



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:58 PM UTC

PDB ID : 8Y54 / pdb_00008y54
Title : Three-dimensional structure of homo-dimer of cystathione beta lyase from lactobacillus delbrueckii(LdPatB)
Authors : Liu, Y.; Yang, C.
Deposited on : 2024-01-31
Resolution : 1.78 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

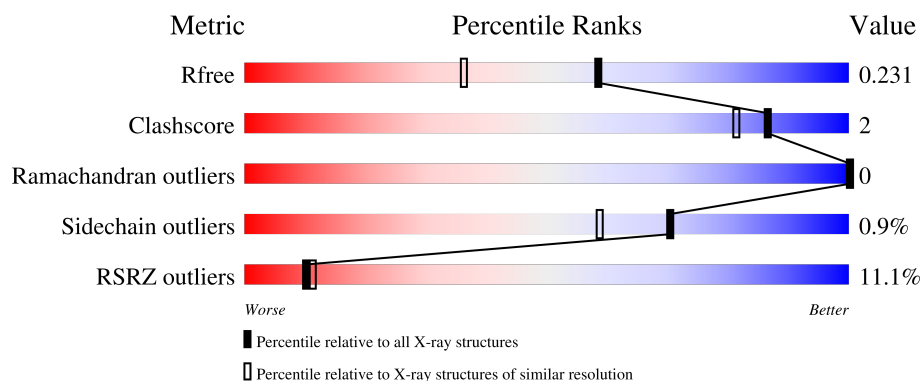
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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	1365 (1.78-1.78)
Clashscore	190562	1395 (1.78-1.78)
Ramachandran outliers	187476	1382 (1.78-1.78)
Sidechain outliers	187428	1382 (1.78-1.78)
RSRZ outliers	180081	1365 (1.78-1.78)

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	390	13% 92% 7% .
1	B	390	9% 91% 7% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6490 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 cysteine-S-conjugate beta-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	387	Total	C	N	O	S	0	0	0
			3078	1970	519	573	16			
1	B	386	Total	C	N	O	S	0	0	0
			3070	1965	517	572	16			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	311	GLU	VAL	engineered mutation	UNP A0AAC9VP02
A	326	ASP	ASN	engineered mutation	UNP A0AAC9VP02
B	311	GLU	VAL	engineered mutation	UNP A0AAC9VP02
B	326	ASP	ASN	engineered mutation	UNP A0AAC9VP02

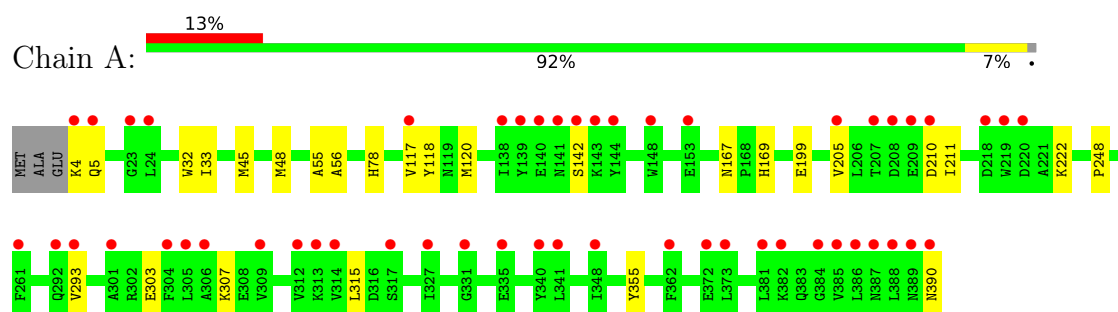
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	165	Total	O	0	0
			165	165		
2	B	177	Total	O	0	0
			177	177		

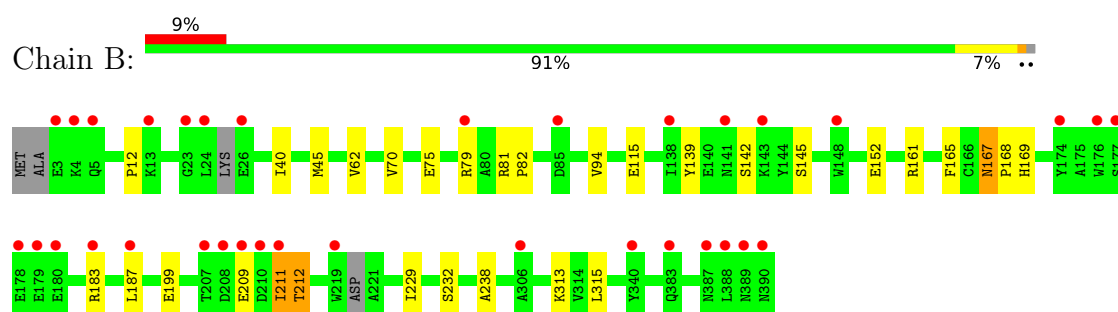
3 Residue-property plots [i](#)

