



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:03 AM UTC

PDB ID : 4J6G / pdb_00004j6g
Title : CRYSTAL STRUCTURE OF LIGHT AND DcR3 COMPLEX
Authors : Liu, W.; Zhan, C.; Bonanno, J.B.; Bhosle, R.C.; Nathenson, S.G.; Almo, S.C.; Atoms-to-Animals: The Immune Function Network (IFN); New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2013-02-11
Resolution : 2.40 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

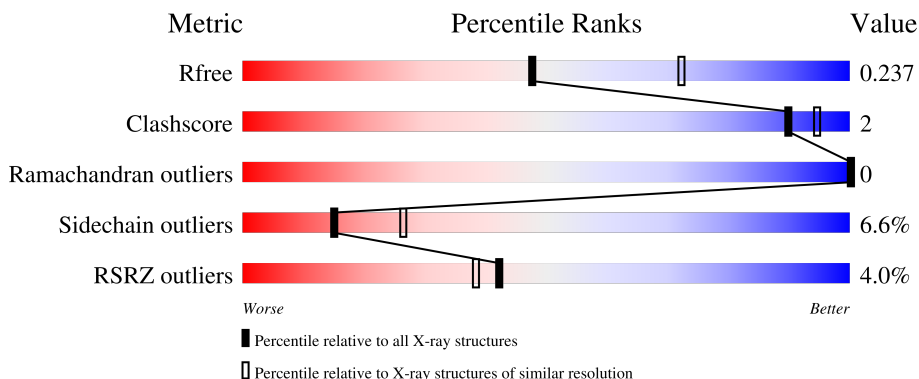
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	165	
1	B	165	
2	C	174	
2	D	174	
3	E	4	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4726 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 Tumor necrosis factor ligand superfamily member 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	139	Total	C	N	O	S	0	0	0
			1072	686	186	197	3			
1	B	139	Total	C	N	O	S	0	1	0
			1080	691	189	197	3			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	76	HIS	-	expression tag	UNP O43557
A	77	HIS	-	expression tag	UNP O43557
A	78	HIS	-	expression tag	UNP O43557
A	79	HIS	-	expression tag	UNP O43557
A	80	HIS	-	expression tag	UNP O43557
A	81	HIS	-	expression tag	UNP O43557
A	82	GLY	-	expression tag	UNP O43557
A	214	GLU	LYS	engineered mutation	UNP O43557
B	76	HIS	-	expression tag	UNP O43557
B	77	HIS	-	expression tag	UNP O43557
B	78	HIS	-	expression tag	UNP O43557
B	79	HIS	-	expression tag	UNP O43557
B	80	HIS	-	expression tag	UNP O43557
B	81	HIS	-	expression tag	UNP O43557
B	82	GLY	-	expression tag	UNP O43557
B	214	GLU	LYS	engineered mutation	UNP O43557

- Molecule 2 is a protein called Tumor necrosis factor receptor superfamily member 6B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	163	Total	C	N	O	S	0	0	0
			1233	747	235	233	18			
2	D	162	Total	C	N	O	S	0	0	0
			1227	744	234	231	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	196	THR	-	expression tag	UNP O95407
C	197	GLY	-	expression tag	UNP O95407
C	198	HIS	-	expression tag	UNP O95407
C	199	HIS	-	expression tag	UNP O95407
C	200	HIS	-	expression tag	UNP O95407
C	201	HIS	-	expression tag	UNP O95407
C	202	HIS	-	expression tag	UNP O95407
C	203	HIS	-	expression tag	UNP O95407
D	196	THR	-	expression tag	UNP O95407
D	197	GLY	-	expression tag	UNP O95407
D	198	HIS	-	expression tag	UNP O95407
D	199	HIS	-	expression tag	UNP O95407
D	200	HIS	-	expression tag	UNP O95407
D	201	HIS	-	expression tag	UNP O95407
D	202	HIS	-	expression tag	UNP O95407
D	203	HIS	-	expression tag	UNP O95407

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	D	1	Total	C	N	O	0	0
			14	8	1	5		

