



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2026 – 04:21 PM EDT

PDB ID : 9EKO / pdb\_00009eko  
Title : A chimeric hybrid protein fused with the FGFR3 Transmembrane Domain  
Authors : Yu, Z.; Kreitler, D.F.; Gellman, S.H.  
Deposited on : 2024-12-03  
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

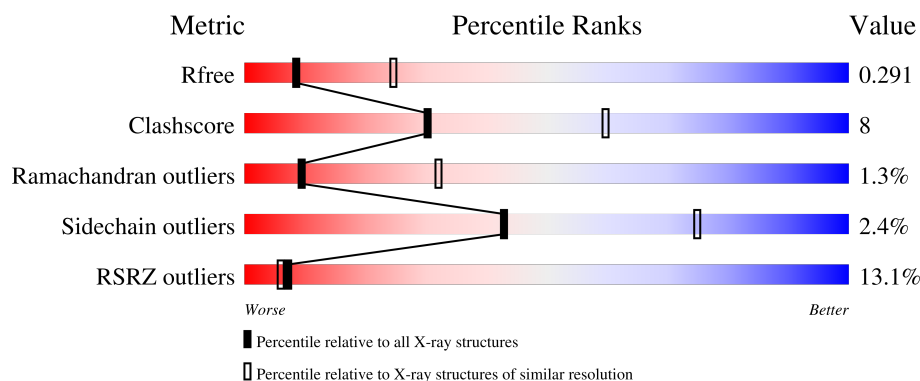
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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  $\geq 3$ , 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	481	
2	B	2	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6607 atoms, of which 3222 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 chimeric protein fused with the FGFR3 Transmembrane Domain, Saposin-A, Fibroblast growth factor receptor 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	452	Total	C	H	N	O	S	0	0	0
			6548	2149	3200	544	641	14			

There are 37 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	2	GLY	-	expression tag	UNP P0AEX9
A	174	ASP	GLU	engineered mutation	UNP P0AEX9
A	182	ALA	ASP	engineered mutation	UNP P0AEX9
A	186	ALA	ASP	engineered mutation	UNP P0AEX9
A	314	VAL	ALA	engineered mutation	UNP P0AEX9
A	337	ALA	GLN	engineered mutation	UNP P0AEX9
A	340	TYR	ALA	engineered mutation	UNP P0AEX9
A	364	ALA	-	linker	UNP P0AEX9
A	365	CYS	-	linker	UNP P0AEX9
A	366	ALA	-	linker	UNP P0AEX9
A	367	ILE	-	linker	UNP P0AEX9
A	368	CYS	-	linker	UNP P0AEX9
A	369	LEU	-	linker	UNP P0AEX9
A	370	ILE	-	linker	UNP P0AEX9
A	371	VAL	-	linker	UNP P0AEX9
A	372	VAL	-	linker	UNP P0AEX9
A	373	ALA	-	linker	UNP P0AEX9
A	374	LYS	-	linker	UNP P0AEX9
A	375	ALA	-	linker	UNP P0AEX9
A	376	GLY	-	linker	UNP P0AEX9
A	377	VAL	-	linker	UNP P0AEX9
A	378	MET	-	linker	UNP P0AEX9
A	379	LEU	-	linker	UNP P0AEX9
A	380	ARG	-	linker	UNP P0AEX9
A	442	ASN	-	linker	UNP P07602

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Chain	Residue	Modelled	Actual	Comment	Reference
A	443	SER	-	linker	UNP P07602
A	444	GLY	-	linker	UNP P07602
A	445	GLY	-	linker	UNP P07602
A	446	SER	-	linker	UNP P07602
A	472	SER	CYS	engineered mutation	UNP P22607
A	476	HIS	-	expression tag	UNP P22607
A	477	HIS	-	expression tag	UNP P22607
A	478	HIS	-	expression tag	UNP P22607
A	479	HIS	-	expression tag	UNP P22607
A	480	HIS	-	expression tag	UNP P22607
A	481	HIS	-	expression tag	UNP P22607

