



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 12, 2024 – 07:26 PM EST

PDB ID : 4FA8
Title : Multi-pronged modulation of cytokine signaling
Authors : He, X.; Shim, A.H.
Deposited on : 2012-05-21
Resolution : 2.20 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

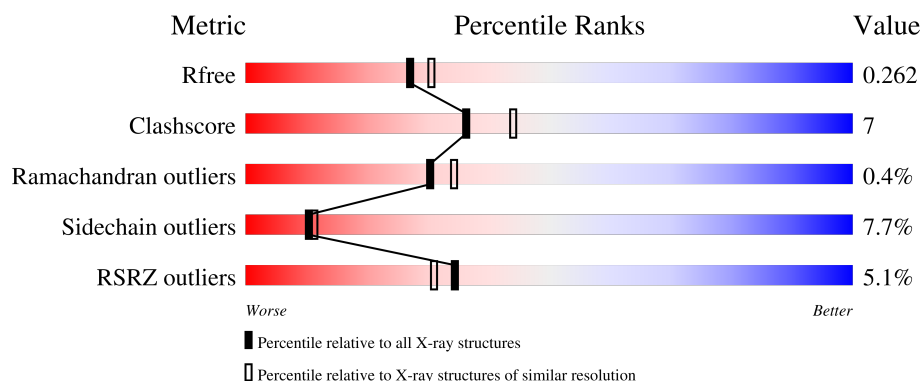
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	203	 2% 75% 16% • 7%
1	B	203	 3% 81% 10% • 7%
1	D	203	 4% 75% 14% • 7%
2	E	147	 15% 75% 20% • •
2	F	147	 3% 79% 14% 5% • •

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Mol	Chain	Length	Quality of chain
2	G	147	<div><div></div><div>3%</div><div>71%</div><div>22%</div><div>6%</div></div>
3	C	3	<div><div></div><div>33%</div><div>67%</div></div>
3	H	3	<div><div></div><div>100%</div></div>
3	I	3	<div><div></div><div>100%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8676 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 Secreted protein BARF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1497	968	255	267	7			
1	B	189	Total	C	N	O	S	0	0	0
			1503	971	256	269	7			
1	D	188	Total	C	N	O	S	0	0	0
			1497	968	255	267	7			

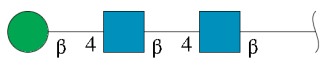
- Molecule 2 is a protein called Macrophage colony-stimulating factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	145	Total	C	N	O	S	0	0	0
			1187	747	197	232	11			
2	F	146	Total	C	N	O	S	0	0	0
			1193	750	198	234	11			
2	G	147	Total	C	N	O	S	0	0	0
			1198	753	199	235	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	2	ASP	-	expression tag	UNP P09603
E	3	PRO	-	expression tag	UNP P09603
F	2	ASP	-	expression tag	UNP P09603
F	3	PRO	-	expression tag	UNP P09603
G	2	ASP	-	expression tag	UNP P09603
G	3	PRO	-	expression tag	UNP P09603

- Molecule 3 is an oligosaccharide called 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	C	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	H	3	Total	C	N	O	0	0	0
			39	22	2	15			
3	I	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		
4	G	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	117	Total	O	0	0
			117	117		

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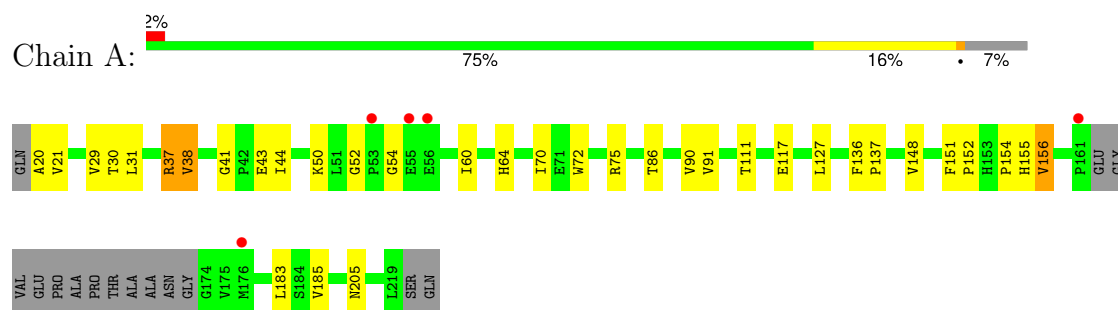
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	101	Total 101	O 101	0	0
5	D	72	Total 72	O 72	0	0
5	E	23	Total 23	O 23	0	0
5	F	63	Total 63	O 63	0	0
5	G	66	Total 66	O 66	0	0

