	1.85	0.42
1:B:18:VAL:HG12	1:B:20:ILE:HD12	2.02	0.42
1:B:128:ARG:HH22	1:B:242:GLY:H	1.68	0.42
1:A:355:TYR:CB	1:A:425:THR:HG21	2.50	0.42
1:A:507:ARG:HD3	1:A:508:LEU:H	1.85	0.42
1:A:27:THR:HG22	1:A:28:SER:N	2.34	0.41
1:B:284:GLN:HB2	1:B:290:PHE:HB3	2.02	0.41
1:A:213:LYS:NZ	4:A:606:SO4:O4	2.53	0.41
1:A:477:TRP:CG	1:A:511:LEU:HB2	2.55	0.41
1:A:2:SER:N	1:A:3:PRO:CD	2.84	0.41
1:A:265:VAL:HG21	1:A:279:ILE:HD11	2.02	0.41
1:B:256:SER:HB2	1:B:260:ASN:HB2	2.02	0.40
1:B:27:THR:HG22	1:B:28:SER:N	2.37	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	531/557 (95%)	505 (95%)	26 (5%)	0	100	100
1	B	528/557 (95%)	500 (95%)	28 (5%)	0	100	100
All	All	1059/1114 (95%)	1005 (95%)	54 (5%)	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	460/476 (97%)	454 (99%)	6 (1%)	69	86
1	B	457/476 (96%)	452 (99%)	5 (1%)	73	88
All	All	917/952 (96%)	906 (99%)	11 (1%)	71	87

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

Mol	Chain	Res	Type
1	A	97	ASN
1	A	160	ASP
1	A	307	CYS
1	A	496	SER
1	A	540	VAL
1	A	545	GLU
1	B	97	ASN
1	B	160	ASP
1	B	174	ARG
1	B	307	CYS
1	B	496	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates i

4 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
2	NAG	C	1	2,1	14,14,15	0.37	0	17,19,21	0.55	0
2	FUC	C	2	2	10,10,11	0.81	0	14,14,16	0.83	0
2	NAG	D	1	2,1	14,14,15	0.64	0	17,19,21	0.81	0
2	FUC	D	2	2	10,10,11	1.15	0	14,14,16	1.04	1 (7%)

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
2	NAG	C	1	2,1	-	3/6/23/26	0/1/1/1
2	FUC	C	2	2	-	-	0/1/1/1
2	NAG	D	1	2,1	-	0/6/23/26	0/1/1/1
2	FUC	D	2	2	-	-	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	FUC	O5-C5-C4	2.21	113.48	109.52

There are no chirality outliers.

All (3) torsion outliers are listed below:

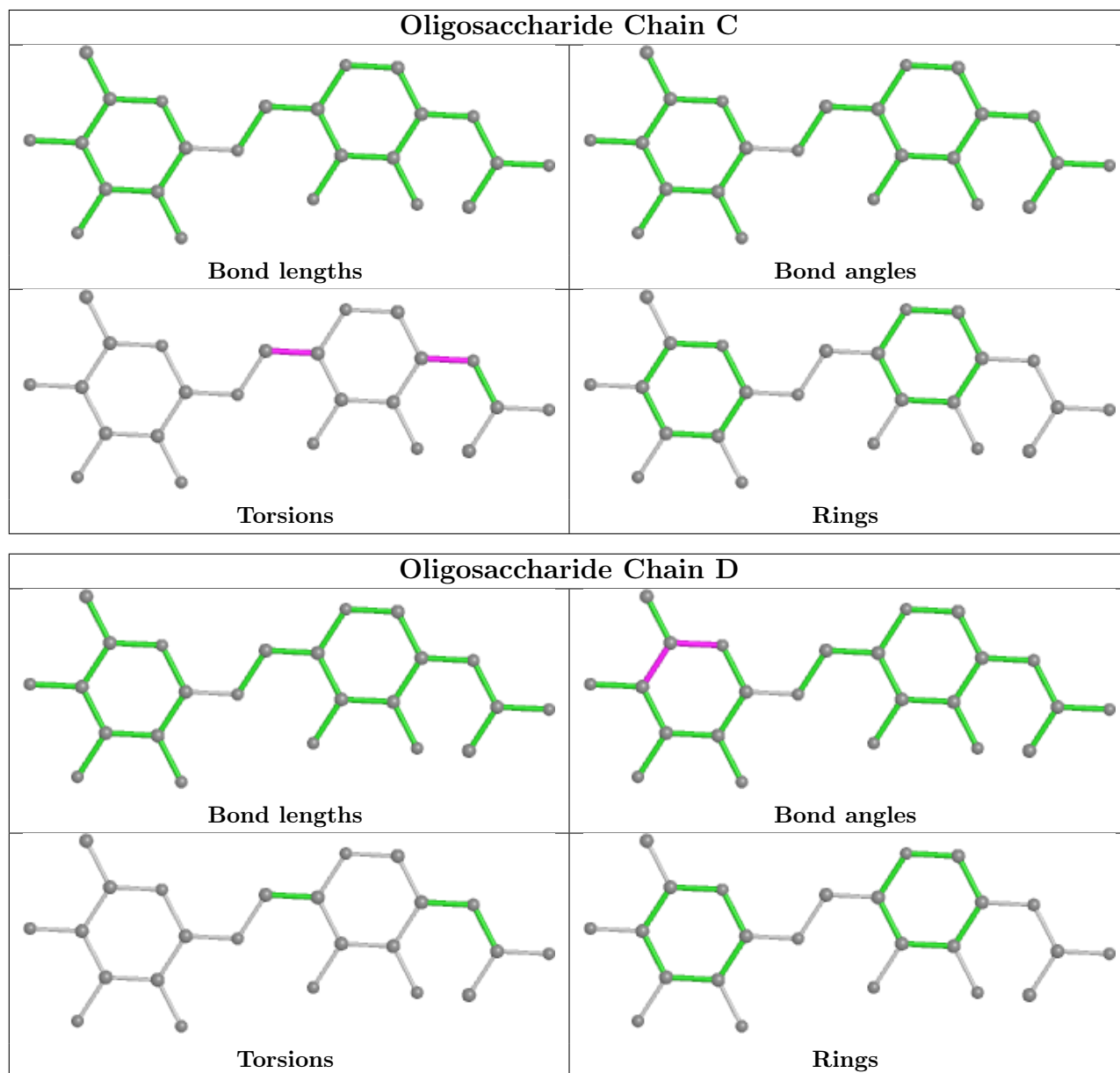
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	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](#)

