



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2022 – 07:39 AM JST

PDB ID : 5YZD
Title : Crystal structure of the prefusion form of measles virus fusion protein in complex with a fusion inhibitor peptide (FIP)
Authors : Hashiguchi, T.; Fukuda, Y.; Matsuoka, R.; Kuroda, D.; Kubota, M.; Shirigane, Y.; Watanabe, S.; Tsumoto, K.; Kohda, D.; Plemper, R.K.; Yanagi, Y.
Deposited on : 2017-12-14
Resolution : 2.64 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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	:	2.27
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)	:	2.27

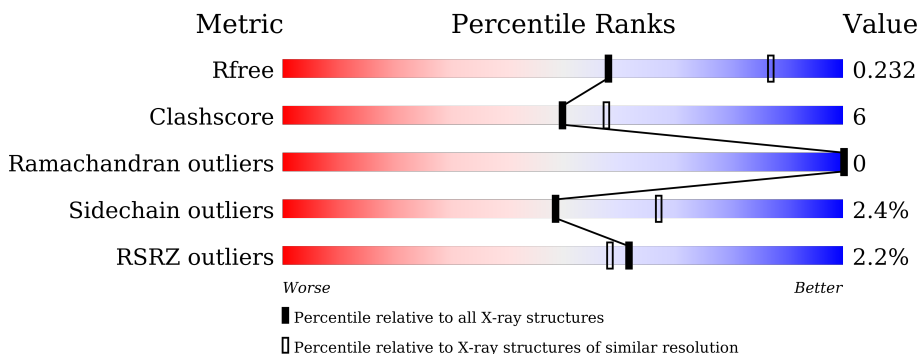
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.64 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	1426 (2.66-2.62)
Clashscore	141614	1472 (2.66-2.62)
Ramachandran outliers	138981	1446 (2.66-2.62)
Sidechain outliers	138945	1446 (2.66-2.62)
RSRZ outliers	127900	1408 (2.66-2.62)

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	94	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>7%</div> <div>•</div> <div>14%</div> </div> </div>
2	C	419	<div> <div>2%</div> <div> <div></div> <div>77%</div> <div>9%</div> <div>•</div> <div>12%</div> </div> </div>
3	B	4	<div> <div></div> <div>100%</div> </div>
4	D	2	<div> <div></div> <div>100%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3525 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 glycoprotein F2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	81	Total	C	N	O	S	0	0	0
			637	400	120	113	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLY	-	expression tag	UNP Q786F3

- Molecule 2 is a protein called glycoprotein F1, measles virus fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	367	Total	C	N	O	S	0	0	0
			2771	1749	467	541	14			

- Molecule 3 is a protein called peptide CBZ-DPN-PHE-GLY.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	4	Total	C	N	O	0	0	0
			36	28	3	5			

- Molecule 4 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
4	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

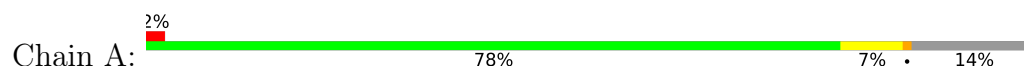
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	O	0	0
			3	3		
6	C	36	Total	O	0	0
			36	36		

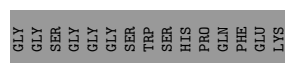
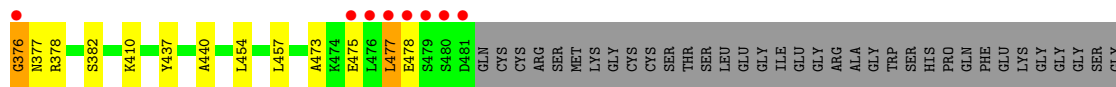
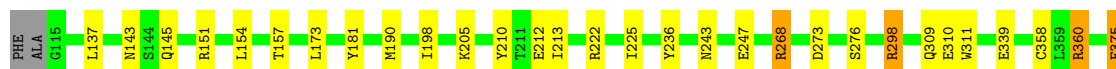
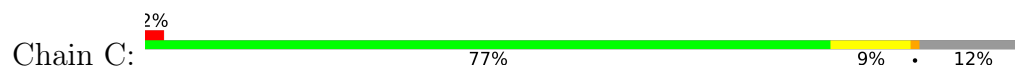
3 Residue-property plots [i](#)

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: glycoprotein F2



- Molecule 2: glycoprotein F1, measles virus fusion protein



- Molecule 3: peptide CBZ-DPN-PHE-GLY



There are no outlier residues recorded for this chain.

