



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 8, 2019 – 11:00 AM EDT

PDB ID : 6C07
Title : Crystal Structure of S-Adenosylmethionine synthetase (MetK/Mat) from *Cryptosporidium parvum*
Authors : Ohren, J.F.; Viola, R.E.
Deposited on : 2017-12-28
Resolution : 1.85 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

<https://www.wwpdb.org/validation/2017/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
Xtriage (Phenix)	:	1.13
EDS	:	rb-20031633
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031633

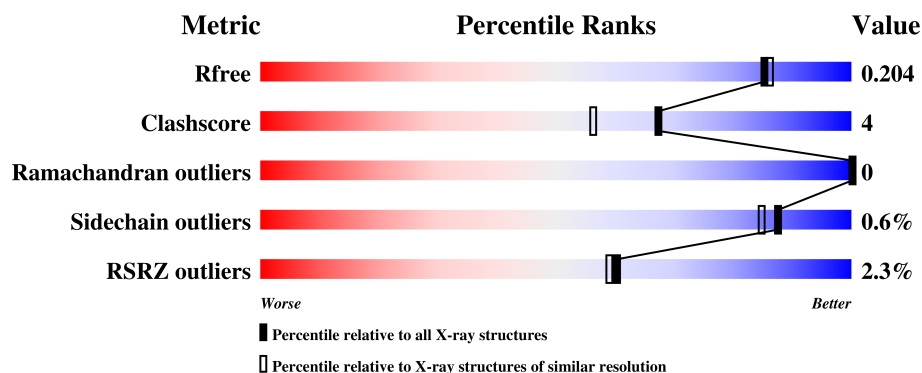
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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}	111664	2111 (1.86-1.86)
Clashscore	122126	2258 (1.86-1.86)
Ramachandran outliers	120053	2234 (1.86-1.86)
Sidechain outliers	120020	2234 (1.86-1.86)
RSRZ outliers	108989	2075 (1.86-1.86)

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	406	<div> <div>2%</div> <div>85% 8% 7%</div> </div>
1	B	406	<div> <div>%</div> <div>83% 8% 9%</div> </div>
1	C	406	<div> <div>%</div> <div>87% 5% 8%</div> </div>
1	D	406	<div> <div>4%</div> <div>83% 7% 9%</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
2	CL	C	502	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23945 atoms, of which 11300 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 S-adenosylmethionine synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	376	Total	C	H	N	O	S	0	0	0
			5777	1832	2884	491	554	16			
1	B	368	Total	C	H	N	O	S	0	10	0
			5607	1795	2779	477	538	18			
1	C	374	Total	C	H	N	O	S	0	7	0
			5802	1840	2893	491	560	18			
1	D	368	Total	C	H	N	O	S	0	5	0
			5548	1777	2744	473	538	16			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		
3	A	2	Total	Mg	0	0
			2	2		
3	D	1	Total	Mg	0	0
			1	1		
3	C	2	Total	Mg	0	0
			2	2		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total K 1 1	0	0

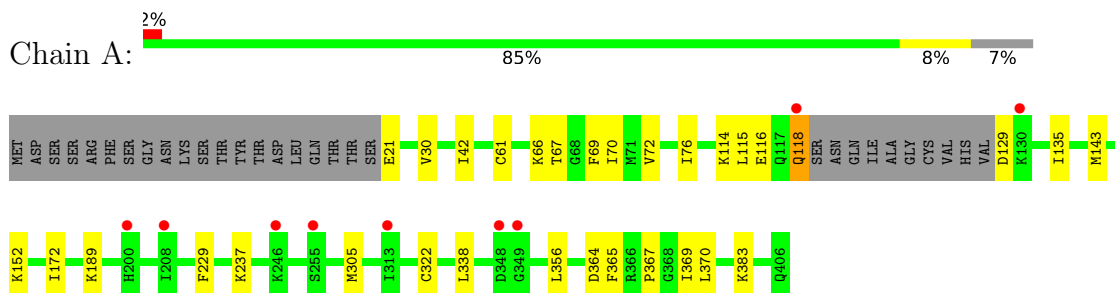
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	327	Total O 327 327	0	0
5	B	306	Total O 306 306	0	0
5	C	335	Total O 335 335	0	0
5	D	233	Total O 233 233	0	0

