wwPDB X-ray Structure Validation Summary Report (i)

Oct 8, 2023 – 09:29 AM EDT

PDB ID	:	6E9O
Title	:	E. coli D-galactonate:proton symporter mutant E133Q in the outward substrate-bound form
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Deposited on	:	2018-08-01
Resolution	:	3.50 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:

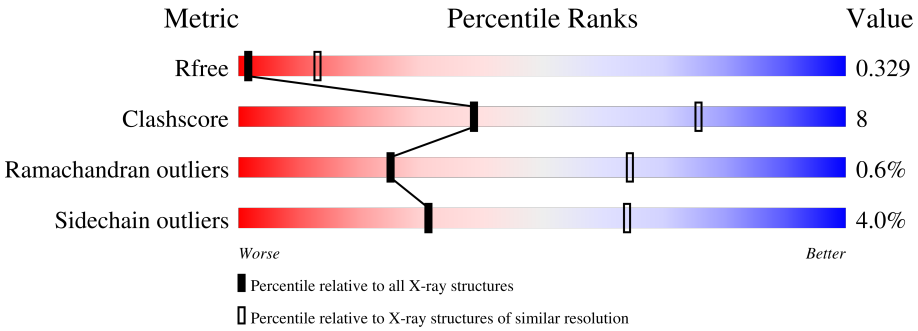
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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%

Mol	Chain	Length	Quality of chain
1	A	460	72% 13% • 15%
1	B	460	67% 19% • 13%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6166 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 D-galactonate transport.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	402	Total	C	N	O	S	0	0	0
			3103	2081	490	515	17			
1	A	393	Total	C	N	O	S	0	0	0
			3035	2032	487	499	17			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	133	GLN	GLU	engineered mutation	UNP J7QAK3
B	446	SER	-	expression tag	UNP J7QAK3
B	447	LEU	-	expression tag	UNP J7QAK3
B	448	VAL	-	expression tag	UNP J7QAK3
B	449	PRO	-	expression tag	UNP J7QAK3
B	450	ARG	-	expression tag	UNP J7QAK3
B	451	GLY	-	expression tag	UNP J7QAK3
B	452	SER	-	expression tag	UNP J7QAK3
B	453	GLY	-	expression tag	UNP J7QAK3
B	454	SER	-	expression tag	UNP J7QAK3
B	455	HIS	-	expression tag	UNP J7QAK3
B	456	HIS	-	expression tag	UNP J7QAK3
B	457	HIS	-	expression tag	UNP J7QAK3
B	458	HIS	-	expression tag	UNP J7QAK3
B	459	HIS	-	expression tag	UNP J7QAK3
B	460	HIS	-	expression tag	UNP J7QAK3
A	133	GLN	GLU	engineered mutation	UNP J7QAK3
A	446	SER	-	expression tag	UNP J7QAK3
A	447	LEU	-	expression tag	UNP J7QAK3
A	448	VAL	-	expression tag	UNP J7QAK3
A	449	PRO	-	expression tag	UNP J7QAK3
A	450	ARG	-	expression tag	UNP J7QAK3
A	451	GLY	-	expression tag	UNP J7QAK3
A	452	SER	-	expression tag	UNP J7QAK3
A	453	GLY	-	expression tag	UNP J7QAK3

