wwPDB X-ray Structure Validation Summary Report (i)

Oct 25, 2022 – 09:36 pm BST

PDB ID	:	7ZG0
Title	:	Murine IL-27 in complex with IL-27Ra and a non-competing Nb
Authors	:	Skladanowska, K.; Bloch, Y.; Savvides, S.N.
Deposited on	:	2022-04-01
Resolution	:	3.18 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:

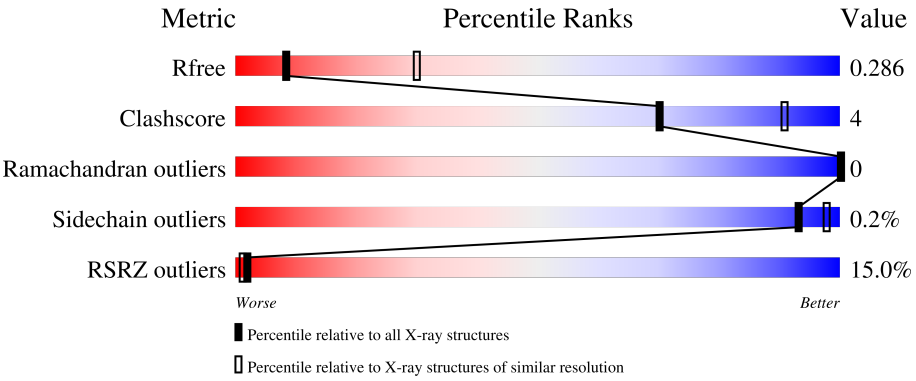
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 3.18 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	1467 (3.20-3.16)
Clashscore	141614	1599 (3.20-3.16)
Ramachandran outliers	138981	1574 (3.20-3.16)
Sidechain outliers	138945	1573 (3.20-3.16)
RSRZ outliers	127900	1423 (3.20-3.16)

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	246	2% 59% 8% 34%
1	B	246	2% 56% 9% 35%
2	C	241	10% 69% 9% 22%
2	D	241	8% 72% 6% 22%
3	E	219	20% 79% 8% 13%

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Mol	Chain	Length	Quality of chain
3	F	219	20% 80% 8% 12%
4	G	166	21% 69% 5% 26%
4	H	166	13% 66% 9% 25%
5	I	2	50% 50%
5	J	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	NAG	I	2	-	-	-	X
5	NAG	J	2	-	-	-	X

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 10641 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 Interleukin-27 subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	S	0	0	0
			1314	849	231	230	4			
1	B	161	Total	C	N	O	S	0	0	0
			1303	843	229	227	4			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP Q8K3I6
A	-1	GLY	-	expression tag	UNP Q8K3I6
A	0	ILE	-	expression tag	UNP Q8K3I6
A	1	LEU	-	expression tag	UNP Q8K3I6
A	2	PRO	-	expression tag	UNP Q8K3I6
A	3	SER	-	expression tag	UNP Q8K3I6
A	4	PRO	-	expression tag	UNP Q8K3I6
A	5	GLY	-	expression tag	UNP Q8K3I6
A	6	MET	-	expression tag	UNP Q8K3I6
A	7	PRO	-	expression tag	UNP Q8K3I6
A	8	ALA	-	expression tag	UNP Q8K3I6
A	9	LEU	-	expression tag	UNP Q8K3I6
A	10	LEU	-	expression tag	UNP Q8K3I6
A	11	SER	-	expression tag	UNP Q8K3I6
A	12	LEU	-	expression tag	UNP Q8K3I6
A	13	VAL	-	expression tag	UNP Q8K3I6
A	14	SER	-	expression tag	UNP Q8K3I6
A	15	LEU	-	expression tag	UNP Q8K3I6
A	16	LEU	-	expression tag	UNP Q8K3I6
A	17	SER	-	expression tag	UNP Q8K3I6
A	18	VAL	-	expression tag	UNP Q8K3I6
A	19	LEU	-	expression tag	UNP Q8K3I6
A	20	LEU	-	expression tag	UNP Q8K3I6
A	21	MET	-	expression tag	UNP Q8K3I6
A	22	GLY	-	expression tag	UNP Q8K3I6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	23	CYS	-	expression tag	UNP Q8K3I6
A	24	VAL	-	expression tag	UNP Q8K3I6
A	25	ALA	-	expression tag	UNP Q8K3I6
A	26	GLU	-	expression tag	UNP Q8K3I6
A	27	THR	-	expression tag	UNP Q8K3I6
A	235	GLY	-	expression tag	UNP Q8K3I6
A	236	THR	-	expression tag	UNP Q8K3I6
A	237	LYS	-	expression tag	UNP Q8K3I6
A	238	HIS	-	expression tag	UNP Q8K3I6
A	239	HIS	-	expression tag	UNP Q8K3I6
A	240	HIS	-	expression tag	UNP Q8K3I6
A	241	HIS	-	expression tag	UNP Q8K3I6
A	242	HIS	-	expression tag	UNP Q8K3I6
A	243	HIS	-	expression tag	UNP Q8K3I6
B	-2	MET	-	initiating methionine	UNP Q8K3I6
B	-1	GLY	-	expression tag	UNP Q8K3I6
B	0	ILE	-	expression tag	UNP Q8K3I6
B	1	LEU	-	expression tag	UNP Q8K3I6
B	2	PRO	-	expression tag	UNP Q8K3I6
B	3	SER	-	expression tag	UNP Q8K3I6
B	4	PRO	-	expression tag	UNP Q8K3I6
B	5	GLY	-	expression tag	UNP Q8K3I6
B	6	MET	-	expression tag	UNP Q8K3I6
B	7	PRO	-	expression tag	UNP Q8K3I6
B	8	ALA	-	expression tag	UNP Q8K3I6
B	9	LEU	-	expression tag	UNP Q8K3I6
B	10	LEU	-	expression tag	UNP Q8K3I6
B	11	SER	-	expression tag	UNP Q8K3I6
B	12	LEU	-	expression tag	UNP Q8K3I6
B	13	VAL	-	expression tag	UNP Q8K3I6
B	14	SER	-	expression tag	UNP Q8K3I6
B	15	LEU	-	expression tag	UNP Q8K3I6
B	16	LEU	-	expression tag	UNP Q8K3I6
B	17	SER	-	expression tag	UNP Q8K3I6
B	18	VAL	-	expression tag	UNP Q8K3I6
B	19	LEU	-	expression tag	UNP Q8K3I6
B	20	LEU	-	expression tag	UNP Q8K3I6
B	21	MET	-	expression tag	UNP Q8K3I6
B	22	GLY	-	expression tag	UNP Q8K3I6
B	23	CYS	-	expression tag	UNP Q8K3I6
B	24	VAL	-	expression tag	UNP Q8K3I6
B	25	ALA	-	expression tag	UNP Q8K3I6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	26	GLU	-	expression tag	UNP Q8K3I6
B	27	THR	-	expression tag	UNP Q8K3I6
B	235	GLY	-	expression tag	UNP Q8K3I6
B	236	THR	-	expression tag	UNP Q8K3I6
B	237	LYS	-	expression tag	UNP Q8K3I6
B	238	HIS	-	expression tag	UNP Q8K3I6
B	239	HIS	-	expression tag	UNP Q8K3I6
B	240	HIS	-	expression tag	UNP Q8K3I6
B	241	HIS	-	expression tag	UNP Q8K3I6
B	242	HIS	-	expression tag	UNP Q8K3I6
B	243	HIS	-	expression tag	UNP Q8K3I6