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	2	Total	C	H	O	0	0	0
			45	12	22	11			

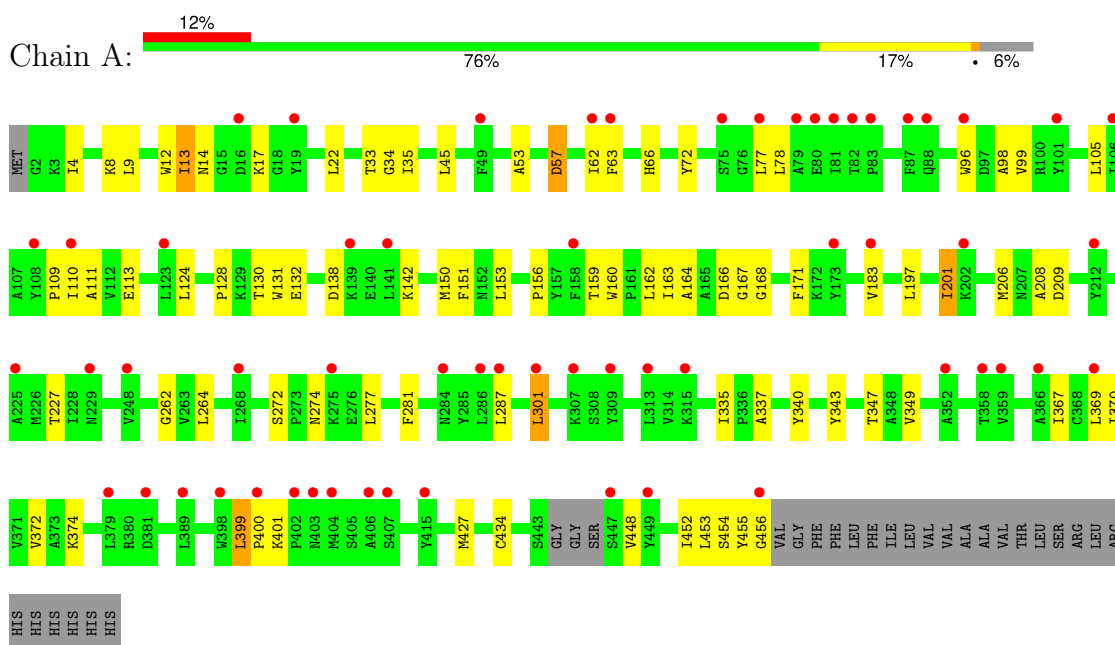
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	14	Total	O	0	0
			14	14		

### 3 Residue-property plots

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: chimeric protein fused with the FGFR3 Transmembrane Domain, Saposin-A, Fibroblast growth factor receptor 3



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	142.00Å 70.26Å 63.58Å 90.00° 114.18° 90.00°	Depositor
Resolution (Å)	64.77 – 2.90 64.77 – 2.90	Depositor EDS
% Data completeness (in resolution range)	54.8 (64.77-2.90) 54.8 (64.77-2.90)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.85 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, $R_{free}$	0.275 , 0.287 0.275 , 0.291	Depositor DCC
$R_{free}$ test set	527 reflections (4.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	82.2	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 76.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.042 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	6607	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC

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	0.09	0/3424	0.23	0/4670

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 [i](#)

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	3348	3200	3197	55	0
2	B	23	22	20	1	0
3	A	14	0	0	0	0
All	All	3385	3222	3217	55	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 8.