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: cysteine-S-conjugate beta-lyase



- Molecule 1: cysteine-S-conjugate beta-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.47Å 91.06Å 80.87Å 90.00° 125.27° 90.00°	Depositor
Resolution (Å)	38.95 – 1.78 38.95 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.7 (38.95-1.78) 99.6 (38.95-1.78)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.78Å)	Xtriage
Refinement program	PHENIX v1.16	Depositor
R, R_{free}	0.207 , 0.232 0.205 , 0.231	Depositor DCC
R_{free} test set	2000 reflections (3.14%)	wwPDB-VP
Wilson B-factor (Å ²)	25.1	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6490	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% 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](#)

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	0.59	0/3153	0.84	3/4279 (0.1%)
1	B	0.68	4/3143 (0.1%)	0.90	9/4263 (0.2%)
All	All	0.64	4/6296 (0.1%)	0.87	12/8542 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	94	VAL	CA-CB	10.57	1.61	1.53
1	B	142	SER	C-N	7.88	1.44	1.33
1	B	62	VAL	CA-C	-6.75	1.47	1.53
1	B	167	ASN	C-O	-6.34	1.19	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	SER	N-CA-C	-9.24	97.58	111.81
1	A	5	GLN	N-CA-C	-8.40	102.80	113.72
1	B	212	THR	CB-CA-C	7.58	118.07	110.33
1	B	165	PHE	CA-CB-CG	6.01	119.81	113.80
1	B	169	HIS	CA-C-N	5.87	130.99	121.83
1	B	169	HIS	C-N-CA	5.87	130.99	121.83
1	B	62	VAL	O-C-N	-5.77	117.74	121.37
1	B	209	GLU	CA-C-N	-5.30	113.56	123.05
1	B	209	GLU	C-N-CA	-5.30	113.56	123.05
1	B	82	PRO	CB-CA-C	-5.21	104.15	110.98
1	B	115	GLU	CA-C-O	-5.14	115.09	120.70
1	A	355	TYR	N-CA-C	-5.13	106.79	113.16

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	3078	0	3025	14	0
1	B	3070	0	3012	13	0
2	A	165	0	0	1	0
2	B	177	0	0	1	0
All	All	6490	0	6037	25	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 (25) 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:78:HIS:HA	1:A:210:ASP:OD2	1.92	0.68
1:B:70:VAL:HG13	1:B:229:ILE:HD11	1.86	0.57
1:A:222:LYS:HG2	1:A:248:PRO:HG2	1.93	0.51
1:B:168:PRO:HD3	1:B:211:ILE:HD13	1.92	0.51
1:B:232:SER:HB2	1:B:238:ALA:HA	1.94	0.50
1:B:313:LYS:NZ	2:B:402:HOH:O	2.26	0.50
1:A:303:GLU:HG2	1:A:307:LYS:HD3	1.95	0.49
1:B:139:TYR:CE1	1:B:315:LEU:HD21	2.48	0.48
1:B:167:ASN:O	1:B:199:GLU:HA	2.14	0.48
1:B:139:TYR:HE1	1:B:315:LEU:HD21	1.80	0.47
1:A:55:ALA:HA	1:B:45:MET:HE1	1.97	0.47
1:A:4:LYS:NZ	1:A:293:VAL:HB	2.30	0.47
1:A:205:VAL:HG21	1:A:211:ILE:HG23	1.97	0.47
1:A:32:TRP:CG	1:A:33:ILE:H	2.33	0.46
1:B:152:GLU:HG3	1:B:187:LEU:HD22	1.96	0.46
1:A:45:MET:HA	1:A:48:MET:HE2	1.98	0.44
1:B:40:ILE:HD11	1:B:45:MET:HE2	1.99	0.44
1:B:75:GLU:HB2	1:B:81:ARG:HB2	2.00	0.43
1:A:390:ASN:C	2:A:401:HOH:O	2.62	0.42
1:A:167:ASN:O	1:A:199:GLU:HA	2.20	0.42
1:A:117:VAL:HG23	1:A:169:HIS:CE1	2.55	0.42
1:A:32:TRP:CG	1:A:33:ILE:N	2.88	0.41
1:A:56:ALA:HB2	1:B:12:PRO:HG2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:TYR:CE2	1:A:120:MET:HB2	2.57	0.40
1:B:211:ILE:HG13	1:B:212:THR:N	2.35	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	385/390 (99%)	372 (97%)	13 (3%)	0	100	100
1	B	380/390 (97%)	373 (98%)	7 (2%)	0	100	100
All	All	765/780 (98%)	745 (97%)	20 (3%)	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	326/328 (99%)	325 (100%)	1 (0%)	86	80
1	B	325/328 (99%)	320 (98%)	5 (2%)	57	41
All	All	651/656 (99%)	645 (99%)	6 (1%)	70	59

