



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3CUX
Title : Atomic Resolution Structures of Escherichia coli and Bacillus anthracis Malate Synthase A: Comparison with Isoform G and Implications for Structure Based Drug Design
Authors : Lohman, J.R.; Remington, S.J.
Deposited on : 2008-04-17
Resolution : 1.70 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
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

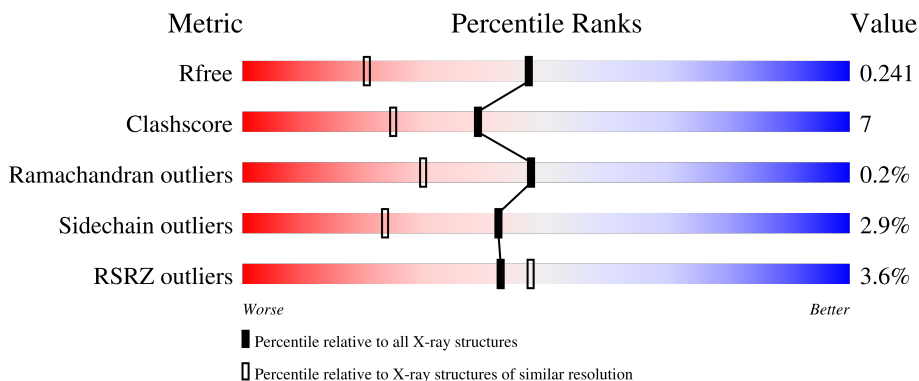
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	528	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4161 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 Malate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	501	3991	2542	694	737	18	0	5	0

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	168	Total	O	0	0
			168	168		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.86Å 52.04Å 89.11Å 90.00° 98.90° 90.00°	Depositor
Resolution (Å)	30.00 – 1.70 29.34 – 1.78	Depositor EDS
% Data completeness (in resolution range)	89.7 (30.00-1.70) 93.5 (29.34-1.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 1.78Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.235 0.205 , 0.241	Depositor DCC
R_{free} test set	2006 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtrriage
Anisotropy	0.232	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 69.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4161	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.66% 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: MG

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	0.80	1/4090 (0.0%)	0.83	5/5525 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	271	CYS	CB-SG	-10.97	1.63	1.82

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	A	97	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	A	415	ARG	NE-CZ-NH2	-5.67	117.46	120.30
1	A	48	ARG	NE-CZ-NH1	-5.25	117.68	120.30
1	A	246	LEU	CA-CB-CG	-5.17	103.42	115.30

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	3991	0	3893	59	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	168	0	0	2	0
All	All	4161	0	3893	59	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 7.

