



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:06 PM UTC

PDB ID : 1A1S / pdb_00001a1s
Title : ORNITHINE CARBAMOYLTRANSFERASE FROM PYROCOCCUS FU-
RIOSUS
Authors : Villeret, V.; Clantin, B.; Tricot, C.; Legrain, C.; Roovers, M.; Stalon, V.;
Glansdorff, N.; Van Beeumen, J.
Deposited on : 1997-12-15
Resolution : 2.70 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	:	4-5-2 with Phenix2.0
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

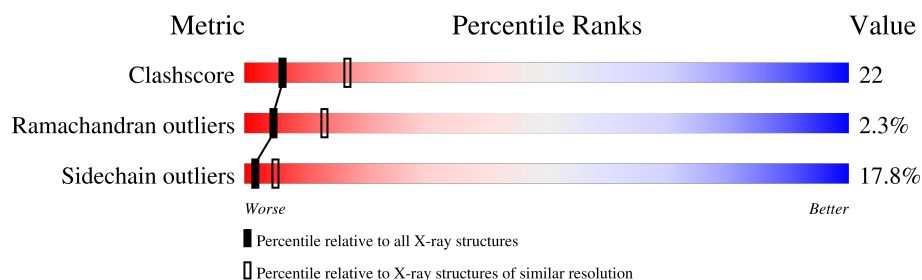
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)

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 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	 54% 33% 11% .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2454 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 ORNITHINE CARBAMOYLTRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	313	Total	C	N	O	S	0	0	0
			2454	1559	425	457	13			

There are 2 discrepancies between the modelled and reference sequences:

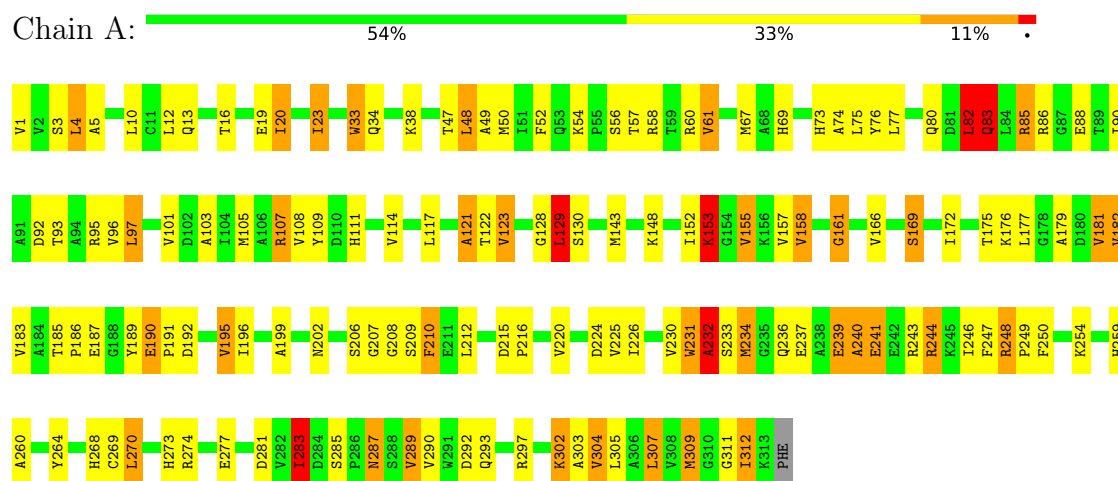
Chain	Residue	Modelled	Actual	Comment	Reference
A	206	SER	ARG	conflict	UNP Q51742
A	207	GLY	SER	conflict	UNP Q51742

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: ORNITHINE CARBAMOYLTRANSFERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	F 2 3	Depositor
Cell constants a, b, c, α , β , γ	186.80Å 186.80Å 186.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70	Depositor
% Data completeness (in resolution range)	99.3 (10.00-2.70)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.85	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.226 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2454	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.80	1/2505 (0.0%)	1.23	24/3394 (0.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	309	MET	SD-CE	-5.40	1.66	1.79

