wwPDB X-ray Structure Validation Summary Report (i)

Mar 5, 2026 – 01:00 AM UTC

PDB ID	:	5NH3 / pdb_00005nh3
Title	:	CRYSTAL STRUCTURE OF THE Activin receptor type-2A LIGAND BINDING DOMAIN IN COMPLEX WITH BIMAGRUMAB FV
Authors	:	Scheufler, C.
Deposited on	:	2017-03-21
Resolution	:	2.35 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 (i) 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 (1)) were used in the production of this report:

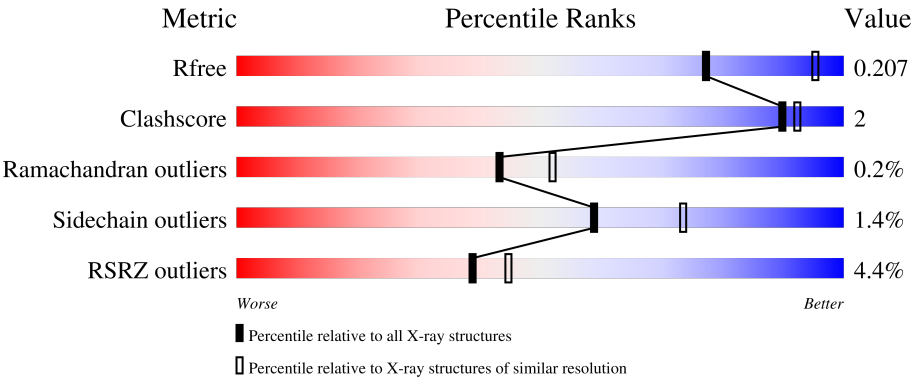
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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 <=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	122	10% 70% 7% 23%
1	B	122	9% 70% 7% 22%
2	H	121	% 88% 6% 6%
2	I	121	% 90% 6%
3	L	119	2% 87% 7% 7%

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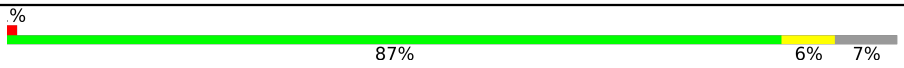
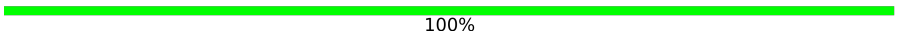
Mol	Chain	Length	Quality of chain
3	M	119	
4	C	2	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5263 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 Activin receptor type-2A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	94	Total	C	N	O	S	0	0	0
			730	455	122	142	11			
1	B	95	Total	C	N	O	S	0	0	0
			745	467	123	144	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	136	GLU	-	expression tag	UNP P27037
A	137	PHE	-	expression tag	UNP P27037
A	138	ARG	-	expression tag	UNP P27037
A	139	HIS	-	expression tag	UNP P27037
A	140	ASP	-	expression tag	UNP P27037
A	141	SER	-	expression tag	UNP P27037
B	136	GLU	-	expression tag	UNP P27037
B	137	PHE	-	expression tag	UNP P27037
B	138	ARG	-	expression tag	UNP P27037
B	139	HIS	-	expression tag	UNP P27037
B	140	ASP	-	expression tag	UNP P27037
B	141	SER	-	expression tag	UNP P27037

- Molecule 2 is a protein called anti-human ActRIIB mAb BYM338 Fv heavy-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	114	Total	C	N	O	S	0	0	0
			871	549	148	169	5			
2	I	114	Total	C	N	O	S	0	0	0
			870	548	148	169	5			

- Molecule 3 is a protein called anti-human ActRIIB mAb BYM338 Fv light-chain.

