



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:16 PM UTC

PDB ID : 1ORT / pdb_00001ort
Title : ORNITHINE TRANSCARBAMOYLASE FROM PSEUDOMONAS
AERUGINOSA
Authors : Villeret, V.; Dideberg, O.
Deposited on : 1995-08-24
Resolution : 3.00 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
Xtrriage (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

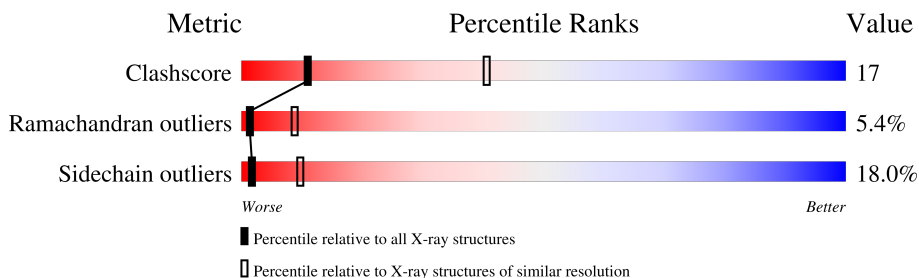
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)




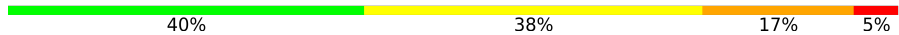
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	335	
1	B	335	
1	C	335	
1	D	335	
1	E	335	
1	F	335	
1	G	335	
1	H	335	

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Mol	Chain	Length	Quality of chain
1	I	335	 40% 38% 16% 5%
1	J	335	 41% 38% 16% 5%
1	K	335	 40% 38% 16% 6%
1	L	335	 40% 38% 17% 5%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 31968 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 TRANSCARBAMOYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	335	2664	1682	466	500	16	0	0	0
1	B	335	2664	1682	466	500	16	0	0	0
1	C	335	2664	1682	466	500	16	0	0	0
1	D	335	2664	1682	466	500	16	0	0	0
1	E	335	2664	1682	466	500	16	0	0	0
1	F	335	2664	1682	466	500	16	0	0	0
1	G	335	2664	1682	466	500	16	0	0	0
1	H	335	2664	1682	466	500	16	0	0	0
1	I	335	2664	1682	466	500	16	0	0	0
1	J	335	2664	1682	466	500	16	0	0	0
1	K	335	2664	1682	466	500	16	0	0	0
1	L	335	2664	1682	466	500	16	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	GLY	GLU	engineered mutation	UNP P08308
B	105	GLY	GLU	engineered mutation	UNP P08308
C	105	GLY	GLU	engineered mutation	UNP P08308
D	105	GLY	GLU	engineered mutation	UNP P08308
E	105	GLY	GLU	engineered mutation	UNP P08308

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Chain	Residue	Modelled	Actual	Comment	Reference
F	105	GLY	GLU	engineered mutation	UNP P08308
G	105	GLY	GLU	engineered mutation	UNP P08308
H	105	GLY	GLU	engineered mutation	UNP P08308
I	105	GLY	GLU	engineered mutation	UNP P08308
J	105	GLY	GLU	engineered mutation	UNP P08308
K	105	GLY	GLU	engineered mutation	UNP P08308
L	105	GLY	GLU	engineered mutation	UNP P08308

