

Full wwPDB X-ray Structure Validation Report (i)

Mar 5, 2024 – 06:27 AM EST

PDB ID	:	2CVP
Title	:	Crystal structure of mouse AMF
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Deposited on	:	2005-06-10
Resolution	:	1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

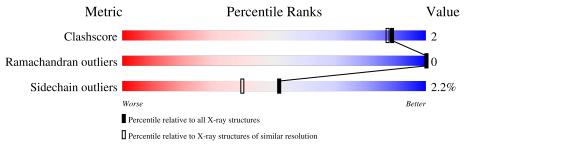
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\hbox{-}RAY\,DIFFRACTION$

The reported resolution of this entry is 1.80 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	Similar resolution
Metric	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain	
1	А	557	93%	7%
1	В	557	92%	8%



2CVP

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9541 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.

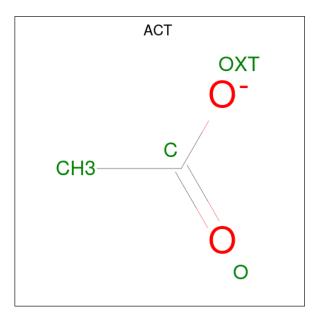
• Molecule 1 is a protein called Glucose-6-phosphate isomerase.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	557	Total	С	Ν	0	\mathbf{S}	0	0	0
	A	557	4416	2826	764	807	19	0	0	0
1	Р	557	Total	С	Ν	0	S	0	0	0
	D	557	4416	2826	764	807	19	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P06745
А	61	SER	ASN	conflict	UNP P06745
В	1	MET	-	initiating methionine	UNP P06745
В	61	SER	ASN	conflict	UNP P06745

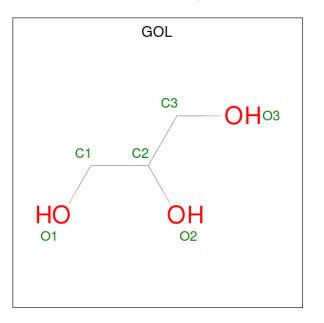
• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).





Mol	Chain	Residues	Ate	oms		ZeroOcc	AltConf
2	A	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0

• Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0

• Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	342	Total O 342 342	0	0
4	В	339	Total O 339 339	0	0

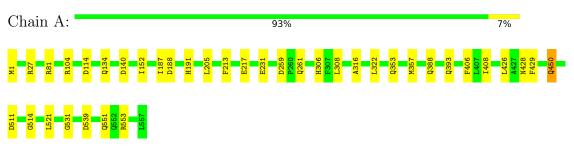


3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Glucose-6-phosphate isomerase



• Molecule 1: Glucose-6-phosphate isomerase

C	hε	aiı	n	B	•															9	2%												8%	-		
M1	D54		A72	K73	RA1		R104	D114		D161	P164	1176	-	F183	D188		K194	S198	F013	0171	E231	L246	K254	8275	1 280	H306	F307 L308	7101	A316	L322	P340	P383	<mark>0388</mark>	03 <mark>333</mark>	F406	L407
	1141/	L426	A427	N428	r429	A435		R446	L462	R479		D511	G514		E530	D539	167	FOOL																		



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	69.97Å 115.88Å 73.27 Å	Depositor			
a, b, c, α , β , γ	90.00° 101.76° 90.00°	Depositor			
Resolution (Å)	40.00 - 1.80	Depositor			
% Data completeness	98.0 (40.00-1.80)	Depositor			
(in resolution range)	30.0 (40.00-1.00)	Depositor			
R_{merge}	(Not available)	Depositor			
R_{sym}	(Not available)	Depositor			
Refinement program	REFMAC 5.1.24	Depositor			
R, R_{free}	0.181 , 0.219	Depositor			
Estimated twinning fraction	No twinning to report.	Xtriage			
Total number of atoms	9541	wwPDB-VP			
Average B, all atoms $(Å^2)$	17.0	wwPDB-VP			



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: ACT, GOL

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	B	ond angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.41	0/4525	0.65	6/6124~(0.1%)
1	В	0.41	0/4525	0.65	6/6124~(0.1%)
All	All	0.41	0/9050	0.65	12/12248~(0.1%)

There are no bond length outliers.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	В	511	ASP	CB-CG-OD2	7.01	124.61	118.30
1	А	511	ASP	CB-CG-OD2	6.77	124.39	118.30
1	А	188	ASP	CB-CG-OD2	6.20	123.88	118.30
1	В	188	ASP	CB-CG-OD2	6.08	123.77	118.30
1	В	539	ASP	CB-CG-OD2	5.97	123.67	118.30
1	В	161	ASP	CB-CG-OD2	5.38	123.14	118.30
1	А	140	ASP	CB-CG-OD2	5.37	123.13	118.30
1	А	259	ASP	CB-CG-OD2	5.34	123.11	118.30
1	А	539	ASP	CB-CG-OD2	5.26	123.03	118.30
1	В	54	ASP	CB-CG-OD2	5.21	122.99	118.30
1	А	114	ASP	CB-CG-OD2	5.12	122.91	118.30
1	В	114	ASP	CB-CG-OD2	5.12	122.91	118.30

All (12) bond angle outliers are listed below:

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	4416	0	4398	19	0
1	В	4416	0	4398	19	0
2	А	4	0	3	0	0
3	А	18	0	24	0	0
3	В	6	0	8	0	0
4	А	342	0	0	2	0
4	В	339	0	0	2	0
All	All	9541	0	8831	33	0

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.

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 2.