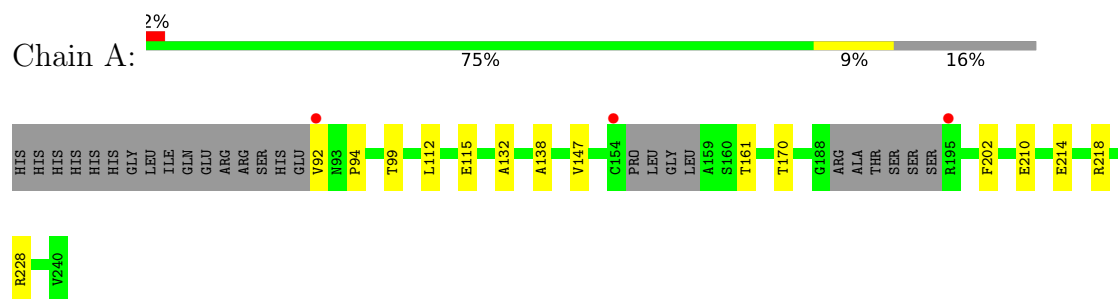
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	18	Total	O	0	0
			18	18		
7	B	15	Total	O	0	0
			15	15		
7	C	7	Total	O	0	0
			7	7		
7	D	6	Total	O	0	0
			6	6		

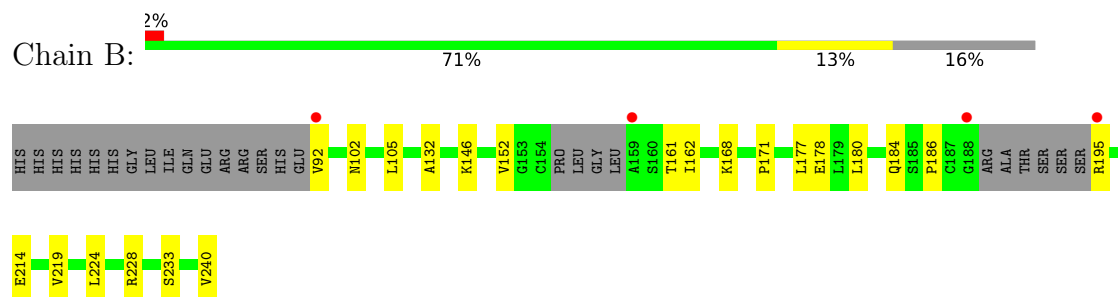
3 Residue-property plots [i](#)

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.

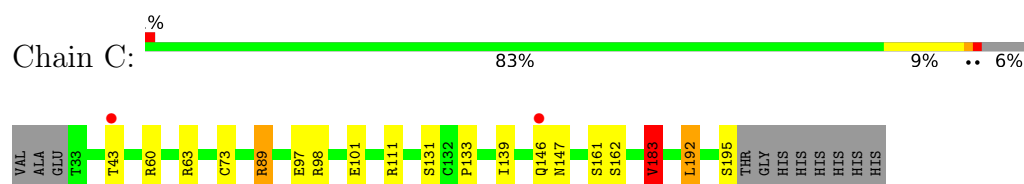
- Molecule 1: Tumor necrosis factor ligand superfamily member 14



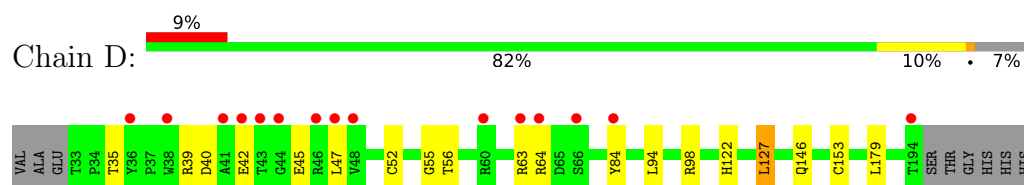
- Molecule 1: Tumor necrosis factor ligand superfamily member 14



- Molecule 2: Tumor necrosis factor receptor superfamily member 6B



- Molecule 2: Tumor necrosis factor receptor superfamily member 6B



- Molecule 3: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

100%

MAG1
MAG2
BGLA3
MAIN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	149.06Å 149.06Å 149.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 2.40 19.93 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (19.93-2.40) 99.8 (19.93-2.40)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.62 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.194 , 0.232 0.200 , 0.237	Depositor DCC
R_{free} test set	2175 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 28.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.028 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4726	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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, BMA, NAG, MG, CL