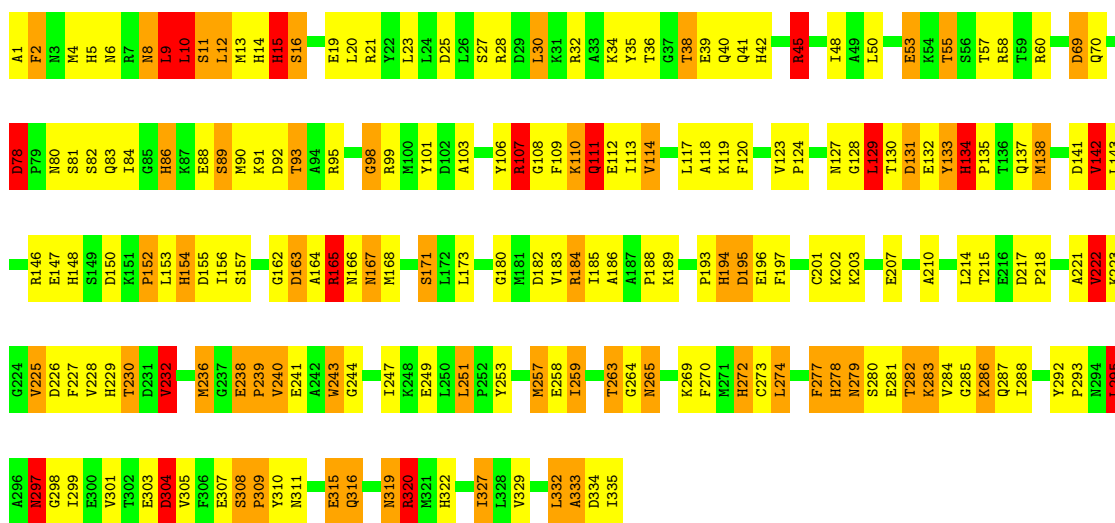
3 Residue-property plots [i](#)

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.

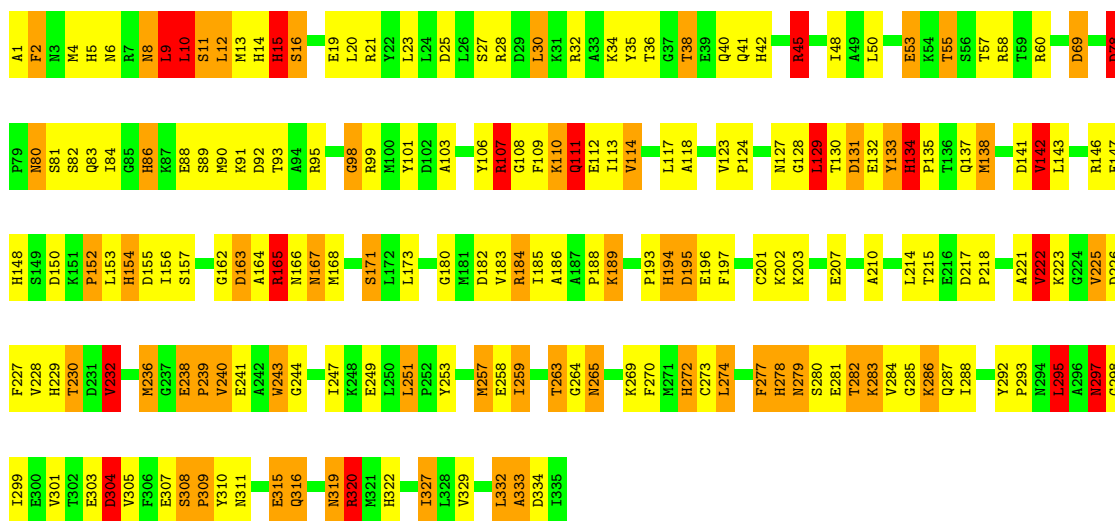
- Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain A: 



