



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4BQC / pdb_00004bqc
Title : Crystal structure of the FN5 and FN6 domains of NEO1 bound to SOS
Authors : Bell, C.H.; Healey, E.; vanErp, S.; Bishop, B.; Tang, C.; Gilbert, R.J.C.; Aricescu, A.R.; Pasterkamp, R.J.; Siebold, C.
Deposited on : 2013-05-30
Resolution : 3.20 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

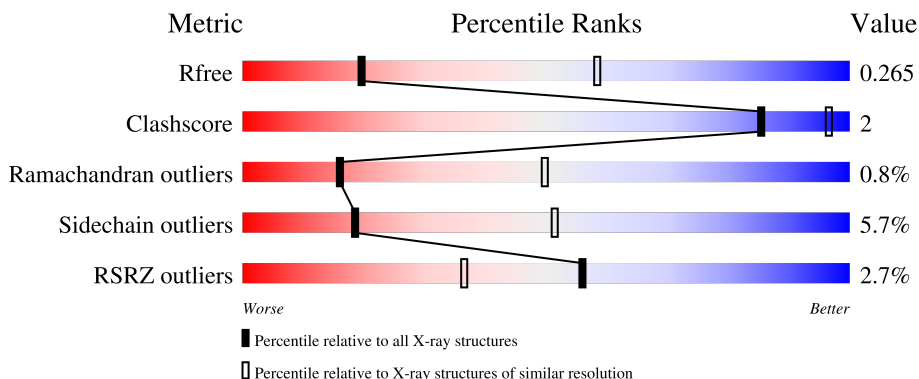
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	264	2% 66% 8% 25%
1	B	264	2% 58% 9% 33%
2	C	2	100%
2	D	2	100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3079 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 NEOGENIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	197	Total	C	N	O	S	0	0	0
			1555	990	265	294	6			
1	B	176	Total	C	N	O	S	0	0	0
			1398	901	233	260	4			

There are 26 discrepancies between the modelled and reference sequences:

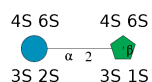
Chain	Residue	Modelled	Actual	Comment	Reference
A	880	GLU	-	expression tag	UNP P97798
A	881	THR	-	expression tag	UNP P97798
A	882	GLY	-	expression tag	UNP P97798
A	1134	ASN	-	expression tag	UNP P97798
A	1135	GLY	-	expression tag	UNP P97798
A	1136	THR	-	expression tag	UNP P97798
A	1137	LYS	-	expression tag	UNP P97798
A	1138	HIS	-	expression tag	UNP P97798
A	1139	HIS	-	expression tag	UNP P97798
A	1140	HIS	-	expression tag	UNP P97798
A	1141	HIS	-	expression tag	UNP P97798
A	1142	HIS	-	expression tag	UNP P97798
A	1143	HIS	-	expression tag	UNP P97798
B	880	GLU	-	expression tag	UNP P97798
B	881	THR	-	expression tag	UNP P97798
B	882	GLY	-	expression tag	UNP P97798
B	1134	ASN	-	expression tag	UNP P97798
B	1135	GLY	-	expression tag	UNP P97798
B	1136	THR	-	expression tag	UNP P97798
B	1137	LYS	-	expression tag	UNP P97798
B	1138	HIS	-	expression tag	UNP P97798
B	1139	HIS	-	expression tag	UNP P97798
B	1140	HIS	-	expression tag	UNP P97798
B	1141	HIS	-	expression tag	UNP P97798
B	1142	HIS	-	expression tag	UNP P97798

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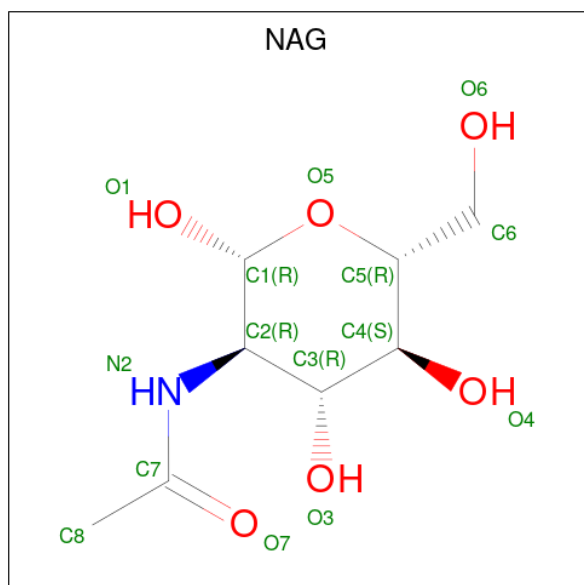
Chain	Residue	Modelled	Actual	Comment	Reference
B	1143	HIS	-	expression tag	UNP P97798