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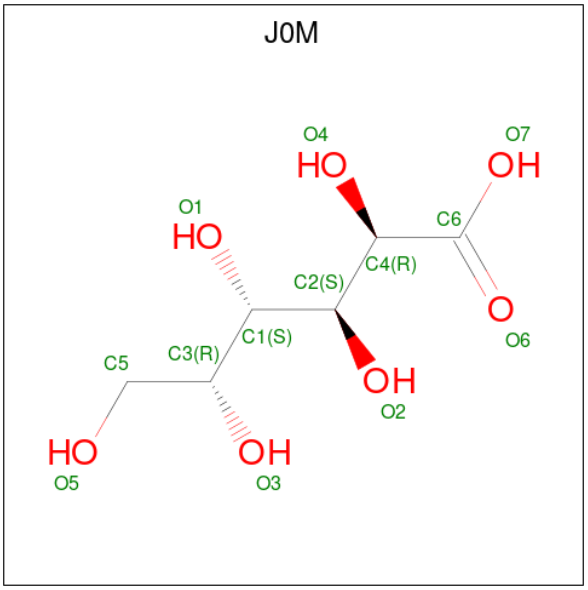
Chain	Residue	Modelled	Actual	Comment	Reference
A	454	SER	-	expression tag	UNP J7QAK3
A	455	HIS	-	expression tag	UNP J7QAK3
A	456	HIS	-	expression tag	UNP J7QAK3
A	457	HIS	-	expression tag	UNP J7QAK3
A	458	HIS	-	expression tag	UNP J7QAK3
A	459	HIS	-	expression tag	UNP J7QAK3
A	460	HIS	-	expression tag	UNP J7QAK3

- Molecule 2 is D-galactonic acid (three-letter code: J0M) (formula: $C_6H_{12}O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 13 6 7	0	0
2	A	1	Total C O 13 6 7	0	0

- Molecule 3 is water.

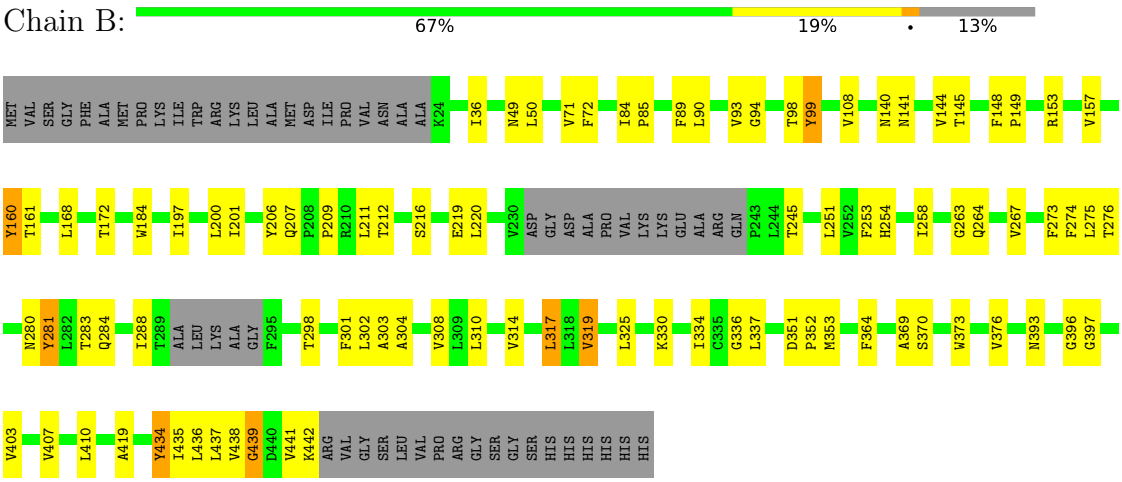
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total O 2 2	0	0

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. 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. 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.