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	1.31	4/1096 (0.4%)	1.14	2/1485 (0.1%)
1	B	1.20	2/1107 (0.2%)	1.15	0/1499
2	C	1.17	3/1271 (0.2%)	1.16	5/1736 (0.3%)
2	D	1.05	0/1265	1.10	5/1728 (0.3%)
All	All	1.18	9/4739 (0.2%)	1.14	12/6448 (0.2%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	GLU	N-CA	7.06	1.53	1.45
2	C	133	PRO	CA-C	6.47	1.58	1.52
1	A	202	PHE	C-O	-6.42	1.15	1.24
1	B	180	LEU	C-O	-5.67	1.17	1.23
1	B	171	PRO	C-O	-5.58	1.16	1.24

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	183	VAL	CB-CA-C	7.81	118.05	110.16
2	D	153	CYS	CA-C-N	-6.41	113.78	120.38
2	D	153	CYS	C-N-CA	-6.41	113.78	120.38
2	D	84	TYR	CA-CB-CG	6.05	124.79	113.90
2	C	89	ARG	NE-CZ-NH2	5.98	124.59	119.20

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	1072	0	1055	2	0
1	B	1080	0	1068	7	0
2	C	1233	0	1123	4	0
2	D	1227	0	1118	4	0
3	E	50	0	43	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	D	14	0	13	0	0
7	A	18	0	0	0	0
7	B	15	0	0	0	0
7	C	7	0	0	0	0
7	D	6	0	0	0	0
All	All	4726	0	4420	16	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 16 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:B:162:ILE:HD11	1:B:224:LEU:HD13	1.89	0.55
2:C:60:ARG:HD2	2:C:63:ARG:NH2	2.23	0.54
1:B:152:VAL:O	1:B:152:VAL:HG23	2.11	0.50
2:D:52:CYS:HB3	2:D:56:THR:OG1	2.15	0.46
1:A:132:ALA:HB1	1:A:214:GLU:HB3	1.97	0.46

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	133/165 (81%)	130 (98%)	3 (2%)	0	100	100
1	B	134/165 (81%)	131 (98%)	3 (2%)	0	100	100
2	C	161/174 (92%)	153 (95%)	8 (5%)	0	100	100
2	D	160/174 (92%)	153 (96%)	7 (4%)	0	100	100
All	All	588/678 (87%)	567 (96%)	21 (4%)	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	112/135 (83%)	107 (96%)	5 (4%)	24	42
1	B	113/135 (84%)	103 (91%)	10 (9%)	9	15
2	C	137/146 (94%)	127 (93%)	10 (7%)	13	22
2	D	136/146 (93%)	127 (93%)	9 (7%)	15	26
All	All	498/562 (89%)	464 (93%)	34 (7%)	15	25

5 of 34 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	63	ARG
2	D	64	ARG
2	D	146	GLN

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Continued from previous page...

Mol	Chain	Res	Type
1	B	228[A]	ARG
1	B	219	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	102	ASN
2	D	109	HIS
2	D	151	GLN
1	A	183	GLN
1	A	93	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 ⓘ

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	$\# Z > 2$
3	NAG	E	1	3,2	14,14,15	1.46	2 (14%)	17,19,21	2.98	10 (58%)
3	NAG	E	2	3	14,14,15	0.90	0	17,19,21	1.87	5 (29%)
3	BMA	E	3	3	11,11,12	1.15	1 (9%)	15,15,17	2.54	4 (26%)
3	MAN	E	4	3	11,11,12	1.03	1 (9%)	15,15,17	1.86	5 (33%)

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	E	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	E	2	3	-	0/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	2/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4	MAN	C2-C3	2.88	1.56	1.52
3	E	1	NAG	C6-C5	2.17	1.59	1.51
3	E	3	BMA	O3-C3	2.09	1.48	1.43
3	E	1	NAG	C4-C5	2.04	1.57	1.53

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	BMA	C1-O5-C5	7.50	122.23	112.19
3	E	1	NAG	C1-O5-C5	6.11	120.38	112.19
3	E	1	NAG	C3-C4-C5	5.18	119.62	110.23
3	E	4	MAN	C1-O5-C5	4.47	118.17	112.19
3	E	3	BMA	O3-C3-C2	4.14	118.51	110.05

There are no chirality outliers.

