wwPDB X-ray Structure Validation Summary Report (i)

Aug 14, 2023 – 05:30 PM EDT

PDB ID	:	1R6Z
Title	:	The Crystal Structure of the Argonaute2 PAZ domain (as a MBP fusion)
Authors	:	Song, J.J.; Liu, J.; Tolia, N.H.; Schneiderman, J.; Smith, S.K.; Martienssen, R.A.; Hannon, G.J.; Joshua-Tor, L.
Deposited on	:	2003-10-17
Resolution	:	2.80 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 (i)) were used in the production of this report:

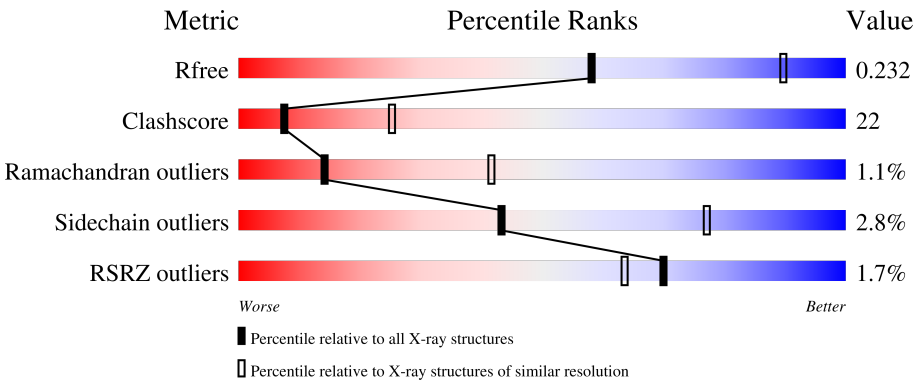
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	509	.% 60% 36% • •
1	P	509	3% 59% 36% • •
1	Z	509	.% 61% 35% • •
2	B	2	100%
2	C	2	50% 50%

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Mol	Chain	Length	Quality of chain
2	D	2	100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11834 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 Chimera of Maltose-binding periplasmic protein and Argonaute 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	P	498	3901	2511	642	738	10	0	0	0
1	A	497	3892	2506	641	735	10	0	0	0
1	Z	499	3906	2512	644	740	10	0	0	0

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-1	MET	-	cloning artifact	UNP P02928
P	366	ASN	-	linker	UNP P02928
P	367	ALA	-	linker	UNP P02928
P	368	ALA	-	linker	UNP P02928
P	369	ALA	-	linker	UNP P02928
P	370	GLU	-	linker	UNP P02928
P	371	PHE	-	linker	UNP P02928
A	-1	MET	-	cloning artifact	UNP P02928
A	366	ASN	-	linker	UNP P02928
A	367	ALA	-	linker	UNP P02928
A	368	ALA	-	linker	UNP P02928
A	369	ALA	-	linker	UNP P02928
A	370	GLU	-	linker	UNP P02928
A	371	PHE	-	linker	UNP P02928
Z	-1	MET	-	cloning artifact	UNP P02928
Z	366	ASN	-	linker	UNP P02928
Z	367	ALA	-	linker	UNP P02928
Z	368	ALA	-	linker	UNP P02928
Z	369	ALA	-	linker	UNP P02928
Z	370	GLU	-	linker	UNP P02928
Z	371	PHE	-	linker	UNP P02928

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

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	B	2	23	12	11	0	0	0
2	C	2	23	12	11	0	0	0
2	D	2	23	12	11	0	0	0

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ni		
3	P	3	3	3	0	0
3	A	3	3	3	0	0
3	Z	3	3	3	0	0

- Molecule 4 is water.

