



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 11:15 PM UTC

PDB ID : 1T5G / pdb_00001t5g
Title : Arginase-F2-L-Arginine complex
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Deposited on : 2004-05-04
Resolution : 2.40 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

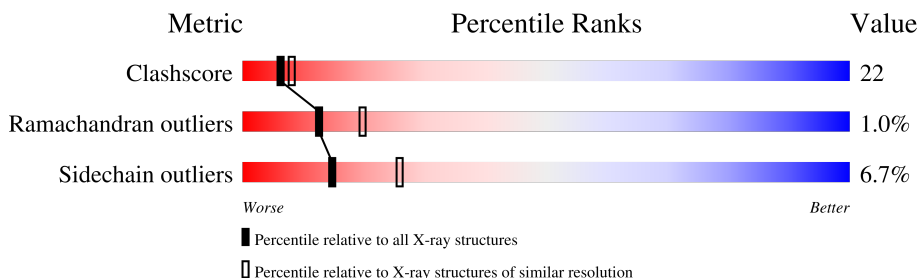
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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	56% 38% 6%
1	B	314	57% 38% 5%
1	C	314	56% 39% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7300 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
			2384	1523	402	455	4			
1	B	314	Total	C	N	O	S	0	0	0
			2384	1523	402	455	4			
1	C	314	Total	C	N	O	S	0	0	0
			2384	1523	402	455	4			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	CYS	GLN	engineered mutation	UNP P07824
A	119	ALA	CYS	engineered mutation	UNP P07824
A	141	ALA	HIS	engineered mutation	UNP P07824
A	168	ALA	CYS	engineered mutation	UNP P07824
A	303	ALA	CYS	engineered mutation	UNP P07824
B	19	CYS	GLN	engineered mutation	UNP P07824
B	119	ALA	CYS	engineered mutation	UNP P07824
B	141	ALA	HIS	engineered mutation	UNP P07824
B	168	ALA	CYS	engineered mutation	UNP P07824
B	303	ALA	CYS	engineered mutation	UNP P07824
C	19	CYS	GLN	engineered mutation	UNP P07824
C	119	ALA	CYS	engineered mutation	UNP P07824
C	141	ALA	HIS	engineered mutation	UNP P07824
C	168	ALA	CYS	engineered mutation	UNP P07824
C	303	ALA	CYS	engineered mutation	UNP P07824

- Molecule 2 is FLUORIDE ION (CCD ID: F) (formula: F).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	F	0	0
			2	2		

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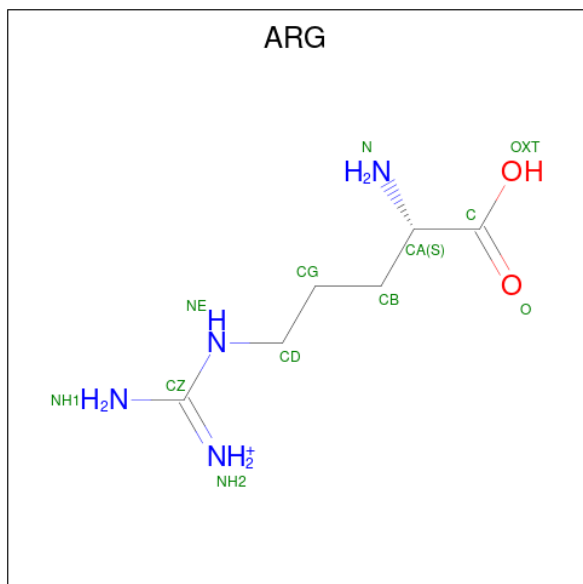
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	F	0	0
			2	2		
2	C	2	Total	F	0	0
			2	2		

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

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

- Molecule 4 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			12	6	4	2		
4	B	1	Total	C	N	O	0	0
			12	6	4	2		
4	C	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 5 is water.