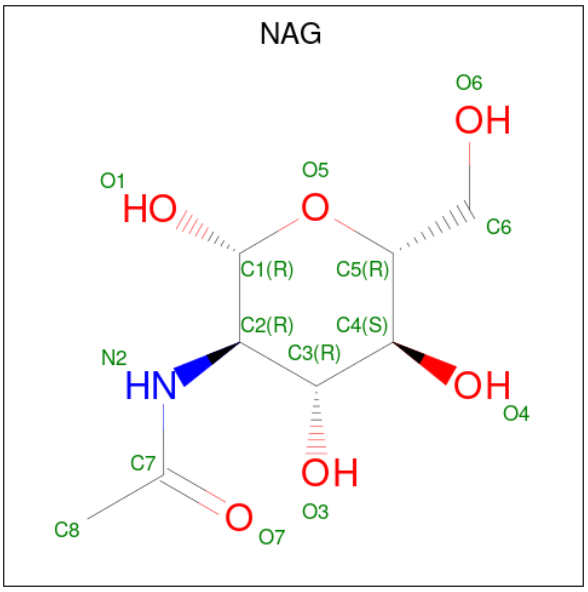
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	111	Total	C	N	O	S	0	0	0
			805	505	133	164	3			
3	M	111	Total	C	N	O	S	0	0	0
			811	508	135	165	3			

- Molecule 4 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
4	C	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

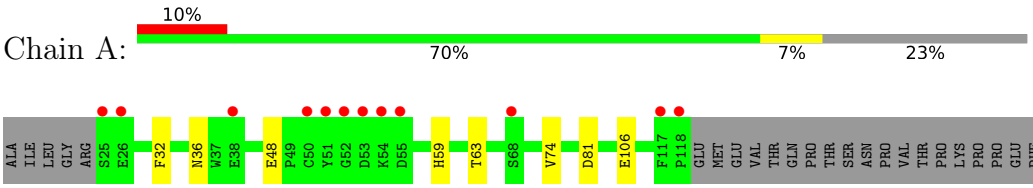
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	37	Total O 37 37	0	0
6	B	28	Total O 28 28	0	0
6	H	78	Total O 78 78	0	0
6	I	71	Total O 71 71	0	0
6	L	77	Total O 77 77	0	0
6	M	70	Total O 70 70	0	0

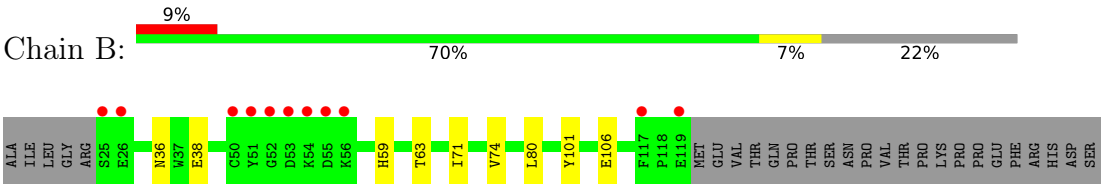
3 Residue-property plots (i)

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.

