

wwPDB X-ray Structure Validation Summary Report (i)

Sep 4, 2024 - 01:25 pm BST

PDB ID : 8QLI

Title : Crystal structure of Paradendryphiella salina PL7C alginate lyase mutant

H124 soaked with with tetra-mannuronic acid

Authors : Wilkens, C. Deposited on : 2023-09-19

Resolution : 1.12 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 (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 3.0

Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)

CCP4 : 9.0.002 (Gargrove)

Density-Fitness : 1.0.11

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

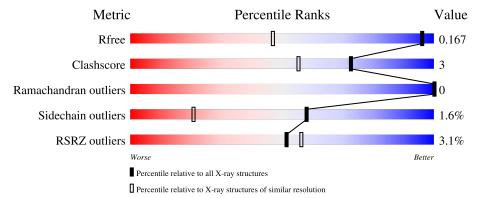
Validation Pipeline (wwPDB-VP) : 2.38.2

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 1.12 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	164625	1652 (1.14-1.10)
Clashscore	180529	1870 (1.14-1.10)
Ramachandran outliers	177936	1828 (1.14-1.10)
Sidechain outliers	177891	1824 (1.14-1.10)
RSRZ outliers	164620	1652 (1.14-1.10)

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	234	91%	6% •		
2	В	4	75%	25%		



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4189 atoms, of which 1831 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 Alginate lyase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace			
1	A	227	Total 3691	C 1199	H 1801	N 304	O 380	S 7	4	26	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLU	=	expression tag	UNP A0A7I9C8Z1
A	0	PHE	-	expression tag	UNP A0A7I9C8Z1
A	124	ASN	HIS	engineered mutation	UNP A0A7I9C8Z1
A	241	VAL	-	expression tag	UNP A0A7I9C8Z1
A	242	ASP	-	expression tag	UNP A0A7I9C8Z1
A	243	HIS	1	expression tag	UNP A0A7I9C8Z1
A	244	HIS	-	expression tag	UNP A0A7I9C8Z1
A	245	HIS	-	expression tag	UNP A0A7I9C8Z1
A	246	HIS	-	expression tag	UNP A0A7I9C8Z1
A	247	HIS	-	expression tag	UNP A0A7I9C8Z1
A	248	HIS	-	expression tag	UNP A0A7I9C8Z1

• Molecule 2 is an oligosaccharide called beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace		
2	В	4	Total 79	C 24	H 30	O 25	0	0	0

• Molecule 3 is water.



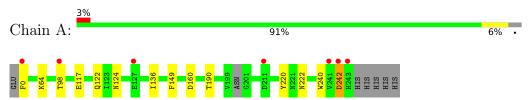
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	419	Total O 419 419	0	0



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: Alginate lyase



• Molecule 2: beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid-(1-4)-beta-D-mannopyranuronic acid

Chain B: 75% 25%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	77.54Å 38.77Å 75.17Å	Depositor
a, b, c, α , β , γ	90.00° 116.91° 90.00°	Depositor
Resolution (Å)	38.67 - 1.12	Depositor
rtesolution (A)	38.67 - 1.12	EDS
% Data completeness	98.3 (38.67-1.12)	Depositor
(in resolution range)	98.3 (38.67-1.12)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.07 (at 1.12Å)	Xtriage
Refinement program	PHENIX dev_4788	Depositor
D D.	0.144 , 0.168	Depositor
R, R_{free}	0.143 , 0.167	DCC
R_{free} test set	2100 reflections (2.78%)	wwPDB-VP
Wilson B-factor (Å ²)	7.6	Xtriage
Anisotropy	0.497	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.40 , 41.6	EDS
L-test for twinning ²	$ < L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4189	wwPDB-VP
Average B, all atoms (Å ²)	11.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.57% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: BEM

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).

Mal	Chain	Bond	lengths	Bond angles	
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.40	0/1988	0.68	0/2696

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
1	A	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
1	A	122	GLN	Peptide

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	1890	1801	1861	12	0
2	В	49	30	26	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	419	0	0	5	7
All	All	2358	1831	1887	12	7

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 3.

The worst 5 of 12 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	$\operatorname{distance}\ (ext{\AA})$	overlap (Å)
1:A:222[B]:ASN:OD1	3:A:301:HOH:O	1.79	0.98
1:A:160:ASP:OD1	3:A:302:HOH:O	2.11	0.67
1:A:190[A]:THR:OG1	3:A:303:HOH:O	2.15	0.64
1:A:220[A]:TYR:OH	2:B:1:BEM:H5	2.00	0.62
1:A:136[B]:ILE:HG23	1:A:149:PHE:CE1	2.42	0.55

The worst 5 of 7 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
3:A:396:HOH:O	ı — ı	1.89	0.31
3:A:494:HOH:O	3:A:695:HOH:O[4_555]	1.91	0.29
3:A:303:HOH:O	3:A:306:HOH:O[1_565]	1.95	0.25
3:A:304:HOH:O	3:A:550:HOH:O[4_555]	2.04	0.16
3:A:390:HOH:O	3:A:630:HOH:O[3_445]	2.05	0.15