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	121	ALA	N-CA-C	13.51	125.70	110.97
1	A	83	GLN	N-CA-C	-10.97	96.05	110.53
1	A	231	TRP	N-CA-C	7.76	122.12	109.85
1	A	169	SER	N-CA-C	7.71	120.76	111.82
1	A	241	GLU	N-CA-C	-7.39	104.65	112.93
1	A	232	ALA	N-CA-C	6.81	125.31	110.80
1	A	82	LEU	N-CA-C	6.78	121.98	107.67
1	A	283	ILE	CB-CA-C	-6.53	102.52	112.05
1	A	292	ASP	N-CA-C	-6.49	104.29	111.36
1	A	297	ARG	N-CA-C	-5.80	105.09	111.82
1	A	290	VAL	N-CA-C	5.51	117.94	111.05
1	A	302	LYS	N-CA-C	-5.46	105.41	111.36
1	A	187	GLU	N-CA-C	5.38	122.25	110.80
1	A	208	GLY	N-CA-C	-5.36	100.48	113.18
1	A	161	GLY	CA-C-O	-5.32	117.80	122.16
1	A	38	LYS	CA-C-N	5.31	125.60	119.92
1	A	38	LYS	C-N-CA	5.31	125.60	119.92
1	A	210	PHE	N-CA-C	-5.25	101.09	109.07
1	A	4	LEU	N-CA-C	-5.23	105.19	112.30
1	A	83	GLN	CA-C-N	-5.22	114.46	121.71
1	A	83	GLN	C-N-CA	-5.22	114.46	121.71
1	A	287	ASN	N-CA-C	-5.16	106.98	113.28
1	A	143	MET	N-CA-C	-5.09	105.64	111.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	TRP	CA-CB-CG	5.06	123.22	113.60

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	2454	0	2454	109	0
All	All	2454	0	2454	109	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.

