



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:17 AM UTC

PDB ID : 9IJF / pdb_00009ijf
Title : Structure of ATP-dependent diazotase CmaA6
Authors : Katsuyama, Y.; Kawai, S.; Ohnishi, Y.
Deposited on : 2024-06-22
Resolution : 2.73 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 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

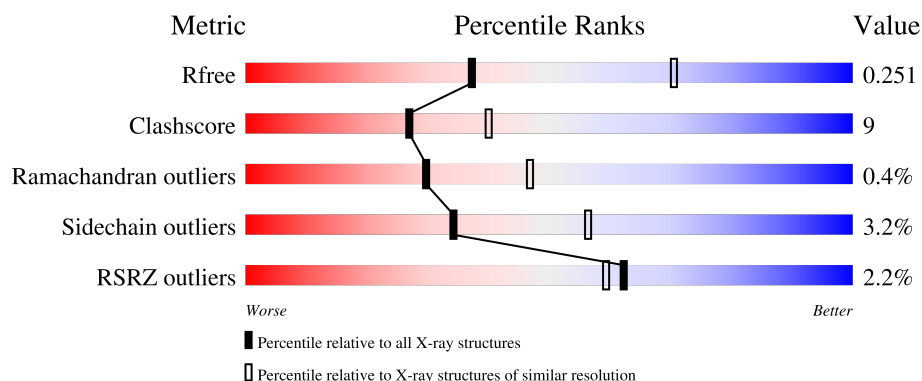
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	569	7% 73% 21% • 5%
1	B	569	% 71% 19% • 8%
1	D	569	% 75% 16% 8%
1	E	569	% 72% 19% • 8%
1	F	569	% 68% 23% • 8%

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Mol	Chain	Length	Quality of chain
1	G	569	3% 71% 20% 8%
1	H	569	2% 70% 22% 8%
1	I	569	71% 21% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 32117 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 AMP-binding enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	0	0
			4104	2581	726	784	13			
1	B	523	Total	C	N	O	S	0	0	0
			3996	2514	706	763	13			
1	D	523	Total	C	N	O	S	0	0	0
			3996	2514	706	763	13			
1	E	521	Total	C	N	O	S	0	0	0
			3982	2507	704	758	13			
1	F	523	Total	C	N	O	S	0	0	0
			3996	2514	706	763	13			
1	G	523	Total	C	N	O	S	0	0	0
			3996	2514	706	763	13			
1	H	523	Total	C	N	O	S	0	0	0
			3996	2514	706	763	13			
1	I	524	Total	C	N	O	S	0	0	0
			4006	2520	709	764	13			