- Molecule 2 is an oligosaccharide called 1,3,4,6-tetra-O-sulfo-beta-D-fructofuranose-(2-1)-2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	O	S	0	0	0
			55	12	35	8			
2	D	2	Total	C	O	S	0	0	0
			55	12	35	8			

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

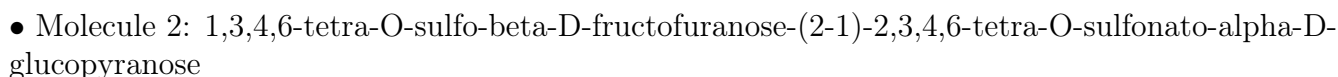
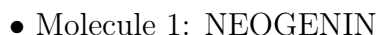


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Na 1	0	0
4	B	1	Total 1	Na 1	0	0

- Molecule 1: NEOGENIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	96.16Å 157.84Å 89.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.20 30.00 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (30.00-3.20) 99.3 (30.00-3.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 3.19Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.217 , 0.259 0.227 , 0.265	Depositor DCC
R_{free} test set	554 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	79.6	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 81.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.000 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.003 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3079	wwPDB-VP
Average B, all atoms (Å ²)	102.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 37.62 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.1721e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: YYJ, NAG, GU4, NA

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	0.84	0/1596	1.20	3/2181 (0.1%)
1	B	0.78	0/1437	1.16	4/1966 (0.2%)
All	All	0.81	0/3033	1.18	7/4147 (0.2%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1067	ASN	CA-CB-CG	6.10	118.70	112.60
1	B	1042	VAL	N-CA-CB	5.87	117.53	110.95
1	A	1067	ASN	CA-CB-CG	5.69	118.29	112.60
1	A	954	ASN	CA-CB-CG	5.44	118.04	112.60
1	B	1061	PHE	N-CA-C	5.34	117.10	108.34

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	1555	0	1545	7	0
1	B	1398	0	1387	7	0
2	C	55	0	6	0	0
2	D	55	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	14	0	13	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
All	All	3079	0	2957	13	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.

The worst 5 of 13 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:1005:ILE:HG13	1:A:1049:GLN:HG3	1.94	0.49
1:B:1064:GLN:HB3	1:B:1074:MET:HG2	1.94	0.49
1:B:953:PRO:HB2	1:B:1015:ASN:HB3	1.95	0.48
1:B:1005:ILE:HG13	1:B:1049:GLN:HG3	1.96	0.48
1:A:1064:GLN:HB3	1:A:1074:MET:HG2	1.97	0.47

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	193/264 (73%)	181 (94%)	10 (5%)	2 (1%)	12	45
1	B	170/264 (64%)	160 (94%)	9 (5%)	1 (1%)	21	56
All	All	363/528 (69%)	341 (94%)	19 (5%)	3 (1%)	16	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1015	ASN

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Mol	Chain	Res	Type
1	B	1015	ASN
1	A	883	THR

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	175/232 (75%)	165 (94%)	10 (6%)	18	51
1	B	156/232 (67%)	147 (94%)	9 (6%)	18	51
All	All	331/464 (71%)	312 (94%)	19 (6%)	18	51

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	996	SER
1	B	1076	GLU
1	B	1082	THR
1	B	1032	GLU
1	A	1076	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	1009	GLN
1	A	1079	GLN
1	B	1009	GLN
1	B	1049	GLN
1	B	1079	GLN

5.3.3 RNA [i](#)

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 ⓘ

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	GU4	C	1	2	27,27,28	1.88	11 (40%)	32,43,45	2.11	9 (28%)
2	YYJ	C	2	2	27,28,28	2.12	3 (11%)	33,46,46	2.06	8 (24%)
2	GU4	D	1	2	27,27,28	1.80	6 (22%)	32,43,45	1.75	6 (18%)
2	YYJ	D	2	2	27,28,28	1.73	3 (11%)	33,46,46	1.61	3 (9%)

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	GU4	C	1	2	-	10/21/38/41	0/1/1/1
2	YYJ	C	2	2	-	11/23/42/42	0/1/1/1
2	GU4	D	1	2	-	8/21/38/41	0/1/1/1
2	YYJ	D	2	2	-	6/23/42/42	0/1/1/1