- Molecule 2 is a protein called Interleukin-27 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	188	Total	C	N	O	S	0	0	0
			1482	941	273	262	6			
2	D	188	Total	C	N	O	S	0	0	0
			1482	941	273	262	6			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-12	MET	-	initiating methionine	UNP O35228
C	-11	GLY	-	expression tag	UNP O35228
C	-10	ILE	-	expression tag	UNP O35228
C	-9	LEU	-	expression tag	UNP O35228
C	-8	PRO	-	expression tag	UNP O35228
C	-7	SER	-	expression tag	UNP O35228
C	-6	PRO	-	expression tag	UNP O35228
C	-5	GLY	-	expression tag	UNP O35228
C	-4	MET	-	expression tag	UNP O35228
C	-3	PRO	-	expression tag	UNP O35228
C	-2	ALA	-	expression tag	UNP O35228
C	-1	LEU	-	expression tag	UNP O35228
C	0	LEU	-	expression tag	UNP O35228
C	1	SER	-	expression tag	UNP O35228
C	2	LEU	-	expression tag	UNP O35228
C	3	VAL	-	expression tag	UNP O35228
C	4	SER	-	expression tag	UNP O35228
C	5	LEU	-	expression tag	UNP O35228
C	6	LEU	-	expression tag	UNP O35228

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Chain	Residue	Modelled	Actual	Comment	Reference
C	7	SER	-	expression tag	UNP O35228
C	8	VAL	-	expression tag	UNP O35228
C	9	LEU	-	expression tag	UNP O35228
C	10	LEU	-	expression tag	UNP O35228
C	11	MET	-	expression tag	UNP O35228
C	12	GLY	-	expression tag	UNP O35228
C	13	CYS	-	expression tag	UNP O35228
C	14	VAL	-	expression tag	UNP O35228
C	15	ALA	-	expression tag	UNP O35228
C	16	GLU	-	expression tag	UNP O35228
C	17	THR	-	expression tag	UNP O35228
D	-12	MET	-	initiating methionine	UNP O35228
D	-11	GLY	-	expression tag	UNP O35228
D	-10	ILE	-	expression tag	UNP O35228
D	-9	LEU	-	expression tag	UNP O35228
D	-8	PRO	-	expression tag	UNP O35228
D	-7	SER	-	expression tag	UNP O35228
D	-6	PRO	-	expression tag	UNP O35228
D	-5	GLY	-	expression tag	UNP O35228
D	-4	MET	-	expression tag	UNP O35228
D	-3	PRO	-	expression tag	UNP O35228
D	-2	ALA	-	expression tag	UNP O35228
D	-1	LEU	-	expression tag	UNP O35228
D	0	LEU	-	expression tag	UNP O35228
D	1	SER	-	expression tag	UNP O35228
D	2	LEU	-	expression tag	UNP O35228
D	3	VAL	-	expression tag	UNP O35228
D	4	SER	-	expression tag	UNP O35228
D	5	LEU	-	expression tag	UNP O35228
D	6	LEU	-	expression tag	UNP O35228
D	7	SER	-	expression tag	UNP O35228
D	8	VAL	-	expression tag	UNP O35228
D	9	LEU	-	expression tag	UNP O35228
D	10	LEU	-	expression tag	UNP O35228
D	11	MET	-	expression tag	UNP O35228
D	12	GLY	-	expression tag	UNP O35228
D	13	CYS	-	expression tag	UNP O35228
D	14	VAL	-	expression tag	UNP O35228
D	15	ALA	-	expression tag	UNP O35228
D	16	GLU	-	expression tag	UNP O35228
D	17	THR	-	expression tag	UNP O35228