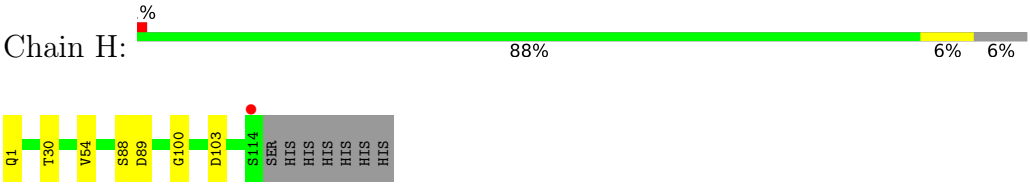
• Molecule 1: Activin receptor type-2A



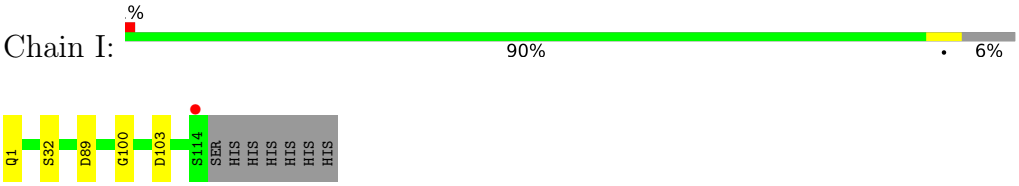
• Molecule 1: Activin receptor type-2A



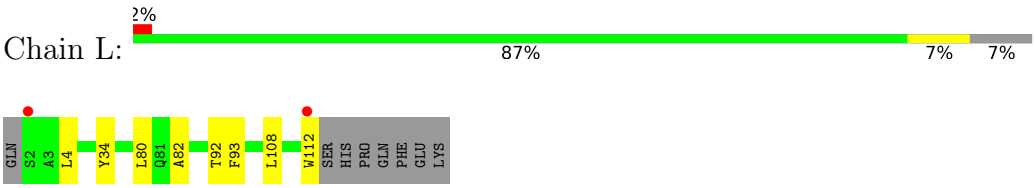
• Molecule 2: anti-human ActRIIB mAb BYM338 Fv heavy-chain



• Molecule 2: anti-human ActRIIB mAb BYM338 Fv heavy-chain

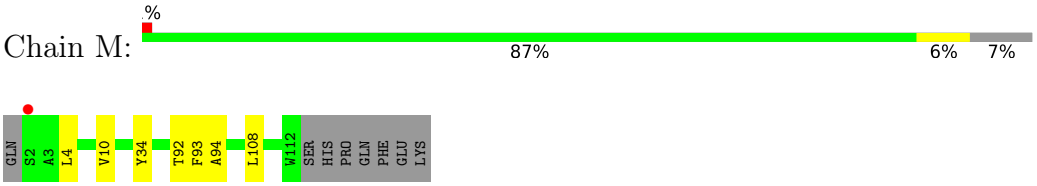


• Molecule 3: anti-human ActRIIB mAb BYM338 Fv light-chain



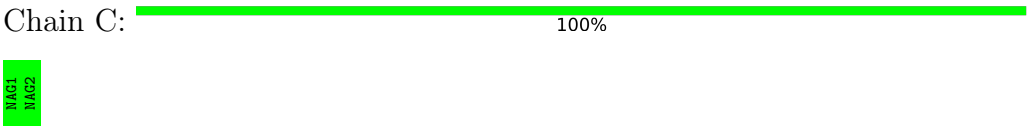
• Molecule 3: anti-human ActRIIB mAb BYM338 Fv light-chain

Chain M:



• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.33Å 108.21Å 100.69Å 90.00° 98.25° 90.00°	Depositor
Resolution (Å)	47.55 – 2.35 47.55 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.9 (47.55-2.35) 97.9 (47.55-2.35)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.90 (at 2.34Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.166 , 0.208 0.164 , 0.207	Depositor DCC
R_{free} test set	1917 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	33.4	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 58.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5263	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.80% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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, PCA

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	0/748	1.13	0/1015
1	B	0.86	0/764	1.17	0/1035
2	H	0.79	0/884	1.07	2/1202 (0.2%)
2	I	0.81	0/883	1.06	2/1201 (0.2%)
3	L	0.86	0/825	1.08	0/1122
3	M	0.83	0/831	1.07	0/1128
All	All	0.83	0/4935	1.09	4/6703 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	89	ASP	CA-CB-CG	5.99	118.59	112.60
2	I	103	ASP	CA-CB-CG	5.99	118.59	112.60
2	I	89	ASP	CA-CB-CG	5.79	118.39	112.60
2	H	103	ASP	CA-CB-CG	5.46	118.06	112.60

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	730	0	617	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	745	0	635	4	0
2	H	871	0	834	3	0
2	I	870	0	832	3	0
3	L	805	0	749	5	0
3	M	811	0	768	4	0
4	C	28	0	25	0	0
5	A	28	0	26	0	0
5	B	14	0	13	0	0
6	A	37	0	0	0	0
6	B	28	0	0	0	0
6	H	78	0	0	0	0
6	I	71	0	0	0	0
6	L	77	0	0	0	0
6	M	70	0	0	0	0
All	All	5263	0	4499	17	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 17 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:32:PHE:HB2	1:A:48:GLU:HB2	1.89	0.55
1:B:63:THR:HG23	1:B:74:VAL:HB	1.91	0.53
1:A:63:THR:HG23	1:A:74:VAL:HB	1.93	0.50
3:L:80:LEU:HD11	3:L:108:LEU:HD21	1.95	0.49
1:A:59:HIS:HD1	1:A:106:GLU:HG2	1.78	0.48