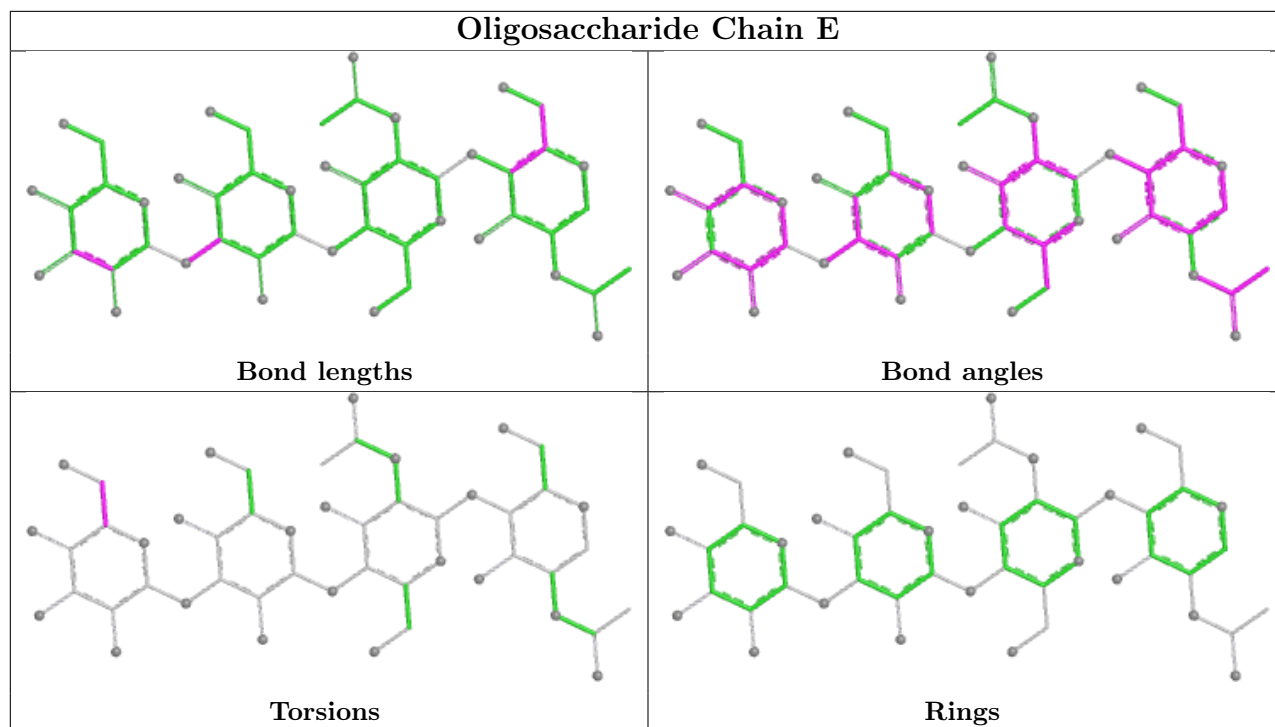
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	4	MAN	O5-C5-C6-O6
3	E	4	MAN	C4-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](#)

Of 5 ligands modelled in this entry, 4 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	$\# Z > 2$
6	NAG	D	301	2	14,14,15	1.31	1 (7%)	17,19,21	2.51	6 (35%)

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	NAG	D	301	2	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	D	301	NAG	C4-C3	2.05	1.57	1.52

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	D	301	NAG	C1-O5-C5	6.45	120.83	112.19
6	D	301	NAG	O5-C1-C2	-3.75	105.49	111.29
6	D	301	NAG	O7-C7-C8	-3.57	115.70	122.05
6	D	301	NAG	O5-C5-C6	3.07	113.64	107.66
6	D	301	NAG	O4-C4-C5	2.62	115.77	109.32

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	301	NAG	C4-C5-C6-O6

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	139/165 (84%)	-0.56	3 (2%) 62 58	18, 28, 54, 84	0
1	B	139/165 (84%)	-0.54	4 (2%) 53 50	21, 31, 51, 73	1 (0%)
2	C	163/174 (93%)	-0.10	2 (1%) 76 73	25, 42, 63, 88	0
2	D	162/174 (93%)	0.34	15 (9%) 14 11	29, 48, 107, 120	0
All	All	603/678 (88%)	-0.19	24 (3%) 42 38	18, 38, 69, 120	1 (0%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	38	TRP	4.2
2	D	41	ALA	4.2
2	D	64	ARG	3.5
2	D	63	ARG	3.3
2	D	46	ARG	3.1

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.

