



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 04:05 pm GMT

PDB ID : 4AF0
Title : Crystal structure of cryptococcal inosine monophosphate dehydrogenase
Authors : Valkov, E.; Stamp, A.; Morrow, C.A.; Kobe, B.; Fraser, J.A.
Deposited on : 2012-01-15
Resolution : 2.20 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	:	trunk28620
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)	:	recalc28949

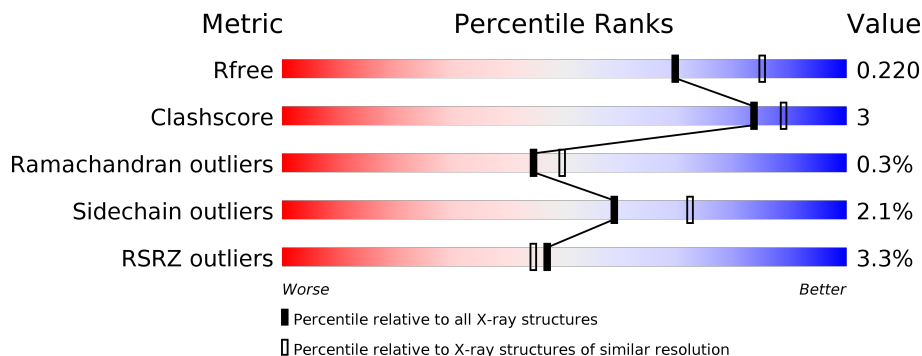
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	556	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>6%</div> <div>29%</div> </div> </div>
2	B	556	<div> <div>3%</div> <div> <div></div> <div>65%</div> <div>6%</div> <div>29%</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
5	SO4	B	1528	-	-	-	X
5	SO4	B	1529	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6526 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 INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			2955	1853	519	568	15			

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	EXPRESSION TAG	UNP E3P6S0
A	-10	ARG	-	EXPRESSION TAG	UNP E3P6S0
A	-9	GLY	-	EXPRESSION TAG	UNP E3P6S0
A	-8	SER	-	EXPRESSION TAG	UNP E3P6S0
A	-7	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-6	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-5	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-4	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-3	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-2	HIS	-	EXPRESSION TAG	UNP E3P6S0
A	-1	GLY	-	EXPRESSION TAG	UNP E3P6S0
A	0	SER	-	EXPRESSION TAG	UNP E3P6S0
A	501	ALA	GLY	CONFLICT	UNP E3P6S0

- Molecule 2 is a protein called INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	395	Total	C	N	O	S	0	0	0
			2954	1852	519	568	15			

There are 12 discrepancies between the modelled and reference sequences:

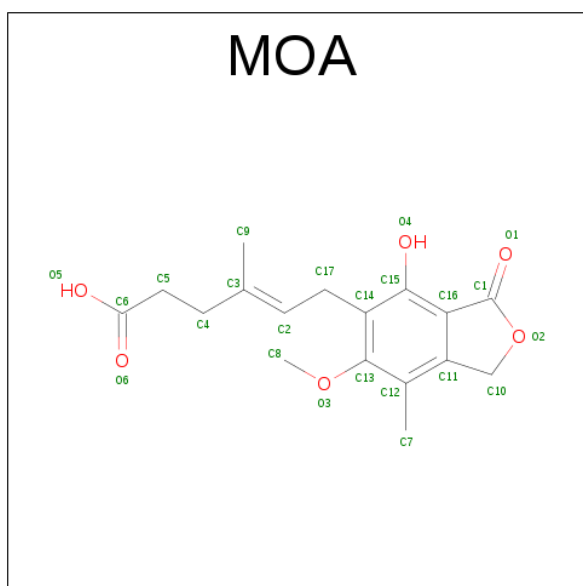
Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	MET	-	EXPRESSION TAG	UNP E3P6S0
B	-10	ARG	-	EXPRESSION TAG	UNP E3P6S0
B	-9	GLY	-	EXPRESSION TAG	UNP E3P6S0

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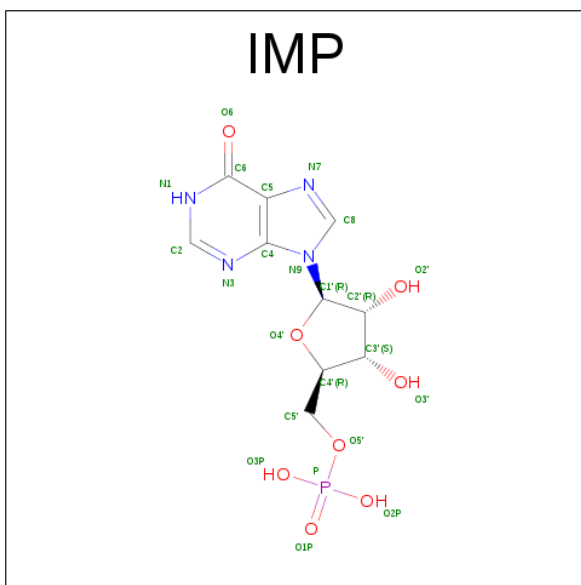
Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	SER	-	EXPRESSION TAG	UNP E3P6S0
B	-7	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-6	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-5	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-4	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-3	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-2	HIS	-	EXPRESSION TAG	UNP E3P6S0
B	-1	GLY	-	EXPRESSION TAG	UNP E3P6S0
B	0	SER	-	EXPRESSION TAG	UNP E3P6S0

- Molecule 3 is MYCOPHENOLIC ACID (three-letter code: MOA) (formula: $C_{17}H_{20}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			23	17	6		
3	B	1	Total	C	O	0	0
			23	17	6		