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



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, α , β , γ	170.41Å 170.41Å 170.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	85.20 – 2.64 85.20 – 2.64	Depositor EDS
% Data completeness (in resolution range)	100.0 (85.20-2.64) 100.0 (85.20-2.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.65Å)	Xtriage
Refinement program	PHENIX (1.11_2567)	Depositor
R, R_{free}	0.191 , 0.232 0.191 , 0.232	Depositor DCC
R_{free} test set	1244 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	57.2	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.027 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3525	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PHQ, DPN, 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	0.50	0/645	0.70	0/873
2	C	0.60	1/2812 (0.0%)	0.83	6/3820 (0.2%)
3	B	0.68	0/15	0.65	0/18
All	All	0.59	1/3472 (0.0%)	0.80	6/4711 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	377	ASN	N-CA	-5.03	1.36	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	268	ARG	NE-CZ-NH1	10.91	125.75	120.30
2	C	377	ASN	N-CA-C	-6.55	93.31	111.00
2	C	360	ARG	NE-CZ-NH1	-6.44	117.08	120.30
2	C	268	ARG	NE-CZ-NH2	-6.11	117.25	120.30
2	C	376	GLY	N-CA-C	-5.25	99.99	113.10
2	C	457	LEU	CB-CG-CD2	-5.03	102.46	111.00

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	637	0	672	10	0
2	C	2771	0	2797	35	0
3	B	36	0	27	0	0
4	D	28	0	25	0	0
5	A	14	0	13	0	0
6	A	3	0	0	0	0
6	C	36	0	0	1	0
All	All	3525	0	3534	41	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 6.

All (41) 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:C:375:PHE:CD1	2:C:376:GLY:O	2.07	1.08
2:C:375:PHE:HD1	2:C:376:GLY:O	1.42	0.99
1:A:101:VAL:HG23	1:A:102:GLN:OE1	1.68	0.91
2:C:151:ARG:HD3	2:C:276:SER:OG	1.85	0.75
1:A:101:VAL:CG2	1:A:102:GLN:OE1	2.38	0.71
1:A:102:GLN:H	1:A:102:GLN:CD	1.94	0.71
2:C:375:PHE:CE1	2:C:376:GLY:O	2.44	0.69
2:C:243:ASN:O	2:C:247:GLU:HG3	1.93	0.68
2:C:190:MET:HE2	2:C:198:ILE:HG13	1.79	0.64
2:C:212:GLU:HG3	2:C:236:TYR:CG	2.33	0.64
2:C:268:ARG:NH1	6:C:601:HOH:O	2.30	0.64
2:C:310:GLU:OE1	2:C:378:ARG:NH1	2.29	0.64
2:C:310:GLU:CD	2:C:378:ARG:HH11	2.00	0.64
2:C:151:ARG:NH2	2:C:273:ASP:OD2	2.32	0.63
2:C:339:GLU:N	2:C:339:GLU:OE1	2.29	0.62
2:C:410:LYS:HD3	2:C:440:ALA:HB3	1.82	0.61
2:C:190:MET:HE1	2:C:198:ILE:HG21	1.83	0.61
1:A:38:ILE:HG13	2:C:298:ARG:HG2	1.88	0.56
2:C:212:GLU:HG3	2:C:236:TYR:CD2	2.41	0.56
1:A:24:GLN:HA	1:A:24:GLN:OE1	2.05	0.56
1:A:102:GLN:CD	1:A:102:GLN:N	2.63	0.53
2:C:375:PHE:CD1	2:C:375:PHE:C	2.84	0.52
1:A:102:GLN:OE1	1:A:102:GLN:N	2.43	0.51
1:A:94:MET:HB2	2:C:225:ILE:HD13	1.94	0.50
2:C:473:ALA:O	2:C:477:LEU:HD22	2.11	0.50
2:C:478:GLU:N	2:C:478:GLU:OE1	2.45	0.49
2:C:475:GLU:HA	2:C:478:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:137:LEU:CA	2:C:268:ARG:HH22	2.28	0.47
2:C:151:ARG:HH22	2:C:273:ASP:CG	2.20	0.44
2:C:309:GLN:HB3	2:C:311:TRP:NE1	2.32	0.44
1:A:79:LEU:HB3	2:C:210:TYR:CE1	2.53	0.44
2:C:190:MET:CE	2:C:198:ILE:HG21	2.48	0.43
1:A:54:LEU:HD12	2:C:173:LEU:HB3	2.01	0.42
2:C:154:LEU:O	2:C:157:THR:HG22	2.20	0.42
2:C:151:ARG:NH2	2:C:273:ASP:CG	2.73	0.42
2:C:454:LEU:HD23	2:C:454:LEU:HA	1.79	0.41
2:C:213:ILE:HD13	2:C:213:ILE:HA	1.86	0.41
2:C:360:ARG:HH11	2:C:360:ARG:HD2	1.59	0.41
2:C:181:TYR:CD2	2:C:205:LYS:HG3	2.55	0.40
2:C:309:GLN:HB3	2:C:311:TRP:HE1	1.86	0.40
2:C:382:SER:HG	2:C:437:TYR:HH	1.67	0.40