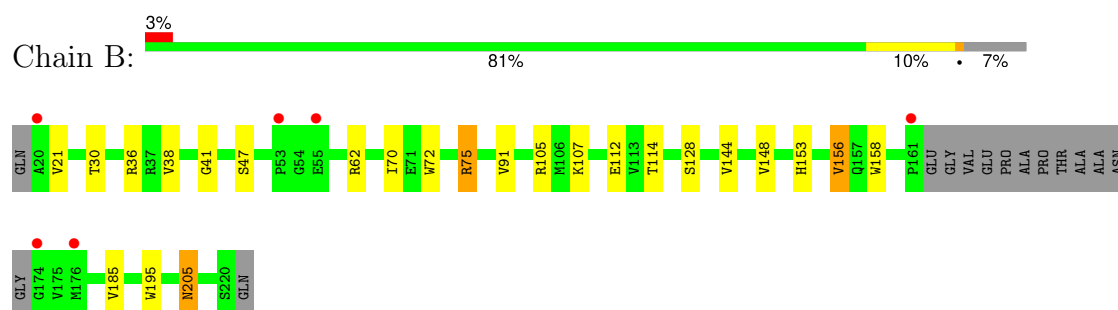
3 Residue-property plots [i](#)

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.

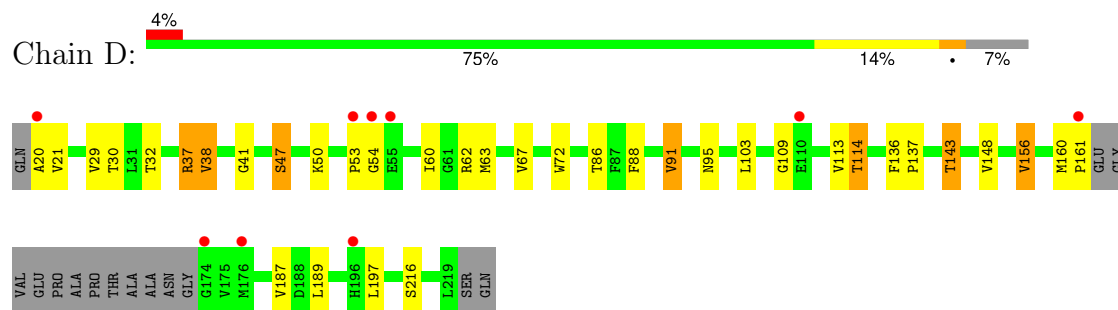
- Molecule 1: Secreted protein BARF1



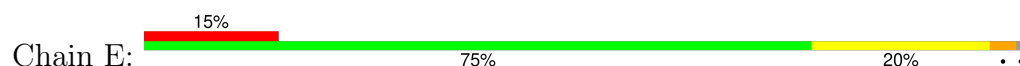
- Molecule 1: Secreted protein BARF1

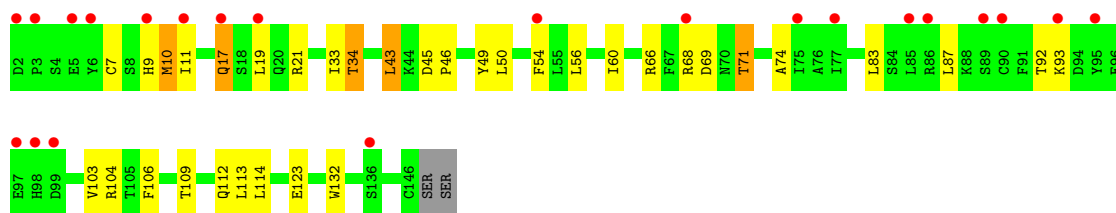


- Molecule 1: Secreted protein BARF1

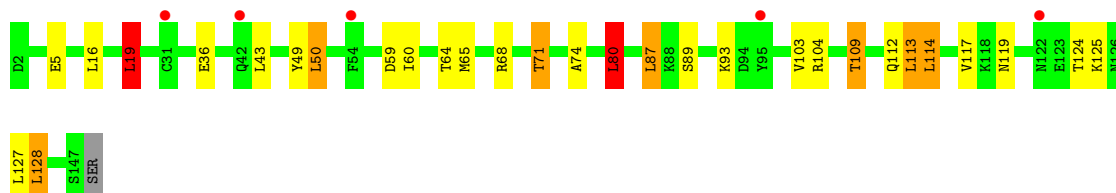
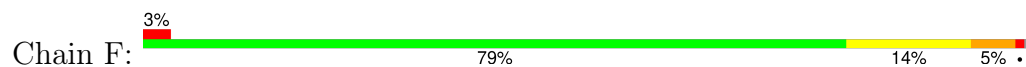


- Molecule 2: Macrophage colony-stimulating factor 1

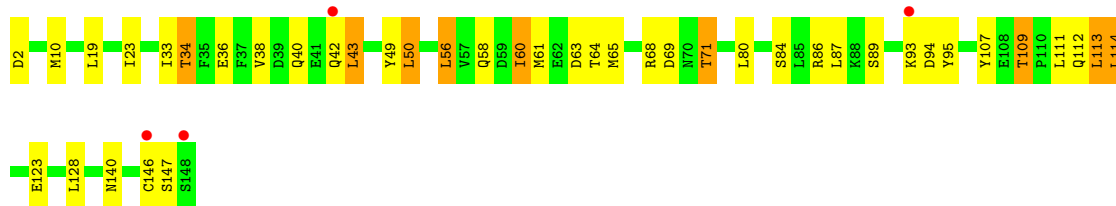




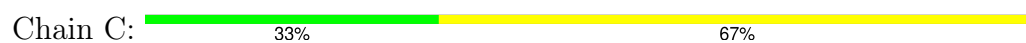
- Molecule 2: Macrophage colony-stimulating factor 1



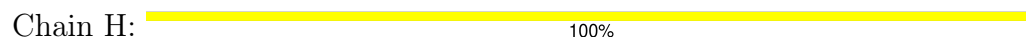
- Molecule 2: Macrophage colony-stimulating factor 1



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



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



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



MAG1
MAG2
BMA3

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	199.55Å 162.70Å 57.34Å 90.00° 95.87° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 20.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.6 (20.00-2.20) 97.6 (20.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.222 , 0.260 0.222 , 0.262	Depositor DCC
