



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 30, 2023 – 08:30 AM EDT

PDB ID : 3OJV
Title : Crystal Structure of FGF1 complexed with the ectodomain of FGFR1c exhibiting an ordered ligand specificity-determining betaC'-betaE loop
Authors : Beenken, A.; Mohammadi, M.
Deposited on : 2010-08-23
Resolution : 2.60 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

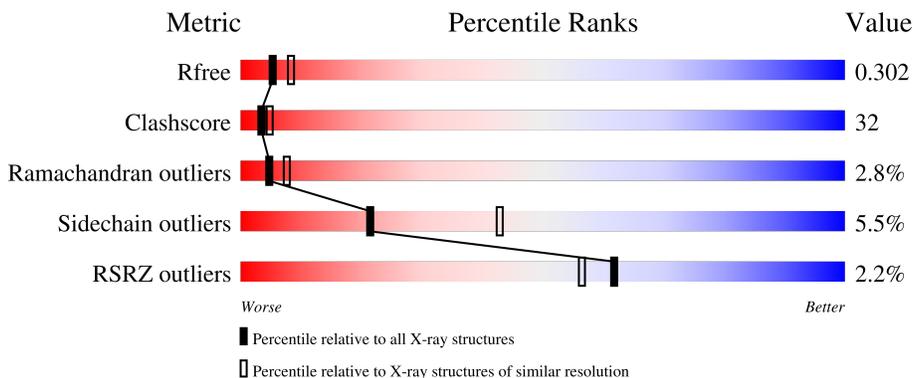
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	136	 50% 44% . .
1	B	136	 3% 44% 51% . .
2	C	226	 3% 49% 42% . 6%
2	D	226	 3% 50% 39% 5% 6%
3	E	6	 17% 83%

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
3	UAP	E	6	X	-	-	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5465 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 Heparin-binding growth factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	133	1052	665	184	199	4	0	0	0
1	B	133	1052	665	184	199	4	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP P05230
B	20	MET	-	initiating methionine	UNP P05230

- Molecule 2 is a protein called Basic fibroblast growth factor receptor 1.

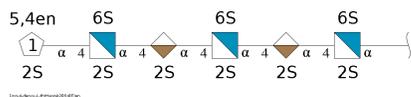
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	213	1608	1026	278	295	9	0	0	0
2	D	213	1617	1028	283	297	9	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	140	MET	-	initiating methionine	UNP P11362
C	141	ALA	-	expression tag	UNP P11362
C	185	GLN	ASN	engineered mutation	UNP P11362
D	140	MET	-	initiating methionine	UNP P11362
D	141	ALA	-	expression tag	UNP P11362
D	185	GLN	ASN	engineered mutation	UNP P11362

- Molecule 3 is an oligosaccharide called 4-deoxy-2-O-sulfo-alpha-L-threo-hex-4-enopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-

2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	6	104	36	3	56	9	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total	O	0	0
			6	6		
4	B	2	Total	O	0	0
			2	2		
4	C	13	Total	O	0	0
			13	13		
4	D	11	Total	O	0	0
			11	11		

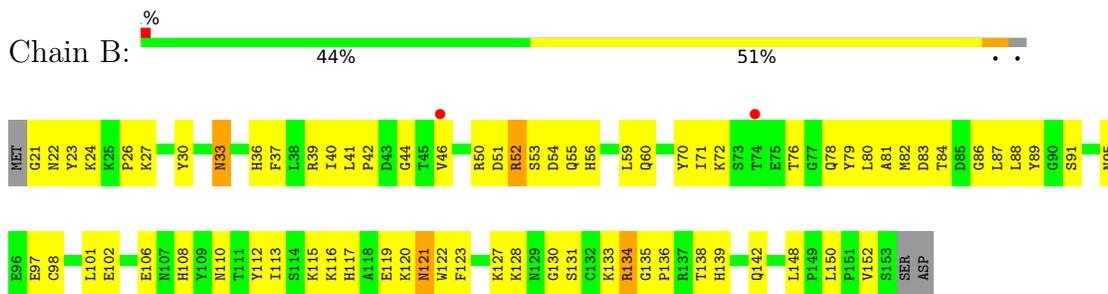
3 Residue-property plots [i](#)

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.