10 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	NAG	B	604	1	14,14,15	0.30	0	17,19,21	0.54	0
3	NAG	B	605	1	14,14,15	0.70	1 (7%)	17,19,21	0.53	0
4	SO4	A	607	-	4,4,4	0.18	0	6,6,6	0.12	0
3	NAG	A	605	1	14,14,15	0.34	0	17,19,21	0.38	0
3	NAG	A	604	1	14,14,15	0.98	2 (14%)	17,19,21	0.71	0
3	NAG	B	601	1	14,14,15	0.38	0	17,19,21	0.54	0
4	SO4	A	606	-	4,4,4	0.16	0	6,6,6	0.19	0
4	SO4	B	606	-	4,4,4	0.15	0	6,6,6	0.13	0
4	SO4	B	607	-	4,4,4	0.28	0	6,6,6	0.38	0
3	NAG	A	601	1	14,14,15	0.49	0	17,19,21	0.42	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	B	604	1	-	0/6/23/26	0/1/1/1
3	NAG	B	605	1	-	0/6/23/26	0/1/1/1
3	NAG	A	605	1	-	0/6/23/26	0/1/1/1
3	NAG	A	604	1	-	0/6/23/26	0/1/1/1
3	NAG	B	601	1	-	0/6/23/26	0/1/1/1
3	NAG	A	601	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	604	NAG	O5-C1	2.71	1.48	1.43
3	A	604	NAG	C1-C2	2.40	1.55	1.52
3	B	605	NAG	C1-C2	2.16	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	NAG	1	0
4	A	606	SO4	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	539/557 (96%)	0.54	34 (6%) 20 15	32, 57, 96, 149	0
1	B	536/557 (96%)	0.57	36 (6%) 17 13	30, 61, 94, 140	0
All	All	1075/1114 (96%)	0.55	70 (6%) 18 14	30, 59, 95, 149	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	360	SER	5.8
1	A	259	GLU	5.8
1	B	358	LYS	5.2
1	B	373	GLN	4.6
1	A	358	LYS	4.6
1	A	361	LYS	4.5
1	A	373	GLN	4.2
1	A	209	ASN	4.1
1	A	357	ARG	4.1
1	B	547	ARG	4.1
1	A	440	ILE	3.9
1	B	31	ARG	3.8
1	A	28	SER	3.8
1	B	372	ALA	3.7
1	B	357	ARG	3.6
1	A	502	CYS	3.5
1	B	28	SER	3.5
1	A	500	VAL	3.4
1	B	500	VAL	3.3
1	A	547	ARG	3.3
1	B	359	GLU	3.3
1	B	101	LEU	3.3
1	A	257	SER	3.2
1	A	286	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	361	LYS	3.1
1	B	5	PHE	3.1
1	A	207	ASP	3.1
1	B	29	VAL	3.0
1	A	441	GLU	3.0
1	B	286	LYS	3.0
1	A	503	ASP	3.0
1	A	457	GLY	2.9
1	B	497	LYS	2.9
1	B	232	ARG	2.9
1	A	232	ARG	2.9
1	A	29	VAL	2.8
1	B	441	GLU	2.8
1	B	3	PRO	2.8
1	A	515	LEU	2.8
1	B	360	SER	2.7
1	B	329	ASN	2.5
1	B	71	GLU	2.5
1	A	25	PRO	2.5
1	A	359	GLU	2.5
1	A	31	ARG	2.5
1	A	426	ASN	2.4
1	B	299	LYS	2.4
1	A	517	THR	2.4
1	B	231	LEU	2.4
1	B	416	ARG	2.4
1	B	30	ASN	2.4
1	A	501	ASN	2.3
1	B	2	SER	2.3
1	B	4	ILE	2.3
1	B	74	THR	2.2
1	B	480	TRP	2.2
1	B	440	ILE	2.2
1	B	283	PRO	2.2
1	A	356	ASN	2.1
1	B	504	GLU	2.1
1	A	3	PRO	2.1
1	B	438	LYS	2.1
1	A	546	GLU	2.1
1	A	418	ALA	2.1
1	B	194	LEU	2.1
1	B	508	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	30	ASN	2.1
1	B	425	THR	2.0
1	A	287	ASP	2.0
1	A	99	ARG	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](#)