R_{free} test set	4494 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	31.5	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8676	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.11% 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: BMA, 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	0.63	1/1541 (0.1%)	0.66	0/2097
1	B	0.60	2/1547 (0.1%)	0.67	0/2105
1	D	0.60	1/1541 (0.1%)	0.62	0/2097
2	E	0.45	1/1208 (0.1%)	0.58	0/1628
2	F	0.57	0/1214	0.77	3/1636 (0.2%)
2	G	0.49	0/1219	0.65	0/1643
All	All	0.57	5/8270 (0.1%)	0.66	3/11206 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	72	TRP	CD2-CE2	5.50	1.48	1.41
1	D	72	TRP	CD2-CE2	5.43	1.47	1.41
1	B	195	TRP	CD2-CE2	5.32	1.47	1.41
2	E	132	TRP	CD2-CE2	5.10	1.47	1.41
1	B	72	TRP	CD2-CE2	5.04	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	F	19	LEU	CA-CB-CG	5.95	128.98	115.30
2	F	80	LEU	CA-CB-CG	5.52	127.99	115.30
2	F	87	LEU	CA-CB-CG	5.24	127.35	115.30

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	1497	0	1471	24	0
1	B	1503	0	1476	13	0
1	D	1497	0	1471	26	0
2	E	1187	0	1150	16	0
2	F	1193	0	1154	20	0
2	G	1198	0	1156	28	0
3	C	39	0	34	0	0
3	H	39	0	34	0	0
3	I	39	0	34	0	0
4	E	14	0	13	0	0
4	F	14	0	13	0	0
4	G	14	0	13	0	0
5	A	117	0	0	1	0
5	B	101	0	0	0	0
5	D	72	0	0	3	0
5	E	23	0	0	2	0
5	F	63	0	0	2	0
5	G	66	0	0	2	0
All	All	8676	0	8019	115	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 7.