All (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 4 1	A +	Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
1:A:514:GLY:H	1:B:393:GLN:HE22	1.15	0.94	
1:B:306:HIS:HE1	1:B:316:ALA:H	1.12	0.94	
1:A:306:HIS:HE1	1:A:316:ALA:H	1.14	0.93	
1:A:393:GLN:HE22	1:B:514:GLY:H	1.24	0.84	
1:B:194:LYS:NZ	4:B:866:HOH:O	2.22	0.72	
1:A:514:GLY:N	1:B:393:GLN:HE22	1.93	0.62	
1:B:406:PHE:HB3	1:B:429:PHE:CE1	2.38	0.58	
1:A:152:ILE:HD12	1:A:205:LEU:HD23	1.86	0.57	
1:B:81:ARG:HD2	1:B:308:LEU:HA	1.87	0.57	
1:B:388:GLN:HE22	1:B:428:ASN:HB3	1.69	0.56	
1:A:187:ILE:HB	1:A:217:GLU:HG3	1.87	0.56	
1:B:306:HIS:CE1	1:B:316:ALA:H	2.05	0.55	
1:A:393:GLN:HE22	1:B:514:GLY:N	2.01	0.55	
1:B:72:ALA:HB2	1:B:322:LEU:HD21	1.92	0.51	
1:A:306:HIS:CE1	1:A:316:ALA:H	2.07	0.51	
1:A:450:GLN:HG3	4:A:1140:HOH:O	2.11	0.50	
1:B:73:LYS:HG3	1:B:312:LEU:HD12	1.97	0.46	
1:A:406:PHE:HB3	1:A:429:PHE:CE1	2.51	0.46	
1:A:353:GLN:O	1:A:357:MET:HB2	2.15	0.46	
1:A:388:GLN:HE22	1:A:428:ASN:HB3	1.80	0.45	
1:A:81:ARG:HD2	1:A:308:LEU:HA	1.98	0.45	
1:B:246:LEU:HD13	1:B:280:ILE:HA	1.98	0.45	
1:B:408:ILE:HD13	1:B:426:LEU:HD23	1.98	0.45	
1:A:531:GLY:O	1:A:553:ARG:NH2	2.51	0.44	

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
1:A:408:ILE:HD13	1:A:426:LEU:HD23	2.01	0.42	
1:B:164:PRO:HB2	1:B:183:PHE:CE2	2.55	0.42	
1:A:191:HIS:HD2	4:A:1125:HOH:O	2.02	0.42	
1:A:521:LEU:HD12	1:B:435:ALA:HB2	2.01	0.41	
1:B:275:SER:O	1:B:280:ILE:HB	2.20	0.41	
1:A:322:LEU:HD23	1:A:322:LEU:HA	1.96	0.41	
1:B:176:LYS:HB3	4:B:768:HOH:O	2.20	0.41	
1:A:187:ILE:HB	1:A:217:GLU:CG	2.49	0.40	
1:B:340:PRO:O	1:B:383:PRO:HA	2.21	0.40	

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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	Analysed Favoured Allowed		Outliers	Percentiles		
1	А	555/557~(100%)	540~(97%)	15 (3%)	0	100	100	
1	В	555/557~(100%)	542 (98%)	13~(2%)	0	100	100	
All	All	1110/1114 (100%)	1082~(98%)	28~(2%)	0	100	100	

There are no Ramachandran outliers to report.

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	Percenti	les
1	А	475/475~(100%)	466~(98%)	9~(2%)	57 46	5
1	В	475/475 (100%)	463 (98%)	12 (2%)	47 34	Ł
All	All	950/950~(100%)	929~(98%)	21 (2%)	52 39)

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	1	MET
1	А	27	ARG
1	А	104	ARG
1	А	134	GLN
1	А	213	PHE
1	А	231	GLU
1	А	261	GLN
1	А	450	GLN
1	А	551	GLN
1	В	1	MET
1	В	104	ARG
1	В	176	LYS
1	В	198	SER
1	В	213	PHE
1	В	231	GLU
1	В	254	LYS
1	В	417	ARG
1	В	446	ARG
1	В	462	LEU
1	В	472	ARG
1	В	530	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	47	ASN
1	А	58	ASN
1	А	134	GLN
1	А	305	GLN
1	А	306	HIS
1	А	388	GLN
1	А	393	GLN
1	А	397	GLN
1	А	475	ASN

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Mol	Chain	Res	Type
1	В	23	ASN
1	В	50	HIS
1	В	58	ASN
1	В	306	HIS
1	В	388	GLN
1	В	393	GLN
1	В	397	GLN
1	В	475	ASN

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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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	Mal Turna Chain Bag		Link	Bond lengths			Bond angles			
	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	GOL	А	704	-	$5,\!5,\!5$	0.35	0	$5,\!5,\!5$	0.40	0
3	GOL	В	703	-	$5,\!5,\!5$	0.40	0	$5,\!5,\!5$	0.25	0
2	ACT	А	801	-	3,3,3	0.75	0	3,3,3	1.41	0
3	GOL	А	701	-	$5,\!5,\!5$	0.36	0	$5,\!5,\!5$	0.38	0
3	GOL	А	702	-	$5,\!5,\!5$	0.35	0	$5,\!5,\!5$	0.39	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	GOL	А	704	-	-	2/4/4/4	-
3	GOL	В	703	-	-	0/4/4/4	-
3	GOL	А	701	-	-	2/4/4/4	-
3	GOL	А	702	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	А	704	GOL	O1-C1-C2-O2
3	А	702	GOL	O1-C1-C2-C3
3	А	704	GOL	O1-C1-C2-C3
3	А	701	GOL	O1-C1-C2-O2
3	А	702	GOL	O1-C1-C2-O2
3	A	701	GOL	O1-C1-C2-C3

There are no ring outliers.

No monomer is involved in short contacts.

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)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