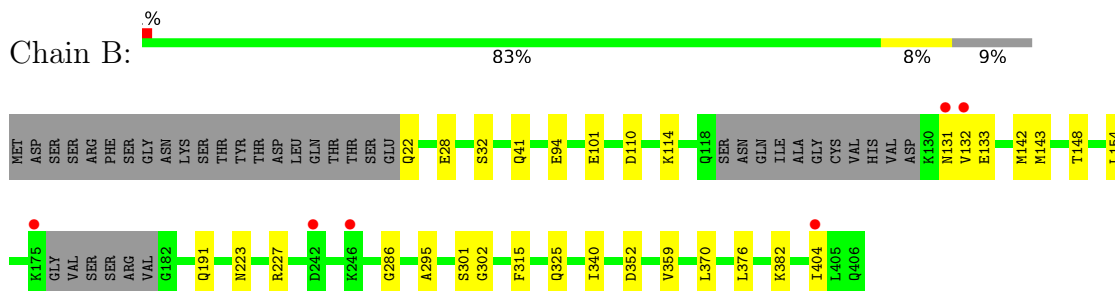
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

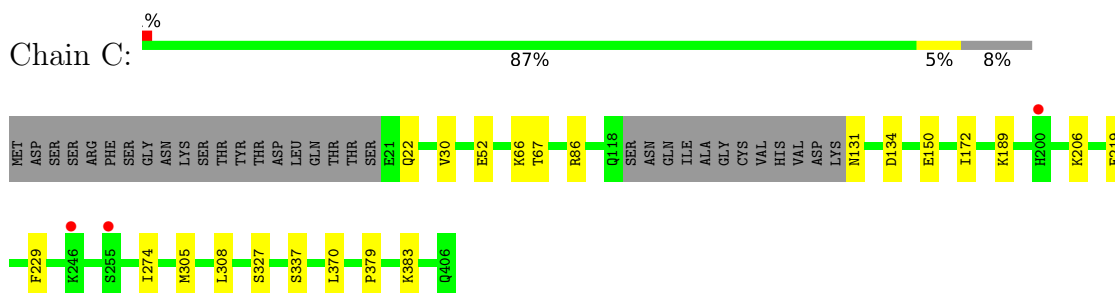
- Molecule 1: S-adenosylmethionine synthase



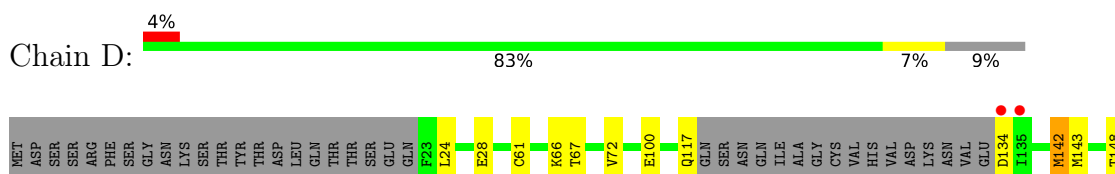
- Molecule 1: S-adenosylmethionine synthase



- Molecule 1: S-adenosylmethionine synthase



- Molecule 1: S-adenosylmethionine synthase





4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	134.39Å 62.06Å 191.58Å 90.00° 90.65° 90.00°	Depositor
Resolution (Å)	19.99 – 1.85 19.99 – 1.85	Depositor EDS
% Data completeness (in resolution range)	94.4 (19.99-1.85) 94.4 (19.99-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 1.85Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.157 , 0.204 0.157 , 0.204	Depositor DCC
R_{free} test set	6388 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	23945	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% 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: K, MG, CL