All (59) 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:235[A]:ILE:HG22	1:A:236:PRO:HD2	1.43	0.96
1:A:235[A]:ILE:HG22	1:A:236:PRO:CD	1.96	0.96
1:A:410:THR:HG22	1:A:413:GLY:H	1.32	0.94
1:A:460:HIS:HD2	1:A:462:GLY:H	1.19	0.90
1:A:288:ASN:O	1:A:460:HIS:HE1	1.54	0.89
1:A:417:ASN:HD21	1:A:453:GLN:HE21	1.24	0.85
1:A:288:ASN:O	1:A:460:HIS:CE1	2.33	0.81
1:A:451[A]:ARG:HD2	1:A:511:LEU:HD13	1.67	0.77
1:A:460:HIS:CD2	1:A:462:GLY:H	2.07	0.72
1:A:145:ASN:OD1	1:A:151:TYR:HE2	1.76	0.69
1:A:310:LEU:HB3	1:A:394:ILE:CD1	2.28	0.63
1:A:419:SER:O	1:A:423:GLN:HG3	1.98	0.63
1:A:417:ASN:HD21	1:A:453:GLN:NE2	1.94	0.62
1:A:68:LYS:O	1:A:72:GLU:HG3	2.01	0.59
1:A:38:ASN:ND2	1:A:179:LYS:HE2	2.17	0.59
1:A:235[A]:ILE:CG2	1:A:236:PRO:CD	2.77	0.57
1:A:294:ASP:OD2	1:A:410:THR:HB	2.06	0.56
1:A:230:GLN:NE2	1:A:240:ILE:H	2.05	0.54
1:A:90:GLU:HB2	1:A:363:TRP:CD1	2.43	0.54
1:A:272:GLY:HA3	3:A:685:HOH:O	2.07	0.53
1:A:134:ARG:HA	1:A:195:ASN:HD21	1.74	0.52
1:A:51:LYS:CD	3:A:698:HOH:O	2.58	0.51
1:A:310:LEU:HB3	1:A:394:ILE:HD12	1.93	0.51
1:A:233:ILE:HG13	1:A:235[A]:ILE:HG13	1.93	0.50
1:A:386:GLN:NE2	1:A:389:ARG:HD3	2.27	0.50
1:A:511:LEU:CD2	1:A:518:VAL:HG11	2.42	0.49
1:A:235[A]:ILE:HG22	1:A:236:PRO:HD3	1.89	0.49
1:A:521:LEU:HD12	1:A:521:LEU:C	2.33	0.49
1:A:306:ARG:NH1	1:A:357:ASP:OD2	2.47	0.48
1:A:230:GLN:NE2	1:A:239:THR:H	2.12	0.48
1:A:460:HIS:HD2	1:A:462:GLY:N	2.00	0.47
1:A:281:LEU:O	1:A:281:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:458:ILE:HD11	1:A:476:MET:HG3	1.96	0.46
1:A:235[A]:ILE:CG2	1:A:236:PRO:HD3	2.45	0.46
1:A:97:ARG:HD3	1:A:142:SER:O	2.16	0.46
1:A:38:ASN:HD22	1:A:179:LYS:CE	2.29	0.46
1:A:238:GLY:H	1:A:265:HIS:HE2	1.63	0.46
1:A:366:HIS:CD2	1:A:368:GLY:H	2.35	0.45
1:A:451[A]:ARG:NH2	1:A:517:PHE:CE2	2.85	0.45
1:A:467:ASP:OD2	1:A:469:ARG:NH2	2.47	0.44
1:A:295:ARG:H	1:A:453:GLN:HE22	1.65	0.44
1:A:38:ASN:HD22	1:A:179:LYS:NZ	2.16	0.44
1:A:207:TYR:CD1	1:A:241:LYS:HB2	2.53	0.44
1:A:192:PHE:CE1	1:A:240:ILE:HD11	2.53	0.44
1:A:192:PHE:CE2	1:A:229:ALA:HB1	2.53	0.44
1:A:124:GLU:H	1:A:124:GLU:CD	2.22	0.43
1:A:281:LEU:HD23	1:A:281:LEU:C	2.39	0.43
1:A:518:VAL:HG21	1:A:524:PRO:HD3	1.99	0.43
1:A:386:GLN:NE2	1:A:389:ARG:HH11	2.17	0.43
1:A:451[A]:ARG:HG3	1:A:452:ALA:N	2.32	0.43
1:A:352:GLU:HG3	1:A:380:ILE:HD11	2.00	0.42
1:A:230:GLN:HE22	1:A:239:THR:H	1.68	0.42
1:A:38:ASN:HD22	1:A:179:LYS:HZ3	1.66	0.41
1:A:386:GLN:HE21	1:A:389:ARG:HD3	1.84	0.41
1:A:38:ASN:ND2	1:A:179:LYS:CE	2.82	0.41
1:A:292:LEU:H	1:A:456:GLN:NE2	2.19	0.41
1:A:415:ARG:NH2	1:A:482:GLU:OE1	2.32	0.41
1:A:41[A]:ARG:HH22	1:A:170:GLU:HG3	1.87	0.40
1:A:366:HIS:HD2	1:A:368:GLY:H	1.70	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	498/528 (94%)	485 (97%)	12 (2%)	1 (0%)	47 30

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	439	ASN

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	412/452 (91%)	398 (97%)	14 (3%)	37 18

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	GLU
1	A	64	LEU
1	A	152	ARG
1	A	179	LYS
1	A	209	TYR
1	A	215	SER
1	A	235[A]	ILE
1	A	235[B]	ILE
1	A	246	LEU
1	A	275	ASP
1	A	410	THR
1	A	451[A]	ARG
1	A	451[B]	ARG
1	A	516	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	102	ASN

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Mol	Chain	Res	Type
1	A	194	HIS
1	A	195	ASN
1	A	223	ASN
1	A	230	GLN
1	A	288	ASN
1	A	366	HIS
1	A	386	GLN
1	A	453	GLN
1	A	456	GLN
1	A	460	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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	501/528 (94%)	0.28	18 (3%) 42 47	14, 24, 38, 47	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	439	ASN	4.7
1	A	369	LEU	4.0
1	A	372	VAL	3.6
1	A	440	LEU	3.3
1	A	346	LYS	3.0
1	A	394	ILE	3.0
1	A	151	TYR	3.0
1	A	234	GLY	2.7
1	A	347	VAL	2.7
1	A	501	PHE	2.7
1	A	145	ASN	2.4
1	A	235[A]	ILE	2.3
1	A	499	GLY	2.2
1	A	438	TYR	2.2
1	A	162	VAL	2.1
1	A	60	PHE	2.1
1	A	161	ILE	2.1
1	A	186	VAL	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 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
2	MG	A	1	1/1	0.99	0.08	23,23,23,23	0
2	MG	A	530	1/1	0.99	0.05	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.