wwPDB X-ray Structure Validation Summary Report (i)

Jun 15, 2020 – 10:34 pm BST

PDB ID	:	1G8M
Title	:	CRYSTAL STRUCTURE OF AVIAN ATIC, A BIFUNCTIONAL TRANSFORMYLASE AND CYCLOHYDROLASE ENZYME IN PURINE BIOSYNTHESIS AT 1.75 ANG. RESOLUTION
Authors	:	Greasley, S.E.; Horton, P.; Beardsley, G.P.; Benkovic, S.J.; Wilson, I.A.
Deposited on	:	2000-11-17
Resolution	:	1.75 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 (i) symbol.

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

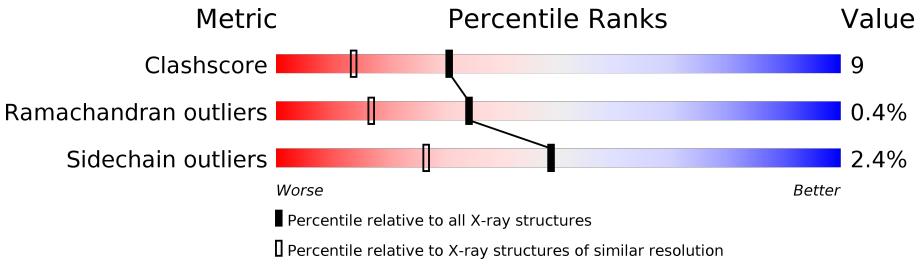
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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))
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	593	82% 17% ...
1	B	593	84% 14% ..

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9795 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 AICAR TRANSFORMYLASE-IMP CYCLOHYDROLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	590	Total	C	N	O	S	Se	0	5	0
			4516	2846	799	852	9	10			
1	B	590	Total	C	N	O	S	Se	0	2	0
			4509	2840	799	851	9	10			

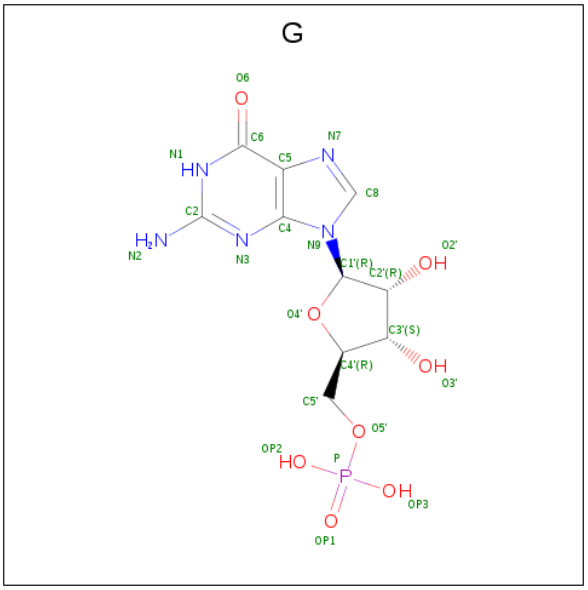
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	MSE	MET	CLONING ARTIFACT	UNP P31335
A	89	MSE	MET	CLONING ARTIFACT	UNP P31335
A	159	MSE	MET	CLONING ARTIFACT	UNP P31335
A	211	MSE	MET	CLONING ARTIFACT	UNP P31335
A	289	MSE	MET	CLONING ARTIFACT	UNP P31335
A	313	MSE	MET	CLONING ARTIFACT	UNP P31335
A	368	MSE	MET	CLONING ARTIFACT	UNP P31335
A	388	MSE	MET	CLONING ARTIFACT	UNP P31335
A	477	MSE	MET	CLONING ARTIFACT	UNP P31335
A	512	MSE	MET	CLONING ARTIFACT	UNP P31335
B	61	MSE	MET	CLONING ARTIFACT	UNP P31335
B	89	MSE	MET	CLONING ARTIFACT	UNP P31335
B	159	MSE	MET	CLONING ARTIFACT	UNP P31335
B	211	MSE	MET	CLONING ARTIFACT	UNP P31335
B	289	MSE	MET	CLONING ARTIFACT	UNP P31335
B	313	MSE	MET	CLONING ARTIFACT	UNP P31335
B	368	MSE	MET	CLONING ARTIFACT	UNP P31335
B	388	MSE	MET	CLONING ARTIFACT	UNP P31335
B	477	MSE	MET	CLONING ARTIFACT	UNP P31335
B	512	MSE	MET	CLONING ARTIFACT	UNP P31335

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total K 1 1	0	0
2	A	1	Total K 1 1	0	0

- Molecule 3 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: G) (formula: $C_{10}H_{14}N_5O_8P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 24 10 5 8 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	383	Total O 383 383	0	0
4	B	361	Total O 361 361	0	0