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	315	LEU
1	B	79	ARG
1	B	145	SER
1	B	161	ARG
1	B	183	ARG
1	B	211	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	114	GLN
1	B	223	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](#)

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	387/390 (99%)	0.87	52 (13%) 7 7	19, 30, 48, 67	0
1	B	386/390 (98%)	0.64	34 (8%) 15 18	19, 26, 43, 69	0
All	All	773/780 (99%)	0.76	86 (11%) 10 11	19, 28, 47, 69	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	219	TRP	7.3
1	A	220	ASP	5.9
1	B	208	ASP	5.5
1	B	24	LEU	5.5
1	B	177	SER	4.9
1	A	4	LYS	4.8
1	B	390	ASN	4.5
1	B	306	ALA	4.1
1	B	388	LEU	4.1
1	B	4	LYS	4.0
1	A	292	GLN	3.7
1	A	309	VAL	3.6
1	B	5	GLN	3.6
1	A	139	TYR	3.5
1	B	207	THR	3.5
1	A	141	ASN	3.4
1	A	293	VAL	3.3
1	A	390	ASN	3.3
1	B	178	GLU	3.2
1	A	219	TRP	3.2
1	A	143	LYS	3.1
1	A	140	GLU	3.1
1	B	179	GLU	3.1
1	A	386	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	306	ALA	3.1
1	B	26	GLU	3.1
1	A	340	TYR	3.0
1	A	207	THR	3.0
1	A	384	GLY	3.0
1	B	387	ASN	2.9
1	B	3	GLU	2.8
1	A	331	GLY	2.8
1	B	23	GLY	2.8
1	A	317	SER	2.8
1	A	138	ILE	2.7
1	A	153	GLU	2.7
1	A	210	ASP	2.7
1	B	79	ARG	2.7
1	A	385	VAL	2.6
1	B	138	ILE	2.6
1	A	312	VAL	2.6
1	A	261	PHE	2.5
1	B	210	ASP	2.5
1	B	174	TYR	2.5
1	B	211	ILE	2.5
1	B	85	ASP	2.4
1	A	142	SER	2.4
1	A	389	ASN	2.4
1	A	304	PHE	2.4
1	A	208	ASP	2.4
1	A	341	LEU	2.4
1	A	313	LYS	2.4
1	A	381	LEU	2.3
1	B	13	LYS	2.3
1	A	362	PHE	2.3
1	A	348	ILE	2.3
1	B	148	TRP	2.3
1	B	176	TRP	2.3
1	A	382	LYS	2.3
1	A	144	TYR	2.3
1	B	340	TYR	2.3
1	A	117	VAL	2.3
1	A	301	ALA	2.2
1	A	305	LEU	2.2
1	A	387	ASN	2.2
1	A	23	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	5	GLN	2.2
1	A	372	GLU	2.2
1	A	148	TRP	2.2
1	B	180	GLU	2.2
1	A	24	LEU	2.2
1	A	327	ILE	2.2
1	B	187	LEU	2.1
1	B	389	ASN	2.1
1	A	218	ASP	2.1
1	A	314	VAL	2.1
1	A	209	GLU	2.1
1	A	335	GLU	2.1
1	B	183	ARG	2.1
1	B	141	ASN	2.1
1	B	383	GLN	2.1
1	A	388	LEU	2.1
1	B	143	LYS	2.1
1	A	205	VAL	2.0
1	A	373	LEU	2.0
1	B	209	GLU	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.