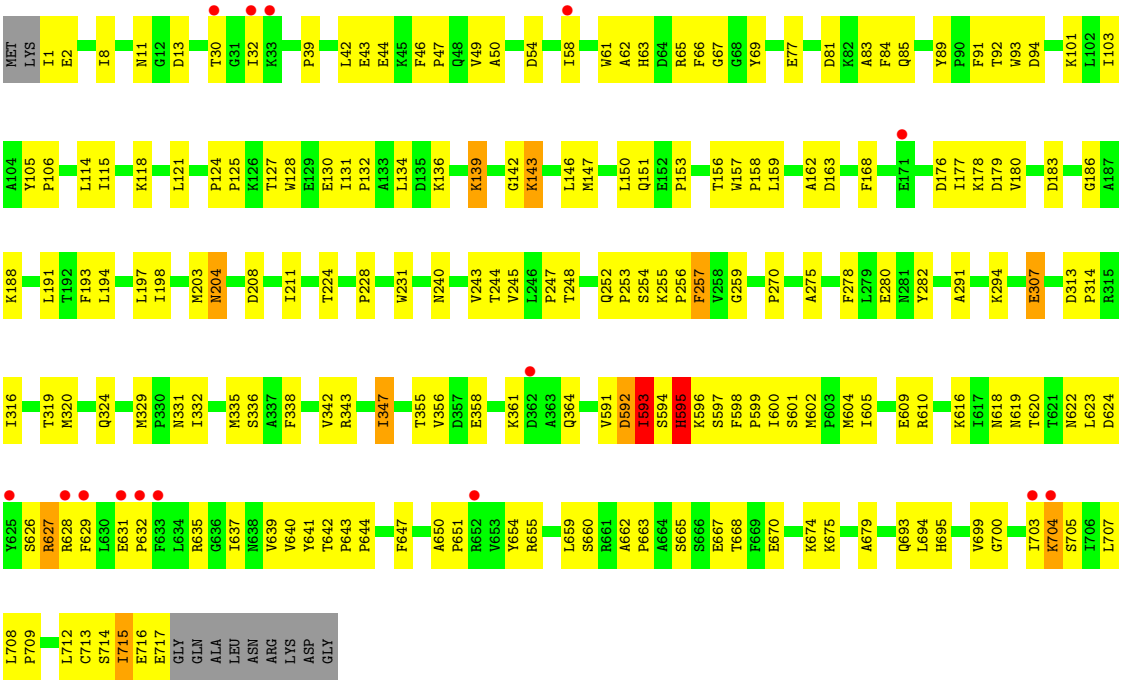
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	P	17	17	17	0	0
4	A	22	22	22	0	0
4	Z	18	18	18	0	0

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.

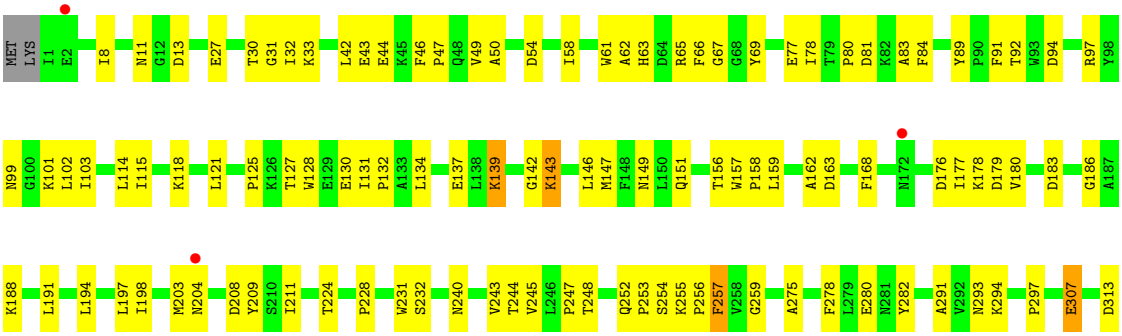
• Molecule 1: Chimera of Maltose-binding periplasmic protein and Argonaute 2

Chain P:



• Molecule 1: Chimera of Maltose-binding periplasmic protein and Argonaute 2

Chain A:



P314 R315 I316 A317 A318 T319 M320 E321 Q324 K325 M329 P330 N331 I332 M335 S336 A337 F338 W339 V342 R343 T344 I347 R353 Q354 T355 V356 D357 E358 K361 D362 A363 Q364 T365 A369 E370 F371 V591 D592 I593 K596 S597 F598 M602 P603 M604 I605 E609 R610

K616 I617 N618 N619 T620 T621 N622 L623 D624 Y625 S626 R627 R628 F629 L630 E631 P632 R635 V639 V640 Y641 T642 P643 P644 F647 Y654 L659 S660 R661 A662 P663 E667 T668 F669 E670 K674 K675 F682 Y687 Q693 L694 H695 V699 G700 S701 S702 I703 K704

S705 I706 L707 L708 P709 L712 C713 S714 I715 E716 GLU GLY GLN ALA LEU ASN ARG LYS ASP GLY

- Molecule 1: Chimera of Maltose-binding periplasmic protein and Argonaute 2

Chain Z:

MET LYS ILE E2 I8 N11 G12 D13 T30 G31 I32 P39 L42 E43 F46 P47 Q48 V49 A50 D54 I58 W61 A62 H63 D64 R65 F66 G67 G68 Y69 E77 D81 K82 A83 F84 Q85 D86 Y89 P90 F91 T92 W93 D94 R97 K101 L102