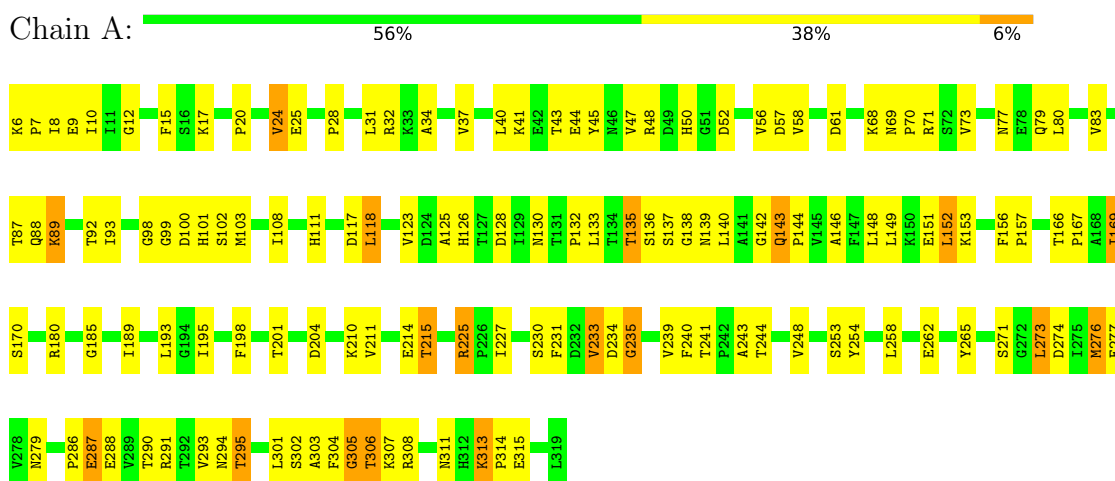
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	30	Total 30	O 30	0	0
5	B	32	Total 32	O 32	0	0
5	C	38	Total 38	O 38	0	0

3 Residue-property plots

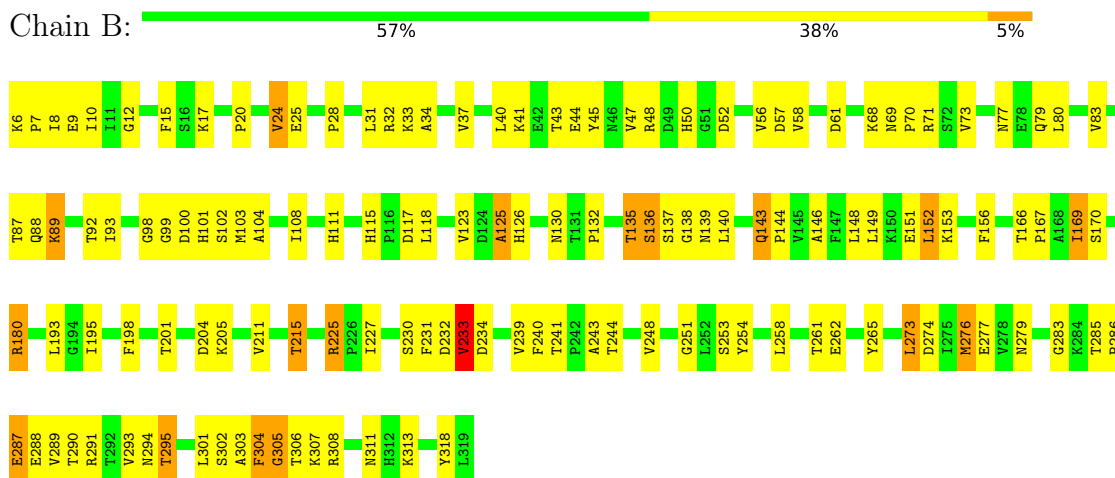
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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	I8	E9	G12	F15	S16	K17	P20	V24	E25	P28	L31	R32	K33	A34	G35	L36	V37	E38	K39	L40	K41	E42	T43	E44	Y45	N46	V47	R48	D49	H50	G51	D52	D57	V58	D61	K68	N69	P70	R71	S72	V73	Q79	L80	V83	T87	Q88		
K89	T92	I93	G99	D100	H101	S102	M103	I108	H111	D117	L118	V123	D124	A125	H126	T127	D128	I129	N130	T131	P132	L133	T134	T135	S136	S137	G138	N139	L140	Q143	P144	V145	A146	F147	L148	L149	K150	E151	L152	K153	F156	P157	T166	P167	A168	I169	S170	L179	R180
D183	P184	G185	E186	H187	Y188	I189	L193	G194	I195	F198	T201	D204	K210	V211	E214	T215	R225	P226	I227	S230	F231	D232	V233	D234	G235	V239	F240	T241	P242	A243	T244	V248	S253	Y254	L258	T261	E262	Y265	S271	G272	L273	D274	I275						
M276	E277	V278	N279	G283	E287	E288	V289	T290	R291	T292	V293	N294	T295	L301	F304	G305	T306	K307	R308	N311	H312	K313	P314	E315	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	87.72Å 87.72Å 104.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	27.69 – 2.40	Depositor
% Data completeness (in resolution range)	95.0 (27.69-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.228 , 0.254	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7300	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: MN, F