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	92/122 (75%)	89 (97%)	2 (2%)	1 (1%)	11 11
1	B	93/122 (76%)	90 (97%)	3 (3%)	0	100 100
2	H	112/121 (93%)	111 (99%)	1 (1%)	0	100 100
2	I	112/121 (93%)	111 (99%)	1 (1%)	0	100 100
3	L	109/119 (92%)	104 (95%)	5 (5%)	0	100 100
3	M	109/119 (92%)	104 (95%)	5 (5%)	0	100 100
All	All	627/724 (87%)	609 (97%)	17 (3%)	1 (0%)	43 52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	ASP

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	75/113 (66%)	74 (99%)	1 (1%)	61 76
1	B	77/113 (68%)	74 (96%)	3 (4%)	28 39
2	H	91/100 (91%)	90 (99%)	1 (1%)	65 79
2	I	91/100 (91%)	91 (100%)	0	100 100
3	L	84/95 (88%)	83 (99%)	1 (1%)	63 77
3	M	87/95 (92%)	86 (99%)	1 (1%)	65 79
All	All	505/616 (82%)	498 (99%)	7 (1%)	59 73

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	71	ILE
2	H	88	SER
3	M	34	TYR
3	L	34	TYR

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Mol	Chain	Res	Type
1	B	38	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	81	GLN
3	M	40	GLN
3	L	40	GLN
2	I	43	GLN
3	L	81	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	PCA	I	1	2	7,8,9	1.31	1 (14%)	9,10,12	1.54	1 (11%)
2	PCA	H	1	2	7,8,9	1.42	1 (14%)	9,10,12	1.86	2 (22%)

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	PCA	I	1	2	-	0/0/11/13	0/1/1/1
2	PCA	H	1	2	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	PCA	CD-N	2.88	1.41	1.34
2	I	1	PCA	CD-N	2.18	1.39	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	1	PCA	CB-CA-C	-3.69	107.60	112.66
2	I	1	PCA	CB-CA-C	-3.21	108.25	112.66
2	H	1	PCA	OE-CD-CG	-2.46	122.33	126.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

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	$\#\|Z\| > 2$
4	NAG	C	1	4,1	14,14,15	0.34	0	17,19,21	0.73	0
4	NAG	C	2	4	14,14,15	0.34	0	17,19,21	0.60	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	C	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	C	2	4	-	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.