All (55) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:PHE:O	1:A:153:LEU:HD12	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:GLU:N	1:A:262:GLY:O	2.26	0.69
1:A:183:VAL:CG1	1:A:370:ILE:HD12	2.27	0.65
1:A:156:PRO:HA	1:A:159:THR:HG22	1.78	0.64
1:A:171:PHE:H	1:A:183:VAL:HG23	1.62	0.64
1:A:372:VAL:HG13	1:A:427:MET:HE3	1.81	0.61
1:A:4:ILE:HD11	1:A:272:SER:HA	1.81	0.60
1:A:369:LEU:HD23	1:A:434:CYS:SG	2.43	0.59
1:A:347:THR:HG21	1:A:369:LEU:CD1	2.34	0.57
1:A:13:ILE:HD11	1:A:22:LEU:HD23	1.86	0.57
1:A:367:ILE:HD13	1:A:370:ILE:HD11	1.87	0.56
1:A:343:TYR:O	1:A:347:THR:HG22	2.06	0.55
1:A:53:ALA:CB	1:A:77:LEU:HD22	2.36	0.55
1:A:13:ILE:HG23	1:A:63:PHE:HB2	1.90	0.53
1:A:159:THR:HG21	1:A:349:VAL:HG11	1.91	0.53
1:A:347:THR:HG21	1:A:369:LEU:HD11	1.91	0.53
1:A:131:TRP:CH2	1:A:162:LEU:HD12	2.44	0.52
1:A:183:VAL:HG11	1:A:370:ILE:HD12	1.92	0.51
1:A:12:TRP:HB3	1:A:45:LEU:HD11	1.91	0.51
1:A:337:ALA:HB1	1:A:340:TYR:CZ	2.45	0.51
1:A:13:ILE:HG23	1:A:63:PHE:CB	2.42	0.49
1:A:162:LEU:C	1:A:162:LEU:HD23	2.37	0.49
1:A:99:VAL:HG21	1:A:109:PRO:HD3	1.95	0.48
1:A:34:GLY:C	1:A:35:ILE:HD12	2.38	0.48
1:A:201:ILE:HG21	1:A:208:ALA:HB2	1.97	0.47
1:A:66:HIS:CD2	1:A:98:ALA:HB1	2.50	0.47
1:A:301:LEU:N	1:A:301:LEU:HD12	2.30	0.47
1:A:399:LEU:CB	1:A:400:PRO:CD	2.92	0.47
1:A:72:TYR:HB3	1:A:78:LEU:HD23	1.95	0.46
1:A:131:TRP:CZ2	1:A:162:LEU:HD12	2.50	0.46
1:A:53:ALA:HB1	1:A:77:LEU:HD22	1.98	0.45
1:A:160:TRP:NE1	1:A:164:ALA:HB2	2.32	0.45
1:A:166:ASP:O	1:A:168:GLY:N	2.49	0.45
1:A:45:LEU:O	1:A:45:LEU:HD23	2.16	0.45
1:A:110:ILE:HD13	1:A:287:LEU:CD2	2.46	0.45
1:A:124:LEU:HD21	1:A:128:PRO:HD3	1.99	0.45
1:A:130:THR:HG22	1:A:132:GLU:OE1	2.16	0.45
1:A:4:ILE:HG23	1:A:57:ASP:HA	1.99	0.44
1:A:96:TRP:CZ3	1:A:105:LEU:HD23	2.53	0.43
1:A:33:THR:HG22	1:A:35:ILE:HD13	1.99	0.43
1:A:163:ILE:HD11	1:A:197:LEU:HD21	2.00	0.43
1:A:110:ILE:HD13	1:A:287:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:PRO:HD2	2:B:2:GLC:O6	2.19	0.43
1:A:17:LYS:HE3	1:A:113:GLU:OE2	2.19	0.43
1:A:62:ILE:HD12	1:A:62:ILE:N	2.34	0.42
1:A:150:MET:O	1:A:227:THR:OG1	2.36	0.42
1:A:277:LEU:O	1:A:281:PHE:N	2.50	0.42
1:A:201:ILE:HG23	1:A:206:MET:O	2.19	0.42
1:A:13:ILE:HG22	1:A:14:ASN:H	1.85	0.42
1:A:8:LYS:N	1:A:274:ASN:OD1	2.52	0.42
1:A:111:ALA:O	1:A:264:LEU:N	2.53	0.42
1:A:335:ILE:HD12	1:A:337:ALA:HB3	2.02	0.42
1:A:454:SER:O	1:A:456:GLY:N	2.46	0.42
1:A:201:ILE:HD13	1:A:208:ALA:HB2	2.02	0.41
1:A:138:ASP:OD1	1:A:142:LYS:NZ	2.35	0.41