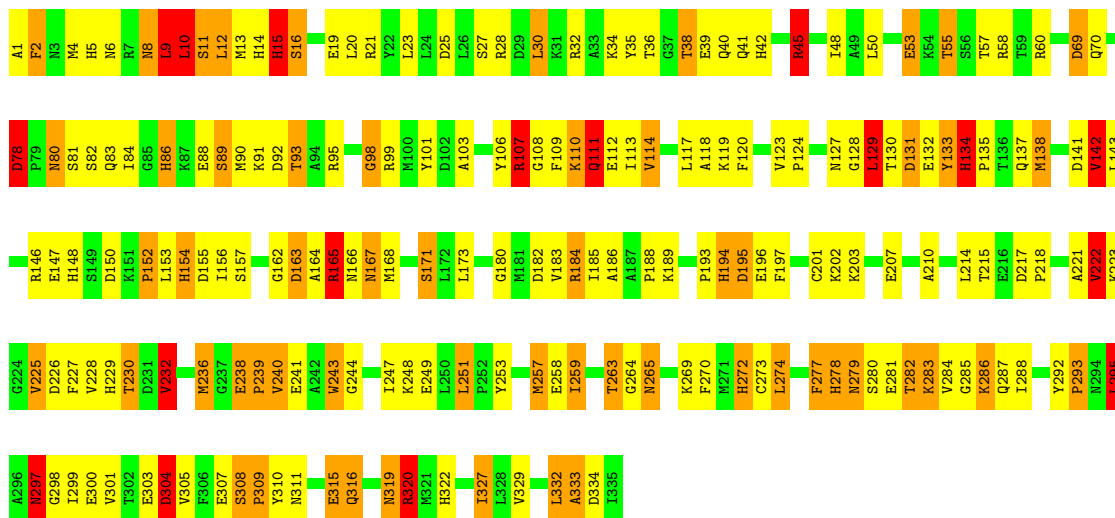
- Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain B: 



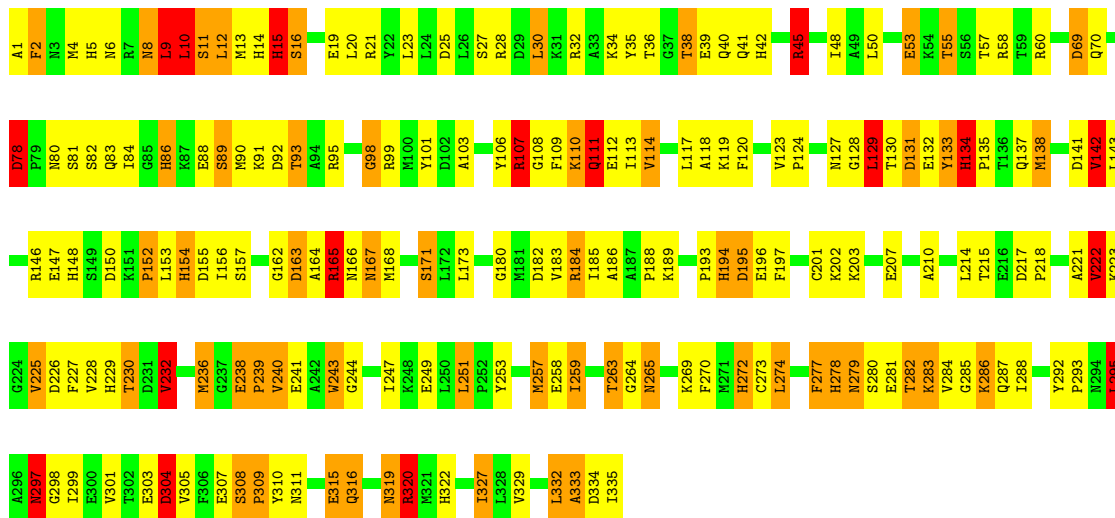
- Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain C: 



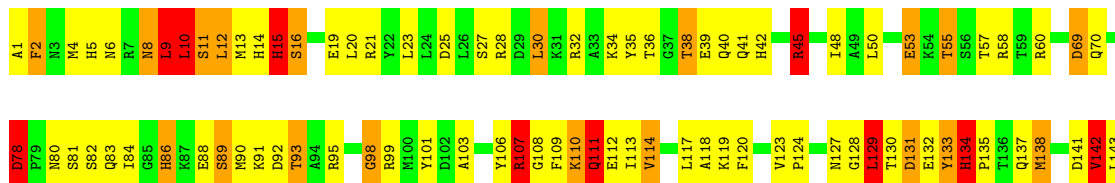
- Molecule 1: ORNITHINE TRANSCARBAMOYLASE