There are 128 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP W5W4E6
A	-14	ASN	-	expression tag	UNP W5W4E6
A	-13	HIS	-	expression tag	UNP W5W4E6
A	-12	LYS	-	expression tag	UNP W5W4E6
A	-11	VAL	-	expression tag	UNP W5W4E6
A	-10	HIS	-	expression tag	UNP W5W4E6
A	-9	HIS	-	expression tag	UNP W5W4E6
A	-8	HIS	-	expression tag	UNP W5W4E6
A	-7	HIS	-	expression tag	UNP W5W4E6
A	-6	HIS	-	expression tag	UNP W5W4E6
A	-5	HIS	-	expression tag	UNP W5W4E6
A	-4	ILE	-	expression tag	UNP W5W4E6
A	-3	GLU	-	expression tag	UNP W5W4E6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP W5W4E6
A	-1	ARG	-	expression tag	UNP W5W4E6
A	0	HIS	-	expression tag	UNP W5W4E6
B	-15	MET	-	initiating methionine	UNP W5W4E6
B	-14	ASN	-	expression tag	UNP W5W4E6
B	-13	HIS	-	expression tag	UNP W5W4E6
B	-12	LYS	-	expression tag	UNP W5W4E6
B	-11	VAL	-	expression tag	UNP W5W4E6
B	-10	HIS	-	expression tag	UNP W5W4E6
B	-9	HIS	-	expression tag	UNP W5W4E6
B	-8	HIS	-	expression tag	UNP W5W4E6
B	-7	HIS	-	expression tag	UNP W5W4E6
B	-6	HIS	-	expression tag	UNP W5W4E6
B	-5	HIS	-	expression tag	UNP W5W4E6
B	-4	ILE	-	expression tag	UNP W5W4E6
B	-3	GLU	-	expression tag	UNP W5W4E6
B	-2	GLY	-	expression tag	UNP W5W4E6
B	-1	ARG	-	expression tag	UNP W5W4E6
B	0	HIS	-	expression tag	UNP W5W4E6
D	-15	MET	-	initiating methionine	UNP W5W4E6
D	-14	ASN	-	expression tag	UNP W5W4E6
D	-13	HIS	-	expression tag	UNP W5W4E6
D	-12	LYS	-	expression tag	UNP W5W4E6
D	-11	VAL	-	expression tag	UNP W5W4E6
D	-10	HIS	-	expression tag	UNP W5W4E6
D	-9	HIS	-	expression tag	UNP W5W4E6
D	-8	HIS	-	expression tag	UNP W5W4E6
D	-7	HIS	-	expression tag	UNP W5W4E6
D	-6	HIS	-	expression tag	UNP W5W4E6
D	-5	HIS	-	expression tag	UNP W5W4E6
D	-4	ILE	-	expression tag	UNP W5W4E6
D	-3	GLU	-	expression tag	UNP W5W4E6
D	-2	GLY	-	expression tag	UNP W5W4E6
D	-1	ARG	-	expression tag	UNP W5W4E6
D	0	HIS	-	expression tag	UNP W5W4E6
E	-15	MET	-	initiating methionine	UNP W5W4E6
E	-14	ASN	-	expression tag	UNP W5W4E6
E	-13	HIS	-	expression tag	UNP W5W4E6
E	-12	LYS	-	expression tag	UNP W5W4E6
E	-11	VAL	-	expression tag	UNP W5W4E6
E	-10	HIS	-	expression tag	UNP W5W4E6
E	-9	HIS	-	expression tag	UNP W5W4E6

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-8	HIS	-	expression tag	UNP W5W4E6
E	-7	HIS	-	expression tag	UNP W5W4E6
E	-6	HIS	-	expression tag	UNP W5W4E6
E	-5	HIS	-	expression tag	UNP W5W4E6
E	-4	ILE	-	expression tag	UNP W5W4E6
E	-3	GLU	-	expression tag	UNP W5W4E6
E	-2	GLY	-	expression tag	UNP W5W4E6
E	-1	ARG	-	expression tag	UNP W5W4E6
E	0	HIS	-	expression tag	UNP W5W4E6
F	-15	MET	-	initiating methionine	UNP W5W4E6
F	-14	ASN	-	expression tag	UNP W5W4E6
F	-13	HIS	-	expression tag	UNP W5W4E6
F	-12	LYS	-	expression tag	UNP W5W4E6
F	-11	VAL	-	expression tag	UNP W5W4E6
F	-10	HIS	-	expression tag	UNP W5W4E6
F	-9	HIS	-	expression tag	UNP W5W4E6
F	-8	HIS	-	expression tag	UNP W5W4E6
F	-7	HIS	-	expression tag	UNP W5W4E6
F	-6	HIS	-	expression tag	UNP W5W4E6
F	-5	HIS	-	expression tag	UNP W5W4E6
F	-4	ILE	-	expression tag	UNP W5W4E6
F	-3	GLU	-	expression tag	UNP W5W4E6
F	-2	GLY	-	expression tag	UNP W5W4E6
F	-1	ARG	-	expression tag	UNP W5W4E6
F	0	HIS	-	expression tag	UNP W5W4E6
G	-15	MET	-	initiating methionine	UNP W5W4E6
G	-14	ASN	-	expression tag	UNP W5W4E6
G	-13	HIS	-	expression tag	UNP W5W4E6
G	-12	LYS	-	expression tag	UNP W5W4E6
G	-11	VAL	-	expression tag	UNP W5W4E6
G	-10	HIS	-	expression tag	UNP W5W4E6
G	-9	HIS	-	expression tag	UNP W5W4E6
G	-8	HIS	-	expression tag	UNP W5W4E6
G	-7	HIS	-	expression tag	UNP W5W4E6
G	-6	HIS	-	expression tag	UNP W5W4E6
G	-5	HIS	-	expression tag	UNP W5W4E6
G	-4	ILE	-	expression tag	UNP W5W4E6
G	-3	GLU	-	expression tag	UNP W5W4E6
G	-2	GLY	-	expression tag	UNP W5W4E6
G	-1	ARG	-	expression tag	UNP W5W4E6
G	0	HIS	-	expression tag	UNP W5W4E6
H	-15	MET	-	initiating methionine	UNP W5W4E6