The worst 5 of 115 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:D:20:ALA:CB	1:D:21:VAL:HA	1.76	1.13
1:A:20:ALA:HB1	1:A:21:VAL:HA	1.31	1.07
1:D:20:ALA:HB1	1:D:21:VAL:CA	1.90	1.01
1:D:20:ALA:HB1	1:D:21:VAL:HA	1.03	0.99
2:F:65:MET:CE	2:F:117:VAL:HG21	2.03	0.89

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	184/203 (91%)	178 (97%)	5 (3%)	1 (0%)	25	28
1	B	185/203 (91%)	177 (96%)	7 (4%)	1 (0%)	25	28
1	D	184/203 (91%)	176 (96%)	6 (3%)	2 (1%)	12	10
2	E	143/147 (97%)	138 (96%)	5 (4%)	0	100	100
2	F	144/147 (98%)	140 (97%)	4 (3%)	0	100	100
2	G	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
All	All	985/1050 (94%)	948 (96%)	33 (3%)	4 (0%)	30	34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	41	GLY
1	A	41	GLY
1	B	41	GLY
1	D	109	GLY

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	167/177 (94%)	162 (97%)	5 (3%)	36	48
1	B	168/177 (95%)	161 (96%)	7 (4%)	25	33
1	D	167/177 (94%)	158 (95%)	9 (5%)	18	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	138/140 (99%)	120 (87%)	18 (13%)	3	3
2	F	139/140 (99%)	125 (90%)	14 (10%)	6	6
2	G	139/140 (99%)	121 (87%)	18 (13%)	3	3
All	All	918/951 (96%)	847 (92%)	71 (8%)	10	11

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	43	LEU
2	G	56	LEU
2	G	93	LYS
2	E	19	LEU
2	E	17	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	141	ASN
2	G	98	HIS
2	G	141	ASN
2	G	119	ASN
2	G	58	GLN

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 ⓘ

9 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	C	1	1,3	14,14,15	0.62	0	17,19,21	1.09	2 (11%)
3	NAG	C	2	3	14,14,15	0.68	0	17,19,21	0.97	0
3	BMA	C	3	3	11,11,12	0.38	0	15,15,17	1.40	3 (20%)
3	NAG	H	1	1,3	14,14,15	0.76	0	17,19,21	1.25	2 (11%)
3	NAG	H	2	3	14,14,15	0.72	0	17,19,21	1.09	2 (11%)
3	BMA	H	3	3	11,11,12	0.63	0	15,15,17	1.80	3 (20%)
3	NAG	I	1	1,3	14,14,15	0.78	0	17,19,21	1.41	2 (11%)
3	NAG	I	2	3	14,14,15	0.54	0	17,19,21	1.22	2 (11%)
3	BMA	I	3	3	11,11,12	0.32	0	15,15,17	0.84	1 (6%)

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	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	2/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	H	2	3	-	2/6/23/26	0/1/1/1
3	BMA	H	3	3	-	2/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	I	2	3	-	2/6/23/26	0/1/1/1
3	BMA	I	3	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	3	BMA	C1-O5-C5	5.14	119.07	112.19
3	I	1	NAG	O5-C1-C2	-3.74	105.50	111.29
3	I	1	NAG	C2-N2-C7	-3.72	117.92	122.90
3	H	1	NAG	C1-O5-C5	3.12	116.37	112.19
3	H	3	BMA	C1-C2-C3	3.10	114.16	109.64

There are no chirality outliers.

