Full wwPDB X-ray Structure Validation Report ⓘ

Apr 2, 2025 – 12:35 am BST

PDB ID	:	1W7L / pdb_00001w7l
Title	:	Crystal structure of human kynurenine aminotransferase I
Authors	:	Rossi, F.; Han, Q.; Li, J.; Li, J.; Rizzi, M.
Deposited on	:	2004-09-06
Resolution	:	2.00 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 ⓘ 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:

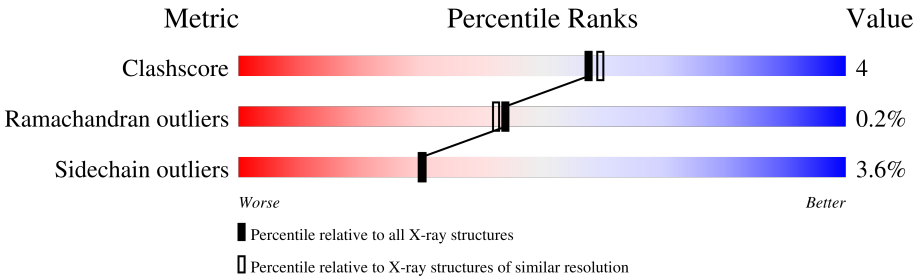
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)

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	A	422	86% 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3773 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.

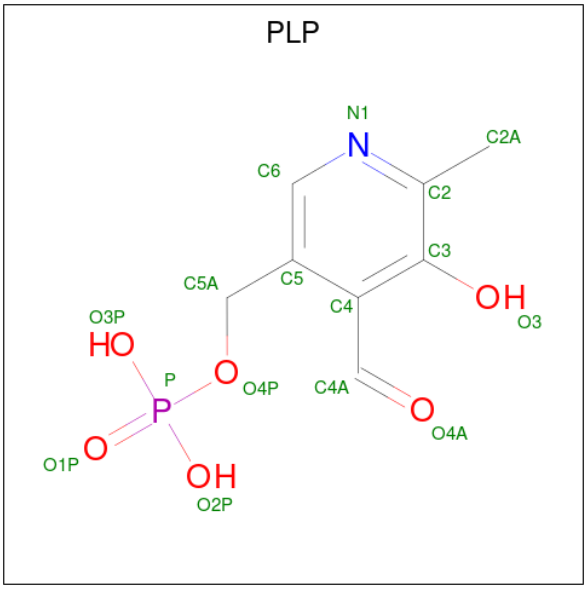
- Molecule 1 is a protein called KYNURENINE--OXOGLUTARATE TRANSAMINASE I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	415	3321	2146	558	598	19	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	332	LEU	ILE	conflict	UNP Q16773

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	15	8	1	5	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	437	Total O 437 437	0	0

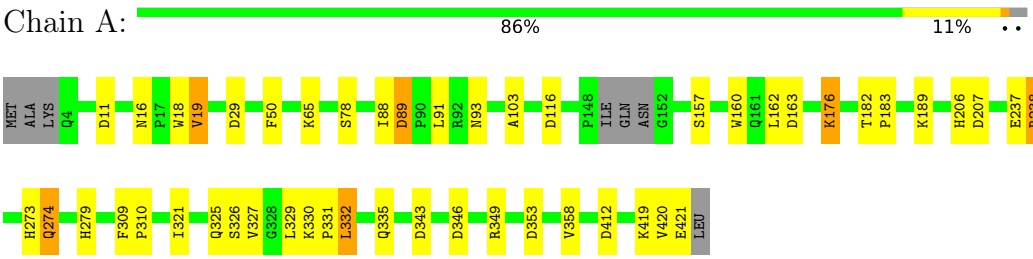
3 Residue-property plots (i)

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: KYNURENINE--OXOGLUTARATE TRANSAMINASE I

Chain A:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	146.37Å 146.37Å 67.45Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.75 – 2.00	Depositor
% Data completeness (in resolution range)	100.0 (29.75-2.00)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.192 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3773	wwPDB-VP
Average B, all atoms (Å^2)	39.0	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: PLP

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	0.49	0/3417	0.69	8/4637 (0.2%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	89	ASP	CB-CG-OD2	6.10	123.79	118.30
1	A	29	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	163	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	263	ASP	CB-CG-OD2	5.32	123.08	118.30
1	A	412	ASP	CB-CG-OD2	5.26	123.03	118.30
1	A	207	ASP	CB-CG-OD2	5.21	122.99	118.30
1	A	346	ASP	CB-CG-OD2	5.04	122.83	118.30
1	A	353	ASP	CB-CG-OD2	5.03	122.82	118.30

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	3321	0	3252	29	0
2	A	15	0	6	0	0
3	A	437	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3773	0	3258	29	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 4.