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	YYJ	O2-C2	6.55	1.52	1.40
2	D	2	YYJ	O2-C2	5.78	1.50	1.40
2	C	2	YYJ	O5-C2	5.73	1.52	1.43
2	C	1	GU4	C3-C4	4.53	1.61	1.52
2	D	1	GU4	C3-C4	4.02	1.60	1.52

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	GU4	O2-C2-C3	7.17	114.59	106.65
2	D	2	YYJ	C3-O3-S3	6.65	125.92	117.69
2	C	2	YYJ	O5-C5-C6	5.75	123.03	109.50
2	D	1	GU4	O2-C2-C3	4.96	112.15	106.65
2	C	2	YYJ	O4-C4-C3	4.50	118.69	108.91

There are no chirality outliers.

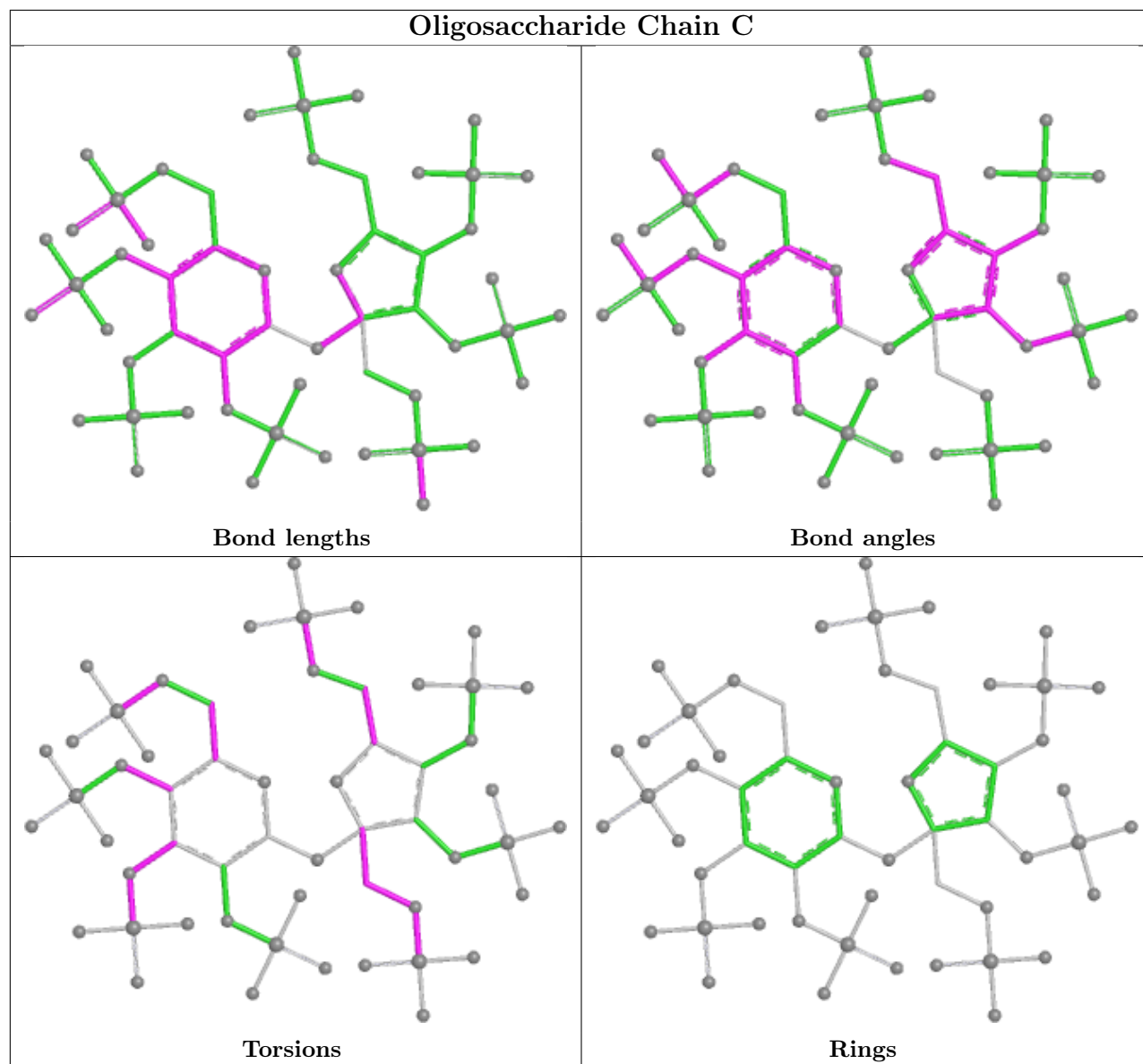
5 of 35 torsion outliers are listed below:

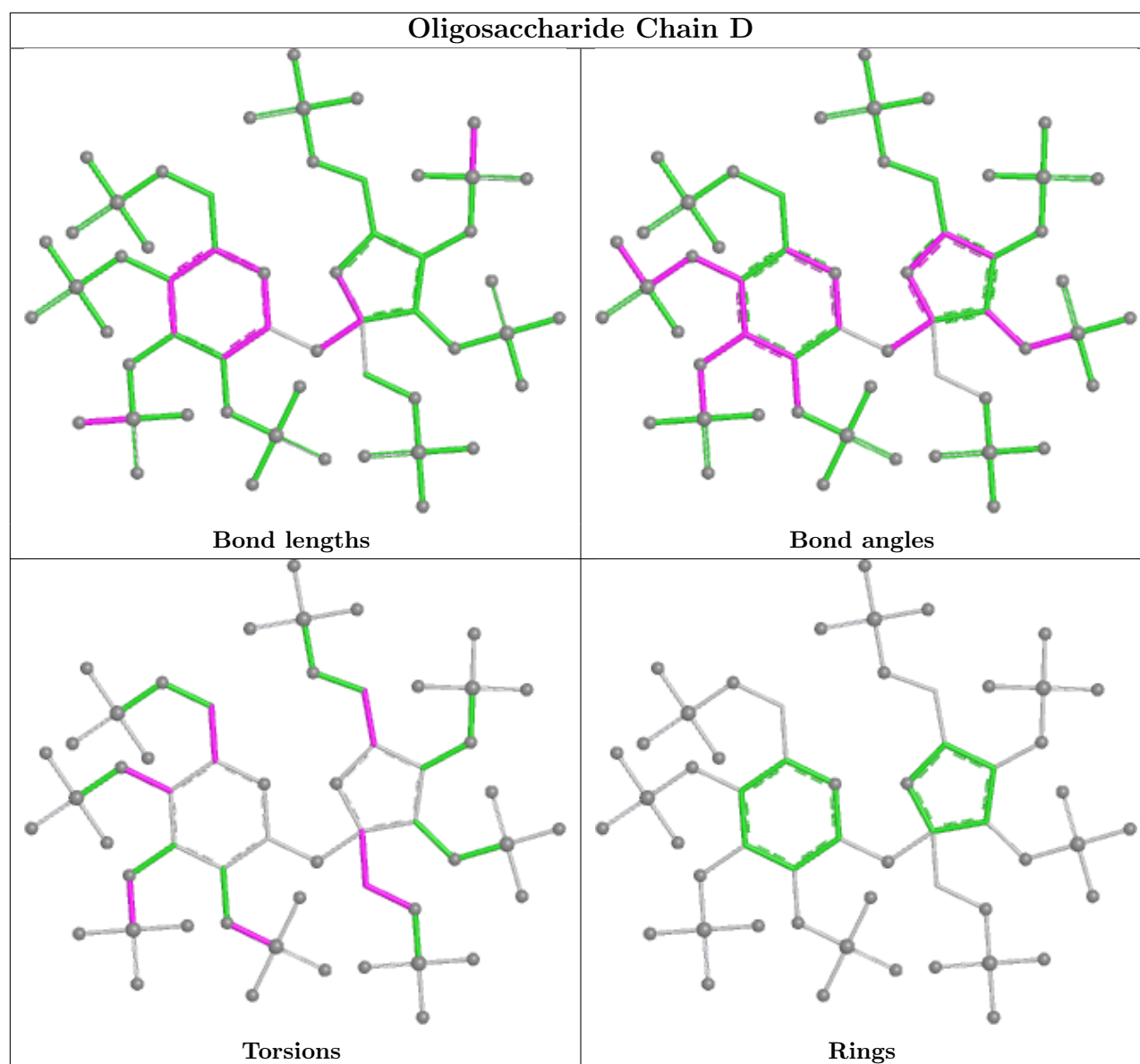
Mol	Chain	Res	Type	Atoms
2	C	1	GU4	O5-C5-C6-O6
2	C	1	GU4	C5-C4-O4-S4
2	C	1	GU4	C3-C4-O4-S4
2	C	1	GU4	C3-O3-S3-O29
2	C	1	GU4	C3-O3-S3-O27