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	79/94 (84%)	77 (98%)	2 (2%)	0	100	100
2	C	365/419 (87%)	360 (99%)	5 (1%)	0	100	100
3	B	1/4 (25%)	1 (100%)	0	0	100	100
All	All	445/517 (86%)	438 (98%)	7 (2%)	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	73/83 (88%)	71 (97%)	2 (3%)	44	63
2	C	305/343 (89%)	298 (98%)	7 (2%)	50	68
3	B	1/1 (100%)	1 (100%)	0	100	100
All	All	379/427 (89%)	370 (98%)	9 (2%)	49	67

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	ARG
1	A	102	GLN
2	C	143	ASN
2	C	145	GLN
2	C	222	ARG
2	C	298	ARG
2	C	358	CYS
2	C	375	PHE
2	C	477	LEU

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	67	ASN
2	C	377	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

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$
4	NAG	D	1	1,4	14,14,15	1.07	2 (14%)	17,19,21	2.23	4 (23%)
4	NAG	D	2	4	14,14,15	1.00	1 (7%)	17,19,21	1.19	2 (11%)

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	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	NAG	C7-N2	2.63	1.43	1.34
4	D	2	NAG	C7-N2	2.49	1.42	1.34
4	D	1	NAG	C2-N2	-2.25	1.42	1.46

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	1	NAG	C1-O5-C5	6.44	120.91	112.19
4	D	1	NAG	C2-N2-C7	-3.71	117.62	122.90
4	D	1	NAG	O5-C1-C2	-3.14	106.33	111.29
4	D	1	NAG	C8-C7-N2	2.58	120.46	116.10
4	D	2	NAG	O5-C5-C6	2.13	110.55	107.20
4	D	2	NAG	C1-O5-C5	2.03	114.94	112.19

There are no chirality outliers.