- Molecule 3 is a protein called Interleukin-27 receptor subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	191	Total	C	N	O	S	0	0	0
			1543	991	255	288	9			
3	F	192	Total	C	N	O	S	0	0	0
			1547	993	256	289	9			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	7	GLU	-	expression tag	UNP O70394
E	8	HIS	-	expression tag	UNP O70394
E	9	HIS	-	expression tag	UNP O70394
E	10	HIS	-	expression tag	UNP O70394
E	11	HIS	-	expression tag	UNP O70394
E	12	HIS	-	expression tag	UNP O70394
E	13	HIS	-	expression tag	UNP O70394
E	14	HIS	-	expression tag	UNP O70394
E	15	HIS	-	expression tag	UNP O70394
E	16	GLU	-	expression tag	UNP O70394
E	17	ASN	-	expression tag	UNP O70394
E	18	LEU	-	expression tag	UNP O70394
E	19	TYR	-	expression tag	UNP O70394
E	20	PHE	-	expression tag	UNP O70394
E	21	GLN	-	expression tag	UNP O70394
E	22	GLY	-	expression tag	UNP O70394
E	23	THR	-	expression tag	UNP O70394
F	7	GLU	-	expression tag	UNP O70394
F	8	HIS	-	expression tag	UNP O70394
F	9	HIS	-	expression tag	UNP O70394
F	10	HIS	-	expression tag	UNP O70394
F	11	HIS	-	expression tag	UNP O70394
F	12	HIS	-	expression tag	UNP O70394
F	13	HIS	-	expression tag	UNP O70394
F	14	HIS	-	expression tag	UNP O70394
F	15	HIS	-	expression tag	UNP O70394
F	16	GLU	-	expression tag	UNP O70394
F	17	ASN	-	expression tag	UNP O70394
F	18	LEU	-	expression tag	UNP O70394
F	19	TYR	-	expression tag	UNP O70394
F	20	PHE	-	expression tag	UNP O70394
F	21	GLN	-	expression tag	UNP O70394
F	22	GLY	-	expression tag	UNP O70394
F	23	THR	-	expression tag	UNP O70394

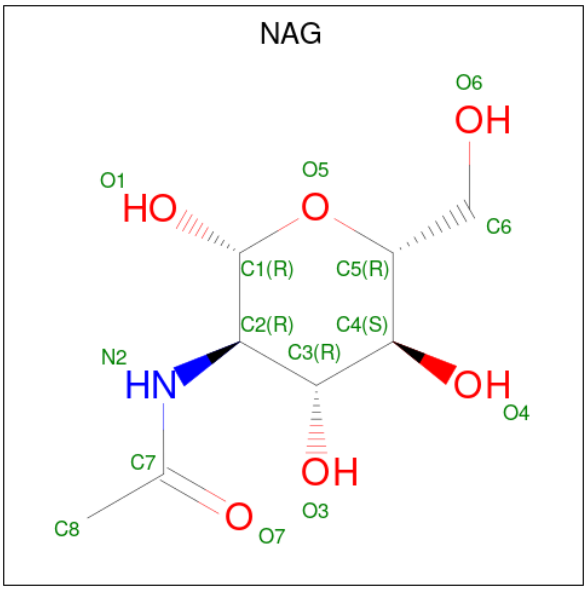
- Molecule 4 is a protein called Nanobody 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	123	Total	C	N	O	S	0	0	0
			922	569	163	185	5			
4	H	124	Total	C	N	O	S	0	0	0
			926	571	164	186	5			

- Molecule 5 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
5	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
5	J	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



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

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

- Molecule 7 is water.

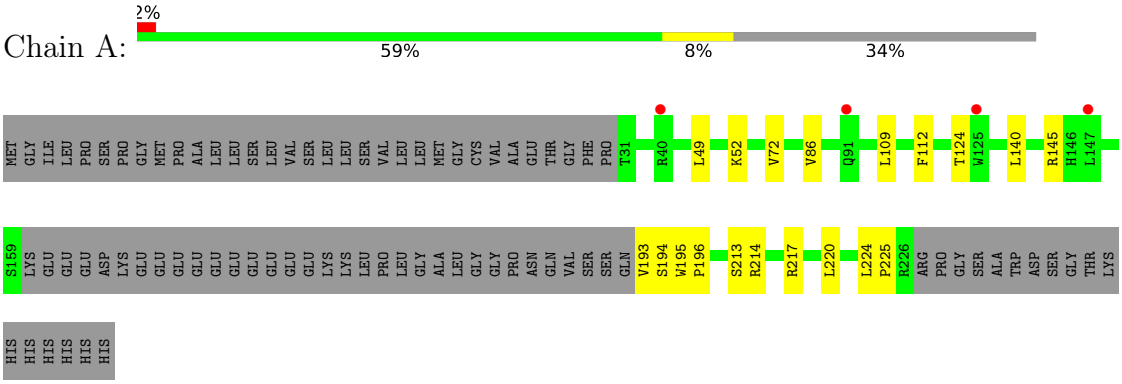
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total O 2 2	0	0
7	B	1	Total O 1 1	0	0
7	C	4	Total O 4 4	0	0
7	D	3	Total O 3 3	0	0

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.

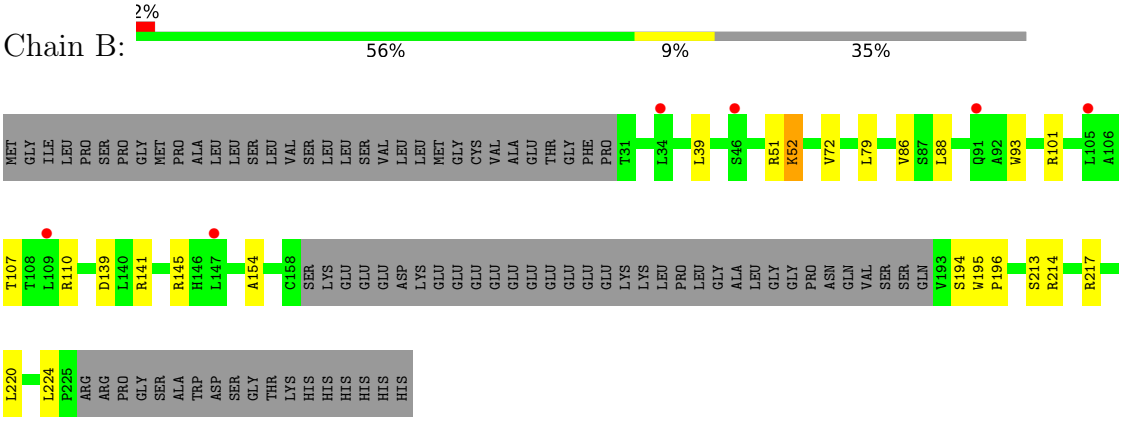
• Molecule 1: Interleukin-27 subunit alpha