- Molecule 4 is INOSINIC ACID (three-letter code: IMP) (formula: $C_{10}H_{13}N_4O_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	4	8	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	4	8	1		

- Molecule 5 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	S	0	0
			5	4	1		
5	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	254	Total 254	O 254	0	0
6	B	261	Total 261	O 261	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, α , β , γ	149.63Å 149.63Å 122.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.44 – 2.20 47.44 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.1 (47.44-2.20) 99.1 (47.44-2.20)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.173 , 0.208 0.185 , 0.220	Depositor DCC
R_{free} test set	3429 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	27.2	Xtriage
Anisotropy	0.858	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.469 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6526	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: IMP, MOA, SO4

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	0.50	0/3007	0.66	0/4066
2	B	0.49	0/3006	0.67	0/4064
All	All	0.49	0/6013	0.66	0/8130

There are no bond length outliers.

There are no bond angle outliers.

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	2955	0	2945	18	0
2	B	2954	0	2943	16	0
3	A	23	0	19	0	0
3	B	23	0	19	1	0
4	A	23	0	11	0	0
4	B	23	0	11	1	0
5	B	10	0	0	0	0
6	A	254	0	0	0	0
6	B	261	0	0	0	0
All	All	6526	0	5948	34	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 3.

The worst 5 of 34 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:59:HIS:N	1:A:501:ALA:HB2	2.03	0.73
2:B:451:LEU:HD21	2:B:472:VAL:HG21	1.73	0.71
1:A:59:HIS:H	1:A:501:ALA:HB2	1.63	0.64
1:A:454:ALA:HB3	1:A:476:VAL:HG12	1.79	0.64
2:B:384:ILE:HD13	2:B:492:GLY:HA3	1.85	0.58

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	389/556 (70%)	371 (95%)	16 (4%)	2 (0%)	32	34
2	B	389/556 (70%)	375 (96%)	14 (4%)	0	100	100
All	All	778/1112 (70%)	746 (96%)	30 (4%)	2 (0%)	44	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	435	GLU
1	A	455	ALA

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	310/445 (70%)	306 (99%)	4 (1%)	73	85
2	B	310/445 (70%)	301 (97%)	9 (3%)	48	60
All	All	620/890 (70%)	607 (98%)	13 (2%)	59	72

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	351	MET
2	B	451	LEU
2	B	460	PHE
2	B	348	GLN
2	B	458	ARG

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

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](#)

6 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	MOA	A	1526	-	21,24,24	2.54	5 (23%)	30,34,34	2.99	10 (33%)
4	IMP	A	1527	-	21,25,25	3.16	9 (42%)	22,38,38	3.48	7 (31%)
3	MOA	B	1526	-	21,24,24	2.58	5 (23%)	30,34,34	3.15	13 (43%)
4	IMP	B	1527	-	21,25,25	3.11	9 (42%)	22,38,38	3.27	7 (31%)
5	SO4	B	1528	-	4,4,4	0.18	0	6,6,6	0.11	0
5	SO4	B	1529	-	4,4,4	0.18	0	6,6,6	0.15	0

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	MOA	A	1526	-	-	0/10/21/21	0/2/2/2
4	IMP	A	1527	-	-	0/6/26/26	0/3/3/3
3	MOA	B	1526	-	-	0/10/21/21	0/2/2/2
4	IMP	B	1527	-	-	0/6/26/26	0/3/3/3
5	SO4	B	1528	-	-	0/0/0/0	0/0/0/0
5	SO4	B	1529	-	-	0/0/0/0	0/0/0/0

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1526	MOA	C16-C1	-3.87	1.40	1.47
4	A	1527	IMP	C2'-C1'	-3.59	1.47	1.53
3	B	1526	MOA	C16-C1	-3.49	1.41	1.47
4	B	1527	IMP	C2'-C1'	-3.35	1.48	1.53
3	A	1526	MOA	O2-C1	-3.25	1.32	1.36

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1527	IMP	N3-C2-N1	-14.16	116.52	128.86
4	B	1527	IMP	N3-C2-N1	-13.09	117.46	128.86
3	B	1526	MOA	C10-O2-C1	-8.60	104.12	110.63
3	A	1526	MOA	C10-O2-C1	-6.97	105.36	110.63
3	A	1526	MOA	O1-C1-C16	-4.38	122.05	130.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1526	MOA	1	0
4	B	1527	IMP	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	395/556 (71%)	-0.31	10 (2%) 58 55	20, 33, 81, 102	0
2	B	395/556 (71%)	-0.25	16 (4%) 38 36	22, 33, 79, 124	0
All	All	790/1112 (71%)	-0.28	26 (3%) 47 44	20, 33, 81, 124	0

The worst 5 of 26 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	454	ALA	9.0
1	A	463	ALA	7.7
2	B	465	ALA	7.4
2	B	459	TYR	7.1
2	B	460	PHE	6.8

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
5	SO4	B	1529	5/5	0.87	0.23	3.65	114,114,115,116	0
5	SO4	B	1528	5/5	0.83	0.14	2.07	134,134,135,135	0
3	MOA	B	1526	23/23	0.97	0.11	-0.04	34,37,42,49	0
3	MOA	A	1526	23/23	0.97	0.11	-0.12	28,35,38,40	0
4	IMP	A	1527	23/23	0.98	0.09	-0.65	21,29,33,34	0
4	IMP	B	1527	23/23	0.99	0.09	-0.78	21,29,31,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.