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-14	ASN	-	expression tag	UNP W5W4E6
H	-13	HIS	-	expression tag	UNP W5W4E6
H	-12	LYS	-	expression tag	UNP W5W4E6
H	-11	VAL	-	expression tag	UNP W5W4E6
H	-10	HIS	-	expression tag	UNP W5W4E6
H	-9	HIS	-	expression tag	UNP W5W4E6
H	-8	HIS	-	expression tag	UNP W5W4E6
H	-7	HIS	-	expression tag	UNP W5W4E6
H	-6	HIS	-	expression tag	UNP W5W4E6
H	-5	HIS	-	expression tag	UNP W5W4E6
H	-4	ILE	-	expression tag	UNP W5W4E6
H	-3	GLU	-	expression tag	UNP W5W4E6
H	-2	GLY	-	expression tag	UNP W5W4E6
H	-1	ARG	-	expression tag	UNP W5W4E6
H	0	HIS	-	expression tag	UNP W5W4E6
I	-15	MET	-	initiating methionine	UNP W5W4E6
I	-14	ASN	-	expression tag	UNP W5W4E6
I	-13	HIS	-	expression tag	UNP W5W4E6
I	-12	LYS	-	expression tag	UNP W5W4E6
I	-11	VAL	-	expression tag	UNP W5W4E6
I	-10	HIS	-	expression tag	UNP W5W4E6
I	-9	HIS	-	expression tag	UNP W5W4E6
I	-8	HIS	-	expression tag	UNP W5W4E6
I	-7	HIS	-	expression tag	UNP W5W4E6
I	-6	HIS	-	expression tag	UNP W5W4E6
I	-5	HIS	-	expression tag	UNP W5W4E6
I	-4	ILE	-	expression tag	UNP W5W4E6
I	-3	GLU	-	expression tag	UNP W5W4E6
I	-2	GLY	-	expression tag	UNP W5W4E6
I	-1	ARG	-	expression tag	UNP W5W4E6
I	0	HIS	-	expression tag	UNP W5W4E6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	10	Total O 10 10	0	0
2	B	3	Total O 3 3	0	0
2	D	11	Total O 11 11	0	0
2	E	4	Total O 4 4	0	0

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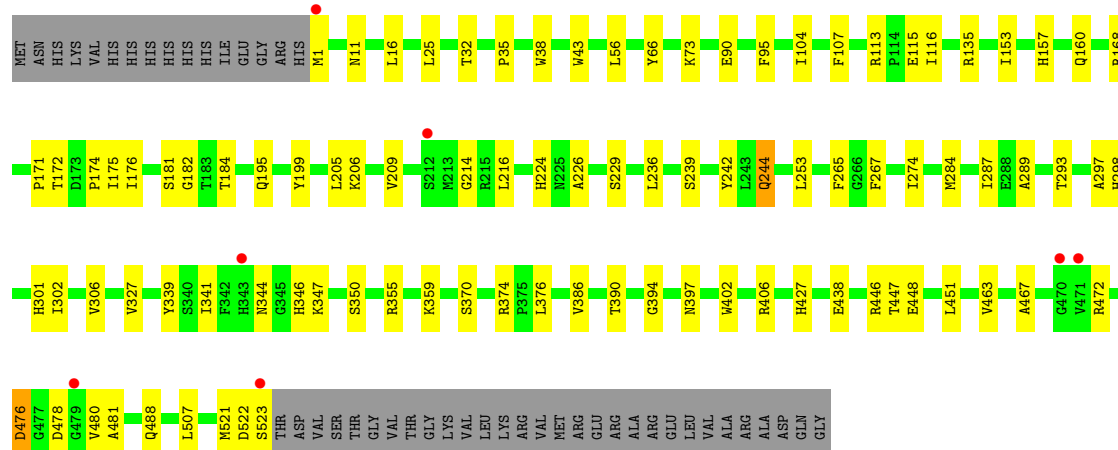
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	3	Total 3	O 3	0	0
2	G	4	Total 4	O 4	0	0
2	H	4	Total 4	O 4	0	0
2	I	6	Total 6	O 6	0	0