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	448/481 (93%)	403 (90%)	39 (9%)	6 (1%)	9	32

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	448	VAL
1	A	167	GLY
1	A	401	LYS
1	A	452	ILE
1	A	453	LEU
1	A	399	LEU

### 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	329/389 (85%)	321 (98%)	8 (2%)	43 75

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	LEU
1	A	13	ILE
1	A	57	ASP
1	A	201	ILE
1	A	209	ASP
1	A	301	LEU
1	A	374	LYS
1	A	455	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	187	ASN

### 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](#)

2 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GLC	B	1	2	12,12,12	1.24	1 (8%)	17,17,17	0.79	0
2	GLC	B	2	2	11,11,12	1.55	3 (27%)	15,15,17	1.19	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	B	1	2	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	GLC	O5-C1	3.77	1.50	1.43
2	B	1	GLC	O5-C1	3.34	1.51	1.42
2	B	2	GLC	O5-C5	2.23	1.47	1.43
2	B	2	GLC	C2-C3	-2.10	1.49	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	GLC	C1-O5-C5	-2.78	108.46	112.19
2	B	2	GLC	C1-C2-C3	2.15	112.77	109.64

There are no chirality outliers.

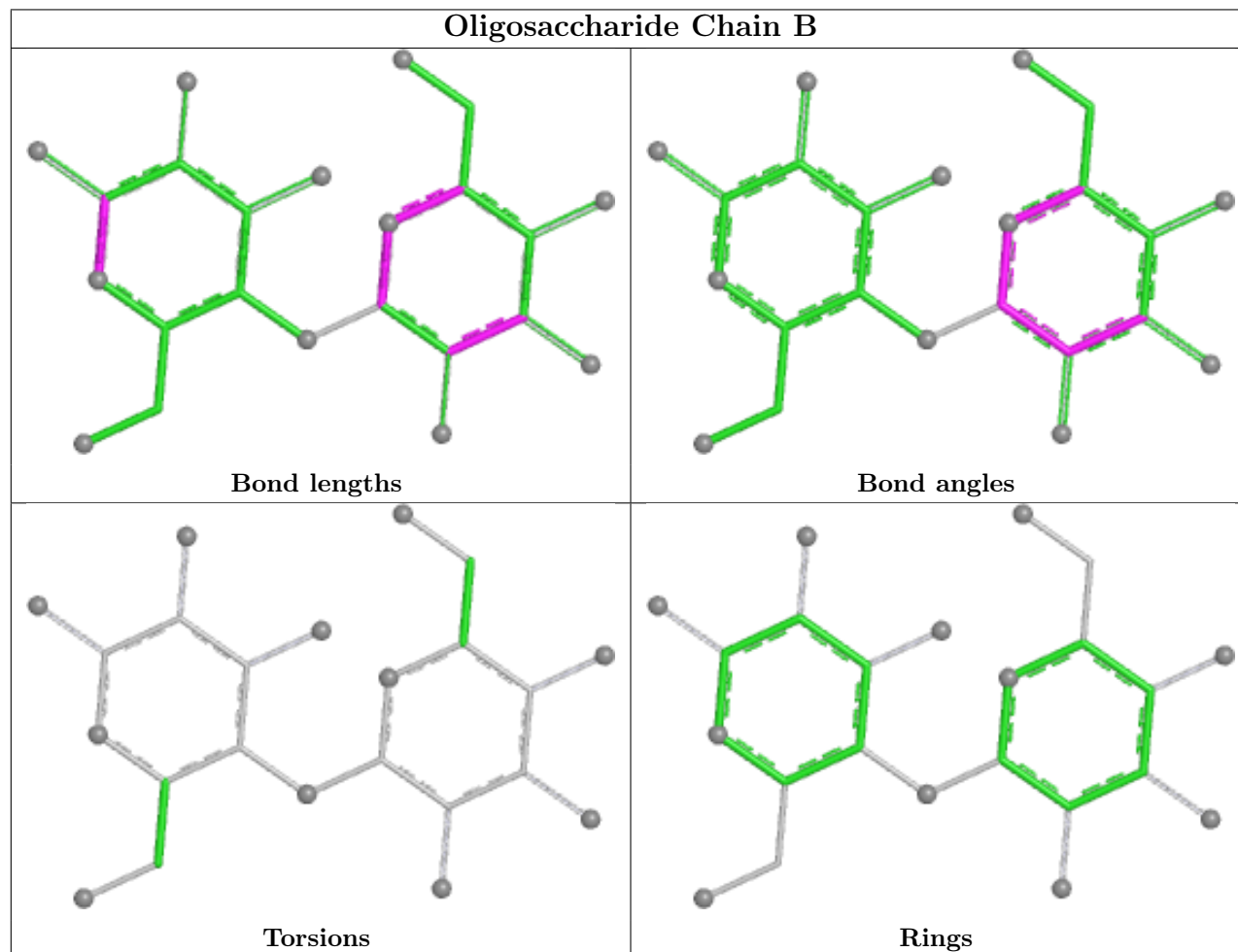
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	GLC	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.