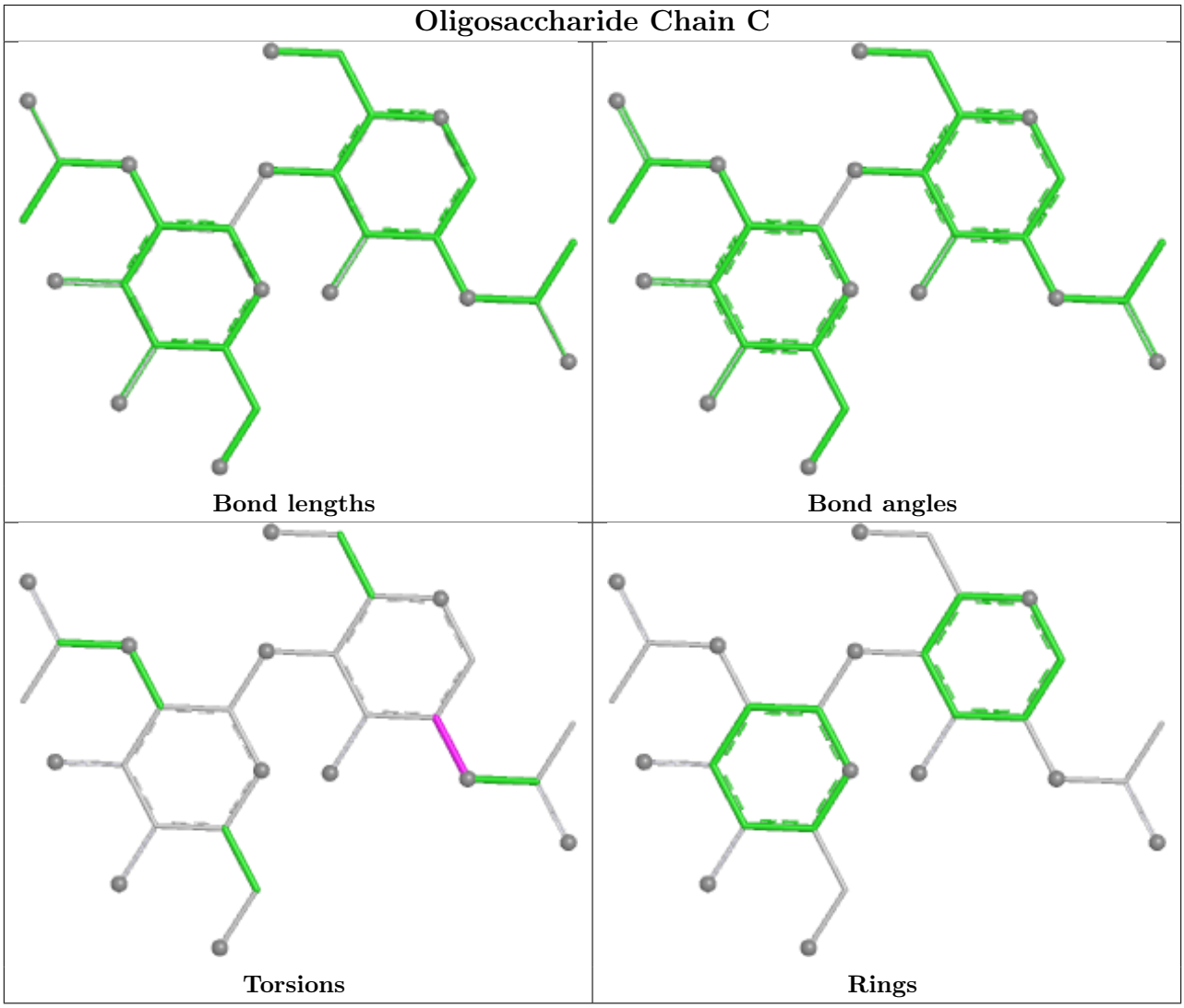
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1	NAG	C1-C2-N2-C7

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)

3 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	$\#\|Z\| > 2$
5	NAG	B	501	1	14,14,15	0.32	0	17,19,21	0.54	0
5	NAG	A	501	1	14,14,15	0.36	0	17,19,21	0.69	1 (5%)
5	NAG	A	502	1	14,14,15	0.33	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
5	NAG	B	501	1	-	0/6/23/26	0/1/1/1
5	NAG	A	501	1	-	2/6/23/26	0/1/1/1
5	NAG	A	502	1	-	1/6/23/26	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(^{o})	Ideal(^{o})
5	A	501	NAG	C1-O5-C5	2.24	115.19	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	NAG	O5-C5-C6-O6
5	A	501	NAG	C4-C5-C6-O6
5	A	502	NAG	C1-C2-N2-C7

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

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	94/122 (77%)	0.26	12 (12%) 7 9	26, 44, 74, 85	0
1	B	95/122 (77%)	0.33	11 (11%) 9 11	27, 45, 76, 90	0
2	H	113/121 (93%)	-0.57	1 (0%) 81 84	20, 31, 49, 70	0
2	I	113/121 (93%)	-0.40	1 (0%) 81 84	24, 36, 55, 88	0
3	L	111/119 (93%)	-0.42	2 (1%) 67 72	21, 30, 48, 93	0
3	M	111/119 (93%)	-0.39	1 (0%) 81 84	25, 33, 50, 58	0
All	All	637/724 (87%)	-0.22	28 (4%) 39 45	20, 36, 65, 93	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	I	114	SER	5.0
1	B	53	ASP	5.0
3	L	2	SER	4.6
1	A	53	ASP	4.5
3	L	112	TRP	4.2

6.2 Non-standard residues in protein, DNA, RNA chains

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.