All (109) 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:158:VAL:HB	1:A:182:VAL:HG22	1.45	0.94
1:A:85:ARG:HH11	1:A:85:ARG:HB3	1.37	0.89
1:A:83:GLN:HG2	1:A:86:ARG:HD3	1.58	0.85
1:A:161:GLY:O	1:A:185:THR:HG22	1.81	0.80
1:A:244:ARG:O	1:A:248:ARG:HB2	1.84	0.77
1:A:216:PRO:HD3	1:A:250:PHE:CE1	2.21	0.76
1:A:236:GLN:HB2	1:A:240:ALA:O	1.84	0.76
1:A:85:ARG:HB3	1:A:85:ARG:NH1	2.04	0.73
1:A:121:ALA:O	1:A:122:THR:HB	1.88	0.72
1:A:254:LYS:HD3	1:A:281:ASP:HB3	1.71	0.71
1:A:236:GLN:HE22	1:A:243:ARG:HB2	1.57	0.70
1:A:309:MET:O	1:A:312:ILE:HG23	1.91	0.69
1:A:274:ARG:HG2	1:A:283:ILE:CD1	2.23	0.68
1:A:231:TRP:O	1:A:234:MET:SD	2.52	0.68
1:A:186:PRO:HG2	1:A:189:TYR:HB2	1.75	0.67
1:A:243:ARG:HG3	1:A:247:PHE:CE2	2.30	0.67
1:A:23:ILE:HD13	1:A:304:VAL:HG12	1.78	0.65
1:A:108:VAL:O	1:A:130:SER:HA	1.98	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ILE:O	1:A:155:VAL:HG13	1.98	0.63
1:A:226:ILE:HD11	1:A:260:ALA:HB2	1.82	0.61
1:A:103:ALA:HA	1:A:123:VAL:HG13	1.82	0.61
1:A:191:PRO:HG2	1:A:196:ILE:HD11	1.82	0.61
1:A:69:HIS:HD2	1:A:302:LYS:HZ3	1.49	0.61
1:A:83:GLN:OE1	1:A:86:ARG:HB3	2.01	0.60
1:A:220:VAL:HG23	1:A:259:HIS:HB2	1.82	0.60
1:A:175:THR:HG21	1:A:199:ALA:HA	1.84	0.60
1:A:175:THR:HG23	1:A:202:ASN:CB	2.32	0.59
1:A:236:GLN:HG3	1:A:237:GLU:H	1.67	0.59
1:A:268:HIS:HE1	1:A:277:GLU:OE2	1.85	0.58
1:A:69:HIS:HD2	1:A:302:LYS:NZ	2.01	0.58
1:A:274:ARG:HG2	1:A:283:ILE:HD11	1.85	0.57
1:A:82:LEU:HD12	1:A:83:GLN:O	2.04	0.57
1:A:83:GLN:CG	1:A:86:ARG:HB3	2.35	0.57
1:A:281:ASP:O	1:A:285:SER:HB3	2.05	0.56
1:A:52:PHE:CZ	1:A:105:MET:HE1	2.41	0.56
1:A:5:ALA:HB1	1:A:311:GLY:O	2.06	0.55
1:A:186:PRO:HG3	1:A:247:PHE:CE1	2.42	0.55
1:A:243:ARG:HG3	1:A:247:PHE:HE2	1.72	0.54
1:A:83:GLN:HG2	1:A:86:ARG:HB3	1.89	0.54
1:A:49:ALA:HB2	1:A:101:VAL:HG11	1.88	0.54
1:A:239:GLU:CD	1:A:239:GLU:H	2.15	0.54
1:A:233:SER:HB2	1:A:243:ARG:NE	2.22	0.54
1:A:3:SER:O	1:A:4:LEU:HD23	2.08	0.53
1:A:128:GLY:O	1:A:129:LEU:HB2	2.07	0.53
1:A:236:GLN:NE2	1:A:243:ARG:HD3	2.23	0.53
1:A:158:VAL:HB	1:A:182:VAL:CG2	2.31	0.52
1:A:52:PHE:CD2	1:A:76:TYR:CE1	2.98	0.52
1:A:57:THR:O	1:A:61:VAL:HG13	2.10	0.52
1:A:243:ARG:O	1:A:247:PHE:HB2	2.09	0.51
1:A:83:GLN:CD	1:A:86:ARG:HB3	2.35	0.51
1:A:175:THR:HG23	1:A:202:ASN:HB3	1.93	0.51
1:A:111:HIS:O	1:A:114:VAL:HG12	2.10	0.51
1:A:153:LYS:O	1:A:179:ALA:HA	2.11	0.50
1:A:88:GLU:HG2	1:A:92:ASP:HB2	1.94	0.50
1:A:181:VAL:O	1:A:210:PHE:HA	2.12	0.49
1:A:183:VAL:HG12	1:A:210:PHE:CE1	2.47	0.49
1:A:186:PRO:HB2	1:A:246:ILE:HD11	1.94	0.49
1:A:246:ILE:O	1:A:249:PRO:HD2	2.13	0.49
1:A:206:SER:O	1:A:207:GLY:C	2.56	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:HIS:CD2	1:A:270:LEU:H	2.31	0.49
1:A:75:LEU:H	1:A:75:LEU:HD12	1.78	0.49
1:A:48:LEU:O	1:A:74:ALA:HA	2.13	0.48
1:A:108:VAL:HG22	1:A:109:TYR:N	2.29	0.48
1:A:20:ILE:HD11	1:A:177:LEU:HD11	1.97	0.47
1:A:52:PHE:CD2	1:A:76:TYR:HE1	2.32	0.47
1:A:196:ILE:HG23	1:A:210:PHE:HE2	1.80	0.47
1:A:175:THR:HG23	1:A:202:ASN:HB2	1.97	0.46
1:A:189:TYR:CE2	1:A:243:ARG:NH2	2.83	0.46
1:A:175:THR:O	1:A:206:SER:OG	2.34	0.46
1:A:248:ARG:HE	1:A:248:ARG:C	2.23	0.46
1:A:289:VAL:O	1:A:289:VAL:HG13	2.15	0.46
1:A:16:THR:OG1	1:A:19:GLU:HG3	2.16	0.45
1:A:48:LEU:HD13	1:A:50:MET:HG2	1.98	0.45
1:A:254:LYS:HD3	1:A:281:ASP:CB	2.45	0.45
1:A:69:HIS:CD2	1:A:302:LYS:NZ	2.84	0.45
1:A:153:LYS:HD2	1:A:153:LYS:C	2.42	0.45
1:A:305:LEU:HD22	1:A:309:MET:CE	2.46	0.45
1:A:189:TYR:HE2	1:A:243:ARG:NH2	2.15	0.45
1:A:48:LEU:HB2	1:A:67:MET:HE2	1.99	0.44
1:A:231:TRP:C	1:A:234:MET:SD	3.00	0.44
1:A:196:ILE:HG23	1:A:210:PHE:CE2	2.52	0.44
1:A:236:GLN:HG3	1:A:237:GLU:N	2.32	0.44
1:A:16:THR:O	1:A:20:ILE:HG23	2.17	0.44
1:A:172:ILE:O	1:A:176:LYS:HG3	2.17	0.44
1:A:190:GLU:HB2	1:A:191:PRO:HD2	2.00	0.44
1:A:96:VAL:HG13	1:A:97:LEU:N	2.33	0.43
1:A:148:LYS:HE2	1:A:289:VAL:HG22	1.99	0.43
1:A:233:SER:HB2	1:A:243:ARG:HE	1.83	0.43
1:A:47:THR:HA	1:A:73:HIS:O	2.19	0.43
1:A:75:LEU:HD12	1:A:75:LEU:N	2.34	0.43
1:A:283:ILE:H	1:A:283:ILE:HG12	1.54	0.42
1:A:232:ALA:HB3	1:A:247:PHE:CE2	2.55	0.42
1:A:231:TRP:CZ3	1:A:277:GLU:HA	2.54	0.42
1:A:215:ASP:HA	1:A:216:PRO:HD2	1.87	0.42
1:A:224:ASP:O	1:A:264:TYR:HA	2.20	0.42
1:A:285:SER:C	1:A:287:ASN:H	2.28	0.42
1:A:117:LEU:HD12	1:A:117:LEU:HA	1.83	0.41
1:A:54:LYS:O	1:A:107:ARG:HD3	2.19	0.41
1:A:105:MET:C	1:A:105:MET:SD	3.03	0.41
1:A:185:THR:HB	1:A:189:TYR:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:HIS:H	1:A:293:GLN:HE22	1.68	0.41
1:A:13:GLN:O	1:A:13:GLN:HG3	2.20	0.41
1:A:233:SER:HB3	1:A:236:GLN:HB3	2.03	0.41
1:A:192:ASP:HB3	1:A:195:VAL:HG13	2.03	0.41
1:A:269:CYS:O	1:A:270:LEU:O	2.39	0.40
1:A:273:HIS:HB2	1:A:277:GLU:OE1	2.21	0.40
1:A:54:LYS:HD3	1:A:109:TYR:OH	2.21	0.40
1:A:303:ALA:O	1:A:307:LEU:HB2	2.22	0.40
1:A:236:GLN:NE2	1:A:243:ARG:HB2	2.31	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	311/314 (99%)	271 (87%)	33 (11%)	7 (2%)	5 13