I103 A104 Y105 P106 K118 L121 P125 K126 T127 W128 E129 E130 I131 P132 A133 L134 K139 G142 K143 L146 M147 L150 Q151 Y154 F155 T156 W157 P158 L159 A162 D163 F168 D176 I177 K178 D179 V180 D183 N184 A185 G186 A187 K188 L191 L194

L197 I198 M203 N204 D208 I211 P228 W229 A230 W231 N240 T244 V245 L246 P247 T248 G251 Q252 P253 S254 K255 P256 F257 V258 G259 A275 F278 L279 E280 N281 Y282 A291 K294 E307 D313 P314 R315 I316 T319 M320 Q324 M329 P330 N331

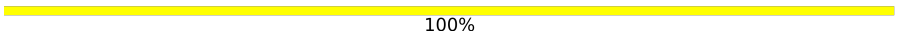
M335 S336 A337 F338 V342 R343 I347 Q354 T355 V356 D357 E358 K361 D362 A363 Q364 F371 V591 D592 I593 S597 F598 P599 M602 P603 M604 I605 E609 R610 K616 I617 N618 N619 T620 T621 N622 L623 D624 Y625 S626 R627 R628 F629 L630 E631 P632 R635 V639

V640 Y641 T642 P643 P644 F647 A650 P651 Y654 R655 L659 S660 S665 S666 E667 T668 F669 E670 K674 K675 A679 F682 Y687 Q693 L694 H695 V699 G700 S701 S702 I703 K704 S705 I706 L707 L708 P709 L712 C713 S714 I715 E716 E717 G718 Q719 ALA LEU ASN

ARG LYS ASP GLY

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

Chain B:



GLC1 GLC2

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

Chain C:

GLC1 GLC2

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

Chain D:

GLC1
GLC2

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	89.81Å 89.81Å 380.33Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.91 – 2.80 44.91 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (44.91-2.80) 97.3 (44.91-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	1.96 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.281 0.240 , 0.232	Depositor DCC
R_{free} test set	2090 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	45.9	Xtriage
Anisotropy	0.093	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 57.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.065 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	11834	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.19% 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 (i)

5.1 Standard geometry (i)

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

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	0.42	0/3990	0.62	0/5417
1	P	0.40	0/3999	0.64	1/5429 (0.0%)
1	Z	0.43	0/4004	0.63	0/5435
All	All	0.42	0/11993	0.63	1/16281 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	P	595	HIS	N-CA-C	-6.06	94.65	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	3892	0	3862	168	0
1	P	3901	0	3868	183	0
1	Z	3906	0	3865	171	0
2	B	23	0	20	0	0
2	C	23	0	20	1	0
2	D	23	0	20	2	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	P	3	0	0	0	0
3	Z	3	0	0	0	0
4	A	22	0	0	3	0
4	P	17	0	0	3	0
4	Z	18	0	0	0	0
All	All	11834	0	11655	518	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 22.

The worst 5 of 518 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:Z:593:ILE:HD12	1:Z:593:ILE:H	1.21	1.06
1:P:313:ASP:HB3	1:P:316:ILE:HD13	1.38	1.03
1:A:596:LYS:O	1:A:596:LYS:HD3	1.57	1.03
1:P:715:ILE:HG22	1:P:716:GLU:H	1.23	1.02
1:Z:313:ASP:HB3	1:Z:316:ILE:HD13	1.39	1.02

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	495/509 (97%)	456 (92%)	34 (7%)	5 (1%)	15 44
1	P	496/509 (97%)	453 (91%)	35 (7%)	8 (2%)	9 31
1	Z	497/509 (98%)	461 (93%)	33 (7%)	3 (1%)	25 56
All	All	1488/1527 (97%)	1370 (92%)	102 (7%)	16 (1%)	14 41

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	P	704	LYS
1	Z	703	ILE
1	P	619	ASN
1	A	619	ASN
1	Z	619	ASN

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	412/421 (98%)	401 (97%)	11 (3%)	44	78
1	P	413/421 (98%)	401 (97%)	12 (3%)	42	76
1	Z	413/421 (98%)	401 (97%)	12 (3%)	42	76
All	All	1238/1263 (98%)	1203 (97%)	35 (3%)	43	77

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Z	307	GLU
1	Z	593	ILE
1	Z	642	THR
1	A	139	LYS
1	P	715	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	172	ASN
1	Z	240	ASN
1	Z	595	HIS
1	A	99	ASN
1	P	240	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)