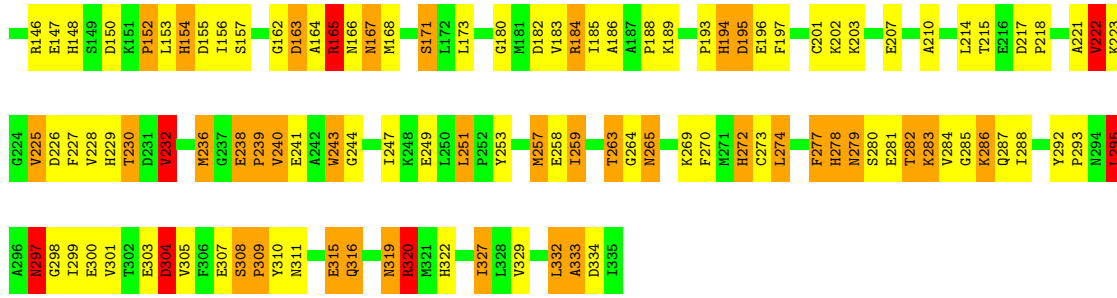
Chain D: 



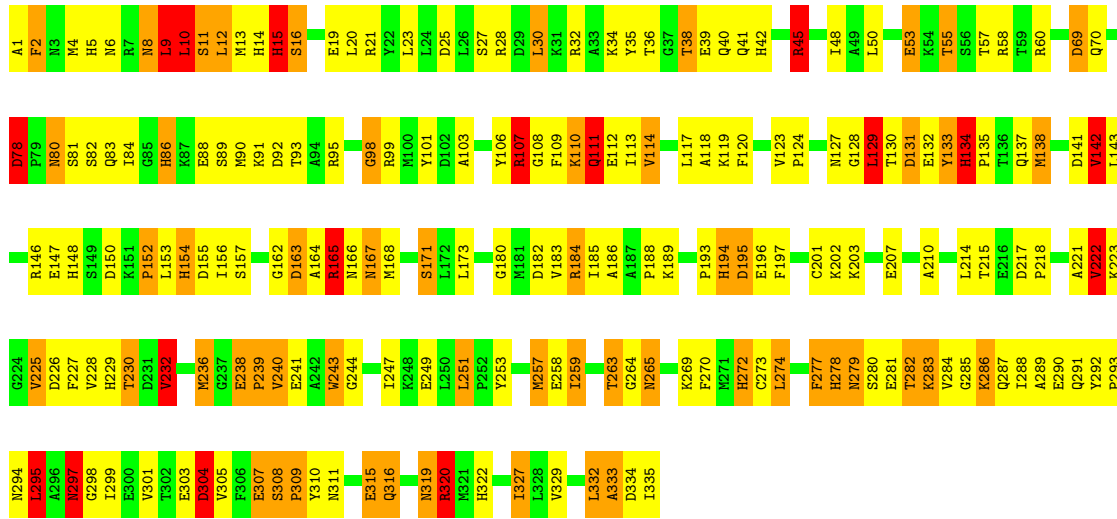
- Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain E: 