ARG
GLU
LEU
VAL
ALA
ARG
ALA
ASP
GLN
GLY

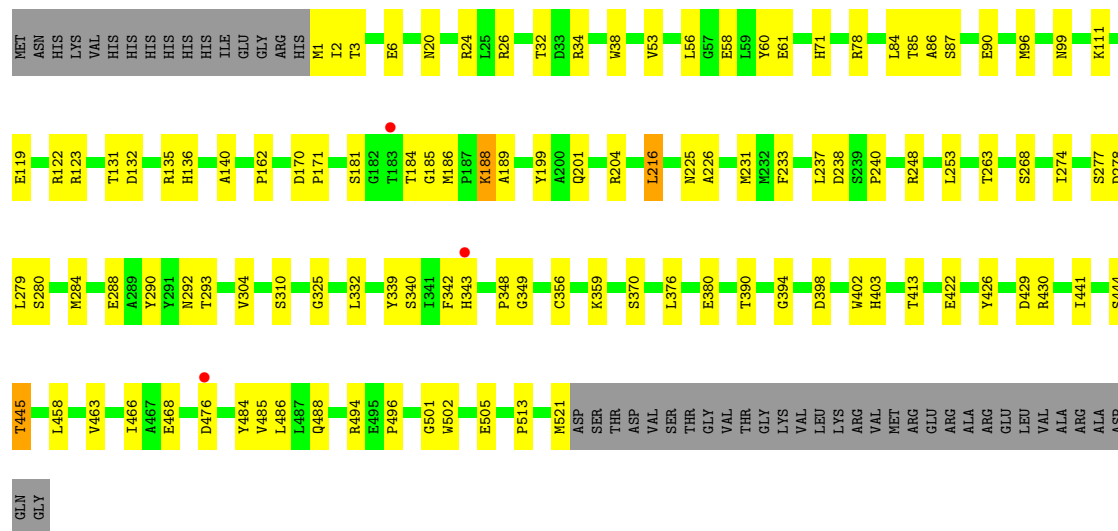
• Molecule 1: Putative AMP-binding enzyme

Chain D: 



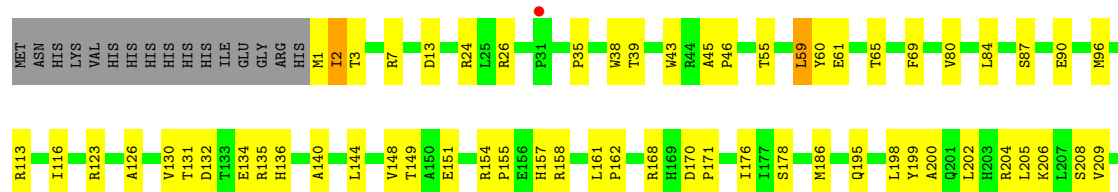
• Molecule 1: Putative AMP-binding enzyme

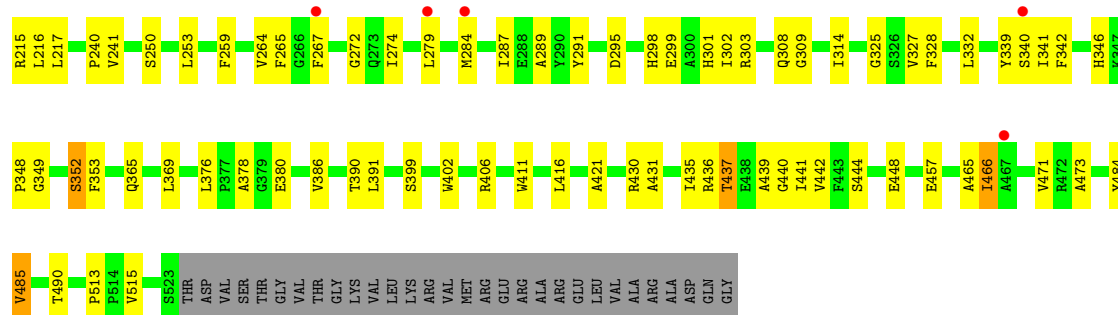
Chain E: 