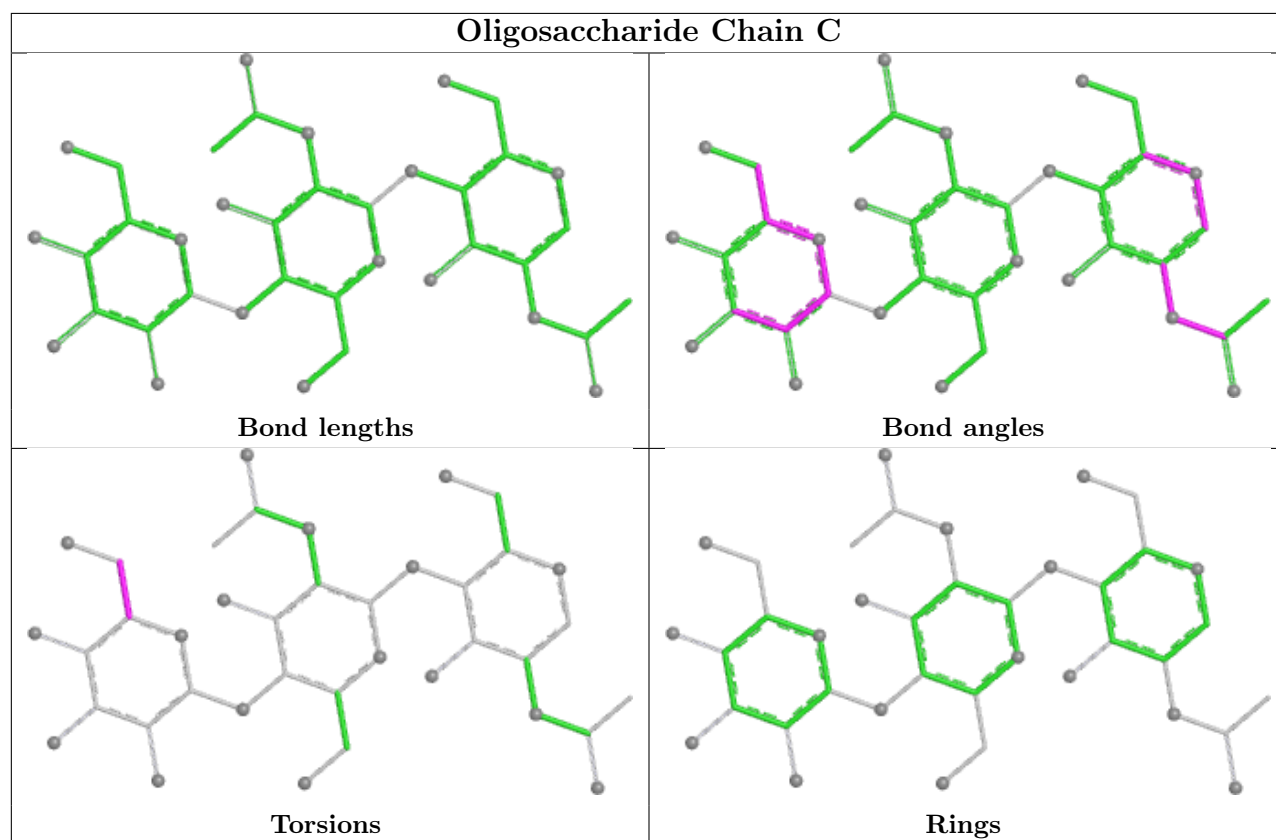
5 of 8 torsion outliers are listed below:

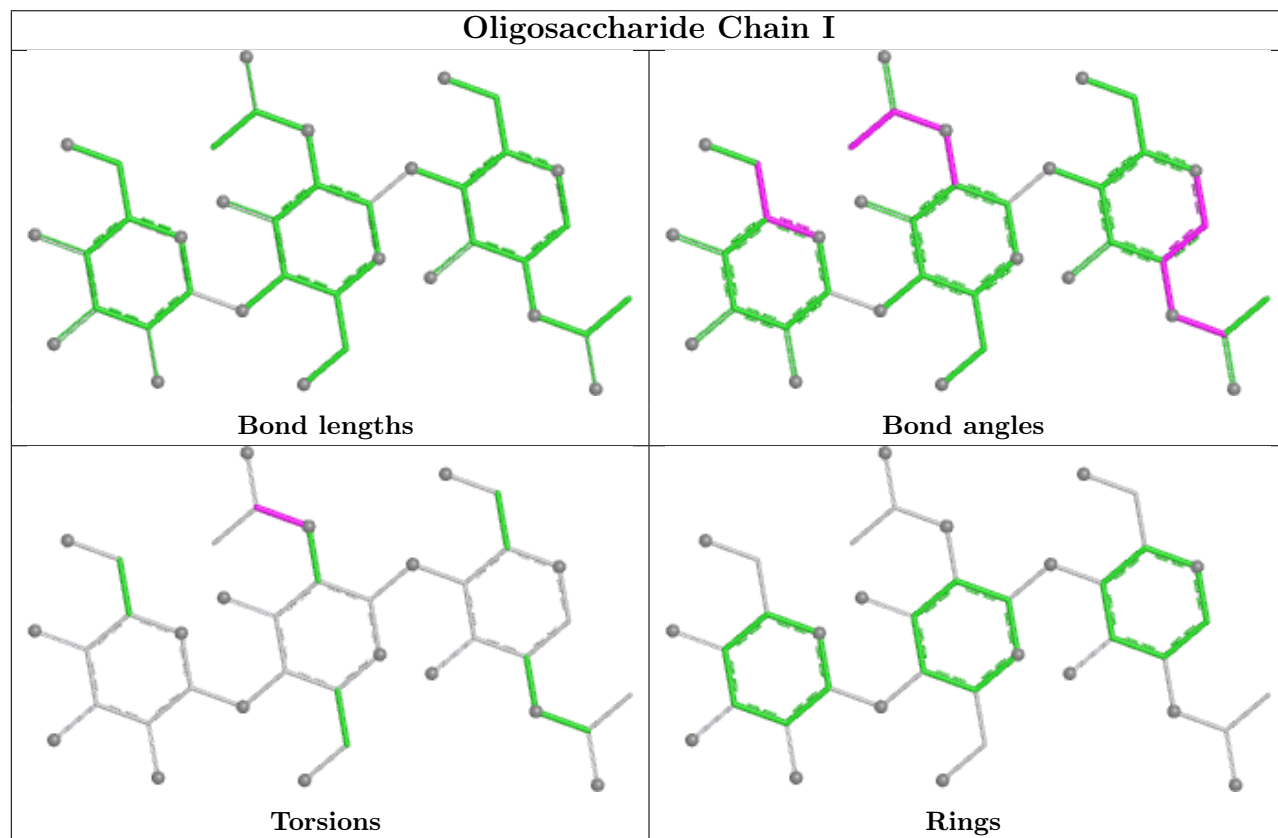
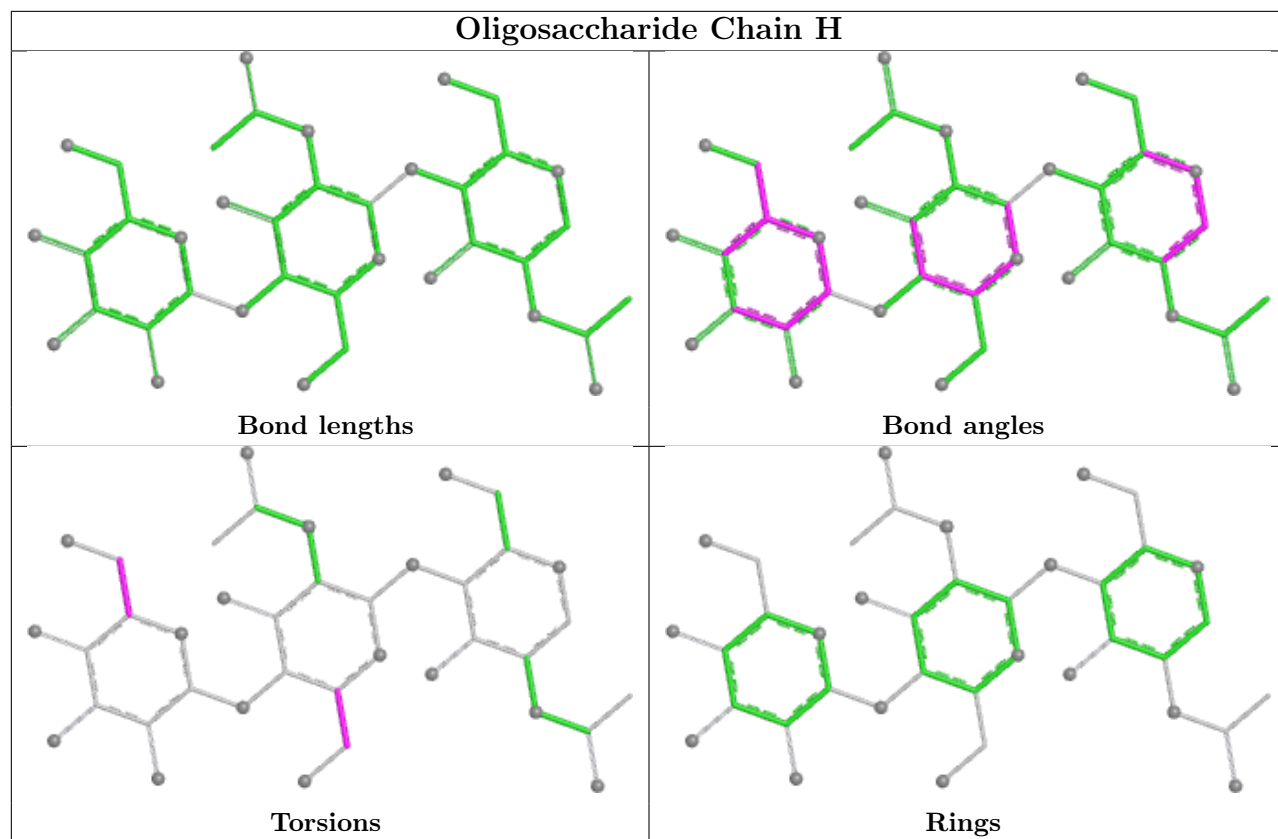
Mol	Chain	Res	Type	Atoms
3	H	2	NAG	O5-C5-C6-O6
3	I	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O7-C7-N2-C2
3	H	2	NAG	C4-C5-C6-O6
3	H	3	BMA	C4-C5-C6-O6