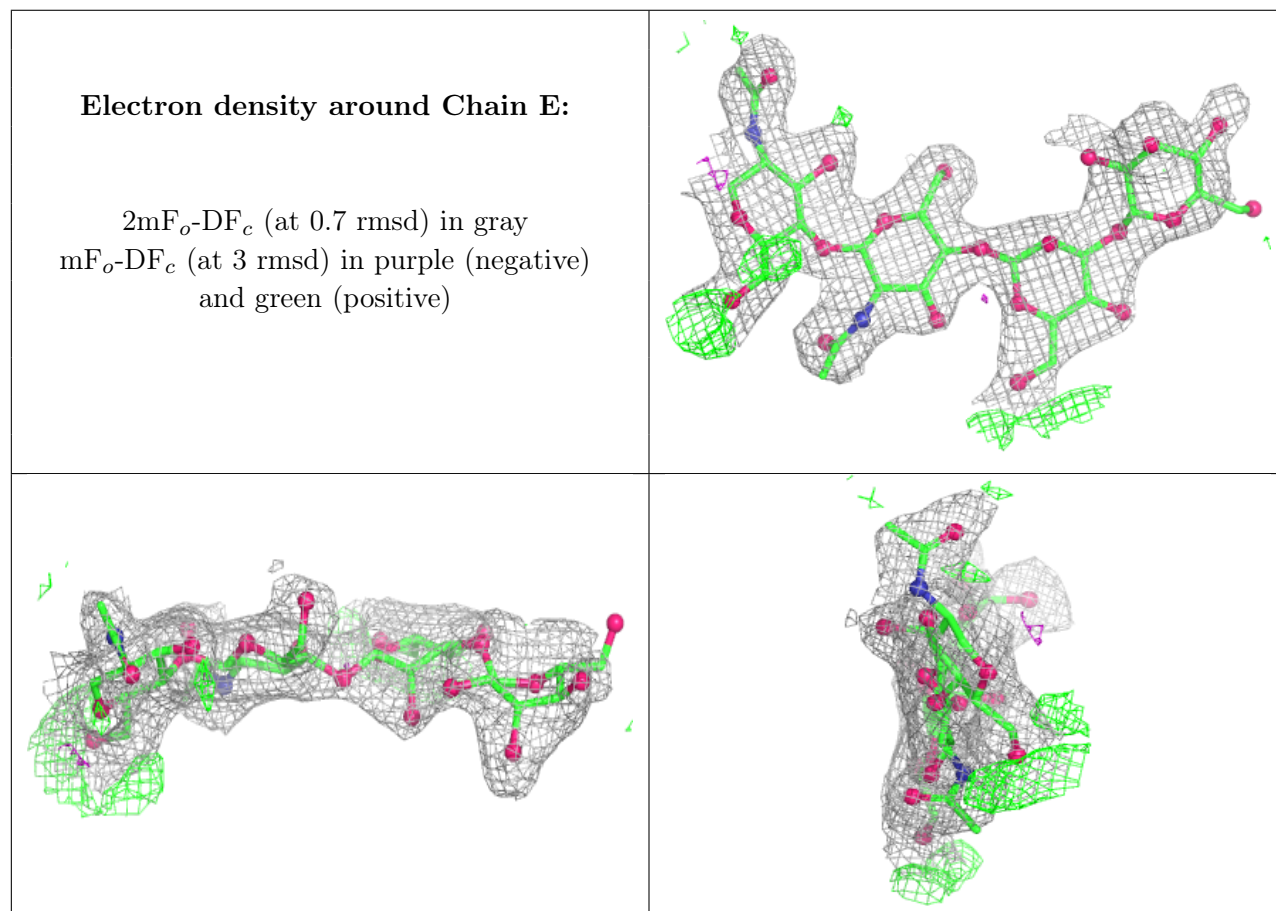
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MAN	E	4	11/12	0.74	0.18	64,85,97,99	0
3	BMA	E	3	11/12	0.79	0.13	65,74,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	E	1	14/15	0.86	0.12	44,53,57,58	0
3	NAG	E	2	14/15	0.90	0.11	49,60,69,71	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	NAG	D	301	14/15	0.82	0.14	47,58,68,69	0
5	MG	C	305	1/1	0.94	0.19	43,43,43,43	0
4	CL	A	301	1/1	0.99	0.03	28,28,28,28	0
5	MG	D	302	1/1	0.99	0.03	48,48,48,48	0
4	CL	B	301	1/1	0.99	0.05	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.