Chain A:



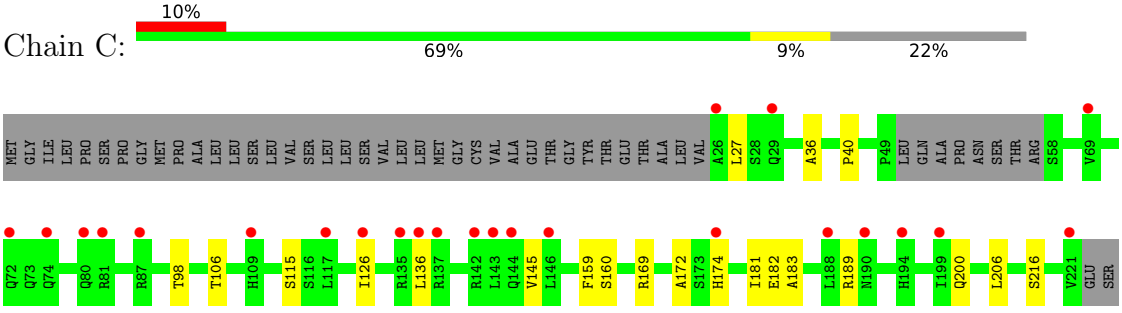
• Molecule 1: Interleukin-27 subunit alpha

Chain B:



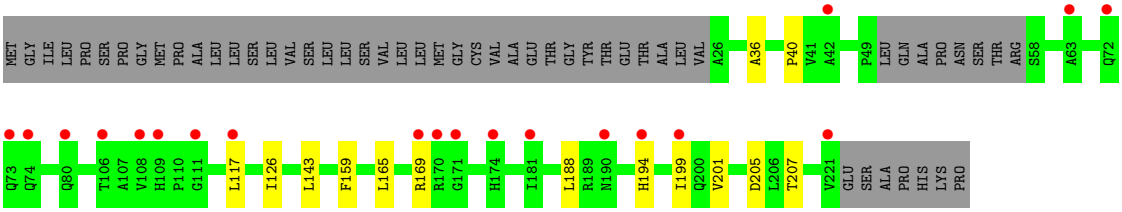
• Molecule 2: Interleukin-27 subunit beta

Chain C:



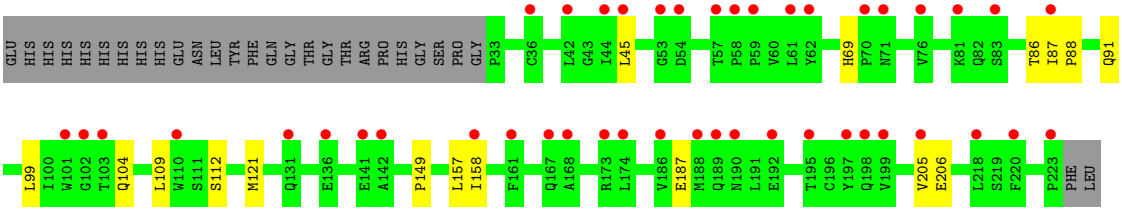
• Molecule 2: Interleukin-27 subunit beta

Chain D:



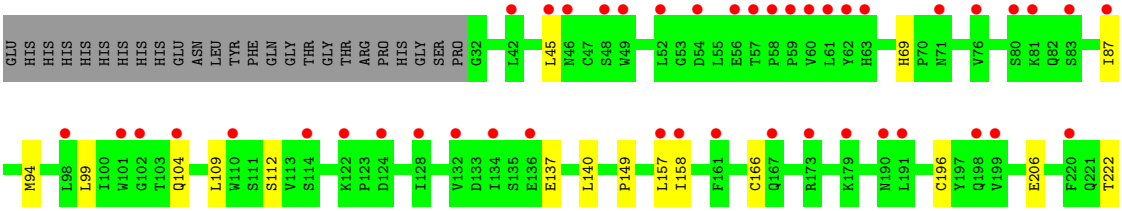
• Molecule 3: Interleukin-27 receptor subunit alpha

Chain E:



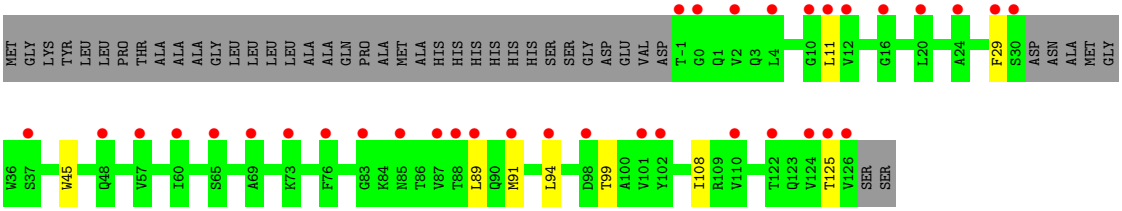
• Molecule 3: Interleukin-27 receptor subunit alpha

Chain F:



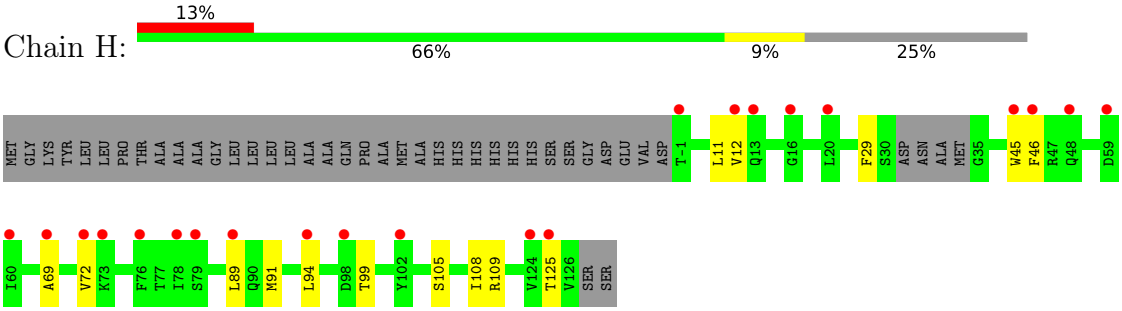
• Molecule 4: Nanobody 5

Chain G:



• Molecule 4: Nanobody 5

Chain H:

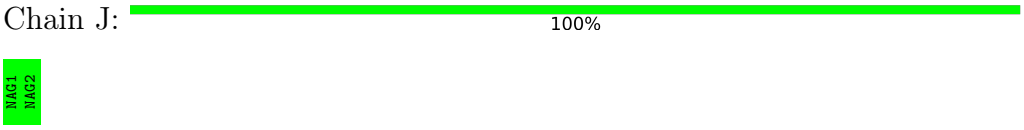


• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:

• Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	167.24Å 137.71Å 111.48Å 90.00° 117.49° 90.00°	Depositor
Resolution (Å)	79.52 – 3.18 100.93 – 3.18	Depositor EDS
% Data completeness (in resolution range)	87.8 (79.52-3.18) 99.1 (100.93-3.18)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.16 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.229 , 0.278 0.257 , 0.286	Depositor DCC
R_{free} test set	2256 reflections (6.01%)	wwPDB-VP
Wilson B-factor (Å^2)	101.5	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	10641	wwPDB-VP
Average B, all atoms (Å^2)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.42% 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

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	0.26	0/1347	0.49	0/1833
1	B	0.25	0/1336	0.48	0/1818
2	C	0.27	0/1527	0.53	0/2085
2	D	0.30	0/1527	0.53	0/2085
3	E	0.25	0/1595	0.47	0/2187
3	F	0.25	0/1599	0.47	0/2193
4	G	0.26	0/938	0.49	0/1271
4	H	0.26	0/942	0.49	0/1276
All	All	0.26	0/10811	0.50	0/14748

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	1314	0	1316	12	0
1	B	1303	0	1309	15	0
2	C	1482	0	1465	13	0
2	D	1482	0	1465	9	0
3	E	1543	0	1491	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1547	0	1493	10	0
4	G	922	0	887	5	0
4	H	926	0	890	9	0
5	I	28	0	25	1	0
5	J	28	0	25	0	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0
6	C	14	0	13	0	0
6	D	14	0	13	2	0
7	A	2	0	0	0	0
7	B	1	0	0	0	0
7	C	4	0	0	0	0
7	D	3	0	0	0	0
All	All	10641	0	10418	75	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 4.

The worst 5 of 75 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)
2:D:117:LEU:HD11	6:D:301:NAG:H82	1.63	0.81
2:D:117:LEU:HD11	6:D:301:NAG:C8	2.20	0.70
3:E:99:LEU:HD11	3:E:112:SER:HB3	1.82	0.62
1:A:86:VAL:HB	1:A:214:ARG:HD2	1.83	0.60
3:F:45:LEU:HD23	3:F:87:ILE:HD12	1.84	0.59

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	159/246 (65%)	157 (99%)	2 (1%)	0	100	100
1	B	157/246 (64%)	156 (99%)	1 (1%)	0	100	100
2	C	184/241 (76%)	181 (98%)	3 (2%)	0	100	100
2	D	184/241 (76%)	182 (99%)	2 (1%)	0	100	100
3	E	189/219 (86%)	186 (98%)	3 (2%)	0	100	100
3	F	190/219 (87%)	186 (98%)	4 (2%)	0	100	100
4	G	119/166 (72%)	118 (99%)	1 (1%)	0	100	100
4	H	120/166 (72%)	119 (99%)	1 (1%)	0	100	100
All	All	1302/1744 (75%)	1285 (99%)	17 (1%)	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	144/216 (67%)	143 (99%)	1 (1%)	84	93
1	B	143/216 (66%)	142 (99%)	1 (1%)	84	93
2	C	163/207 (79%)	163 (100%)	0	100	100
2	D	163/207 (79%)	163 (100%)	0	100	100
3	E	176/200 (88%)	176 (100%)	0	100	100
3	F	176/200 (88%)	176 (100%)	0	100	100
4	G	100/131 (76%)	100 (100%)	0	100	100
4	H	100/131 (76%)	100 (100%)	0	100	100
All	All	1165/1508 (77%)	1163 (100%)	2 (0%)	93	98

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
1	B	52	LYS

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

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	$\#\|Z\| > 2$
5	NAG	I	1	5,3	14,14,15	0.19	0	17,19,21	0.45	0
5	NAG	I	2	5	14,14,15	0.30	0	17,19,21	0.49	0
5	NAG	J	1	5,3	14,14,15	0.20	0	17,19,21	0.43	0
5	NAG	J	2	5	14,14,15	0.28	0	17,19,21	0.45	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	I	1	5,3	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	0/6/23/26	0/1/1/1
5	NAG	J	1	5,3	-	2/6/23/26	0/1/1/1
5	NAG	J	2	5	-	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 (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	I	1	NAG	O5-C5-C6-O6
5	J	1	NAG	O5-C5-C6-O6
5	J	1	NAG	C4-C5-C6-O6
5	I	1	NAG	C4-C5-C6-O6