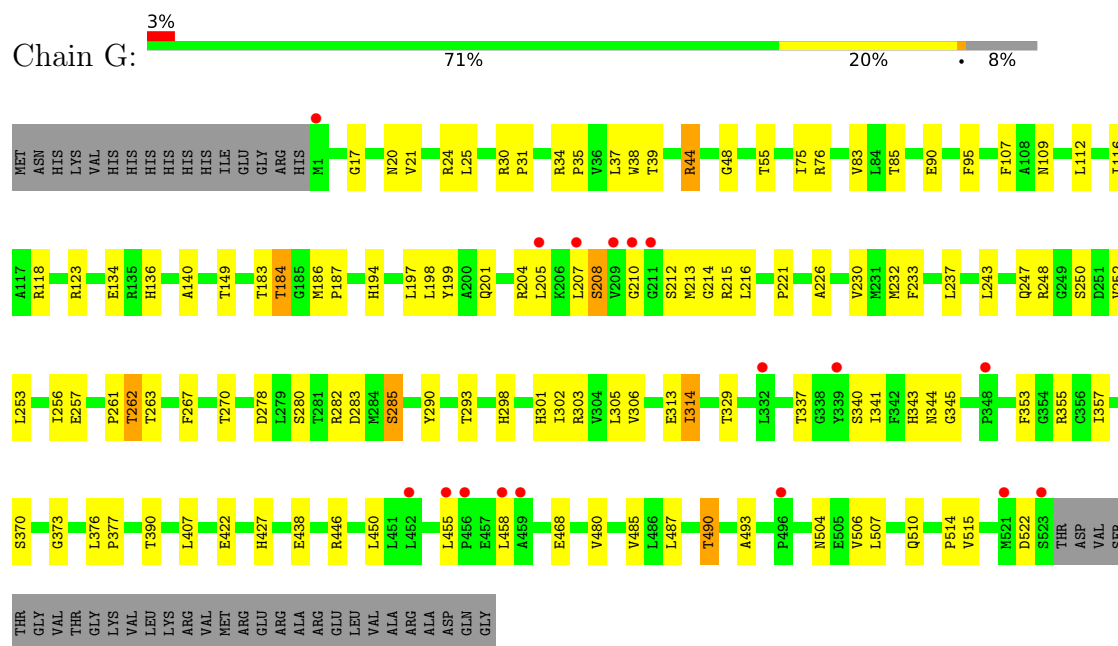
• Molecule 1: Putative AMP-binding enzyme

Chain F: 