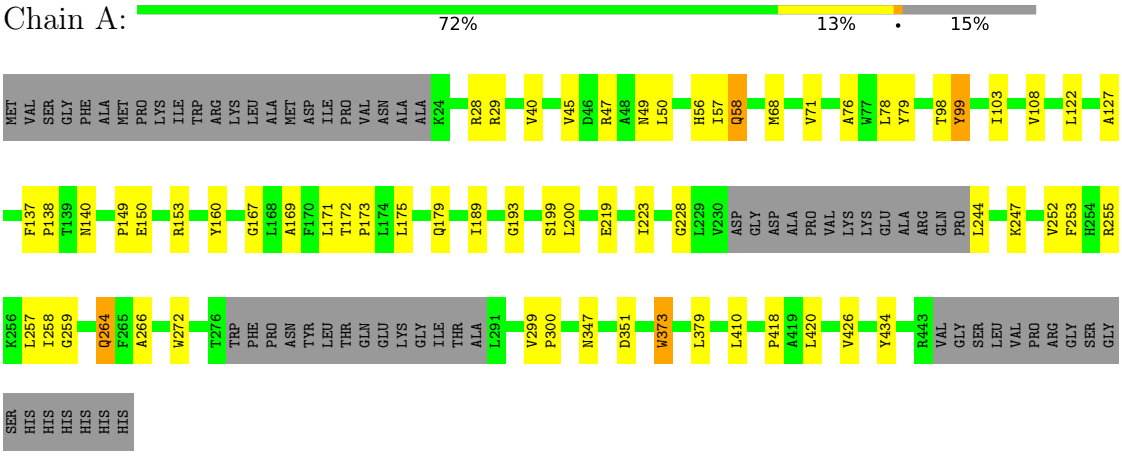
• Molecule 1: D-galactonate transport

Chain B:



• Molecule 1: D-galactonate transport

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	217.07Å 70.71Å 107.16Å 90.00° 101.81° 90.00°	Depositor
Resolution (Å)	14.98 – 3.50 106.24 – 3.50	Depositor EDS
% Data completeness (in resolution range)	91.7 (14.98-3.50) 82.3 (106.24-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.13 (at 3.49Å)	Xtriage
Refinement program	PHENIX (1.13_2998)	Depositor
R, R_{free}	0.285 , 0.300 0.307 , 0.329	Depositor DCC
R_{free} test set	2040 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å^2)	149.3	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.24 , 119.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.77	EDS
Total number of atoms	6166	wwPDB-VP
Average B, all atoms (Å^2)	203.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: J0M

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	0.27	0/3122	0.43	0/4250
1	B	0.27	0/3196	0.44	0/4357
All	All	0.27	0/6318	0.44	0/8607

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

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	3035	0	3093	36	0
1	B	3103	0	3132	59	0
2	A	13	0	0	1	0
2	B	13	0	0	0	0
3	B	2	0	0	0	0
All	All	6166	0	6225	93	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.

The worst 5 of 93 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:57:ILE:HD11	1:A:68:MET:SD	2.26	0.75
1:B:351:ASP:O	1:B:353:MET:N	2.28	0.67
1:B:168:LEU:HD23	1:B:168:LEU:O	1.95	0.65
1:B:149:PRO:O	1:B:153:ARG:NH2	2.30	0.65
1:B:330:LYS:HD3	1:B:438:VAL:HG21	1.79	0.65

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	387/460 (84%)	369 (95%)	17 (4%)	1 (0%)	41 75
1	B	396/460 (86%)	368 (93%)	24 (6%)	4 (1%)	15 54
All	All	783/920 (85%)	737 (94%)	41 (5%)	5 (1%)	25 64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	441	VAL
1	B	439	GLY
1	B	288	ILE
1	B	352	PRO
1	A	149	PRO

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	309/366 (84%)	301 (97%)	8 (3%)	46	74
1	B	316/366 (86%)	299 (95%)	17 (5%)	22	55
All	All	625/732 (85%)	600 (96%)	25 (4%)	31	64

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	319	VAL
1	A	58	GLN
1	A	434	TYR
1	B	442	LYS
1	A	99	TYR

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)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands 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	J0M	B	501	-	12,12,12	0.76	0	16,16,16	0.86	0
2	J0M	A	501	-	12,12,12	0.73	0	16,16,16	0.92	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	J0M	B	501	-	-	2/18/18/18	-
2	J0M	A	501	-	-	4/18/18/18	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	J0M	O6-C6-C4	-2.08	116.16	121.63

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	J0M	C2-C4-C6-O6
2	A	501	J0M	C2-C4-C6-O7
2	B	501	J0M	C2-C4-C6-O6
2	B	501	J0M	C2-C4-C6-O7
2	A	501	J0M	O4-C4-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	J0M	1	0

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.