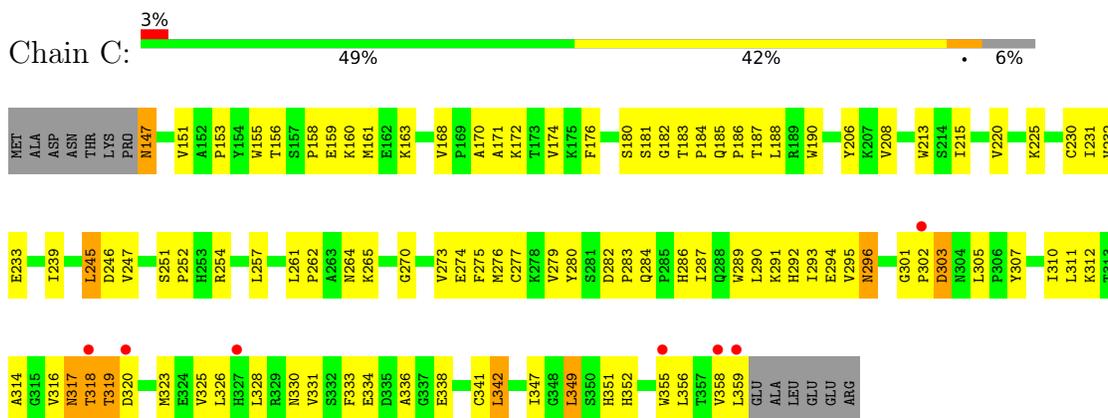
- Molecule 1: Heparin-binding growth factor 1



- Molecule 1: Heparin-binding growth factor 1

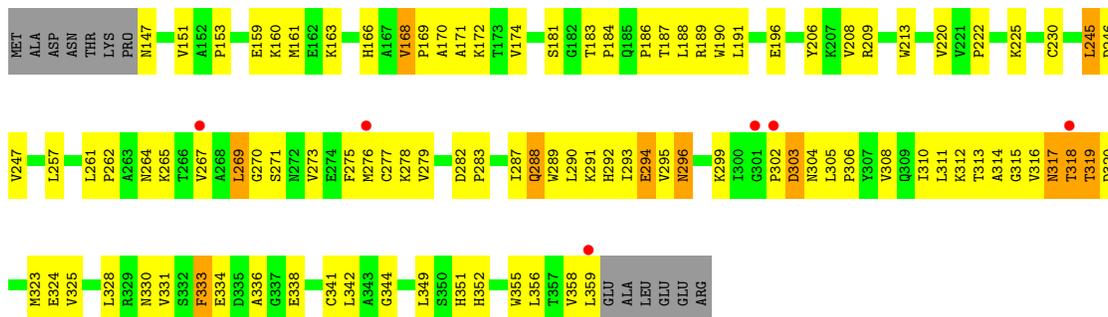


- Molecule 2: Basic fibroblast growth factor receptor 1



- Molecule 2: Basic fibroblast growth factor receptor 1





- Molecule 3: 4-deoxy-2-O-sulfo-alpha-L-threo-hex-4-enopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose-(1-4)-2-O-sulfo-alpha-L-idopyranuronic acid-(1-4)-2-deoxy-6-O-sulfo-2-(sulfoamino)-alpha-D-glucopyranose

Chain E: 17% 83%

SGN1
IDS2
SGN3
IDS4
SGN5
UAPE

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.32Å 53.42Å 80.46Å 106.44° 106.40° 94.44°	Depositor
Resolution (Å)	25.00 – 2.60 36.58 – 2.59	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.60) 95.1 (36.58-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.58Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.251 , 0.309 0.247 , 0.302	Depositor DCC
R_{free} test set	2405 reflections (9.77%)	wwPDB-VP
Wilson B-factor (Å ²)	45.8	Xtrriage
Anisotropy	0.124	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 26.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.018 for k,h,-h-k-l 0.478 for -k,-h,-l 0.017 for -h,-k,h+k+l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	5465	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.95% 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: IDS, SGN, UAP