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	$\#\|Z\| > 2$
2	GLC	B	1	2	12,12,12	1.07	1 (8%)	17,17,17	2.00	5 (29%)
2	GLC	B	2	2	11,11,12	1.59	2 (18%)	15,15,17	1.43	1 (6%)
2	GLC	C	1	2	12,12,12	1.14	1 (8%)	17,17,17	2.09	5 (29%)
2	GLC	C	2	2	11,11,12	1.38	2 (18%)	15,15,17	1.41	1 (6%)
2	GLC	D	1	2	12,12,12	1.05	1 (8%)	17,17,17	2.01	5 (29%)
2	GLC	D	2	2	11,11,12	1.43	2 (18%)	15,15,17	1.19	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
2	GLC	B	1	2	-	0/2/22/22	0/1/1/1
2	GLC	B	2	2	-	2/2/19/22	0/1/1/1
2	GLC	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2	GLC	O5-C1	-3.81	1.37	1.43
2	C	1	GLC	C4-C5	2.80	1.58	1.53
2	D	2	GLC	O5-C1	-2.80	1.39	1.43
2	C	2	GLC	O5-C1	-2.74	1.39	1.43
2	B	1	GLC	C4-C5	2.46	1.58	1.53

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1	GLC	C1-O5-C5	5.90	124.80	113.66
2	B	1	GLC	C1-O5-C5	5.62	124.26	113.66
2	D	1	GLC	C1-O5-C5	5.48	124.01	113.66
2	C	2	GLC	C1-O5-C5	4.50	118.29	112.19
2	B	2	GLC	C1-O5-C5	4.32	118.04	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	GLC	C4-C5-C6-O6
2	B	2	GLC	O5-C5-C6-O6

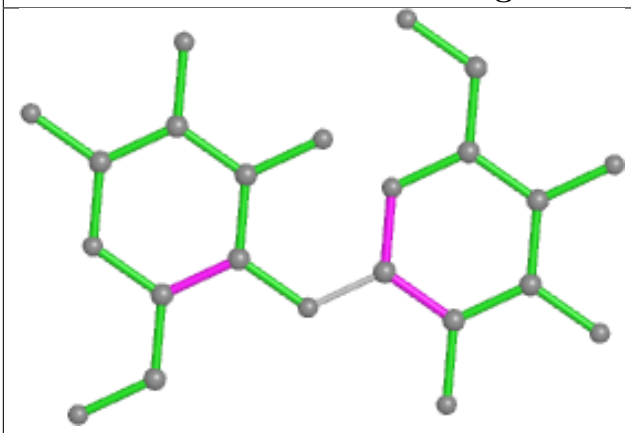
There are no ring outliers.

3 monomers are involved in 3 short contacts:

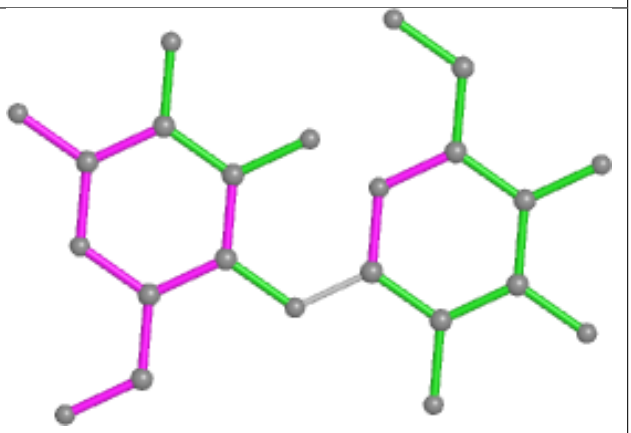
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	2	GLC	1	0
2	C	2	GLC	1	0
2	D	1	GLC	1	0