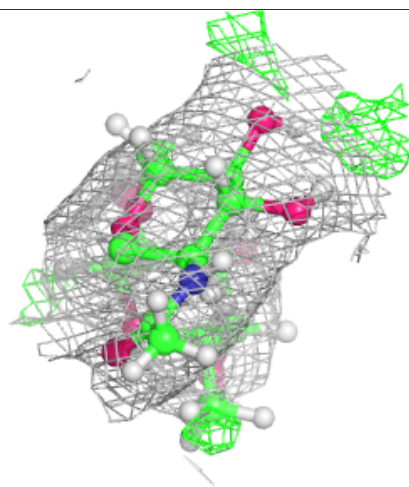
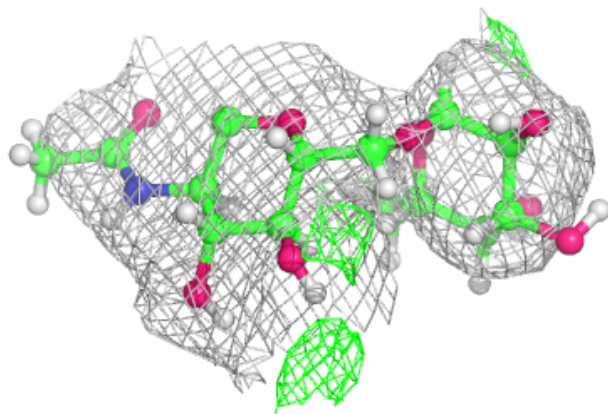
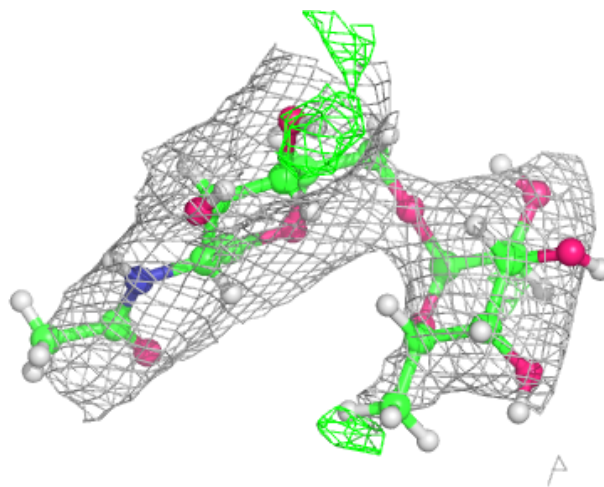
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