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	0.51	0/2436	0.99	9/3309 (0.3%)
1	B	0.50	0/2436	0.99	11/3309 (0.3%)
1	C	0.54	0/2436	1.00	9/3309 (0.3%)
All	All	0.52	0/7308	0.99	29/9927 (0.3%)

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	235	GLY	N-CA-C	-8.06	104.67	114.66
1	A	235	GLY	N-CA-C	-7.16	105.79	114.66
1	C	153	LYS	CD-CE-NZ	6.87	133.89	111.90
1	B	305	GLY	N-CA-C	6.85	121.81	113.79
1	A	305	GLY	N-CA-C	6.58	121.49	113.79

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 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	2384	0	2412	108	0
1	B	2384	0	2412	115	0
1	C	2384	0	2412	114	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	1	0
2	B	2	0	0	1	0
2	C	2	0	0	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
4	A	12	0	12	0	0
4	B	12	0	12	0	0
4	C	12	0	12	0	0
5	A	30	0	0	3	0
5	B	32	0	0	5	0
5	C	38	0	0	6	0
All	All	7300	0	7272	322	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 22.

The worst 5 of 322 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:C:146:ALA:HA	1:C:152:LEU:HD23	1.55	0.89
1:A:146:ALA:HA	1:A:152:LEU:HD23	1.54	0.88
1:B:146:ALA:HA	1:B:152:LEU:HD23	1.55	0.87
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

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%)	289 (93%)	21 (7%)	2 (1%)	21	32
1	B	312/314 (99%)	292 (94%)	16 (5%)	4 (1%)	9	14
1	C	312/314 (99%)	291 (93%)	18 (6%)	3 (1%)	12	20
All	All	936/942 (99%)	872 (93%)	55 (6%)	9 (1%)	12	20

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	233	VAL
1	A	44	GLU
1	B	44	GLU
1	B	143	GLN
1	C	44	GLU

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	259/260 (100%)	242 (93%)	17 (7%)	15	26
1	B	259/260 (100%)	243 (94%)	16 (6%)	16	29
1	C	259/260 (100%)	243 (94%)	16 (6%)	16	29
All	All	777/780 (100%)	728 (94%)	49 (6%)	15	29

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	286	PRO
1	C	87	THR
1	B	287	GLU
1	B	313	LYS
1	C	118	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	294	ASN
1	C	311	ASN
1	A	311	ASN
1	B	311	ASN
1	C	88	GLN

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 15 ligands modelled in this entry, 12 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	$\# Z > 2$
4	ARG	B	1001	-	10,11,11	1.14	1 (10%)	9,13,13	0.66	0
4	ARG	A	1000	-	10,11,11	1.16	1 (10%)	9,13,13	0.72	0
4	ARG	C	1002	-	10,11,11	1.17	1 (10%)	9,13,13	0.57	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
4	ARG	B	1001	-	-	4/11/11/11	-
4	ARG	A	1000	-	-	4/11/11/11	-
4	ARG	C	1002	-	-	4/11/11/11	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1000	ARG	CD-NE	2.30	1.51	1.46
4	B	1001	ARG	CD-NE	2.10	1.50	1.46
4	C	1002	ARG	CD-NE	2.04	1.50	1.46

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1002	ARG	NE-CD-CG-CB
4	B	1001	ARG	NE-CD-CG-CB
4	A	1000	ARG	NE-CD-CG-CB
4	A	1000	ARG	N-CA-CB-CG
4	B	1001	ARG	N-CA-CB-CG

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.