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

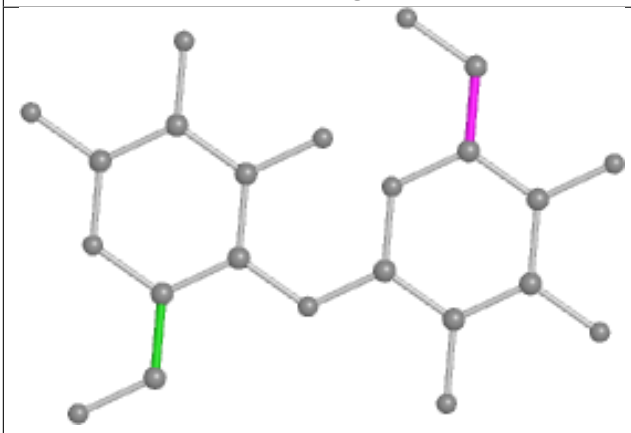
Oligosaccharide Chain B



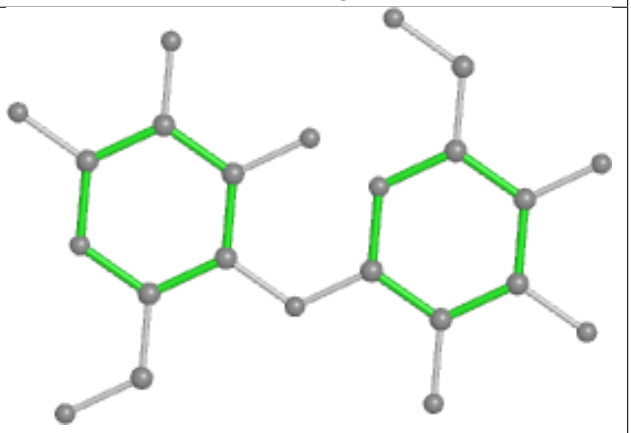
Bond lengths



Bond angles

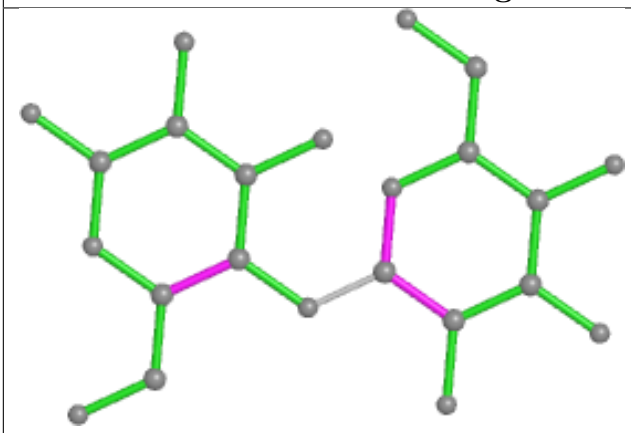


Torsions

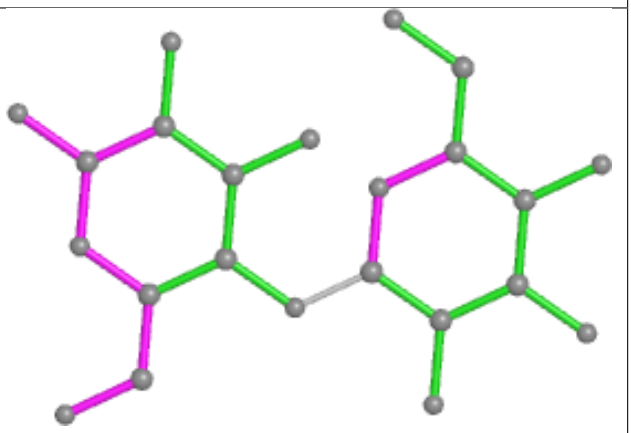


Rings

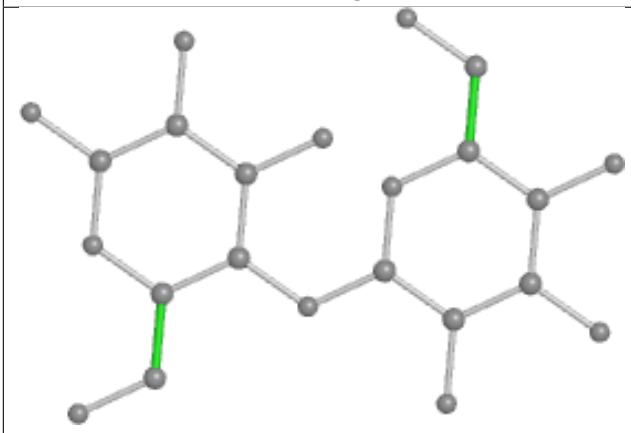
Oligosaccharide Chain C



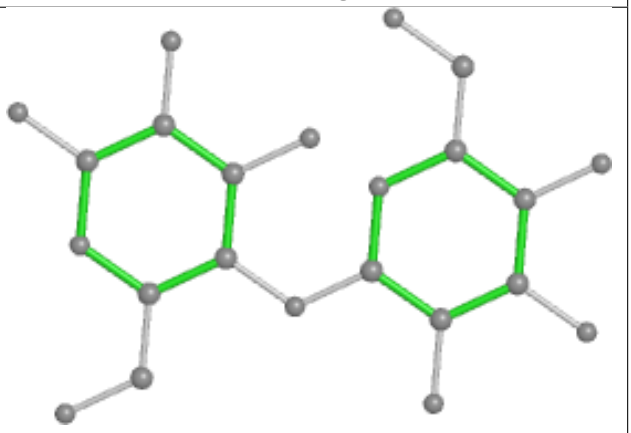
Bond lengths



Bond angles

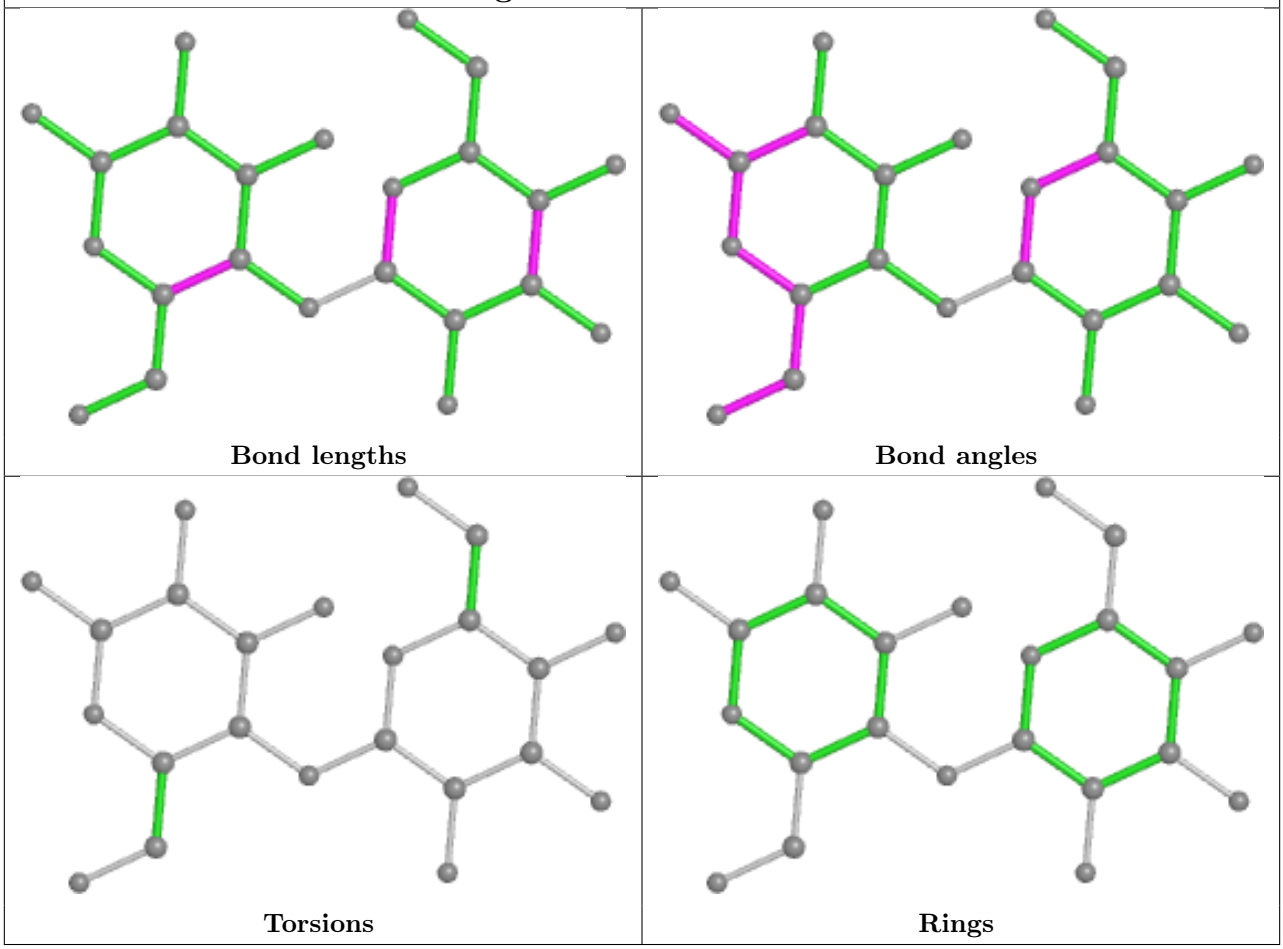


Torsions



Rings

Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 9 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 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	497/509 (97%)	-0.07	7 (1%)	75	70	15, 43, 98, 176	0
1	P	498/509 (97%)	0.08	15 (3%)	50	40	9, 46, 100, 192	0
1	Z	499/509 (98%)	-0.07	4 (0%)	86	81	12, 38, 91, 152	0
All	All	1494/1527 (97%)	-0.02	26 (1%)	70	63	9, 42, 94, 192	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	P	625	TYR	4.2
1	A	172	ASN	3.6
1	P	30	THR	3.5
1	Z	674	LYS	3.2
1	P	631	GLU	3.0