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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
3	NAG	A	2085	1	14,14,15	0.37	0	17,19,21	0.62	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	A	2085	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 [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	197/264 (74%)	-0.13	4 (2%) 65 45	47, 77, 126, 145	0
1	B	176/264 (66%)	0.23	6 (3%) 48 30	57, 116, 178, 201	0
All	All	373/528 (70%)	0.04	10 (2%) 56 36	47, 91, 167, 201	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1044	ASN	3.8
1	A	881	THR	3.4
1	B	887	PRO	2.9
1	B	922	TYR	2.7
1	A	910	LEU	2.6

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](#)

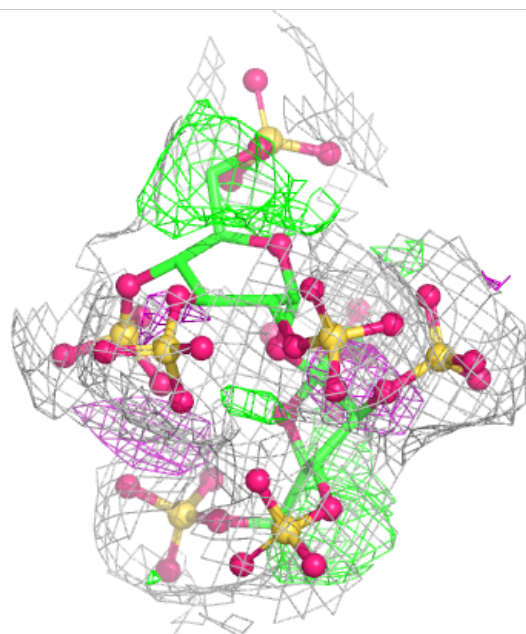
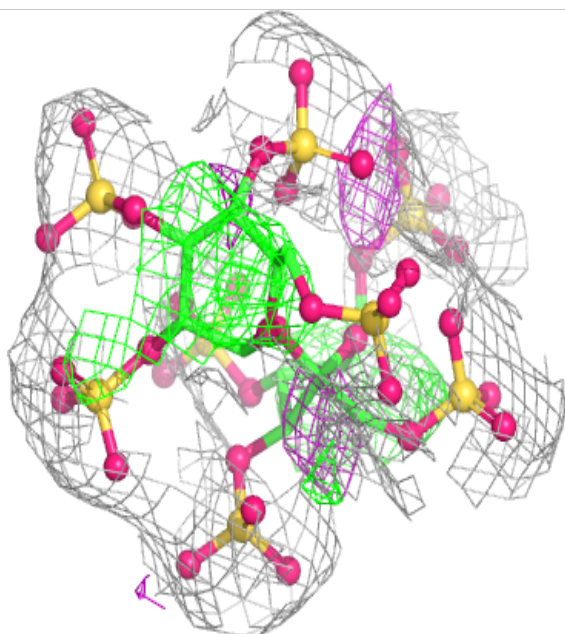
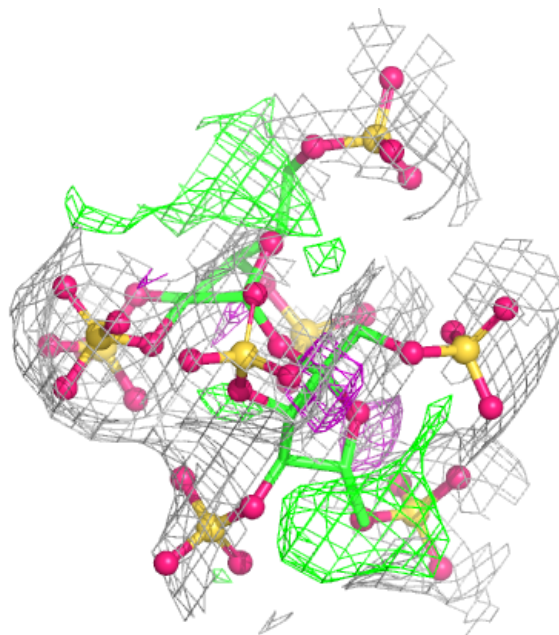
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