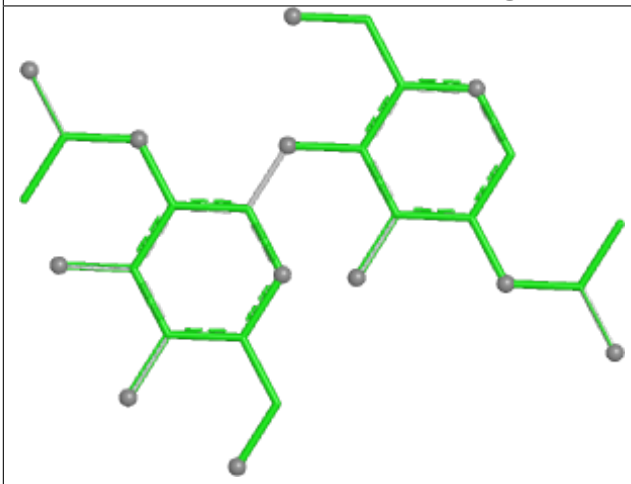
There are no ring outliers.

1 monomer is involved in 1 short contact:

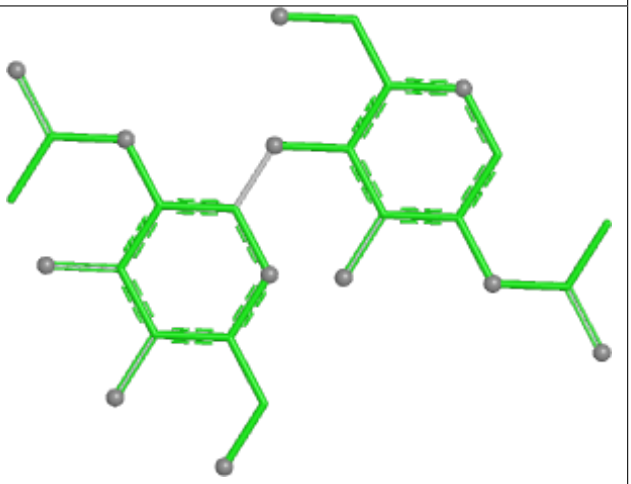
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