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, 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
2	GLC	B	1	12/12	0.94	0.17	29,29,29,29	0
2	GLC	C	1	12/12	0.94	0.13	23,23,23,23	0
2	GLC	B	2	11/12	0.95	0.17	29,29,29,45	0

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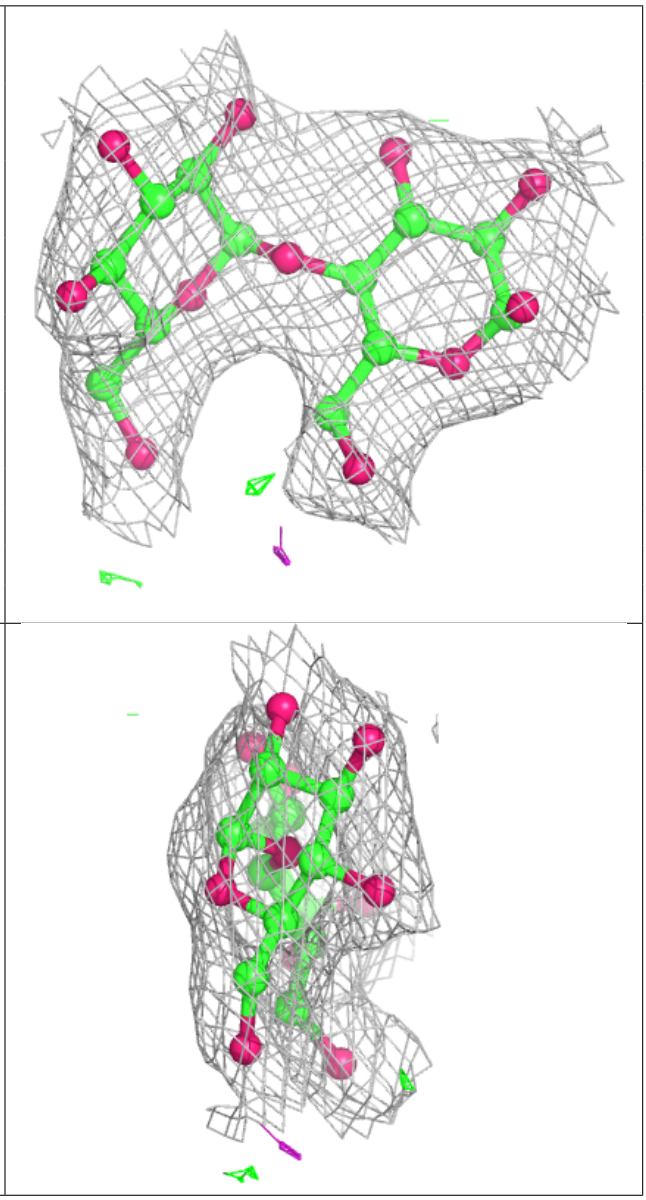
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GLC	C	2	11/12	0.95	0.17	23,23,23,23	0
2	GLC	D	1	12/12	0.95	0.19	30,30,30,30	0
2	GLC	D	2	11/12	0.96	0.18	30,30,30,30	0

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.

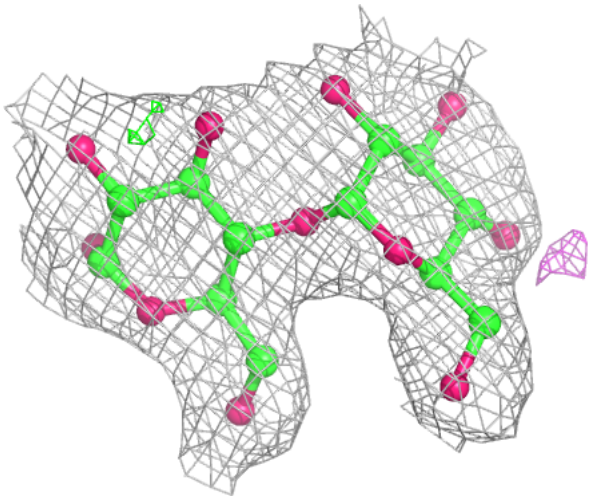
Electron density around Chain B:

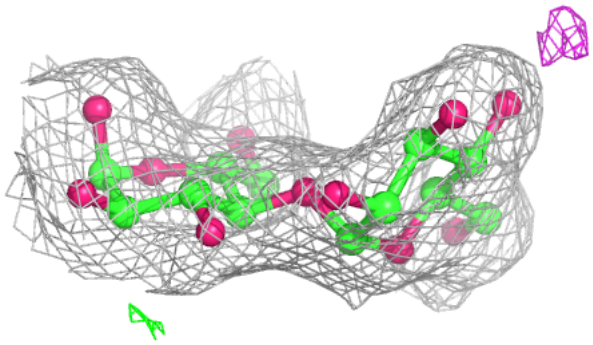
2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

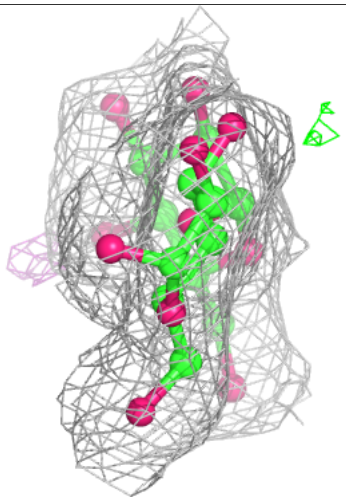


Electron density around Chain C:

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

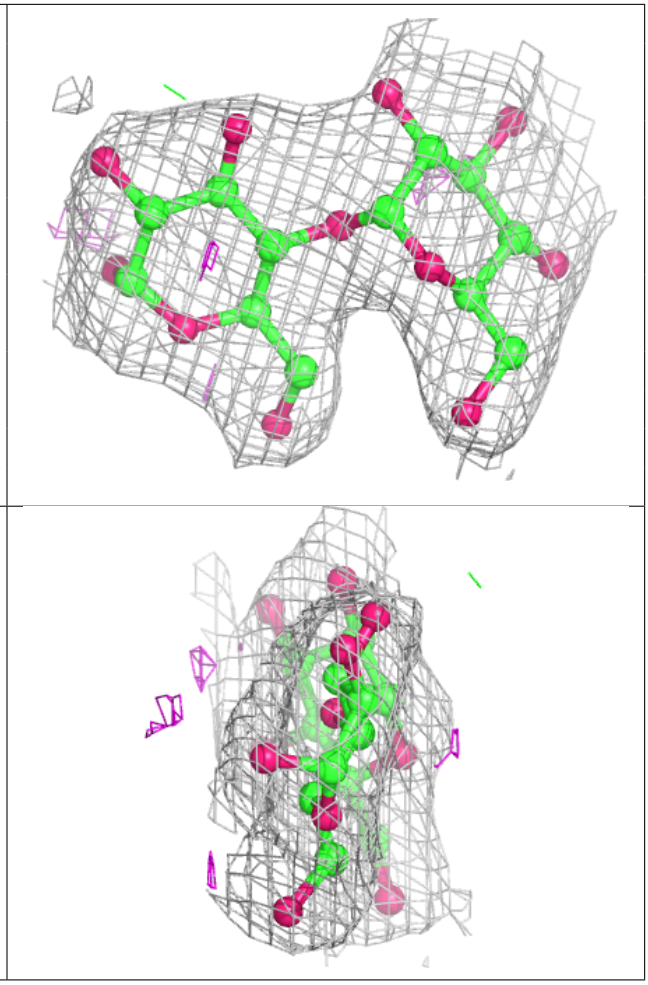






Electron density around Chain D:

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



6.4 Ligands (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	NI	Z	730	1/1	0.49	0.18	123,123,123,123	0
3	NI	P	730	1/1	0.83	0.12	91,91,91,91	0
3	NI	P	729	1/1	0.83	0.20	100,100,100,100	0
3	NI	A	730	1/1	0.85	0.17	106,106,106,106	0
3	NI	A	729	1/1	0.94	0.27	77,77,77,77	0
3	NI	Z	728	1/1	0.96	0.13	67,67,67,67	0
3	NI	Z	729	1/1	0.97	0.15	58,58,58,58	0
3	NI	A	728	1/1	0.98	0.29	61,61,61,61	0
3	NI	P	728	1/1	0.99	0.14	39,39,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.