



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:16 PM UTC

PDB ID : 5HU7 / pdb_00005hu7
Title : Crystal structure of the trans-AT PKS dehydratase domain of C0ZGQ4 from *Brevibacillus brevis*
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Deposited on : 2016-01-27
Resolution : 2.40 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

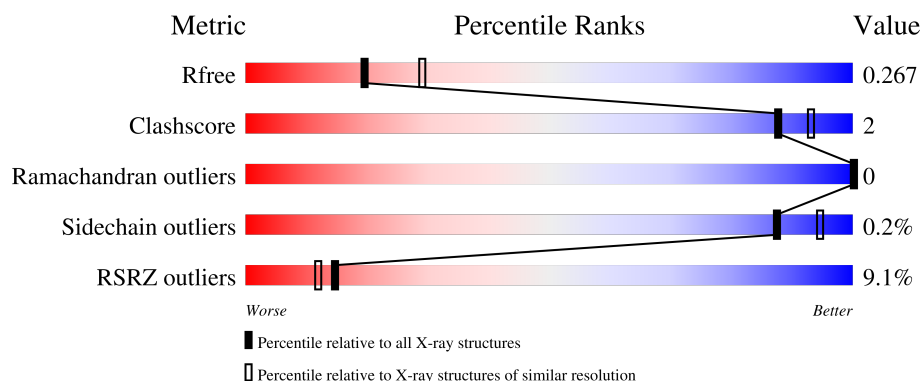
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	322	5% 73% 7% • 19%
1	B	322	9% 75% • 20%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4124 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 Putative polyketide synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2050	1302	338	400	10			
1	B	256	Total	C	N	O	S	0	0	0
			2009	1282	331	387	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2839	SER	-	expression tag	UNP C0ZGQ4
A	2840	MET	-	expression tag	UNP C0ZGQ4
B	2839	SER	-	expression tag	UNP C0ZGQ4
B	2840	MET	-	expression tag	UNP C0ZGQ4

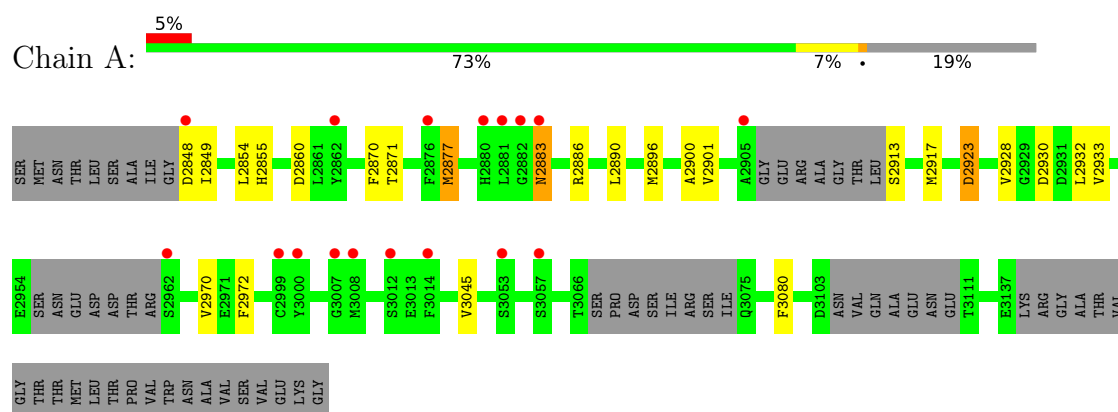
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	42	Total	O	0	0
			42	42		
2	B	23	Total	O	0	0
			23	23		