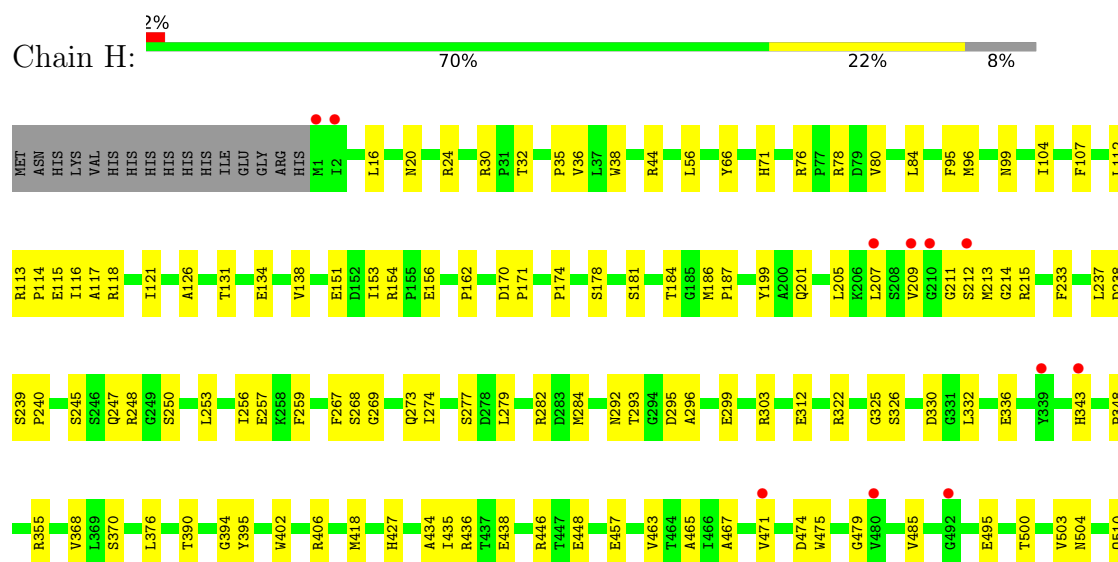


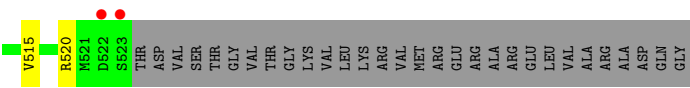


● Molecule 1: Putative AMP-binding enzyme

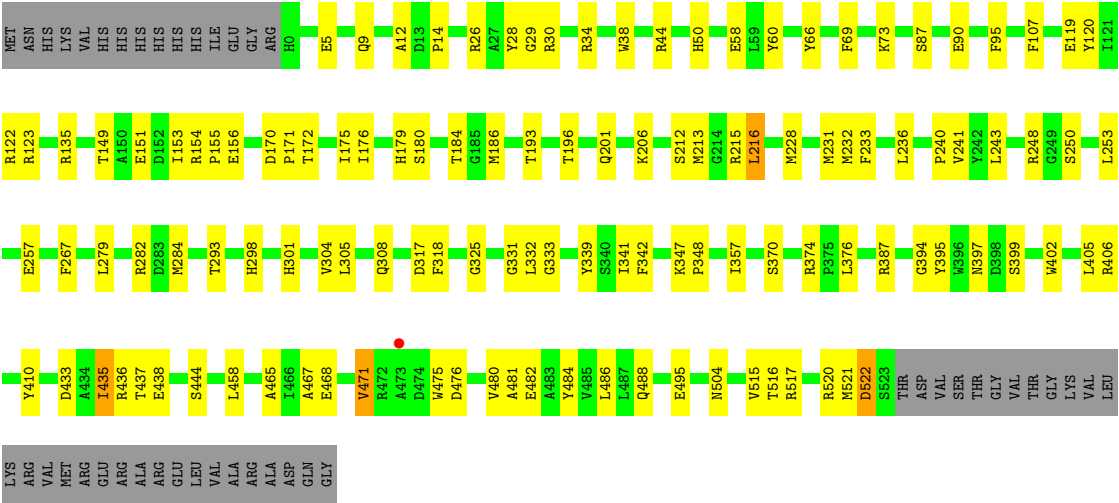


● Molecule 1: Putative AMP-binding enzyme





● Molecule 1: Putative AMP-binding enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	94.16Å 101.07Å 157.41Å 76.31° 88.05° 62.28°	Depositor
Resolution (Å)	65.95 – 2.73 65.95 – 2.73	Depositor EDS
% Data completeness (in resolution range)	98.6 (65.95-2.73) 98.6 (65.95-2.73)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.73Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.194 , 0.251 0.197 , 0.251	Depositor DCC
R_{free} test set	1957 reflections (1.48%)	wwPDB-VP
Wilson B-factor (Å ²)	47.4	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.048 for h,h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	32117	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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	0.40	0/4204	0.55	0/5720
1	B	0.38	0/4096	0.60	2/5574 (0.0%)
1	D	0.41	0/4096	0.60	2/5574 (0.0%)
1	E	0.41	0/4082	0.62	0/5555
1	F	0.35	0/4096	0.56	0/5574
1	G	0.37	0/4096	0.56	0/5574
1	H	0.39	0/4096	0.56	0/5574
1	I	0.40	0/4107	0.60	0/5589
All	All	0.39	0/32873	0.58	4/44734 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
1	H	0	1
All	All	0	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	181	SER	CA-C-N	-8.03	105.68	121.41
1	D	181	SER	C-N-CA	-8.03	105.68	121.41
1	B	237	LEU	CA-C-N	-6.57	109.00	121.54
1	B	237	LEU	C-N-CA	-6.57	109.00	121.54

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	182	GLY	Peptide
1	H	78	ARG	Sidechain

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	4104	0	3997	82	0
1	B	3996	0	3878	70	0
1	D	3996	0	3878	63	0
1	E	3982	0	3869	69	1
1	F	3996	0	3878	82	0
1	G	3996	0	3878	79	0
1	H	3996	0	3878	79	0
1	I	4006	0	3885	81	1
2	A	10	0	0	1	0
2	B	3	0	0	0	0
2	D	11	0	0	0	0
2	E	4	0	0	0	0
2	F	3	0	0	0	0
2	G	4	0	0	0	0
2	H	4	0	0	0	0
2	I	6	0	0	0	0
All	All	32117	0	31141	584	1

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 9.