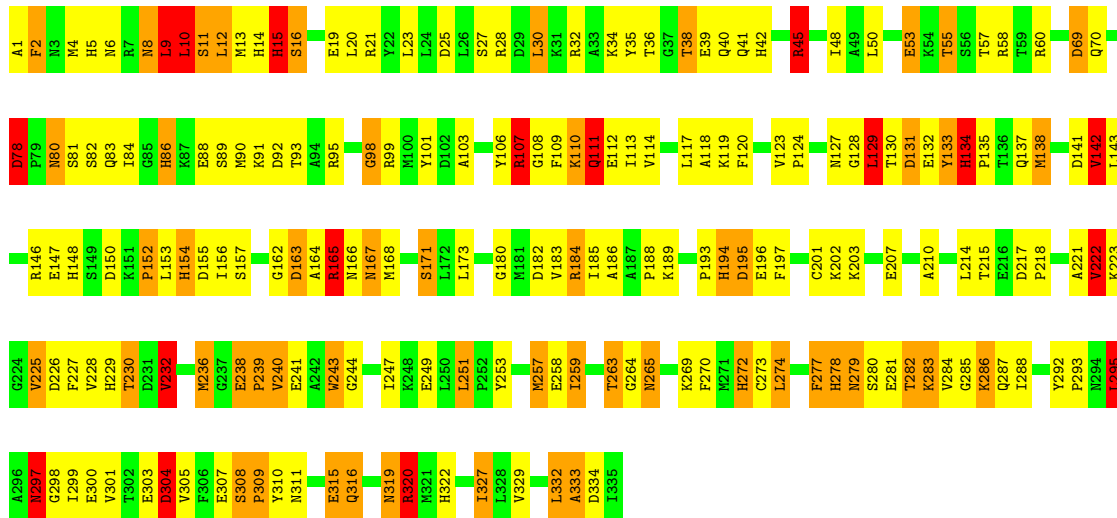




• Molecule 1: ORNITHINE TRANSCARBAMOYLASE

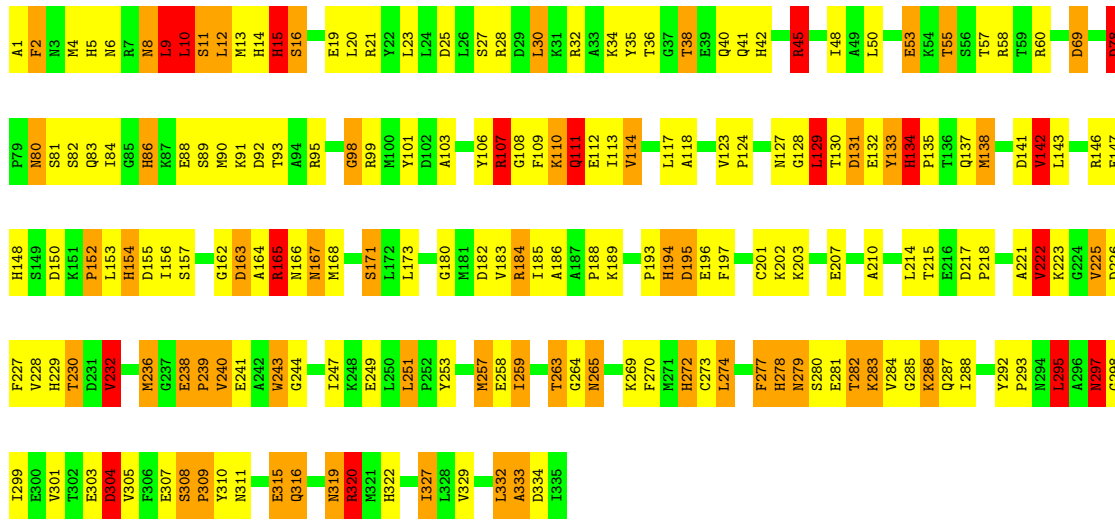


• Molecule 1: ORNITHINE TRANSCARBAMOYLASE



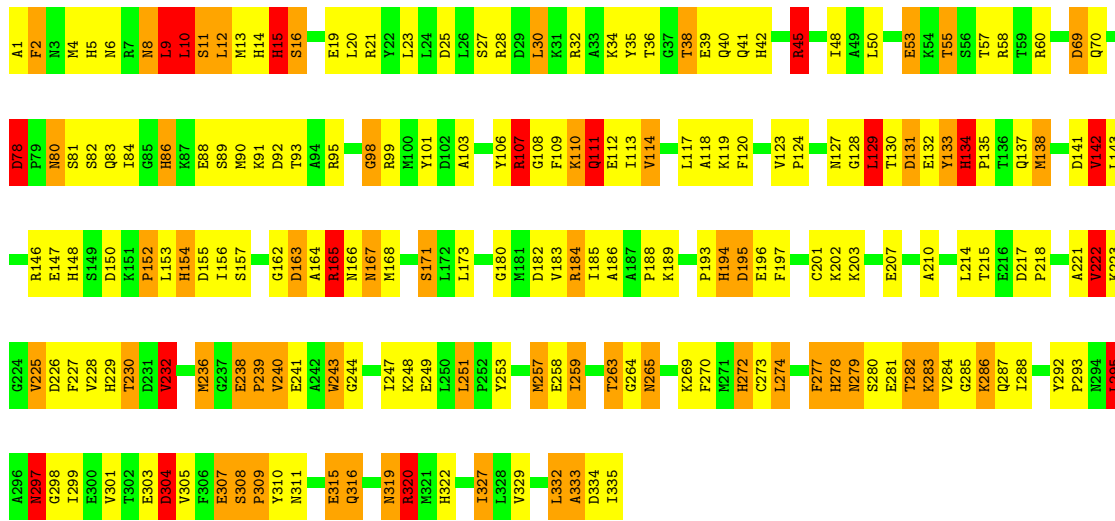
• Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain H: 42% 37% 16% 5%