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	0.40	0/1076	0.68	0/1453
1	B	0.41	0/1076	0.69	0/1453
2	C	0.41	0/1655	0.70	0/2268
2	D	0.41	0/1664	0.70	0/2279
All	All	0.41	0/5471	0.69	0/7453

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	280	TYR	Sidechain

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	1052	0	1023	79	0
1	B	1052	0	1023	72	0
2	C	1608	0	1531	94	0
2	D	1617	0	1537	97	0
3	E	104	0	37	10	0
4	A	6	0	0	2	0
4	B	2	0	0	0	0
4	C	13	0	0	0	0
4	D	11	0	0	0	0
All	All	5465	0	5151	339	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 32.

The worst 5 of 339 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)
3:E:1:SGN:H4	3:E:2:IDS:H5	1.30	1.09
1:B:128:LYS:HD2	3:E:2:IDS:H4	1.32	1.06
1:A:123:PHE:HB2	1:A:138:THR:HG21	1.37	1.05
1:B:123:PHE:HB2	1:B:138:THR:HG21	1.37	1.02
2:D:318:THR:HG23	2:D:319:THR:H	1.33	0.93

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	131/136 (96%)	113 (86%)	15 (12%)	3 (2%)	6 11
1	B	131/136 (96%)	113 (86%)	14 (11%)	4 (3%)	4 6
2	C	211/226 (93%)	184 (87%)	21 (10%)	6 (3%)	5 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	211/226 (93%)	185 (88%)	20 (10%)	6 (3%)	5	7
All	All	684/724 (94%)	595 (87%)	70 (10%)	19 (3%)	5	7

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	134	ARG
1	B	33	ASN
1	B	134	ARG
2	C	160	LYS

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	113/119 (95%)	109 (96%)	4 (4%)	36	62
1	B	113/119 (95%)	108 (96%)	5 (4%)	28	53
2	C	170/198 (86%)	160 (94%)	10 (6%)	19	39
2	D	171/198 (86%)	159 (93%)	12 (7%)	15	30
All	All	567/634 (89%)	536 (94%)	31 (6%)	21	43

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	320	ASP
2	D	334	GLU
2	C	351	HIS
2	D	351	HIS
2	D	304	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	288	GLN
2	D	166	HIS
2	D	330	ASN
2	C	330	ASN
2	D	185	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](#)

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

5.5 Carbohydrates [i](#)

6 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	SGN	E	1	3	18,19,20	2.38	5 (27%)	22,29,31	1.55	4 (18%)
3	IDS	E	2	3	16,16,17	1.93	6 (37%)	17,24,26	2.00	2 (11%)
3	SGN	E	3	3	18,19,20	2.09	4 (22%)	22,29,31	1.97	6 (27%)
3	IDS	E	4	3	16,16,17	2.03	5 (31%)	17,24,26	2.93	6 (35%)
3	SGN	E	5	3	18,19,20	2.38	4 (22%)	22,29,31	1.80	7 (31%)
3	UAP	E	6	3	15,15,16	2.95	9 (60%)	18,22,24	1.81	4 (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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SGN	E	1	3	-	2/11/28/31	0/1/1/1
3	IDS	E	2	3	-	0/9/26/29	0/1/1/1
3	SGN	E	3	3	-	1/11/28/31	0/1/1/1
3	IDS	E	4	3	-	0/9/26/29	0/1/1/1
3	SGN	E	5	3	-	0/11/28/31	0/1/1/1
3	UAP	E	6	3	1/1/5/7	0/9/22/25	0/1/1/1

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	5	SGN	S1-N2	7.83	1.70	1.59
3	E	1	SGN	O2S-S1	5.99	1.49	1.42
3	E	6	UAP	O6A-C6	5.75	1.37	1.22
3	E	3	SGN	O2S-S1	5.63	1.48	1.42
3	E	6	UAP	C1-C2	5.12	1.60	1.51