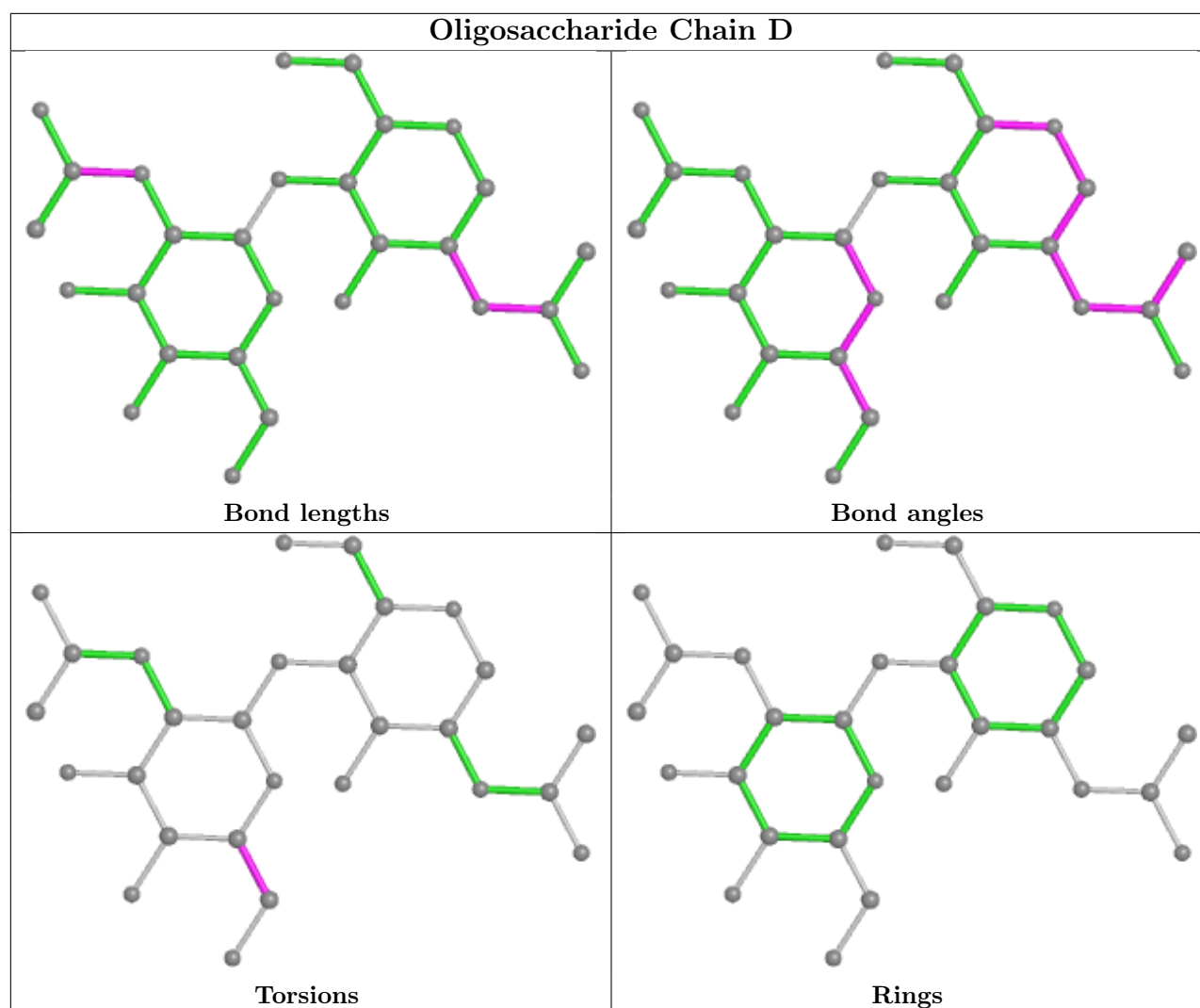
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	2	NAG	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

1 ligand is 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	A	203	1	14,14,15	1.11	1 (7%)	17,19,21	2.30	5 (29%)

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	A	203	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	203	NAG	C2-N2	-3.01	1.41	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	203	NAG	C1-C2-N2	-5.72	100.72	110.49
5	A	203	NAG	C1-O5-C5	4.20	117.89	112.19
5	A	203	NAG	O5-C1-C2	2.54	115.31	111.29
5	A	203	NAG	C4-C3-C2	2.46	114.62	111.02
5	A	203	NAG	C3-C4-C5	-2.36	106.03	110.24

There are no chirality outliers.

There are no torsion outliers.

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	81/94 (86%)	0.29	2 (2%) 57 53	43, 53, 81, 113	0
2	C	367/419 (87%)	0.11	8 (2%) 62 58	38, 52, 85, 140	0
3	B	2/4 (50%)	0.38	0 100 100	54, 54, 54, 66	0
All	All	450/517 (87%)	0.14	10 (2%) 62 58	38, 52, 85, 140	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	104	VAL	6.9
1	A	103	SER	5.4
2	C	479	SER	5.4
2	C	481	ASP	4.9
2	C	476	LEU	4.6
2	C	477	LEU	4.2
2	C	480	SER	4.1
2	C	478	GLU	2.7
2	C	475	GLU	2.7
2	C	376	GLY	2.3

