



# Full wwPDB X-ray Structure Validation Report i

Feb 28, 2014 – 05:17 AM GMT

PDB ID : 1D3V  
Title : CRYSTAL STRUCTURE OF THE BINUCLEAR MANGANESE METALLOENZYME ARGINASE COMPLEXED WITH 2(S)-AMINO-6-BORONO HEXANOICACID, AN L-ARGININE ANALOG  
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Deposited on : 1999-10-01  
Resolution : 1.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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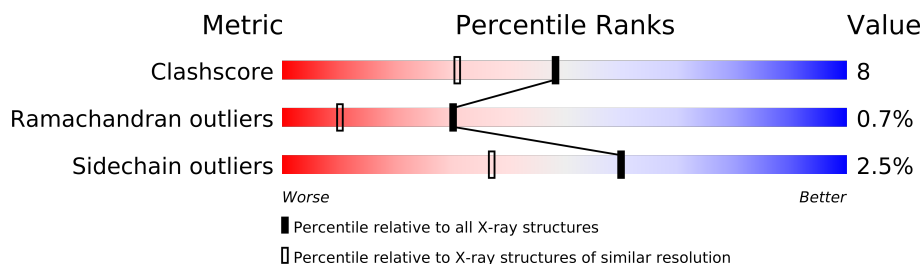
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.70 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	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	323	
1	B	323	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 5015 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

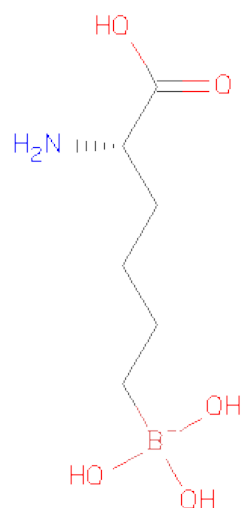
- Molecule 1 is a protein called PROTEIN (ARGINASE).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2344	1495	399	443	7			
1	B	308	Total	C	N	O	S	0	0	0
			2344	1495	399	443	7			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Mn	0	0
			2	2		
2	A	2	Total	Mn	0	0
			2	2		

- Molecule 3 is 2(S)-AMINO-6-BORONOHEXOICACID (three-letter code: ABH) (formula: C<sub>6</sub>H<sub>15</sub>BN<sub>1</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 13	B 1	C 6	N 1	O 5	0	0
3	B	1	Total 13	B 1	C 6	N 1	O 5	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	157	Total 157	O 157	0	0
4	B	140	Total 140	O 140	0	0



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.30Å 91.30Å 69.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.70	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.70)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.157 , 0.179	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5015	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	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: ABH, MN

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	0.41	0/2395	0.69	0/3251
1	B	0.45	2/2395 (0.1%)	0.67	1/3251 (0.0%)
All	All	0.43	2/4790 (0.0%)	0.68	1/6502 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	99	GLY	CA-C	5.54	1.60	1.51
1	B	98	GLY	C-N	-5.33	1.23	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	GLY	CA-C-N	5.10	126.40	116.20