## 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 ⓘ

### 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	452/481 (93%)	0.98	59 (13%) 7 6	53, 83, 134, 209	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	108	TYR	8.6
1	A	402	PRO	6.7
1	A	80	GLU	5.8
1	A	284	ASN	5.8
1	A	87	PHE	5.3
1	A	106	ILE	4.4
1	A	313	LEU	4.1
1	A	77	LEU	3.9
1	A	403	ASN	3.9
1	A	81	ILE	3.7
1	A	141	LEU	3.6
1	A	447	SER	3.6
1	A	406	ALA	3.6
1	A	398	TRP	3.5
1	A	139	LYS	3.5
1	A	123	LEU	3.4
1	A	79	ALA	3.4
1	A	62	ILE	3.3
1	A	301	LEU	3.3
1	A	449	TYR	3.3
1	A	404	MET	3.2
1	A	287	LEU	3.1
1	A	96	TRP	3.1
1	A	225	ALA	3.1
1	A	16	ASP	3.0
1	A	63	PHE	3.0
1	A	359	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	202	LYS	2.9
1	A	212	TYR	2.9
1	A	268	ILE	2.8
1	A	75	SER	2.8
1	A	456	GLY	2.8
1	A	49	PHE	2.7
1	A	415	TYR	2.7
1	A	358	THR	2.6
1	A	83	PRO	2.5
1	A	315	LYS	2.5
1	A	19	TYR	2.5
1	A	158	PHE	2.5
1	A	82	THR	2.5
1	A	379	LEU	2.4
1	A	101	TYR	2.4
1	A	173	TYR	2.4
1	A	286	LEU	2.4
1	A	229	ASN	2.3
1	A	275	LYS	2.3
1	A	183	VAL	2.3
1	A	248	VAL	2.2
1	A	407	SER	2.1
1	A	307	LYS	2.1
1	A	389	LEU	2.1
1	A	88	GLN	2.1
1	A	381	ASP	2.1
1	A	366	ALA	2.1
1	A	309	TYR	2.1
1	A	400	PRO	2.1
1	A	110	ILE	2.0
1	A	352	ALA	2.0
1	A	369	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

