



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1P8Q / pdb_00001p8q
Title : Structural and Functional Importance of First-Shell Metal Ligands in the Binuclear Cluster of Arginase I.
Authors : Cama, E.; Emig, F.A.; Ash, D.E.; Christianson, D.W.
Deposited on : 2003-05-07
Resolution : 2.95 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

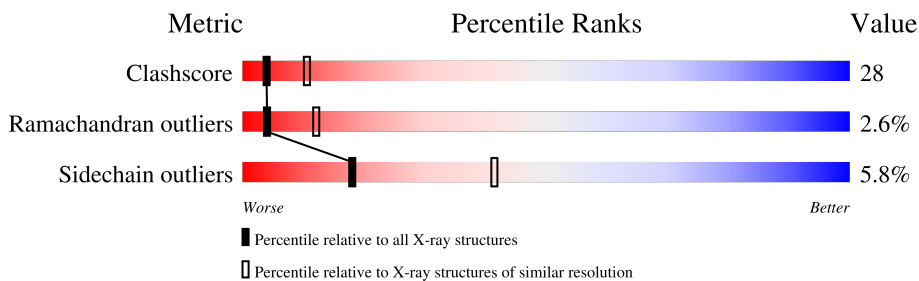
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	314	52% 41% 7%
1	B	314	52% 42% 5%
1	C	314	51% 42% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7262 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 Arginase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2397	1529	405	456	7			
1	B	314	Total	C	N	O	S	0	0	0
			2397	1529	405	456	7			
1	C	314	Total	C	N	O	S	0	0	0
			2397	1529	405	456	7			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	234	GLU	ASP	engineered mutation	UNP P07824
B	234	GLU	ASP	engineered mutation	UNP P07824
C	234	GLU	ASP	engineered mutation	UNP P07824

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is water.

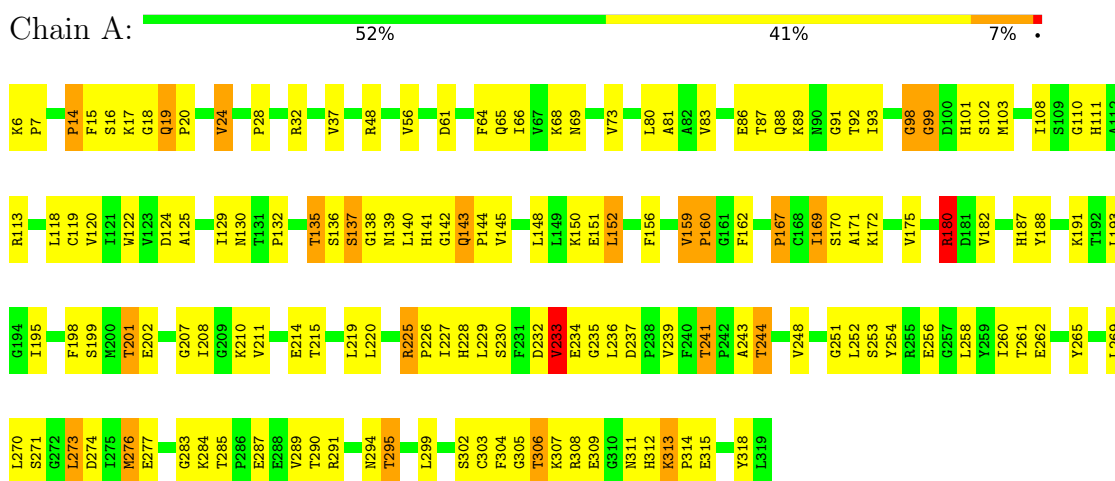
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	O	0	0
			13	13		
4	B	20	Total	O	0	0
			20	20		
4	C	14	Total	O	0	0
			14	14		

3 Residue-property plots

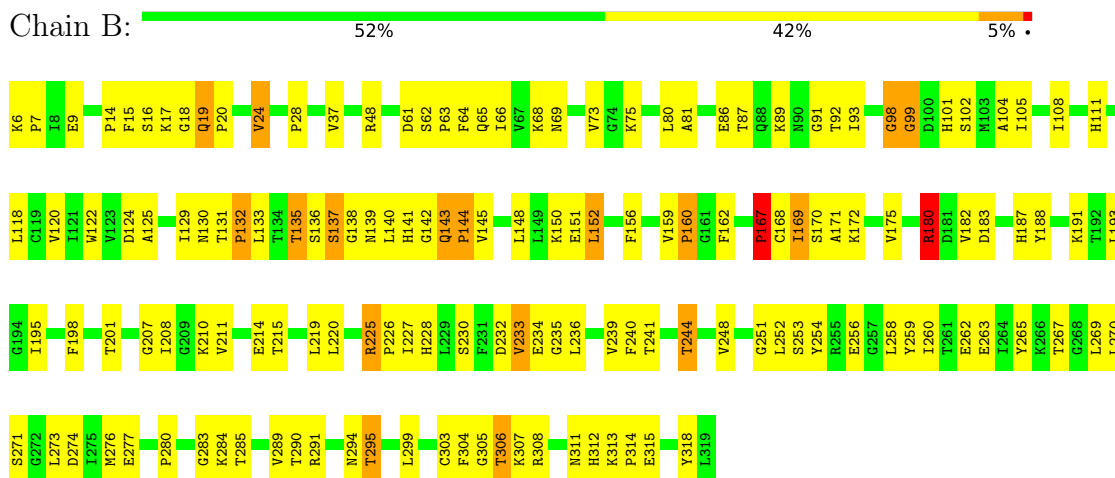
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Arginase 1



