



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2017 – 07:29 PM EDT

PDB ID : 1K0E
Title : THE CRYSTAL STRUCTURE OF AMINODEOXYCHORISMATE SYNTHASE FROM FORMATE GROWN CRYSTALS
Authors : Parsons, J.F.; Jensen, P.Y.; Pachikara, A.S.; Howard, A.J.; Eisenstein, E.; Ladner, J.E.
Deposited on : unknown
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

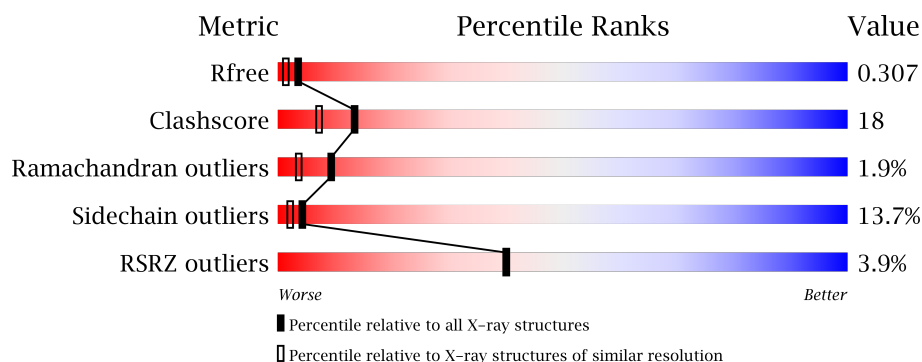
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	453	<div> <div>2%</div> <div> <div></div> <div>43%</div> <div>39%</div> <div>11%</div> <div>• •</div> </div> </div>
1	B	453	<div> <div>6%</div> <div> <div></div> <div>36%</div> <div>37%</div> <div>13%</div> <div>5%</div> <div>9%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	FMT	A	1701	-	-	X	X

2 Entry composition [i](#)

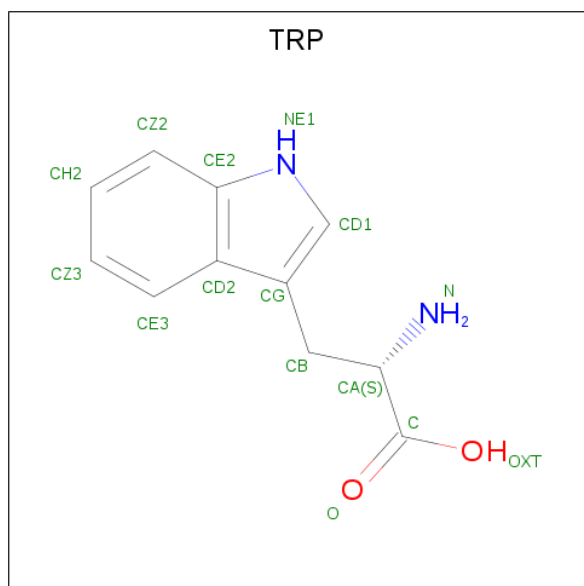
There are 4 unique types of molecules in this entry. The entry contains 7106 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 p-aminobenzoate synthase component I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3466	2186	605	662	13			
1	B	414	Total	C	N	O	S	0	0	0
			3289	2067	574	634	14			

- Molecule 2 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	11	2	2		
2	B	1	Total	C	N	O	0	0
			15	11	2	2		

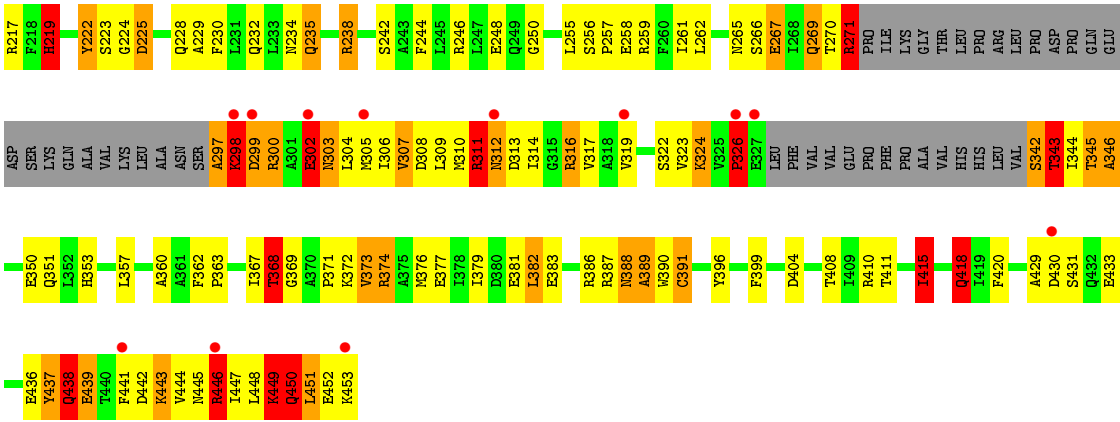
- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	186	Total	O	0	0
			186	186		
4	B	132	Total	O	0	0
			132	132		