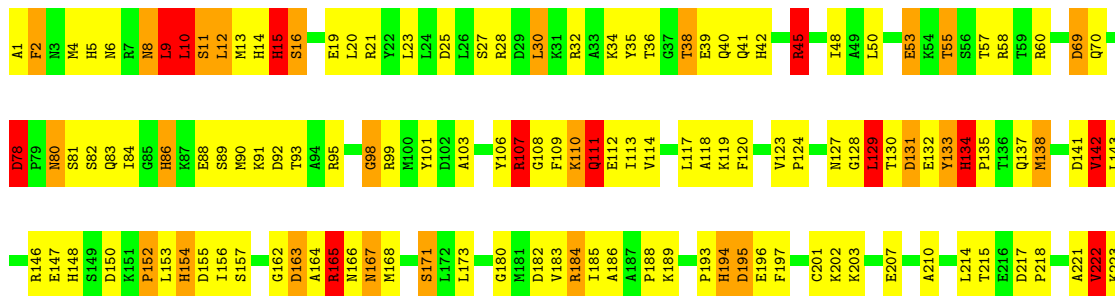
● Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain I: 40% 38% 16% 5%



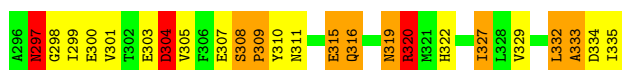
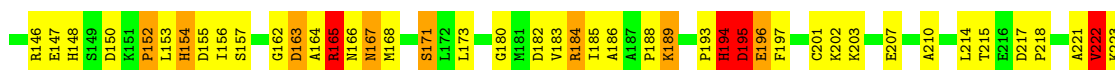
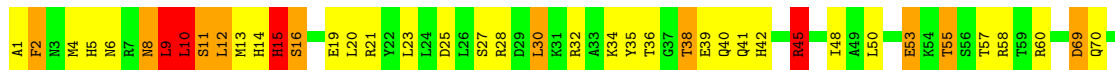
● Molecule 1: ORNITHINE TRANSCARBAMOYLASE

Chain J: 41% 38% 16% 5%

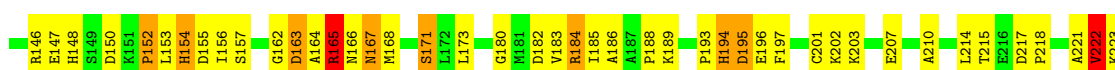
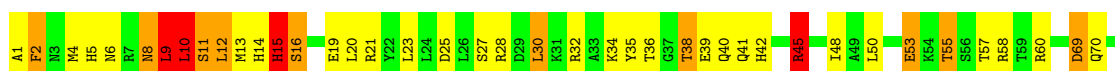




• Molecule 1: ORNITHINE TRANSCARBAMOYLASE



• Molecule 1: ORNITHINE TRANSCARBAMOYLASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	110.36Å 126.42Å 134.54Å 85.07° 59.24° 111.97°	Depositor
Resolution (Å)	5.50 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (5.50-3.00)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.0	Depositor
R, R_{free}	0.216 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	31968	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality i

5.1 Standard geometry i

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	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	B	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	C	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	D	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	E	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	F	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	G	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	H	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	I	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	J	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	K	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
1	L	1.21	20/2720 (0.7%)	2.37	156/3673 (4.2%)
All	All	1.21	240/32640 (0.7%)	2.37	1872/44076 (4.2%)

