



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 01:43 AM UTC

PDB ID : 1T4S / pdb_00001t4s
Title : arginase-L-valine complex
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Deposited on : 2004-04-30
Resolution : 2.80 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

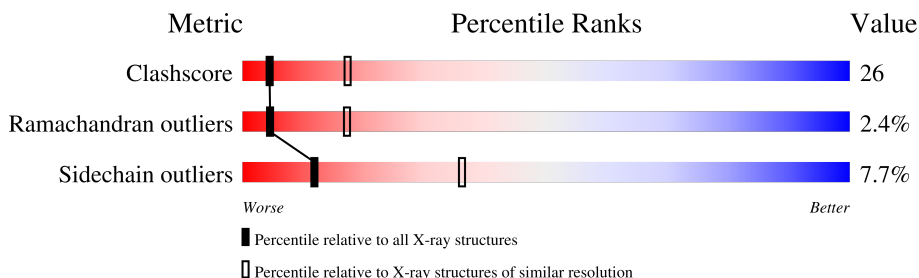
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	314	
1	B	314	
1	C	314	

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
3	VAL	A	1000	-	X	-	-
3	VAL	B	1001	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	VAL	C	1002	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7249 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.

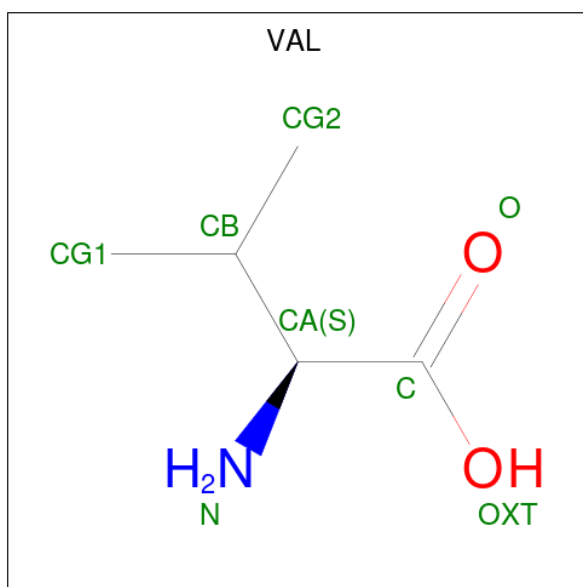
- Molecule 1 is a protein called Arginase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2396	1528	405	456	7			
1	B	314	Total	C	N	O	S	0	0	0
			2396	1528	405	456	7			
1	C	314	Total	C	N	O	S	0	0	0
			2396	1528	405	456	7			

- 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 VALINE (CCD ID: VAL) (formula: C₅H₁₁NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	5	1	2		
3	B	1	Total	C	N	O	0	0
			8	5	1	2		
3	C	1	Total	C	N	O	0	0
			8	5	1	2		

- Molecule 4 is water.

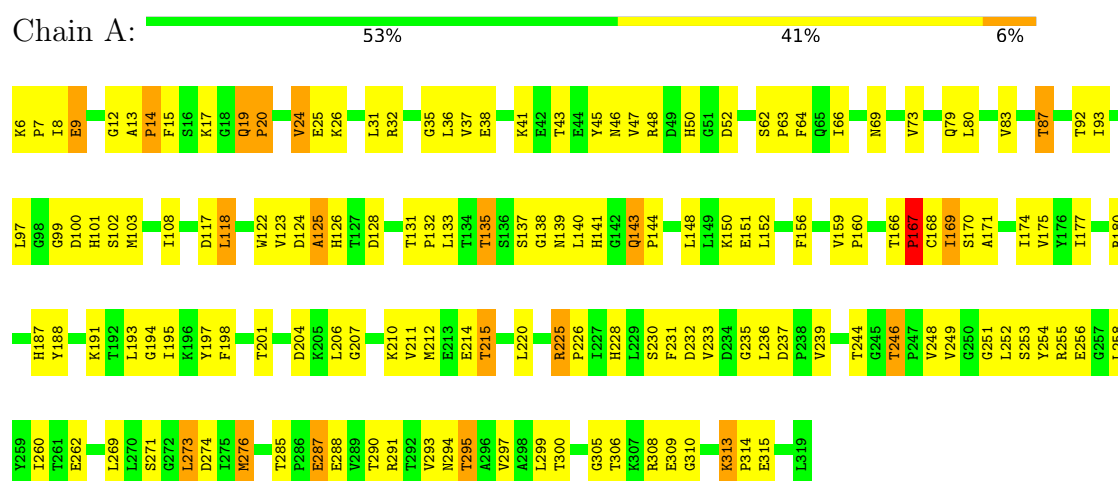
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	10	Total	O	0	0
			10	10		
4	B	14	Total	O	0	0
			14	14		
4	C	7	Total	O	0	0
			7	7		