The worst 5 of 584 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:E:458:LEU:O	1:I:34:ARG:NH1	1.90	1.05
1:G:31:PRO:HG2	1:G:34:ARG:HD2	1.50	0.94
1:B:39:THR:HB	1:B:89:THR:HG21	1.50	0.93
1:H:186:MET:HE3	1:H:187:PRO:HD2	1.51	0.91
1:H:279:LEU:HD21	1:H:284:MET:HE3	1.55	0.88

All (1) 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)
1:E:34:ARG:NH2	1:I:458:LEU:O[1_655]	2.09	0.11

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	536/569 (94%)	499 (93%)	31 (6%)	6 (1%)	11	20
1	B	521/569 (92%)	490 (94%)	29 (6%)	2 (0%)	30	47
1	D	521/569 (92%)	498 (96%)	21 (4%)	2 (0%)	30	47
1	E	519/569 (91%)	498 (96%)	21 (4%)	0	100	100
1	F	521/569 (92%)	489 (94%)	32 (6%)	0	100	100
1	G	521/569 (92%)	494 (95%)	22 (4%)	5 (1%)	12	22
1	H	521/569 (92%)	501 (96%)	18 (4%)	2 (0%)	30	47
1	I	522/569 (92%)	502 (96%)	20 (4%)	0	100	100
All	All	4182/4552 (92%)	3971 (95%)	194 (5%)	17 (0%)	30	47

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	339	TYR
1	G	422	GLU
1	A	211	GLY
1	A	438	GLU
1	A	469	GLU

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	429/455 (94%)	416 (97%)	13 (3%)	36	58
1	B	416/455 (91%)	394 (95%)	22 (5%)	20	37
1	D	416/455 (91%)	409 (98%)	7 (2%)	53	71
1	E	414/455 (91%)	406 (98%)	8 (2%)	50	68
1	F	416/455 (91%)	394 (95%)	22 (5%)	20	37
1	G	416/455 (91%)	405 (97%)	11 (3%)	40	62
1	H	416/455 (91%)	404 (97%)	12 (3%)	37	59
1	I	417/455 (92%)	405 (97%)	12 (3%)	37	59
All	All	3340/3640 (92%)	3233 (97%)	107 (3%)	34	56

5 of 107 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	178	SER
1	F	485	VAL
1	I	216	LEU
1	F	241	VAL
1	F	369	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	343	HIS
1	H	510	GLN
1	G	344	ASN
1	H	365	GLN
1	I	163	GLN

5.3.3 RNA ⓘ

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 [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	538/569 (94%)	0.10	41 (7%)	20 19	17, 44, 92, 118	0
1	B	523/569 (91%)	-0.03	6 (1%)	78 77	21, 44, 74, 94	0
1	D	523/569 (91%)	-0.27	7 (1%)	75 74	16, 36, 68, 97	0
1	E	521/569 (91%)	-0.28	3 (0%)	85 85	19, 35, 59, 93	0
1	F	523/569 (91%)	0.17	6 (1%)	78 77	24, 51, 84, 104	0
1	G	523/569 (91%)	0.12	17 (3%)	49 47	21, 50, 80, 114	0
1	H	523/569 (91%)	-0.12	13 (2%)	58 55	20, 43, 75, 106	0
1	I	524/569 (92%)	-0.28	1 (0%)	91 92	21, 36, 62, 94	0
All	All	4198/4552 (92%)	-0.07	94 (2%)	62 59	16, 42, 79, 118	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	210	GLY	5.4
1	A	209	VAL	4.1
1	A	526	VAL	4.0
1	A	470	GLY	3.9
1	G	339	TYR	3.7

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 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.