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	6
1	B	0	6
1	C	0	6
1	D	0	6
1	E	0	6
1	F	0	6
1	G	0	6
1	H	0	6
1	I	0	6
1	J	0	6
1	K	0	6
1	L	0	6
All	All	0	72

The worst 5 of 240 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	272	HIS	CD2-NE2	-7.77	1.29	1.37
1	B	272	HIS	CD2-NE2	-7.77	1.29	1.37
1	C	272	HIS	CD2-NE2	-7.77	1.29	1.37
1	D	272	HIS	CD2-NE2	-7.77	1.29	1.37
1	E	272	HIS	CD2-NE2	-7.77	1.29	1.37

The worst 5 of 1872 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	6	ASN	CA-CB-CG	-15.31	97.29	112.60
1	B	6	ASN	CA-CB-CG	-15.31	97.29	112.60
1	C	6	ASN	CA-CB-CG	-15.31	97.29	112.60
1	D	6	ASN	CA-CB-CG	-15.31	97.29	112.60
1	E	6	ASN	CA-CB-CG	-15.31	97.29	112.60

There are no chirality outliers.

5 of 72 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	134	HIS	Peptide
1	A	238	GLU	Peptide
1	A	264	GLY	Peptide
1	A	45	ARG	Sidechain
1	A	78	ASP	Peptide

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	2664	0	2637	98	0
1	B	2664	0	2637	95	5
1	C	2664	0	2637	100	4
1	D	2664	0	2637	98	0
1	E	2664	0	2637	99	0
1	F	2664	0	2637	101	40
1	G	2664	0	2637	94	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	2664	0	2637	95	0
1	I	2664	0	2637	100	5
1	J	2664	0	2637	95	0
1	K	2664	0	2637	99	40
1	L	2664	0	2637	101	4
All	All	31968	0	31644	1051	49

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 17.

The worst 5 of 1051 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:81:SER:HB2	1:E:55:THR:HG21	1.57	0.87
1:D:81:SER:HB2	1:K:55:THR:HG21	1.57	0.87
1:A:55:THR:HG21	1:L:81:SER:HB2	1.57	0.87
1:C:81:SER:HB2	1:D:55:THR:HG21	1.57	0.87
1:F:81:SER:HB2	1:J:55:THR:HG21	1.57	0.86

The worst 5 of 49 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:LYS:NZ	1:I:248:LYS:CE[1_654]	0.62	1.58
1:F:291:GLN:O	1:K:194:HIS:NE2[1_654]	0.69	1.51
1:F:289:ALA:O	1:K:195:ASP:OD2[1_654]	0.88	1.32
1:F:291:GLN:O	1:K:194:HIS:CE1[1_654]	0.90	1.30
1:F:291:GLN:C	1:K:194:HIS:NE2[1_654]	1.10	1.10

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	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	B	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	C	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	D	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	E	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	F	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	G	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	H	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	I	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	J	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	K	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
1	L	333/335 (99%)	270 (81%)	45 (14%)	18 (5%)	1	9
All	All	3996/4020 (99%)	3240 (81%)	540 (14%)	216 (5%)	1	9

5 of 216 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	ASP
1	A	240	VAL
1	A	244	GLY
1	A	274	LEU
1	A	297	ASN

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	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	B	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	C	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	D	284/284 (100%)	233 (82%)	51 (18%)	2	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	F	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	G	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	H	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	I	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	J	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	K	284/284 (100%)	233 (82%)	51 (18%)	2	10
1	L	284/284 (100%)	233 (82%)	51 (18%)	2	10
All	All	3408/3408 (100%)	2796 (82%)	612 (18%)	2	10

5 of 612 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	27	SER
1	L	93	THR
1	J	138	MET
1	J	23	LEU
1	K	55	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 129 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	291	GLN
1	L	80	ASN
1	E	86	HIS
1	E	80	ASN
1	L	127	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](#)

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.