3 Residue-property plots

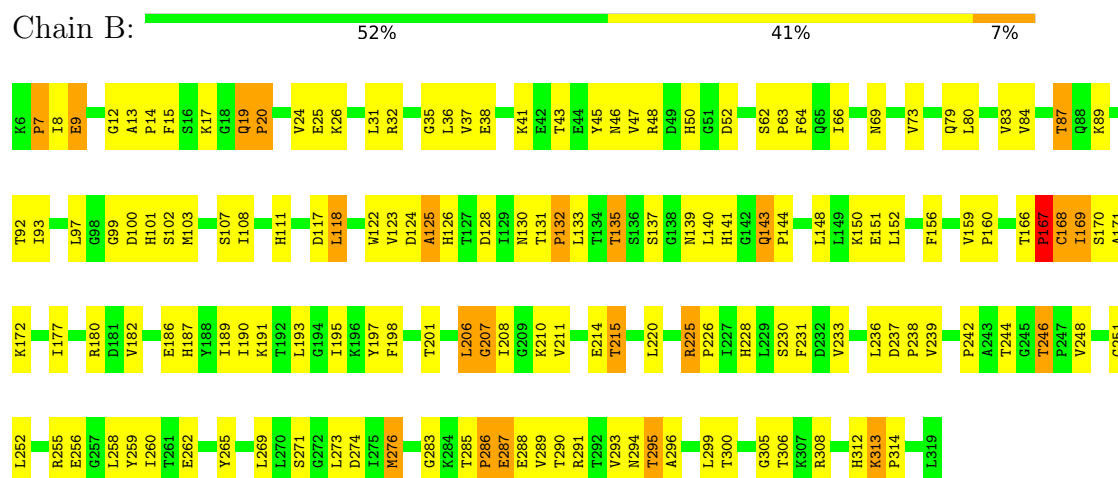
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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	A13	P14	F15	S16	K17	G18	Q19	P20	V24	E25	K26	G27	P28	L31	R32	G35	L36	V37	E38	K41	Y45	N46	V47	R48	D49	H50	G51	D52	F64	Q65	I66	N69	V73	Q79	L80	V83	T87	T92	I93	L97	G98						
G99	D100	H101	S102	M103	I108	H111	H111	D117	L118	V123	D124	A125	H126	T127	D128	T131	P132	L133	T134	T135	S136	G138	N139	L140	H141	G142	Q143	P144	L148	L149	K150	E151	L152	F156	V159	P160	G161	W164	V165	T166	P167	C168	I169	S170	A171	I174	V175	R180			
I190	K191	T192	L193	G194	I195	K196	Y197	F198	T201	D204	K205	L206	G207	I208	G209	K210	V211	E214	T215	L220	G221	R222	R225	H228	L229	S230	F231	D232	V233	D234	G235	L236	D237	P238	V239	T244	G245	T246	P247	V248	V249	G250	G251	L252	S253	Y254	R255	E256	G257	L258	Y259
L260	T261	E262	L269	L270	S271	G272	L273	D274	I275	M276	G283	K284	T285	P286	E287	E288	V289	T290	R291	T292	V293	N294	T295	L299	F304	G305	T306	K307	R308	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	87.80Å 87.80Å 110.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.74 – 2.80	Depositor
% Data completeness (in resolution range)	95.7 (28.74-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.258 , 0.292	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7249	wwPDB-VP
Average B, all atoms (Å ²)	86.0	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: 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	0.54	0/2449	1.04	9/3325 (0.3%)
1	B	0.58	0/2449	1.08	12/3325 (0.4%)
1	C	0.64	1/2449 (0.0%)	1.08	12/3325 (0.4%)
All	All	0.59	1/7347 (0.0%)	1.07	33/9975 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	138	GLY	N-CA	13.28	1.64	1.45