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	Percentile	\mathbf{s}
1	A	249/234 (106%)	241 (97%)	8 (3%)	0	100 100	П



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	214/195 (110%)	209 (98%)	5 (2%)	45 9

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64[A]	LYS
1	A	64[B]	LYS
1	A	240[A]	TRP
1	A	240[B]	TRP
1	A	242	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

4 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	Mol Type Chain Res		Link	Bond lengths			Bond angles			
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BEM	В	1	2	13,13,13	1.27	2 (15%)	18,19,19	2.39	5 (27%)
2	BEM	В	2	2	12,12,13	1.22	1 (8%)	14,17,19	1.34	3 (21%)
2	BEM	В	3	2	12,12,13	1.37	2 (16%)	14,17,19	0.89	0
2	BEM	В	4	2	12,12,13	1.71	3 (25%)	14,17,19	1.12	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
2	BEM	В	1	2	-	1/4/24/24	0/1/1/1
2	BEM	В	2	2	-	0/4/21/24	0/1/1/1
2	BEM	В	3	2	-	0/4/21/24	0/1/1/1
2	BEM	В	4	2	-	1/4/21/24	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	В	4	BEM	O5-C1	3.79	1.49	1.43
2	В	3	BEM	O5-C1	2.62	1.47	1.43
2	В	1	BEM	O5-C1	2.47	1.49	1.42
2	В	4	BEM	C2-C3	-2.45	1.48	1.52
2	В	4	BEM	O5-C5	2.42	1.47	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
2	В	1	BEM	C3-C4-C5	6.15	119.76	109.25
2	В	1	BEM	O4-C4-C5	-4.48	99.69	109.74
2	В	1	BEM	C4-C3-C2	3.84	117.53	110.82
2	В	1	BEM	O5-C5-C4	3.32	115.50	109.57
2	В	1	BEM	O4-C4-C3	-3.10	103.18	110.35

There are no chirality outliers.

All (2) torsion outliers are listed below:



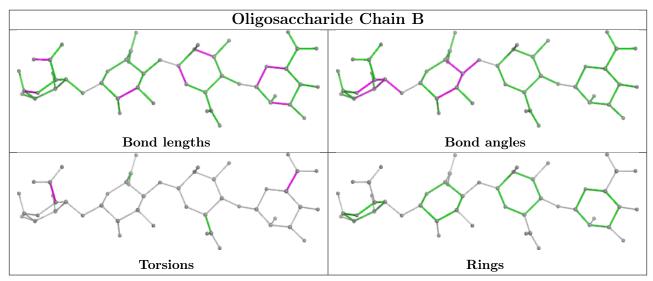
Mol	Chain	Res	Type	Atoms
2	В	1	BEM	C4-C5-C6-O6A
2	В	4	BEM	C4-C5-C6-O6B

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	1	BEM	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, 95^{th} 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	$\langle { m RSRZ} \rangle$	# RSRZ > 2	$OWAB(Å^2)$	Q < 0.9
1	A	227/234 (97%)	-0.00	7 (3%) 51 56	3, 9, 16, 41	26 (11%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	0	PHE	7.1
1	A	242	ASP	5.5
1	A	243	HIS	5.0
1	A	241	VAL	3.7
1	A	98	THR	2.7

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

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

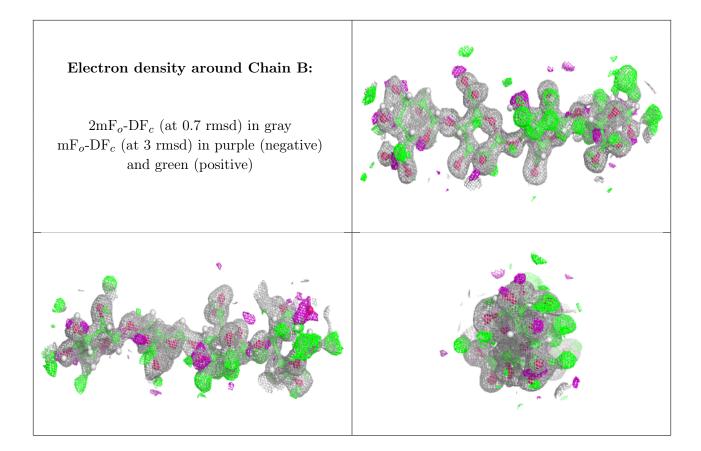
6.3 Carbohydrates (i)

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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	BEM	В	1	13/13	0.87	0.18	10,21,36,44	21
2	BEM	В	2	12/13	0.89	0.12	8,14,18,20	19
2	BEM	В	4	12/13	0.89	0.11	16,23,31,31	0
2	BEM	В	3	12/13	0.95	0.08	10,13,23,23	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.