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	111.99 Å 185.72 Å 45.08 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 28.75 – 1.84	Depositor EDS
% Data completeness (in resolution range)	86.7 (10.00-2.00) 87.2 (28.75-1.84)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 1.84 Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.205 , 0.315 0.203 , 0.307	Depositor DCC
R_{free} test set	2880 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.383	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 82.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7106	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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: FMT

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	1.09	6/3543 (0.2%)	2.67	256/4813 (5.3%)
1	B	1.02	1/3357 (0.0%)	2.71	248/4552 (5.4%)
All	All	1.05	7/6900 (0.1%)	2.69	504/9365 (5.4%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	342	SER	CB-OG	6.96	1.51	1.42
1	B	186	SER	CB-OG	6.28	1.50	1.42
1	A	296	SER	CB-OG	5.84	1.49	1.42
1	A	406	SER	CB-OG	5.35	1.49	1.42
1	A	321	GLY	N-CA	5.33	1.54	1.46

The worst 5 of 504 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	89	ARG	NE-CZ-NH2	-25.30	107.65	120.30
1	A	410	ARG	NE-CZ-NH1	25.21	132.91	120.30
1	B	89	ARG	NE-CZ-NH1	23.25	131.93	120.30
1	A	316	ARG	NE-CZ-NH2	-21.38	109.61	120.30
1	B	311	ARG	CD-NE-CZ	20.15	151.81	123.60

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	3466	0	3367	109	0
1	B	3289	0	3189	131	0
2	A	15	0	9	0	0
2	B	15	0	9	1	0
3	A	3	0	2	4	0
4	A	186	0	0	10	0
4	B	132	0	0	5	0
All	All	7106	0	6576	240	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 18.

The worst 5 of 240 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:B:225:ASP:HB3	1:B:228:GLN:HG2	1.40	0.99
1:A:176:GLU:HG3	1:A:224:GLY:HA2	1.45	0.95
1:B:121:LEU:HD11	1:B:376:MET:HE3	1.51	0.93
1:B:176:GLU:HB2	1:B:225:ASP:HB2	1.56	0.84
1:A:236:ALA:HB1	1:A:446:ARG:HH22	1.40	0.84

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	433/453 (96%)	401 (93%)	25 (6%)	7 (2%)	11	5
1	B	408/453 (90%)	372 (91%)	27 (7%)	9 (2%)	8	3
All	All	841/906 (93%)	773 (92%)	52 (6%)	16 (2%)	9	4

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	175	GLN
1	A	301	ALA
1	B	170	GLN
1	B	173	SER
1	B	298	LYS

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	375/390 (96%)	334 (89%)	41 (11%)	7	4
1	B	355/390 (91%)	296 (83%)	59 (17%)	2	1
All	All	730/780 (94%)	630 (86%)	100 (14%)	4	2

5 of 100 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	12	LEU
1	B	91	ASP
1	B	439	GLU
1	B	15	GLN
1	B	62	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	35	HIS
1	B	103	GLN
1	B	388	ASN
1	B	81	GLN
1	A	199	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	$\# Z > 2$
3	FMT	A	1701	-	0,2,2	0.00	-	0,1,1	0.00	-
2	TRP	A	601	-	11,16,16	1.19	1 (9%)	11,22,22	1.98	5 (45%)
2	TRP	B	602	-	11,16,16	0.95	1 (9%)	11,22,22	3.71	7 (63%)

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
3	FMT	A	1701	-	-	0/0/0/0	0/0/0/0
2	TRP	A	601	-	-	0/3/8/8	0/2/2/2
2	TRP	B	602	-	-	0/3/8/8	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	602	TRP	CD1-NE1	2.14	1.41	1.36
2	A	601	TRP	CH2-CZ3	3.20	1.45	1.38

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	TRP	CH2-CZ2-CE2	-6.98	109.56	120.07
2	B	602	TRP	CZ3-CE3-CD2	-6.56	111.50	120.88
2	A	601	TRP	CZ3-CH2-CZ2	-2.64	116.68	120.45
2	B	602	TRP	CE3-CD2-CG	-2.46	129.90	134.42
2	A	601	TRP	CE3-CD2-CE2	-2.33	115.07	118.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1701	FMT	4	0
2	B	602	TRP	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	437/453 (96%)	-0.11	8 (1%) 69 68	9, 23, 51, 73	0
1	B	414/453 (91%)	0.17	25 (6%) 23 23	11, 27, 66, 144	0
All	All	851/906 (93%)	0.03	33 (3%) 40 40	9, 24, 60, 144	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	172	PHE	9.2
1	B	1	MET	8.3
1	B	173	SER	8.1
1	B	175	GLN	6.1
1	B	171	GLN	5.7

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	FMT	A	1701	3/3	0.88	0.28	3.53	22,22,25,30	0
2	TRP	B	602	15/15	0.94	0.12	-0.24	11,17,22,22	0
2	TRP	A	601	15/15	0.94	0.11	-0.40	8,15,19,21	0

6.5 Other polymers ⓘ

There are no such residues in this entry.