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

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$
4	NAG	E	201	2	14,14,15	0.65	0	17,19,21	1.15	1 (5%)
4	NAG	F	201	2	14,14,15	0.44	0	17,19,21	0.80	1 (5%)
4	NAG	G	201	2	14,14,15	0.51	0	17,19,21	0.77	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	E	201	2	-	0/6/23/26	0/1/1/1
4	NAG	F	201	2	-	0/6/23/26	0/1/1/1
4	NAG	G	201	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	201	NAG	C4-C3-C2	2.97	115.36	111.02
4	F	201	NAG	O5-C5-C6	2.22	111.97	107.66

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	201	NAG	C4-C5-C6-O6
4	G	201	NAG	O5-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	188/203 (92%)	-0.15	5 (2%) 56 53	21, 33, 57, 71	0
1	B	189/203 (93%)	-0.13	6 (3%) 50 47	26, 34, 57, 85	0
1	D	188/203 (92%)	0.04	9 (4%) 36 33	24, 42, 69, 85	0
2	E	145/147 (98%)	1.00	22 (15%) 6 5	34, 65, 104, 117	0
2	F	146/147 (99%)	0.17	5 (3%) 48 45	24, 37, 74, 95	0
2	G	147/147 (100%)	0.12	4 (2%) 56 53	28, 40, 71, 97	0
All	All	1003/1050 (95%)	0.14	51 (5%) 34 31	21, 39, 82, 117	0

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	148	SER	8.5
2	E	95	TYR	5.4
1	A	53	PRO	3.9
1	A	55	GLU	3.8
1	D	53	PRO	3.6

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](#)

SUGAR-RSR INFOmissingINFO

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
4	NAG	G	201	14/15	0.45	0.20	82,90,100,101	0
4	NAG	E	201	14/15	0.54	0.19	91,98,104,106	0
4	NAG	F	201	14/15	0.68	0.17	51,67,70,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.