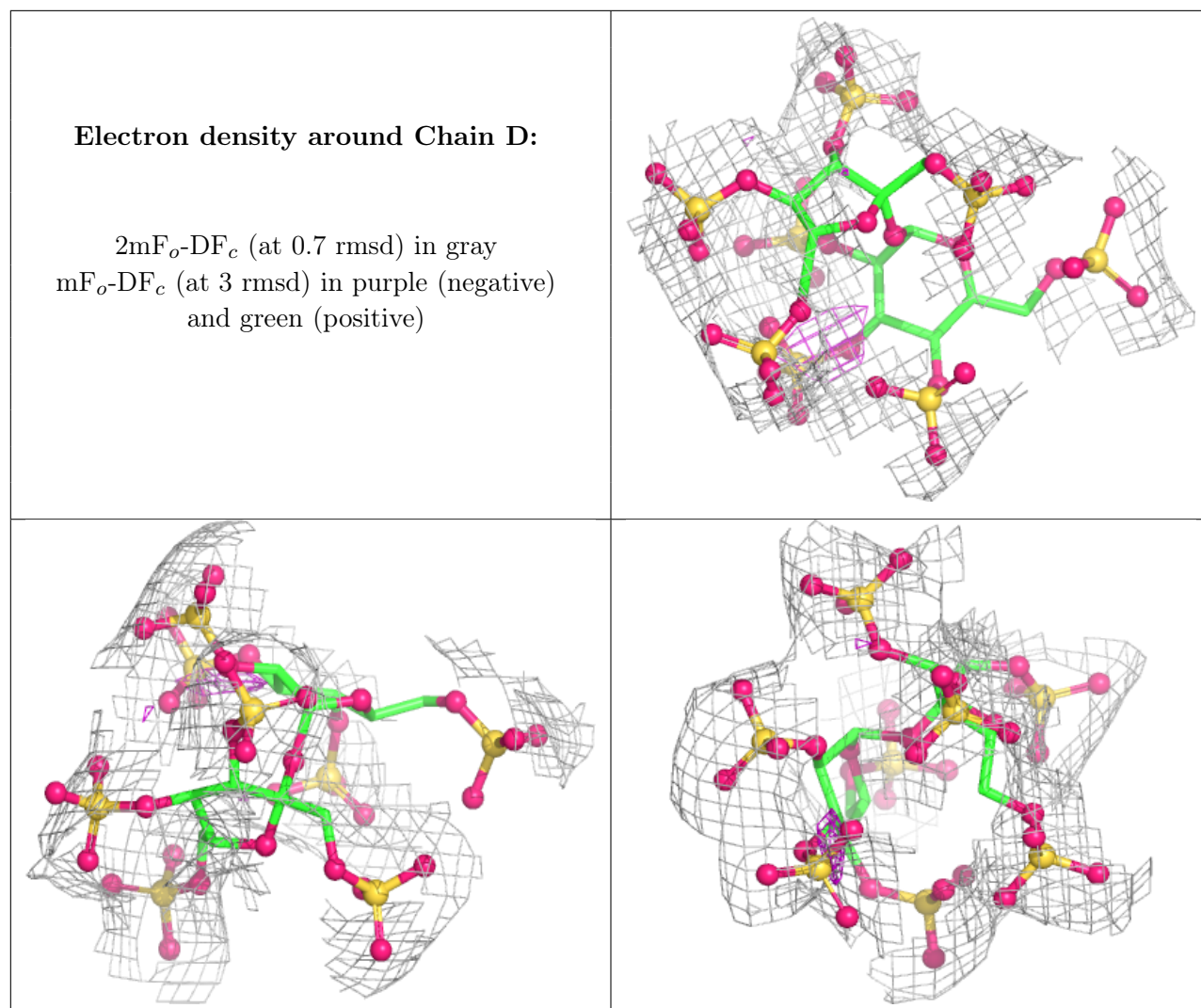
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	YYJ	D	2	28/28	0.52	0.11	233,238,243,243	0
2	GU4	D	1	27/28	0.54	0.10	228,235,245,246	0
2	GU4	C	1	27/28	0.71	0.13	136,151,180,180	0
2	YYJ	C	2	28/28	0.71	0.14	142,169,177,178	0

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($\text{\AA}^2$)	Q<0.9
3	NAG	A	2085	14/15	0.81	0.11	102,107,115,119	0
4	NA	B	2084	1/1	0.89	0.11	71,71,71,71	0
4	NA	A	2086	1/1	0.98	0.08	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.