• Molecule 1: Arginase 1



• Molecule 1: Arginase 1



K6	P7	T8	E9	A13	F14	F15	S16	K17	G18	Q19	P20	V24	P28	R32	V37	R48	D52	D61	F64	Q65	I66	I67	K68	N69	P70	V73	V83	E86	T87	Q88	K89	I90	G91	T92	I93	G98	G99	D100	H101	S102	M103	A104	I105	I108						
H111	G114	I115	A112	L118	C119	V120	I121	W122	V123	D124	A125	I129	N130	T131	T135	S136	S137	G138	N139	L140	H141	G142	Q143	P144	V145	L148	I149	K150	E151	L152	F156	V159	P160	G161	F162	P167	C168	I169	S170	A171	K172	V175	R180	H187	Y188	I189	I190	K191	T192	L193
G194	I195	K196	Y197	F198	S199	M200	T201	E202	K205	L206	G207	K210	V211	E214	T215	L219	L220	R225	P226	I227	H228	L229	S230	F231	D232	V233	E234	G235	L236	V239	F240	T241	T244	V248	G251	L252	S253	Y254	R255	E256	G257	L258	T261	E262	Y265	L269	L270			
S271	G272	L273	D274	I275	M276	E277	G283	K284	T285	P286	E287	E288	V289	T290	R291	N294	T295	L299	S302	C303	F304	G305	T306	K307	R308	N311	H312	K313	P314	E315	T316	D317	Y318	L319																

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	88.33Å 88.33Å 111.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.95	Depositor
% Data completeness (in resolution range)	84.7 (30.00-2.95)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.262 , 0.287	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7262	wwPDB-VP
Average B, all atoms (Å ²)	67.0	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: GOL, 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	0.55	1/2450 (0.0%)	1.03	13/3326 (0.4%)
1	B	0.60	1/2450 (0.0%)	1.05	12/3326 (0.4%)
1	C	0.54	0/2450	1.03	15/3326 (0.5%)
All	All	0.56	2/7350 (0.0%)	1.04	40/9978 (0.4%)

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	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	14	PRO	CA-C	-6.01	1.43	1.52
1	A	233	VAL	CA-C	5.75	1.60	1.52

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	136	SER	N-CA-C	-9.49	101.83	113.41
1	C	136	SER	N-CA-C	-7.45	103.81	113.12
1	B	159	VAL	CA-C-N	6.58	128.07	119.84
1	B	159	VAL	C-N-CA	6.58	128.07	119.84
1	A	159	VAL	CA-C-N	6.20	127.59	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	98	GLY	Peptide
1	B	98	GLY	Peptide
1	C	98	GLY	Peptide

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	2397	0	2422	141	0
1	B	2397	0	2422	135	0
1	C	2397	0	2422	143	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	6	0	8	2	0
3	B	6	0	8	3	0
3	C	6	0	8	1	0
4	A	13	0	0	2	0
4	B	20	0	0	5	0
4	C	14	0	0	2	0
All	All	7262	0	7290	407	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 28.

The worst 5 of 407 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:B:140:LEU:O	1:B:144:PRO:HD3	1.71	0.91
1:B:135:THR:HB	1:B:137:SER:O	1.76	0.85
1:C:135:THR:HB	1:C:137:SER:O	1.76	0.85
1:A:135:THR:HB	1:A:137:SER:O	1.77	0.85
1:B:169:ILE:HD13	1:B:169:ILE:H	1.45	0.82

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	312/314 (99%)	277 (89%)	27 (9%)	8 (3%)	4	12
1	B	312/314 (99%)	273 (88%)	31 (10%)	8 (3%)	4	12
1	C	312/314 (99%)	272 (87%)	32 (10%)	8 (3%)	4	12
All	All	936/942 (99%)	822 (88%)	90 (10%)	24 (3%)	4	12

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	VAL
1	B	233	VAL
1	C	233	VAL
1	A	99	GLY
1	B	99	GLY

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	264/264 (100%)	249 (94%)	15 (6%)	18	42
1	B	264/264 (100%)	247 (94%)	17 (6%)	16	38
1	C	264/264 (100%)	250 (95%)	14 (5%)	20	45
All	All	792/792 (100%)	746 (94%)	46 (6%)	18	41

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	244	THR
1	C	135	THR
1	B	273	LEU
1	C	14	PRO
1	C	169	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	294	ASN
1	B	311	ASN
1	C	311	ASN
1	C	139	ASN
1	C	294	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 6 are monoatomic - leaving 3 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	GOL	C	1002	-	5,5,5	1.12	0	5,5,5	0.43	0
3	GOL	B	1001	-	5,5,5	1.04	0	5,5,5	0.37	0
3	GOL	A	1000	-	5,5,5	1.09	0	5,5,5	0.42	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	C	1002	-	-	2/4/4/4	-
3	GOL	B	1001	-	-	0/4/4/4	-
3	GOL	A	1000	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1000	GOL	C1-C2-C3-O3
3	C	1002	GOL	C1-C2-C3-O3
3	C	1002	GOL	O2-C2-C3-O3
3	A	1000	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1002	GOL	1	0
3	B	1001	GOL	3	0
3	A	1000	GOL	2	0

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 [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.