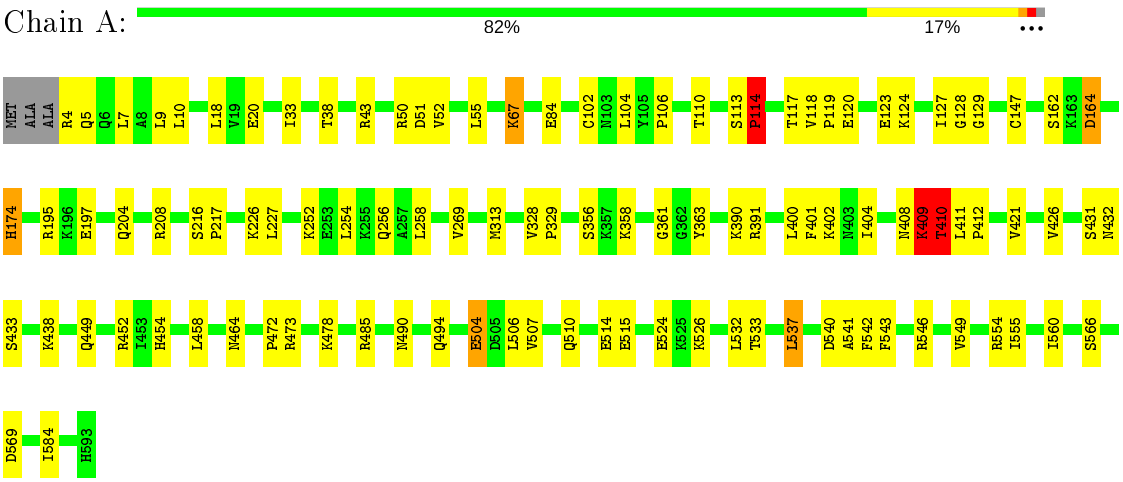
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

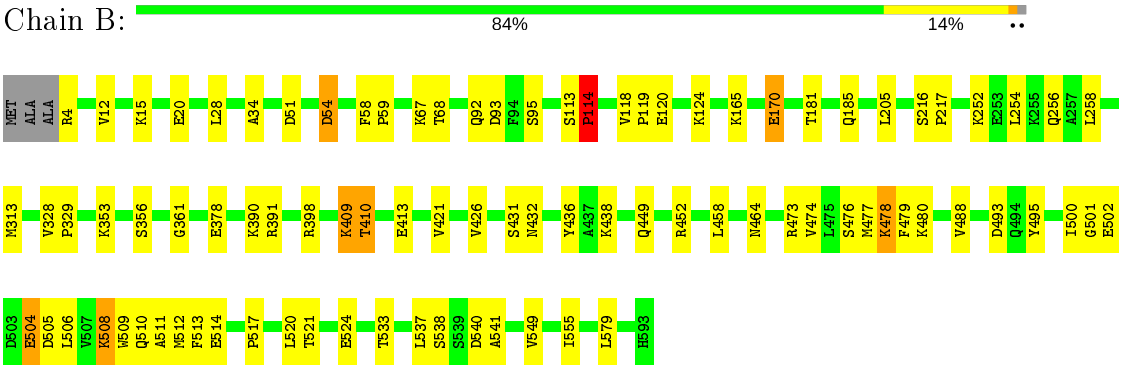
- Molecule 1: AICAR TRANSFORMYLASE-IMP CYCLOHYDROLASE

Chain A:



- Molecule 1: AICAR TRANSFORMYLASE-IMP CYCLOHYDROLASE

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	65.10Å 106.00Å 103.50Å 90.00° 108.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.75	Depositor
% Data completeness (in resolution range)	89.1 (50.00-1.75)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.200 , 0.216	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9795	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K

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	0.32	0/4615	0.61	1/6243 (0.0%)
1	B	0.33	1/4593 (0.0%)	0.59	0/6213
All	All	0.33	1/9208 (0.0%)	0.60	1/12456 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	504	GLU	CD-OE2	7.67	1.34	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	104	LEU	N-CA-C	5.41	125.61	111.00

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	4516	0	4566	92	0
1	B	4509	0	4552	77	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	24	0	12	4	0
4	A	383	0	0	15	0
4	B	361	0	0	6	0
All	All	9795	0	9130	167	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 9.

The worst 5 of 167 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:404:ILE:HD12	1:A:409:LYS:HG2	1.35	1.05
1:A:478:LYS:HG3	1:A:515:GLU:OE2	1.75	0.85
4:A:2099:HOH:O	1:B:390:LYS:HD2	1.77	0.85
1:A:404:ILE:CD1	1:A:409:LYS:HG2	2.08	0.83
1:A:504:GLU:OE1	1:A:507:VAL:HB	1.80	0.81

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	593/593 (100%)	574 (97%)	16 (3%)	3 (0%)	29	12
1	B	590/593 (100%)	571 (97%)	17 (3%)	2 (0%)	41	22
All	All	1183/1186 (100%)	1145 (97%)	33 (3%)	5 (0%)	34	17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	409	LYS

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Mol	Chain	Res	Type
1	A	410	THR
1	B	114	PRO
1	A	114	PRO
1	B	410	THR

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	488/475 (103%)	472 (97%)	16 (3%)	38 15
1	B	485/475 (102%)	478 (99%)	7 (1%)	67 52
All	All	973/950 (102%)	950 (98%)	23 (2%)	49 26

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	410	THR
1	A	472	PRO
1	B	478	LYS
1	A	433	SER
1	A	504	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	HIS
1	B	408	ASN
1	B	90	ASN
1	A	92	GLN
1	B	185	GLN

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 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.