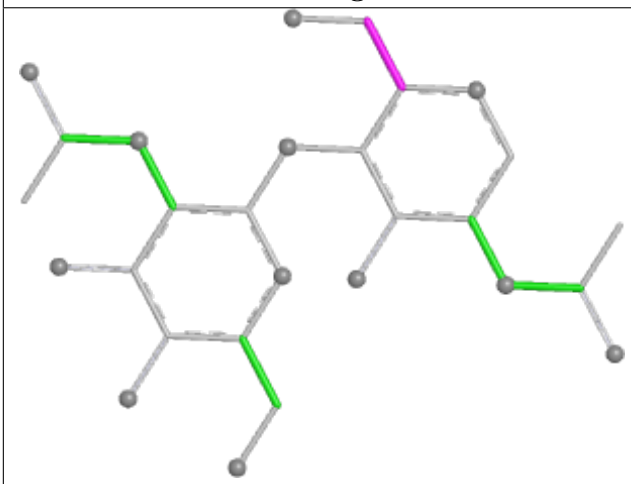
Oligosaccharide Chain I



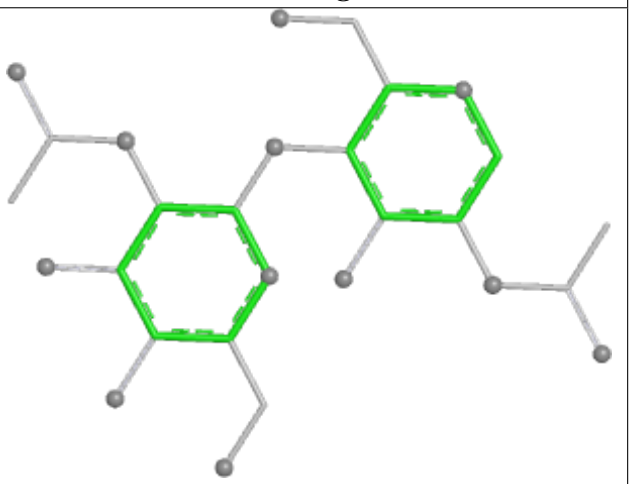
Bond lengths



Bond angles

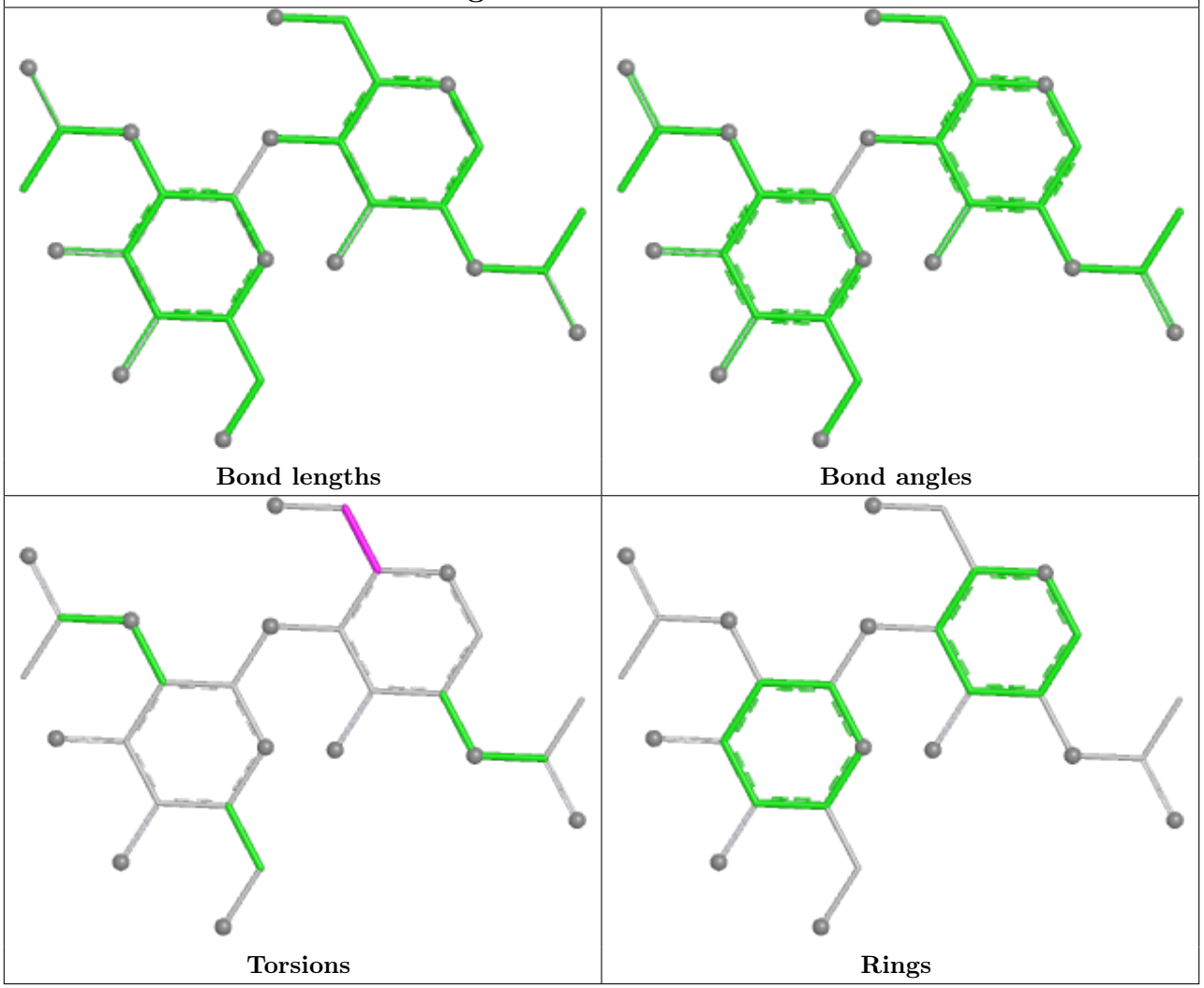


Torsions



Rings

Oligosaccharide Chain J



5.6 Ligand geometry (i)

4 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	NAG	B	301	1	14,14,15	0.33	0	17,19,21	0.49	0
6	NAG	A	301	1	14,14,15	0.35	0	17,19,21	0.51	0
6	NAG	C	301	2	14,14,15	0.39	0	17,19,21	0.75	1 (5%)

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	0.31	0	17,19,21	0.70	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
6	NAG	B	301	1	-	2/6/23/26	0/1/1/1
6	NAG	A	301	1	-	1/6/23/26	0/1/1/1
6	NAG	C	301	2	-	0/6/23/26	0/1/1/1
6	NAG	D	301	2	-	0/6/23/26	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})
6	C	301	NAG	C1-O5-C5	2.67	115.80	112.19

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	301	NAG	O5-C5-C6-O6
6	B	301	NAG	C4-C5-C6-O6
6	A	301	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	301	NAG	2	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, 95^{th} 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	163/246 (66%)	0.78	4 (2%) 57 43	50, 77, 122, 147	0
1	B	161/246 (65%)	0.85	6 (3%) 41 26	55, 81, 121, 144	0
2	C	188/241 (78%)	0.98	24 (12%) 3 2	55, 88, 142, 166	0
2	D	188/241 (78%)	0.98	20 (10%) 6 3	50, 85, 147, 168	0
3	E	191/219 (87%)	1.37	44 (23%) 0 0	84, 118, 172, 222	0
3	F	192/219 (87%)	1.36	44 (22%) 0 0	88, 117, 162, 193	0
4	G	123/166 (74%)	1.46	35 (28%) 0 0	76, 130, 160, 173	0
4	H	124/166 (74%)	1.22	22 (17%) 1 1	63, 105, 152, 174	0
All	All	1330/1744 (76%)	1.12	199 (14%) 2 1	50, 101, 155, 222	0

The worst 5 of 199 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	136	GLU	7.5
3	F	83	SER	7.0
3	F	58	PRO	6.3
4	H	13	GLN	6.3
3	E	198	GLN	6.2

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

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

6.3 Carbohydrates

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,

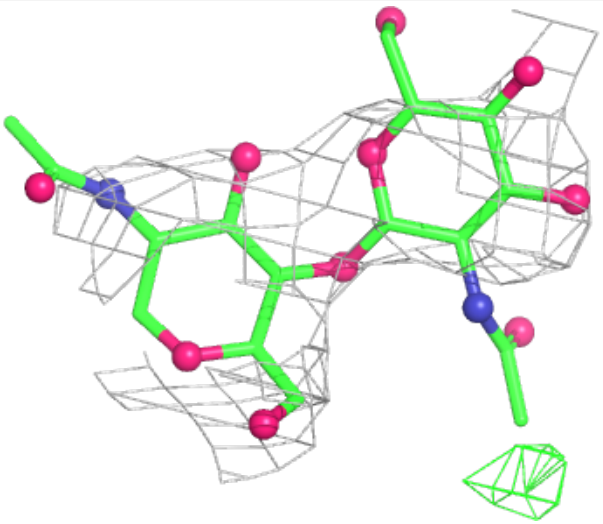
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