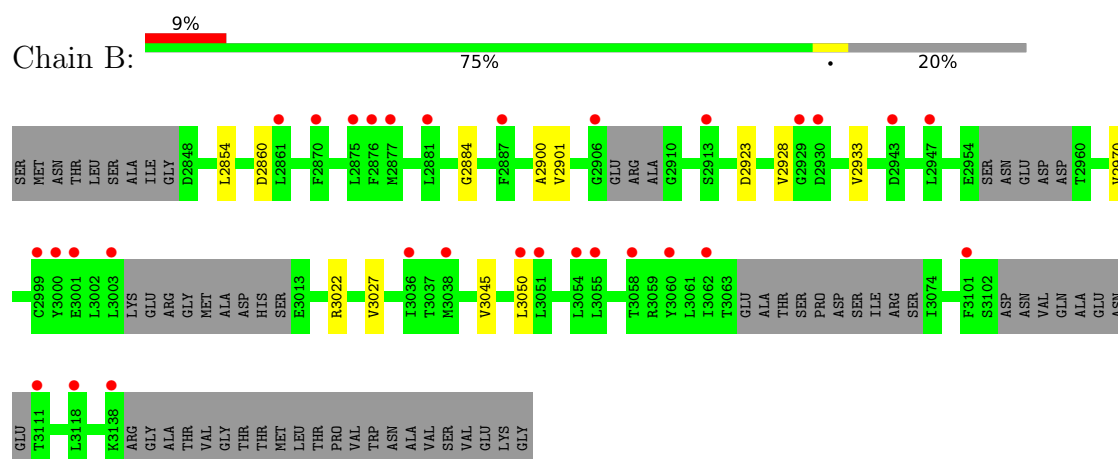
3 Residue-property plots [i](#)

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: Putative polyketide synthase



• Molecule 1: Putative polyketide synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	160.61Å 83.01Å 48.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.44 – 2.40 28.44 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (28.44-2.40) 99.5 (28.44-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.05 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.224 , 0.264 0.233 , 0.267	Depositor DCC
R_{free} test set	1311 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	66.4	Xtriage
Anisotropy	0.697	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4124	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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

5.1 Standard geometry

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	0.90	2/2089 (0.1%)	1.18	9/2828 (0.3%)
1	B	0.85	0/2046	1.12	6/2769 (0.2%)
All	All	0.87	2/4135 (0.0%)	1.15	15/5597 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2896	MET	SD-CE	-6.59	1.63	1.79
1	A	2877	MET	SD-CE	-6.55	1.63	1.79

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3045	VAL	N-CA-C	-8.63	103.47	111.67
1	A	2883	ASN	CA-CB-CG	7.90	120.50	112.60
1	A	3045	VAL	N-CA-C	-7.13	105.42	111.56
1	A	2930	ASP	CA-CB-CG	6.86	119.46	112.60
1	A	2913	SER	CA-C-N	6.63	126.28	119.92
1	A	2913	SER	C-N-CA	6.63	126.28	119.92
1	A	2883	ASN	CA-C-N	6.23	130.37	120.97
1	A	2883	ASN	C-N-CA	6.23	130.37	120.97
1	A	2860	ASP	CA-CB-CG	5.67	118.27	112.60
1	B	2860	ASP	CA-CB-CG	5.57	118.17	112.60
1	B	3050	LEU	N-CA-C	-5.54	105.33	111.36
1	B	2923	ASP	CA-CB-CG	5.41	118.01	112.60
1	B	2884	GLY	CA-C-N	5.38	128.49	120.90
1	B	2884	GLY	C-N-CA	5.38	128.49	120.90
1	A	2923	ASP	CA-CB-CG	5.10	117.70	112.60

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	2050	0	2002	12	0
1	B	2009	0	1982	4	0
2	A	42	0	0	0	0
2	B	23	0	0	0	0
All	All	4124	0	3984	16	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 2.