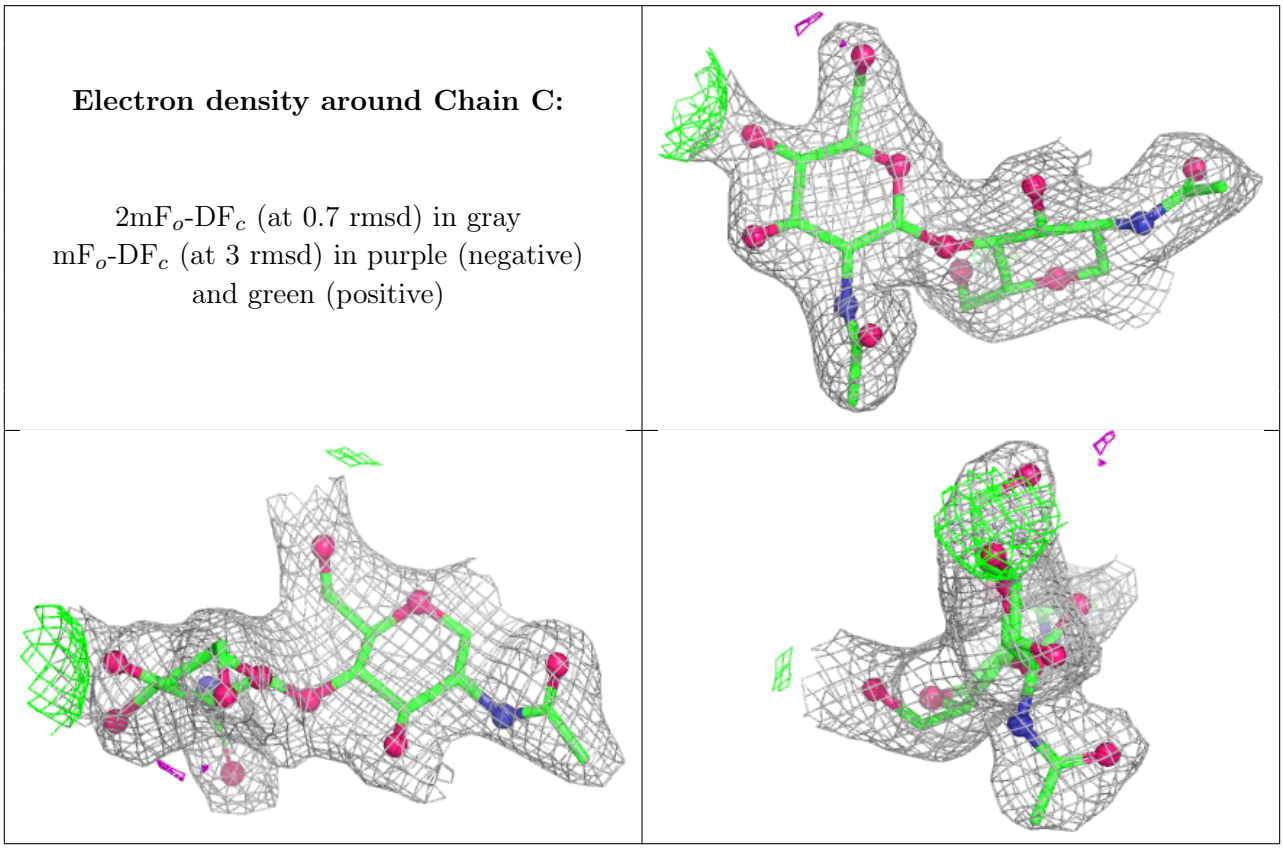
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	PCA	H	1	8/9	0.82	0.16	47,57,62,66	0
2	PCA	I	1	8/9	0.84	0.14	51,58,63,66	0

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	C	1	14/15	-	-	25,40,52,55	0
4	NAG	C	2	14/15	-	-	57,67,70,75	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(Å^2)	Q<0.9
5	NAG	B	501	14/15	0.57	0.16	100,104,108,112	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NAG	A	501	14/15	0.78	0.14	69,75,81,84	0
5	NAG	A	502	14/15	0.84	0.16	49,72,85,87	0

6.5 Other polymers (i)

There are no such residues in this entry.