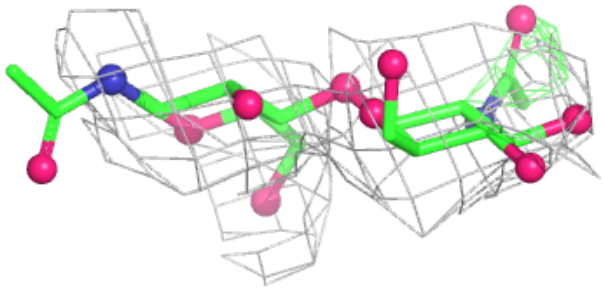
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	NAG	J	2	14/15	0.61	0.45	142,161,173,189	0
5	NAG	I	2	14/15	0.62	0.41	149,174,193,199	0
5	NAG	I	1	14/15	0.83	0.34	126,145,170,174	0
5	NAG	J	1	14/15	0.85	0.29	134,150,160,168	0

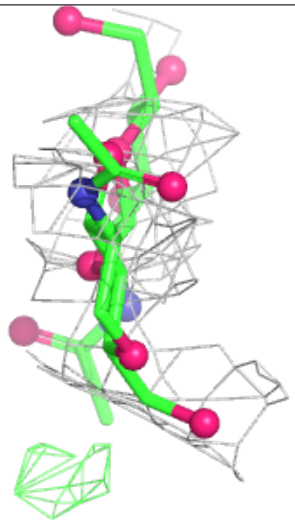
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain I:

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

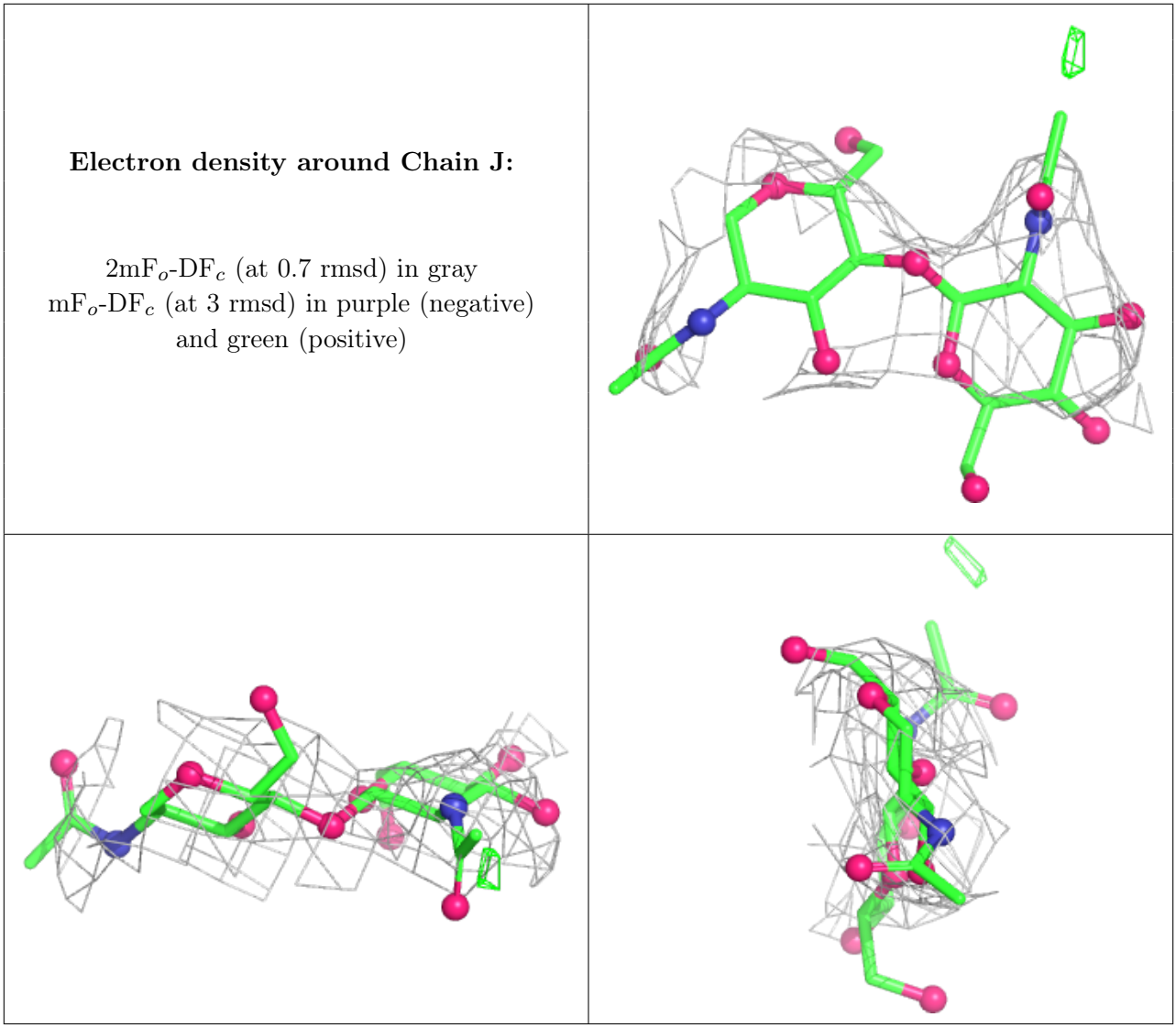






Electron density around Chain J:

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



6.4 Ligands

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, 95^{th} 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
6	NAG	D	301	14/15	0.69	0.38	140,181,200,204	0
6	NAG	B	301	14/15	0.78	0.27	106,126,146,153	0
6	NAG	C	301	14/15	0.83	0.24	141,165,173,192	0
6	NAG	A	301	14/15	0.85	0.31	85,102,121,137	0

6.5 Other polymers (i)

There are no such residues in this entry.