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	138	GLY	N-CA-C	-12.47	83.62	113.18
1	A	20	PRO	N-CA-C	8.17	124.56	114.35
1	C	137	SER	CA-C-N	-7.88	105.97	121.41
1	C	137	SER	C-N-CA	-7.88	105.97	121.41
1	B	20	PRO	N-CA-C	7.86	124.18	114.35

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	2396	0	2420	134	0
1	B	2396	0	2420	131	0
1	C	2396	0	2420	137	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
3	A	8	0	8	1	0
3	B	8	0	8	1	0
3	C	8	0	8	1	0
4	A	10	0	0	2	0
4	B	14	0	0	3	0
4	C	7	0	0	3	0
All	All	7249	0	7284	383	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 26.

The worst 5 of 383 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:143:GLN:N	1:C:144:PRO:HD3	1.95	0.81
1:A:143:GLN:N	1:A:144:PRO:HD3	1.95	0.81
1:A:143:GLN:H	1:A:144:PRO:HD3	1.47	0.80
1:B:143:GLN:N	1:B:144:PRO:HD3	1.96	0.80
1:B:12:GLY:HA3	1:B:52:ASP:OD1	1.81	0.80

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%)	29 (9%)	6 (2%)	6 22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	312/314 (99%)	276 (88%)	29 (9%)	7 (2%)	5	19
1	C	312/314 (99%)	278 (89%)	25 (8%)	9 (3%)	3	13
All	All	936/942 (99%)	831 (89%)	83 (9%)	22 (2%)	4	17

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	160	PRO
1	A	14	PRO
1	A	160	PRO
1	A	167	PRO
1	B	167	PRO

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	264/264 (100%)	245 (93%)	19 (7%)	13	39
1	B	264/264 (100%)	244 (92%)	20 (8%)	12	36
1	C	264/264 (100%)	245 (93%)	19 (7%)	13	39
All	All	792/792 (100%)	734 (93%)	58 (7%)	12	38

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	169	ILE
1	C	287	GLU
1	B	286	PRO
1	C	285	THR
1	C	225	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	19	GLN
1	C	90	ASN
1	C	294	ASN
1	C	115	HIS
1	B	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	VAL	C	1002	-	6,7,7	2.30	2 (33%)	8,9,9	2.17	2 (25%)
3	VAL	A	1000	-	6,7,7	2.48	3 (50%)	8,9,9	2.13	2 (25%)
3	VAL	B	1001	-	6,7,7	2.27	2 (33%)	8,9,9	2.10	2 (25%)

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	VAL	C	1002	-	-	8/8/8/8	-
3	VAL	A	1000	-	-	7/8/8/8	-
3	VAL	B	1001	-	-	7/8/8/8	-

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1000	VAL	O-C	4.65	1.35	1.22
3	C	1002	VAL	O-C	4.28	1.34	1.22
3	B	1001	VAL	O-C	4.24	1.34	1.22
3	A	1000	VAL	CA-C	2.89	1.58	1.52
3	B	1001	VAL	OXT-C	-2.80	1.21	1.30

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1002	VAL	CB-CA-C	4.46	122.64	110.97
3	A	1000	VAL	CB-CA-C	4.42	122.51	110.97
3	B	1001	VAL	CB-CA-C	4.40	122.48	110.97
3	A	1000	VAL	OXT-C-CA	2.87	124.06	114.15
3	C	1002	VAL	OXT-C-CA	2.87	124.05	114.15

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1000	VAL	N-CA-CB-CG1
3	A	1000	VAL	N-CA-CB-CG2
3	A	1000	VAL	C-CA-CB-CG1
3	A	1000	VAL	C-CA-CB-CG2
3	B	1001	VAL	N-CA-CB-CG1

There are no ring outliers.

3 monomers are involved in 3 short contacts:

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.