



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2024 – 07:19 AM EST

PDB ID : 4XFE
Title : Crystal structure of a TRAP periplasmic solute binding protein from *Pseudomonas putida* F1 (Pput_1203), Target EFI-500184, with bound D-glucuronate
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Deposited on : 2014-12-26
Resolution : 1.40 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)

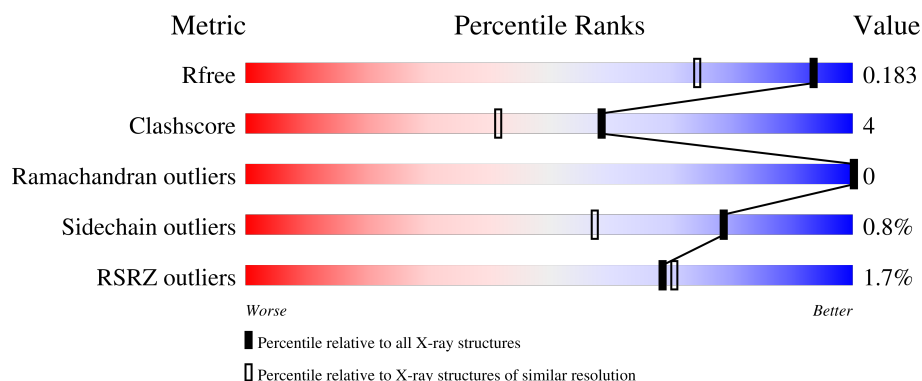
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 1.40 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}	164625	2247 (1.40-1.40)
Clashscore	180529	2446 (1.40-1.40)
Ramachandran outliers	177936	2398 (1.40-1.40)
Sidechain outliers	177891	2397 (1.40-1.40)
RSRZ outliers	164620	2246 (1.40-1.40)

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	341	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
 Validation Pipeline (wwPDB-VP) : 2.39

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5164 atoms, of which 2425 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.

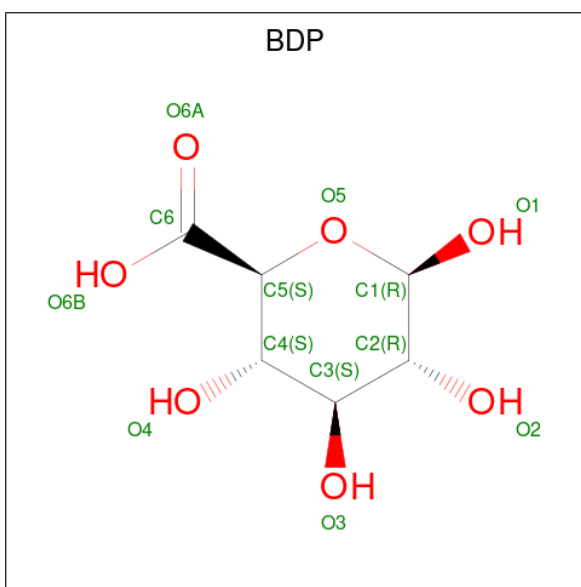
- Molecule 1 is a protein called TRAP dicarboxylate transporter subunit DctP.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	306	Total	C	H	N	O	Se	0	4	0
			4799	1521	2406	406	452	14			

There are 19 discrepancies between the modelled and reference sequences:

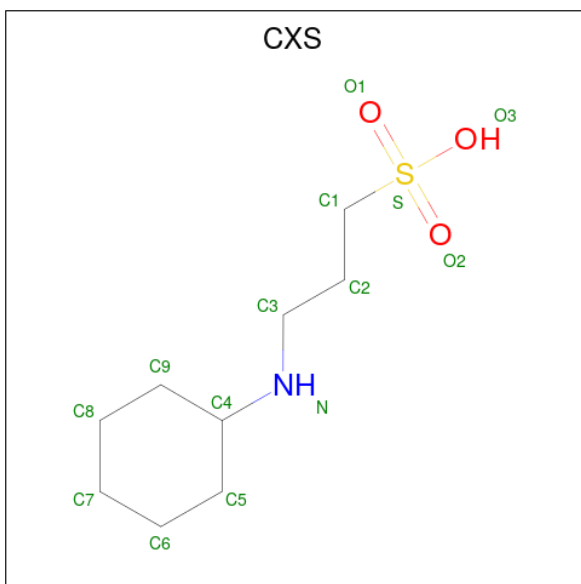
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP I3UZ52
A	324	ALA	-	expression tag	UNP I3UZ52
A	325	GLU	-	expression tag	UNP I3UZ52
A	326	ASN	-	expression tag	UNP I3UZ52
A	327	LEU	-	expression tag	UNP I3UZ52
A	328	TYR	-	expression tag	UNP I3UZ52
A	329	PHE	-	expression tag	UNP I3UZ52
A	330	GLN	-	expression tag	UNP I3UZ52
A	331	GLY	-	expression tag	UNP I3UZ52
A	332	HIS	-	expression tag	UNP I3UZ52
A	333	HIS	-	expression tag	UNP I3UZ52
A	334	HIS	-	expression tag	UNP I3UZ52
A	335	HIS	-	expression tag	UNP I3UZ52
A	336	HIS	-	expression tag	UNP I3UZ52
A	337	HIS	-	expression tag	UNP I3UZ52
A	338	HIS	-	expression tag	UNP I3UZ52
A	339	HIS	-	expression tag	UNP I3UZ52
A	340	HIS	-	expression tag	UNP I3UZ52
A	341	HIS	-	expression tag	UNP I3UZ52

- Molecule 2 is beta-D-glucopyranuronic acid (three-letter code: BDP) (formula: C₆H₁₀O₇).



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

- Molecule 3 is 3-CYCLOHEXYL-1-PROPYLSULFONIC ACID (three-letter code: CXS) (formula: $C_9H_{19}NO_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	S	0	0
			33	9	19	1	3	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

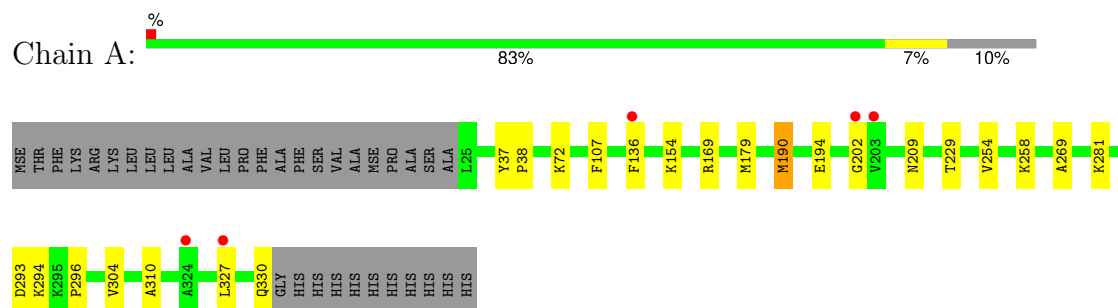
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	309	Total	O	0	0
			309	309		

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: TRAP dicarboxylate transporter subunit DctP



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.00Å 35.05Å 60.83Å 90.00° 99.54° 90.00°	Depositor
Resolution (Å)	26.50 – 1.40 26.50 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (26.50-1.40) 99.1 (26.50-1.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 1.40Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.156 , 0.186 0.157 , 0.183	Depositor DCC
R_{free} test set	2699 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	10.5	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5164	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.75% 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: BDP, SO4, CXS

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	0.46	0/2438	0.65	1/3267 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	327	LEU	CB-CG-CD1	-5.75	101.23	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	2393	2406	2388	20	0
2	A	13	0	8	0	0
3	A	14	19	19	1	0
4	A	10	0	0	1	0
5	A	309	0	0	6	0
All	All	2739	2425	2415	21	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 4.