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4	IDS	O2-C2-C3	8.87	119.34	106.95
3	E	2	IDS	C2-O2-S	-6.10	109.96	117.91
3	E	3	SGN	C4-C3-C2	-5.55	102.88	111.02
3	E	4	IDS	C2-O2-S	-5.38	110.90	117.91
3	E	6	UAP	C2-O2-S	-4.34	112.25	117.91

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	E	6	UAP	C1

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	1	SGN	C6-O6-S2-O6S
3	E	1	SGN	C6-O6-S2-O4S
3	E	3	SGN	C6-O6-S2-O5S

There are no ring outliers.

5 monomers are involved in 10 short contacts:

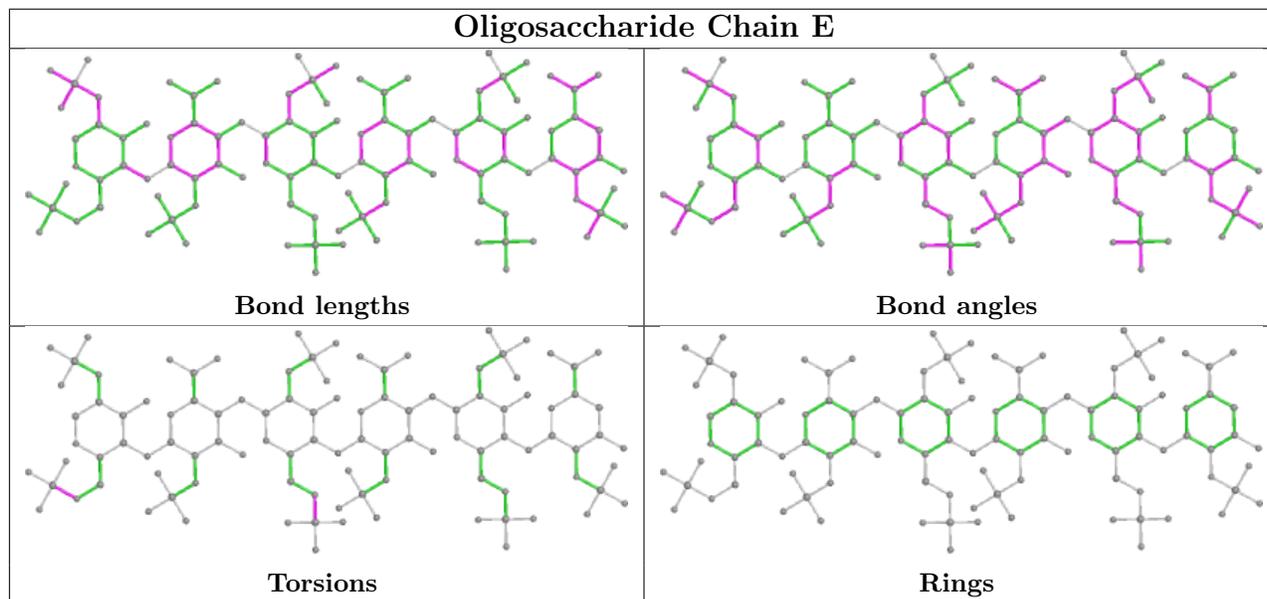
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	4	IDS	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2	IDS	4	0
3	E	5	SGN	3	0
3	E	3	SGN	1	0
3	E	1	SGN	3	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.



5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	133/136 (97%)	-0.11	0 100 100	21, 44, 60, 63	0
1	B	133/136 (97%)	0.01	2 (1%) 73 70	23, 44, 59, 65	0
2	C	213/226 (94%)	0.01	7 (3%) 46 39	19, 38, 74, 79	0
2	D	213/226 (94%)	-0.03	6 (2%) 53 46	20, 37, 74, 79	0
All	All	692/724 (95%)	-0.03	15 (2%) 62 56	19, 40, 69, 79	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	358	VAL	3.7
2	D	267	VAL	3.4
2	C	318	THR	3.3
2	D	302	PRO	3.1
2	C	302	PRO	2.9

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.