All (16) 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:2901:VAL:HG11	1:A:2970:VAL:HG11	1.71	0.72
1:A:2890:LEU:HD22	1:A:3080:PHE:HD2	1.63	0.63
1:A:2890:LEU:HD22	1:A:3080:PHE:CD2	2.33	0.63
1:A:2848:ASP:O	1:A:2849:ILE:HD13	2.09	0.51
1:A:2917:MET:HG2	1:A:2970:VAL:HG22	1.95	0.49
1:A:2883:ASN:HB2	1:A:2886:ARG:HH12	1.80	0.47
1:A:2871:THR:HG22	1:A:2932:LEU:CD1	2.46	0.46
1:B:3022:ARG:HG3	1:B:3027:VAL:HG12	1.98	0.46
1:A:2901:VAL:HG13	1:A:2972:PHE:CZ	2.52	0.45
1:B:2854:LEU:HD11	1:B:2900:ALA:HA	2.00	0.44
1:A:2854:LEU:HD11	1:A:2900:ALA:HA	2.01	0.43
1:A:2928:VAL:HG12	1:A:2933:VAL:HG21	2.02	0.41
1:A:2849:ILE:HG23	1:A:2855:HIS:HA	2.02	0.41
1:B:2901:VAL:HG11	1:B:2970:VAL:HG11	2.03	0.41
1:A:2870:PHE:HB3	1:A:2877:MET:HE2	2.03	0.41
1:B:2928:VAL:HG12	1:B:2933:VAL:HG21	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	251/322 (78%)	244 (97%)	7 (3%)	0	100	100
1	B	244/322 (76%)	237 (97%)	7 (3%)	0	100	100
All	All	495/644 (77%)	481 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	225/275 (82%)	224 (100%)	1 (0%)	84	92
1	B	221/275 (80%)	221 (100%)	0	100	100
All	All	446/550 (81%)	445 (100%)	1 (0%)	87	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2923	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3015	GLN
1	B	2873	GLN

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Mol	Chain	Res	Type
1	B	2885	GLN
1	B	2967	HIS

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](#)

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

6.1 Protein, DNA and RNA chains

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	261/322 (81%)	0.38	17 (6%) 25 21	51, 80, 140, 172	0
1	B	256/322 (79%)	0.76	30 (11%) 9 7	72, 103, 161, 197	0
All	All	517/644 (80%)	0.57	47 (9%) 15 12	51, 91, 155, 197	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2881	LEU	5.8
1	B	3051	LEU	4.3
1	B	2881	LEU	4.0
1	A	3014	PHE	3.9
1	A	3007	GLY	3.8
1	B	3060	TYR	3.4
1	B	2861	LEU	3.3
1	B	3058	THR	3.2
1	B	2906	GLY	3.1
1	A	3012	SER	3.0
1	B	3062	ILE	3.0
1	A	2882	GLY	2.8
1	B	3055	LEU	2.7
1	A	2999	CYS	2.7
1	B	2887	PHE	2.6
1	B	3054	LEU	2.6
1	B	2947	LEU	2.5
1	A	3008	MET	2.5
1	B	2876	PHE	2.5
1	B	2999	CYS	2.4
1	B	3003	LEU	2.4
1	B	3118	LEU	2.4
1	B	3138	LYS	2.4
1	B	3101	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	2905	ALA	2.3
1	B	2877	MET	2.3
1	A	2876	PHE	2.3
1	A	3000	TYR	2.3
1	B	2943	ASP	2.3
1	B	3050	LEU	2.3
1	A	2848	ASP	2.3
1	A	3053	SER	2.2
1	A	2883	ASN	2.2
1	A	2880	HIS	2.2
1	B	2870	PHE	2.1
1	B	2875	LEU	2.1
1	B	3036	ILE	2.1
1	B	3001	GLU	2.1
1	B	3111	THR	2.1
1	A	2862	TYR	2.1
1	A	3057	SER	2.1
1	B	2913	SER	2.1
1	B	2930	ASP	2.0
1	B	2929	GLY	2.0
1	B	3038	MET	2.0
1	A	2962	SER	2.0
1	B	3000	TYR	2.0

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](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.