All (21) 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:72:LYS:HD3	5:A:701:HOH:O	1.69	0.92
1:A:154:LYS:NZ	1:A:202:GLY:HA2	2.03	0.73
1:A:281:LYS:HD2	5:A:771:HOH:O	1.96	0.65
1:A:154:LYS:HZ1	1:A:202:GLY:HA2	1.60	0.65
1:A:254:VAL:CG1	1:A:258:LYS:HE3	2.29	0.63
1:A:190:MSE:HG2	1:A:194:GLU:HB2	1.83	0.60
1:A:229:THR:O	1:A:294:LYS:NZ	2.29	0.58
1:A:254:VAL:HG12	1:A:258:LYS:HE3	1.86	0.56
1:A:107:PHE:HE1	1:A:294:LYS:HE3	1.72	0.55
1:A:154:LYS:NZ	1:A:202:GLY:CA	2.70	0.54
1:A:330:GLN:O	5:A:501:HOH:O	2.19	0.51
1:A:154:LYS:HZ3	1:A:202:GLY:HA2	1.76	0.49
1:A:154:LYS:HZ1	1:A:202:GLY:CA	2.23	0.48
1:A:136:PHE:CE1	5:A:567:HOH:O	2.56	0.46
3:A:402:CXS:N	4:A:403:SO4:O4	2.51	0.44
1:A:169:ARG:C	1:A:169:ARG:HD3	2.38	0.43
1:A:37:TYR:CG	1:A:38:PRO:HD2	2.54	0.43
1:A:269:ALA:HB2	5:A:502:HOH:O	2.21	0.41
1:A:179:MSE:HA	1:A:304:VAL:HG21	2.03	0.41
1:A:293:ASP:O	1:A:296:PRO:HD2	2.21	0.40
1:A:310:ALA:HB3	5:A:761:HOH:O	2.20	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	308/341 (90%)	304 (99%)	4 (1%)	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	257/267 (96%)	255 (99%)	2 (1%)	79	57

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	190	MSE
1	A	209	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	BDP	A	401	-	13,13,13	1.47	2 (15%)	18,19,19	1.00	2 (11%)
3	CXS	A	402	-	14,14,14	0.57	0	18,18,18	1.15	3 (16%)
4	SO4	A	404	-	4,4,4	0.21	0	6,6,6	0.40	0
4	SO4	A	403	-	4,4,4	0.26	0	6,6,6	0.40	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	BDP	A	401	-	-	0/4/24/24	0/1/1/1
3	CXS	A	402	-	-	1/8/16/16	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	BDP	C5-C6	-2.98	1.46	1.53
2	A	401	BDP	C4-C3	-2.20	1.46	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	CXS	O2-S-O1	-2.50	105.69	113.82
3	A	402	CXS	C2-C1-S	-2.40	109.57	113.25
2	A	401	BDP	O6B-C6-O6A	-2.38	118.68	124.08
2	A	401	BDP	O6B-C6-C5	2.13	121.31	113.64
3	A	402	CXS	O2-S-C1	2.10	109.90	106.73

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	CXS	C2-C3-N-C4

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	CXS	1	0
4	A	403	SO4	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 [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	292/341 (85%)	-0.51	5 (1%) 69 70	4, 10, 26, 40	2 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	324	ALA	6.6
1	A	203	VAL	3.3
1	A	327	LEU	2.7
1	A	202	GLY	2.4
1	A	136	PHE	2.1

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](#)

There are no monosaccharides in this entry.

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
4	SO4	A	404	5/5	0.87	0.13	14,21,28,34	0
4	SO4	A	403	5/5	0.96	0.09	19,20,31,33	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CXS	A	402	14/14	0.96	0.07	10,14,20,20	0
2	BDP	A	401	13/13	0.97	0.03	3,4,6,6	0

6.5 Other polymers [i](#)

There are no such residues in this entry.