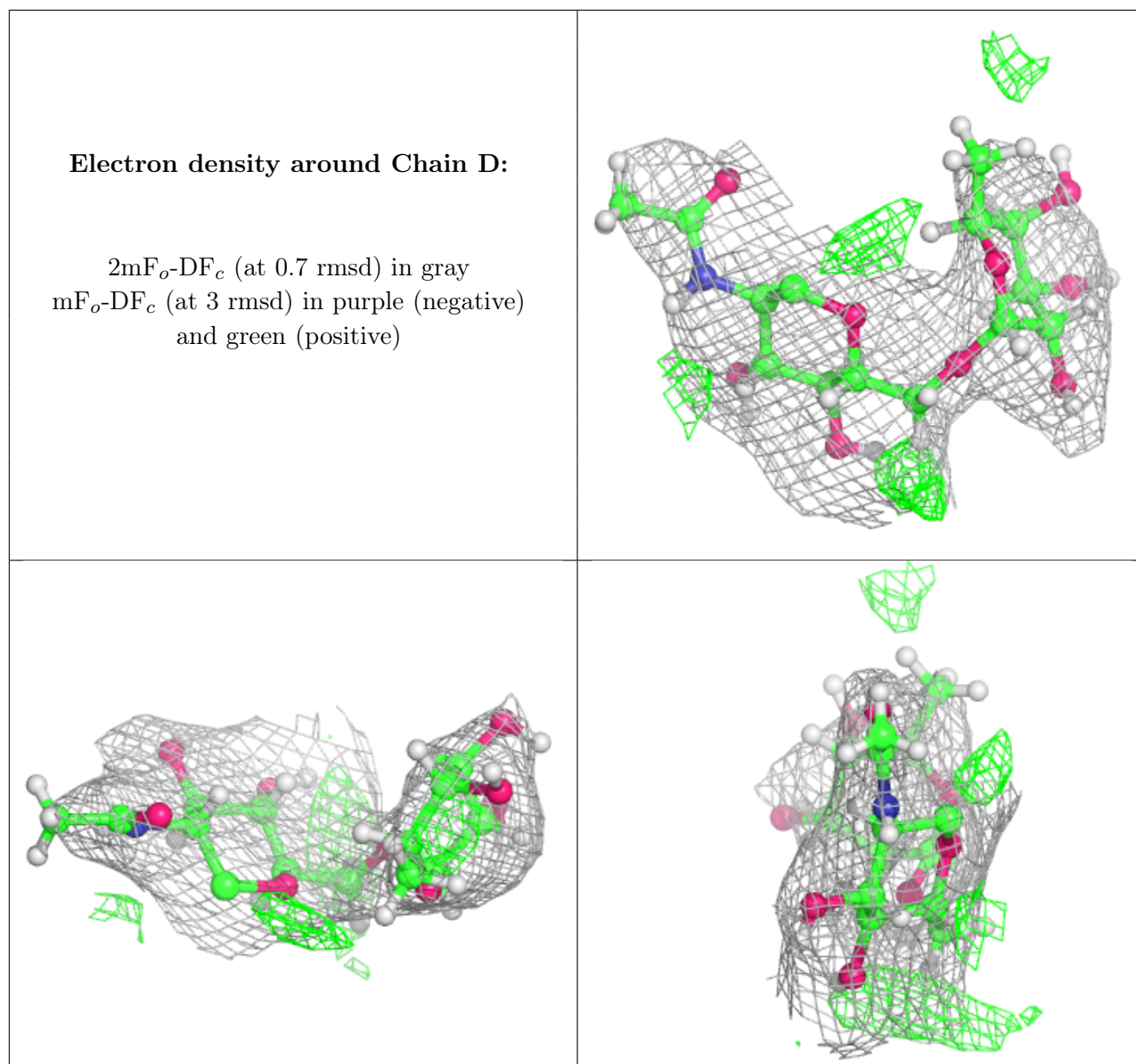
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FUC	C	2	10/11	0.82	0.22	100,112,130,134	0
2	NAG	D	1	14/15	0.87	0.19	66,81,96,96	0
2	NAG	C	1	14/15	0.90	0.18	59,75,94,103	0
2	FUC	D	2	10/11	0.90	0.20	80,93,109,110	0

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.

Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





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
3	NAG	B	601	14/15	0.66	0.36	107,131,168,190	0
3	NAG	A	601	14/15	0.69	0.28	78,107,135,137	0
3	NAG	A	605	14/15	0.78	0.31	97,116,136,156	0
3	NAG	B	605	14/15	0.78	0.21	72,108,126,146	0
3	NAG	A	604	14/15	0.83	0.22	76,96,115,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAG	B	604	14/15	0.85	0.26	67,89,111,116	0
4	SO4	A	607	5/5	0.97	0.15	62,65,73,79	0
4	SO4	B	607	5/5	0.97	0.20	53,54,65,73	0
4	SO4	B	606	5/5	0.98	0.14	58,63,67,74	0
4	SO4	A	606	5/5	0.98	0.14	62,65,73,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.