All (29) 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:A:89:ASP:H	1:A:93:ASN:HD22	1.25	0.85
1:A:237:GLU:HG2	3:A:2319:HOH:O	1.76	0.85
1:A:327:VAL:HB	3:A:2386:HOH:O	1.80	0.81
1:A:160:TRP:O	1:A:189:LYS:HE3	1.86	0.75
1:A:160:TRP:HE1	1:A:332:LEU:HD21	1.63	0.63
1:A:89:ASP:H	1:A:93:ASN:ND2	1.95	0.61
1:A:327:VAL:HG12	1:A:327:VAL:O	1.99	0.61
1:A:273:HIS:HD2	3:A:2160:HOH:O	1.86	0.57
1:A:160:TRP:NE1	1:A:332:LEU:HD21	2.20	0.55
1:A:238:ARG:NE	3:A:2321:HOH:O	2.15	0.54
1:A:182:THR:HA	1:A:183:PRO:C	2.30	0.53
1:A:238:ARG:NH2	3:A:2321:HOH:O	2.38	0.51
1:A:206:HIS:O	3:A:2284:HOH:O	2.20	0.50
1:A:326:SER:HB3	3:A:2390:HOH:O	2.10	0.50
1:A:329:LEU:O	1:A:331:PRO:HD3	2.11	0.49
1:A:89:ASP:N	1:A:93:ASN:HD22	2.03	0.49
1:A:11:ASP:OD1	3:A:2021:HOH:O	2.19	0.48
1:A:274:GLN:HB2	3:A:2113:HOH:O	2.15	0.45
1:A:330:LYS:HB2	1:A:343:ASP:HB3	1.99	0.45
1:A:16:ASN:O	1:A:19:VAL:HG23	2.19	0.42
1:A:321:ILE:O	1:A:325:GLN:HB2	2.19	0.42
1:A:309:PHE:HB3	1:A:310:PRO:HD3	2.02	0.42
1:A:88:ILE:HG23	1:A:93:ASN:HB2	2.02	0.42
1:A:162:LEU:CB	3:A:2265:HOH:O	2.68	0.42
1:A:116:ASP:HB3	1:A:176:LYS:HB2	2.02	0.41
1:A:18:TRP:HZ2	3:A:2189:HOH:O	2.03	0.41
1:A:65:LYS:HE3	3:A:2044:HOH:O	2.19	0.41
1:A:103:ALA:HB1	1:A:259:VAL:HG22	2.03	0.41
1:A:157:SER:HB2	1:A:335:GLN:OE1	2.21	0.40

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	411/422 (97%)	397 (97%)	13 (3%)	1 (0%)	44 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	420	VAL

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	362/368 (98%)	349 (96%)	13 (4%)	30 30

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

Mol	Chain	Res	Type
1	A	19	VAL
1	A	50	PHE
1	A	78	SER
1	A	91	LEU
1	A	176	LYS
1	A	238	ARG
1	A	274	GLN
1	A	279	HIS
1	A	332	LEU
1	A	349	ARG

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Mol	Chain	Res	Type
1	A	358	VAL
1	A	419	LYS
1	A	421	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	ASN
1	A	62	GLN
1	A	93	ASN
1	A	273	HIS
1	A	325	GLN
1	A	395	HIS

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)

1 ligand is 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	PLP	A	1247	1	15,15,16	1.80	2 (13%)	20,22,23	2.02	4 (20%)

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
2	PLP	A	1247	1	-	0/6/6/8	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1247	PLP	O3-C3	-5.20	1.24	1.37
2	A	1247	PLP	C2-N1	2.72	1.39	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1247	PLP	O4P-C5A-C5	6.60	121.92	109.35
2	A	1247	PLP	C6-C5-C4	3.23	120.70	118.16
2	A	1247	PLP	C5-C6-N1	-2.98	118.85	123.82
2	A	1247	PLP	O4P-P-O1P	-2.50	99.47	106.47

There are no chirality outliers.

There are no torsion outliers.

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

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.