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	LYS
1	A	232	ALA
1	A	240	ALA
1	A	56	SER
1	A	129	LEU
1	A	209	SER
1	A	270	LEU

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%)	213 (82%)	46 (18%)	2 5

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	VAL
1	A	10	LEU
1	A	12	LEU
1	A	20	ILE
1	A	23	ILE
1	A	33	TRP
1	A	34	GLN
1	A	48	LEU
1	A	58	ARG
1	A	60	ARG
1	A	61	VAL
1	A	77	LEU
1	A	80	GLN
1	A	82	LEU
1	A	83	GLN
1	A	85	ARG
1	A	90	ILE
1	A	93	THR
1	A	95	ARG
1	A	97	LEU
1	A	107	ARG
1	A	123	VAL
1	A	129	LEU
1	A	153	LYS
1	A	155	VAL
1	A	157	VAL
1	A	158	VAL
1	A	166	VAL
1	A	169	SER
1	A	181	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	182	VAL
1	A	190	GLU
1	A	195	VAL
1	A	212	LEU
1	A	225	VAL
1	A	230	VAL
1	A	234	MET
1	A	239	GLU
1	A	241	GLU
1	A	244	ARG
1	A	248	ARG
1	A	283	ILE
1	A	289	VAL
1	A	304	VAL
1	A	307	LEU
1	A	312	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	34	GLN
1	A	69	HIS
1	A	80	GLN
1	A	137	GLN
1	A	202	ASN
1	A	236	GLN
1	A	268	HIS
1	A	293	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.