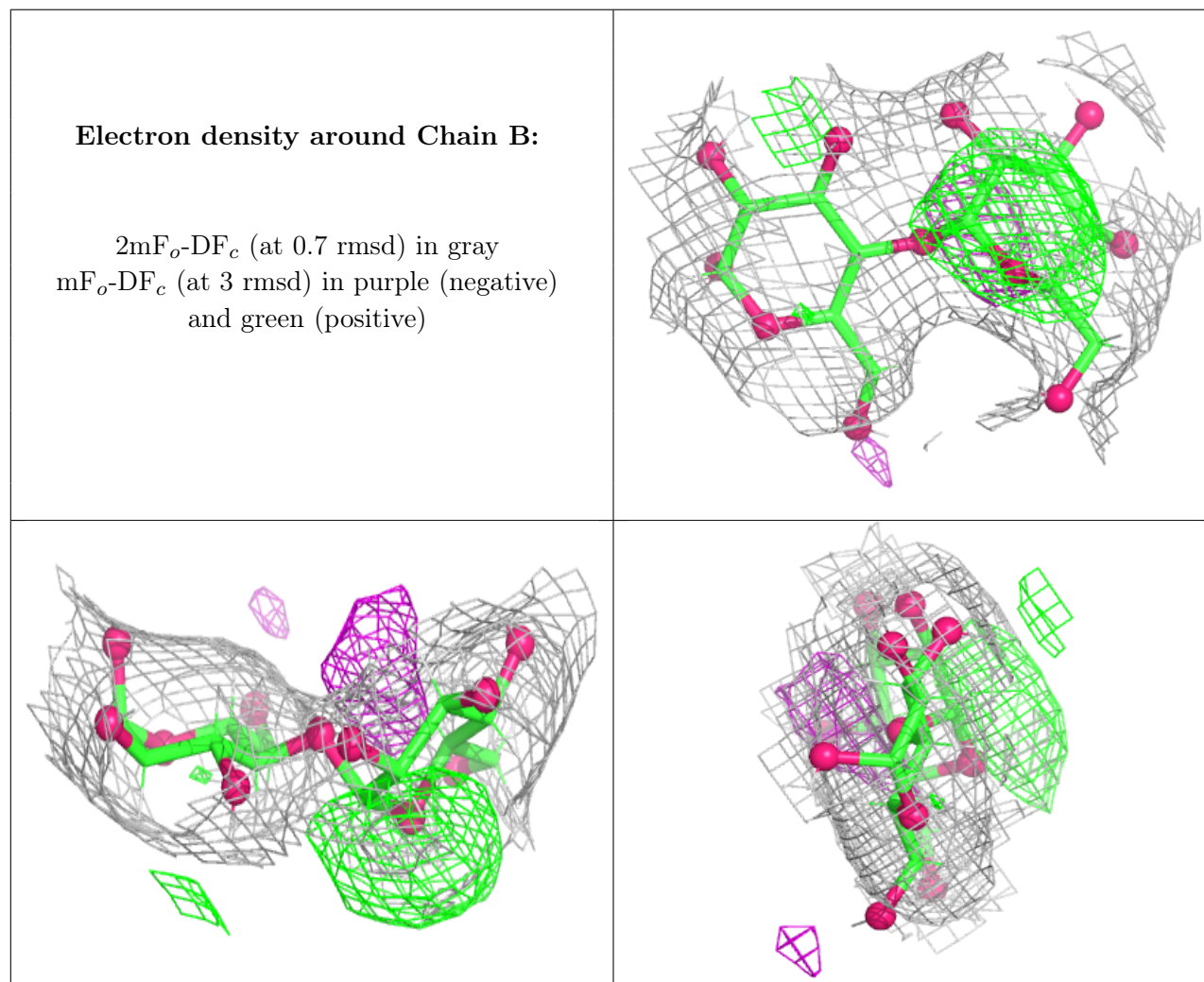
## 6.3 Carbohydrates [i](#)

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, 95<sup>th</sup> 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
2	GLC	B	2	11/12	0.68	0.17	25,56,61,64	0
2	GLC	B	1	12/12	0.81	0.15	39,62,67,71	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.