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2344	0	2376	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2344	0	2376	36	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	13	0	12	0	0
3	B	13	0	12	0	0
4	A	157	0	0	1	0
4	B	140	0	0	0	0
All	All	5015	0	4776	74	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (74) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:7:PRO:HG2	1:B:92:THR:HG22	1.54	0.88
1:A:211:VAL:O	1:A:215:THR:HG23	1.77	0.84
1:B:307:LYS:H	1:B:311:ASN:HD21	1.30	0.79
1:B:117:ASP:O	1:B:225:ARG:HD2	1.86	0.76
1:A:7:PRO:HG2	1:A:92:THR:HG22	1.67	0.76
1:B:211:VAL:O	1:B:215:THR:HG23	1.86	0.75
1:A:15:PHE:CZ	1:A:17:LYS:HB2	2.24	0.73
1:A:307:LYS:H	1:A:311:ASN:HD21	1.34	0.72
1:B:244:THR:HG22	1:B:277:GLU:O	1.91	0.70
1:A:117:ASP:O	1:A:225:ARG:HD2	1.91	0.70
1:B:224:LYS:N	1:B:224:LYS:HE3	2.07	0.69
1:A:33:LYS:HD3	4:A:628:HOH:O	1.92	0.68
1:B:15:PHE:CZ	1:B:17:LYS:HB2	2.29	0.68
1:A:198:PHE:CE1	1:A:215:THR:HG22	2.28	0.68
1:A:180:ARG:NH2	1:A:235:GLY:O	2.29	0.66
1:A:22:GLY:O	1:A:25:GLU:HG3	2.00	0.62
1:A:75:LYS:O	1:A:79:GLN:HG3	2.00	0.62
1:A:37:VAL:HG12	1:A:41:LYS:HE3	1.81	0.62
1:B:180:ARG:NH2	1:B:235:GLY:O	2.33	0.61
1:A:143:GLN:N	1:A:144:PRO:CD	2.64	0.60
1:B:143:GLN:N	1:B:144:PRO:CD	2.65	0.60
1:B:75:LYS:O	1:B:79:GLN:HG3	2.02	0.60
1:B:258:LEU:O	1:B:262:GLU:HG3	2.02	0.59
1:A:6:LYS:HD2	1:A:91:GLY:O	2.04	0.58
1:A:143:GLN:N	1:A:144:PRO:HD2	2.18	0.58
1:A:56:VAL:HG22	1:A:79:GLN:NE2	2.21	0.56
1:A:258:LEU:O	1:A:262:GLU:HG3	2.04	0.56
1:A:224:LYS:N	1:A:224:LYS:HE3	2.21	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:187:HIS:O	1:A:191:LYS:HG2	2.05	0.56
1:A:56:VAL:HG23	1:A:56:VAL:O	2.06	0.55
1:B:143:GLN:N	1:B:144:PRO:HD2	2.22	0.55
1:B:56:VAL:HG23	1:B:56:VAL:O	2.08	0.54
1:B:56:VAL:HG22	1:B:79:GLN:NE2	2.24	0.53
1:B:7:PRO:CG	1:B:92:THR:HG22	2.33	0.52
1:B:118:LEU:HD12	1:B:118:LEU:C	2.30	0.52
1:A:89:LYS:NZ	1:A:89:LYS:HB2	2.25	0.52
1:A:32:ARG:NH1	1:A:52:ASP:OD1	2.44	0.50
1:B:59:PRO:HG2	1:B:60:ASN:H	1.76	0.50
1:B:187:HIS:O	1:B:191:LYS:HG2	2.11	0.50
1:A:56:VAL:H	1:A:79:GLN:HE22	1.59	0.50
1:A:222:ARG:O	1:A:223:LYS:HD3	2.12	0.49
1:B:32:ARG:NH1	1:B:52:ASP:OD1	2.47	0.48
1:B:64:PHE:O	1:B:65:GLN:HB2	2.14	0.48
1:A:109:SER:O	1:A:113:ARG:HG3	2.14	0.47
1:A:7:PRO:CG	1:A:92:THR:HG22	2.42	0.47
1:A:152:LEU:O	1:A:155:LYS:HG2	2.15	0.47
1:B:273:LEU:HD22	1:B:274:ASP:N	2.30	0.46
1:B:223:LYS:C	1:B:224:LYS:HE3	2.35	0.46
1:A:143:GLN:H	1:A:144:PRO:CD	2.25	0.46
1:A:285:THR:OG1	1:A:288:GLU:HG3	2.15	0.46
1:B:143:GLN:H	1:B:144:PRO:CD	2.26	0.46
1:A:223:LYS:C	1:A:224:LYS:HE3	2.36	0.46
1:B:156:PHE:HB2	1:B:157:PRO:HD2	1.98	0.46
1:B:6:LYS:HD2	1:B:91:GLY:O	2.15	0.45
1:B:198:PHE:CE1	1:B:215:THR:HG22	2.51	0.45
1:A:117:ASP:O	1:A:225:ARG:CD	2.62	0.45
1:A:37:VAL:CG1	1:A:41:LYS:HE3	2.47	0.45
1:A:149:LEU:HD12	1:A:152:LEU:HD22	1.99	0.45
1:B:22:GLY:O	1:B:25:GLU:HG3	2.18	0.44
1:B:69:ASN:O	1:B:73:VAL:HG23	2.18	0.44
1:A:89:LYS:NZ	1:A:89:LYS:CB	2.82	0.43
1:B:222:ARG:O	1:B:223:LYS:HD3	2.18	0.43
1:A:149:LEU:HD11	1:A:195:ILE:HD11	1.99	0.42
1:A:118:LEU:C	1:A:118:LEU:HD12	2.39	0.42
1:B:86:GLU:O	1:B:89:LYS:HB3	2.20	0.42
1:B:287:GLU:OE2	1:B:291:ARG:NH2	2.51	0.42
1:A:152:LEU:C	1:A:155:LYS:HG2	2.39	0.42
1:A:244:THR:HG22	1:A:277:GLU:O	2.19	0.42
1:B:56:VAL:H	1:B:79:GLN:HE22	1.67	0.41
1:B:273:LEU:CD2	1:B:274:ASP:N	2.83	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:155:LYS:HA	1:B:155:LYS:HD3	1.91	0.41
1:B:10:ILE:CD1	1:B:10:ILE:N	2.84	0.41
1:A:156:PHE:HB2	1:A:157:PRO:HD2	2.03	0.41
1:B:58:VAL:HA	1:B:59:PRO:HD2	1.89	0.40

There are no symmetry-related clashes.

## 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	306/323 (95%)	295 (96%)	9 (3%)	2 (1%)	30	10
1	B	306/323 (95%)	298 (97%)	6 (2%)	2 (1%)	30	10
All	All	612/646 (95%)	593 (97%)	15 (2%)	4 (1%)	30	10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	143	GLN
1	A	180	ARG
1	B	143	GLN
1	B	180	ARG

### 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	258/273 (94%)	252 (98%)	6 (2%)	63	41
1	B	258/273 (94%)	251 (97%)	7 (3%)	57	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	516/546 (94%)	503 (98%)	13 (2%)	60	37

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	ARG
1	A	52	ASP
1	A	141	HIS
1	A	152	LEU
1	A	244	THR
1	A	273	LEU
1	B	48	ARG
1	B	52	ASP
1	B	141	HIS
1	B	152	LEU
1	B	224	LYS
1	B	244	THR
1	B	273	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	79	GLN
1	A	311	ASN
1	B	65	GLN
1	B	79	GLN
1	B	88	GLN
1	B	115	HIS
1	B	311	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	ABH	A	551	2	12,12,12	0.56	0	13,16,16	1.44	3 (23%)
3	ABH	B	552	2	12,12,12	0.53	0	13,16,16	1.36	3 (23%)

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	ABH	A	551	2	-	0/9/12/12	0/0/0/0
3	ABH	B	552	2	-	0/9/12/12	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	551	ABH	C-CA-N	-3.15	104.16	109.36
3	B	552	ABH	O-C-CA	2.97	126.94	118.36
3	A	551	ABH	O-C-CA	2.88	126.69	118.36
3	B	552	ABH	OT-C-CA	-2.82	110.56	116.88
3	A	551	ABH	OT-C-CA	-2.69	110.85	116.88
3	B	552	ABH	C-CA-N	-2.45	105.31	109.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.