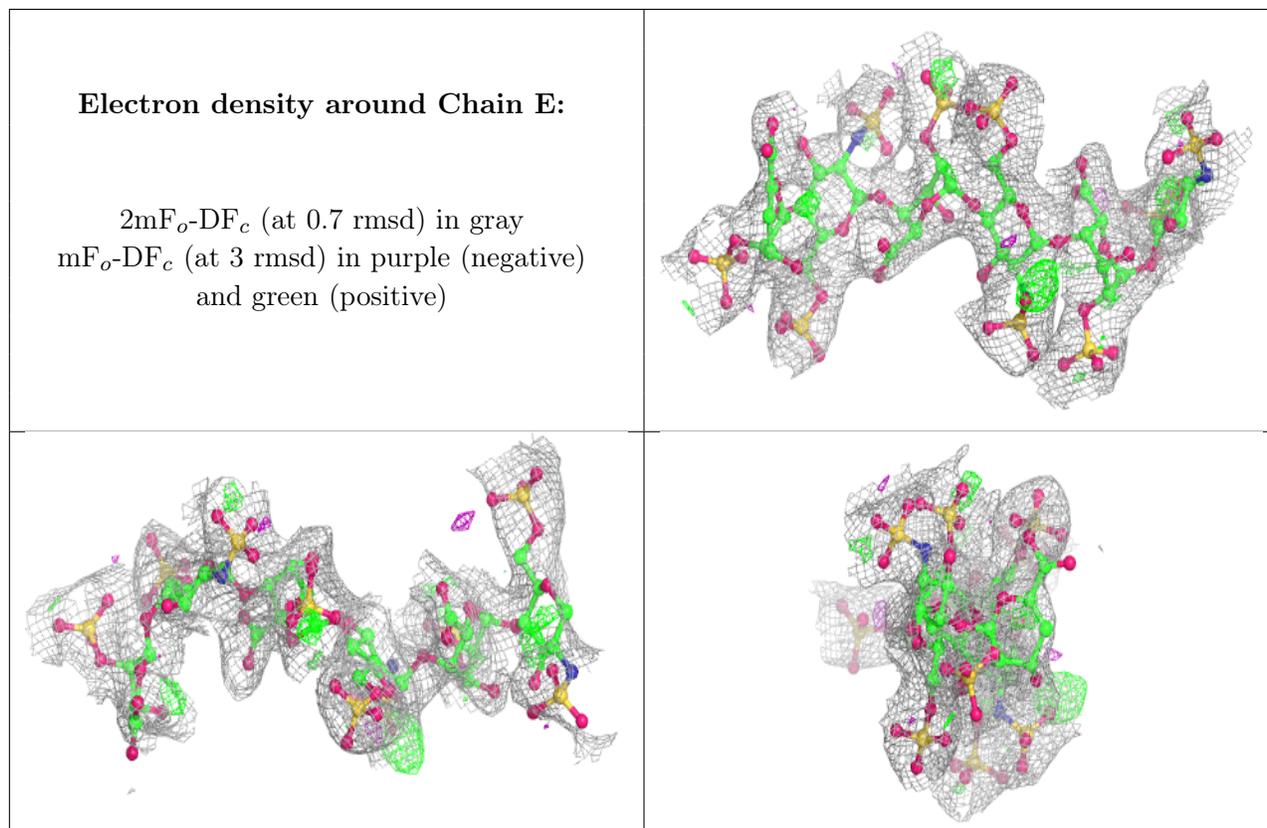
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	UAP	E	6	15/16	0.66	0.21	84,86,87,87	0
3	SGN	E	1	19/20	0.75	0.22	87,90,94,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IDS	E	2	16/17	0.81	0.22	82,83,84,85	0
3	SGN	E	5	19/20	0.87	0.18	78,81,85,85	0
3	SGN	E	3	19/20	0.88	0.17	78,79,81,81	0
3	IDS	E	4	16/17	0.88	0.18	74,79,79,80	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.