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

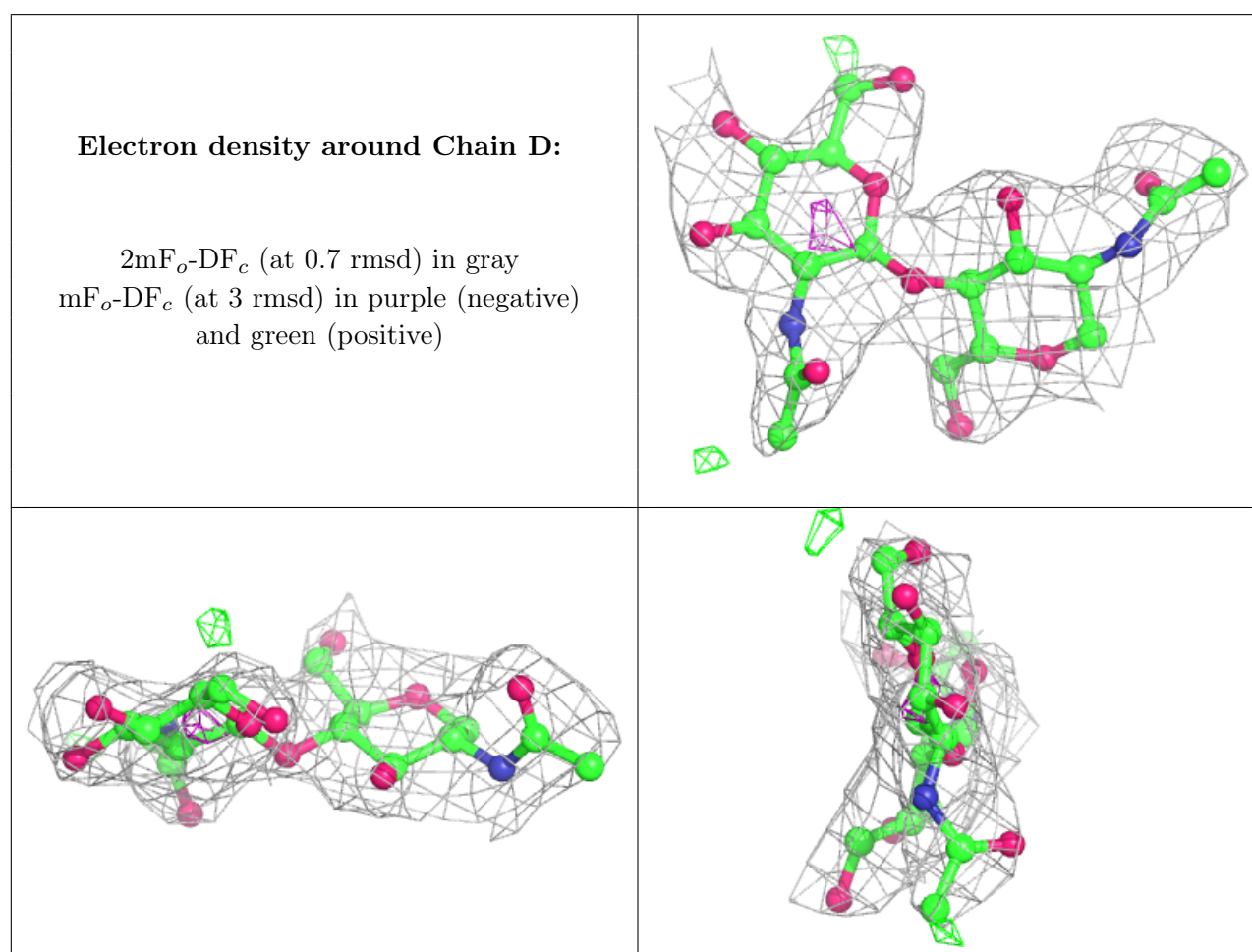
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	DPN	B	2	11/12	0.98	0.17	43,46,54,54	0

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
4	NAG	D	2	14/15	0.79	0.20	73,92,96,98	0
4	NAG	D	1	14/15	0.93	0.12	63,67,76,83	0

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



6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NAG	A	203	14/15	0.88	0.25	61,68,74,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.