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	0.60	1/2942 (0.0%)	0.72	0/3971
1	B	0.54	0/2926	0.71	1/3958 (0.0%)
1	C	0.54	1/2987 (0.0%)	0.69	0/4031
1	D	0.48	0/2861	0.68	0/3876
All	All	0.54	2/11716 (0.0%)	0.70	1/15836 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	322	CYS	CB-SG	-10.19	1.65	1.82
1	C	150	GLU	CB-CG	-5.39	1.42	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	352	ASP	CB-CG-OD2	5.24	123.01	118.30

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	2893	2884	2884	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2828	2779	2734	21	0
1	C	2909	2893	2867	19	0
1	D	2804	2744	2740	31	0
2	A	1	0	0	0	0
2	C	1	0	0	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	C	1	0	0	0	0
5	A	327	0	0	5	0
5	B	306	0	0	7	2
5	C	335	0	0	9	0
5	D	233	0	0	7	0
All	All	12645	11300	11225	95	2

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.

The worst 5 of 95 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:C:52:GLU:OE2	5:C:601:HOH:O	1.60	1.17
2:C:502:CL:CL	5:C:797:HOH:O	1.98	1.13
1:D:340:ILE:HD12	1:D:356:LEU:HD23	1.48	0.94
1:D:356:LEU:HD11	5:D:734:HOH:O	1.69	0.90
1:C:131:ASN:N	5:C:602:HOH:O	2.06	0.87

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:857:HOH:O	5:B:892:HOH:O[1_545]	2.08	0.12
5:B:862:HOH:O	5:B:898:HOH:O[4_554]	2.15	0.05

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	372/406 (92%)	365 (98%)	7 (2%)	0	100	100
1	B	372/406 (92%)	367 (99%)	5 (1%)	0	100	100
1	C	377/406 (93%)	369 (98%)	8 (2%)	0	100	100
1	D	369/406 (91%)	363 (98%)	6 (2%)	0	100	100
All	All	1490/1624 (92%)	1464 (98%)	26 (2%)	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	314/348 (90%)	311 (99%)	3 (1%)	78	72
1	B	305/348 (88%)	302 (99%)	3 (1%)	78	72
1	C	320/348 (92%)	320 (100%)	0	100	100
1	D	298/348 (86%)	296 (99%)	2 (1%)	85	81
All	All	1237/1392 (89%)	1229 (99%)	8 (1%)	87	85

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	101	GLU
1	D	143	MET
1	B	143[B]	MET

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Mol	Chain	Res	Type
1	A	152	LYS
1	B	143[A]	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 10 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 ⓘ

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	376/406 (92%)	-0.24	9 (2%) 59 57	16, 26, 49, 69	0
1	B	368/406 (90%)	-0.22	6 (1%) 72 72	16, 27, 45, 75	0
1	C	374/406 (92%)	-0.27	3 (0%) 86 87	17, 27, 47, 74	0
1	D	368/406 (90%)	0.00	16 (4%) 35 34	18, 33, 52, 79	0
All	All	1486/1624 (91%)	-0.18	34 (2%) 60 59	16, 28, 49, 79	0

The worst 5 of 34 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	202	VAL	4.9
1	D	200	HIS	4.8
1	A	348	ASP	4.4
1	C	200	HIS	4.3
1	D	198	CYS	4.1

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 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. 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(\AA^2)	Q<0.9
3	MG	A	503	1/1	0.87	0.06	47,47,47,47	0
3	MG	C	504	1/1	0.93	0.11	44,44,44,44	1
3	MG	D	501	1/1	0.94	0.11	24,24,24,24	1
2	CL	C	502	1/1	0.95	0.13	47,47,47,47	0
3	MG	B	501	1/1	0.97	0.07	30,30,30,30	1
3	MG	C	503	1/1	0.98	0.05	37,37,37,37	1
4	K	C	501	1/1	0.99	0.07	23,23,23,23	1
3	MG	B	502	1/1	0.99	0.05	27,27,27,27	1
2	CL	A	501	1/1	0.99	0.04	26,26,26,26	1
3	MG	A	502	1/1	1.00	0.03	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.