



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:29 PM GMT

PDB ID : 1TYC  
Title : STRUCTURAL ANALYSIS OF A SERIES OF MUTANTS OF TYROSYL-  
TRNA SYNTHETASE: ENHANCEMENT OF CATALYSIS BY HY-  
DROPHOBIC INTERACTIONS  
Authors : Brown, K.A.; Brick, P.; De Meester, P.; Blow, D.M.  
Deposited on : 1992-07-06  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

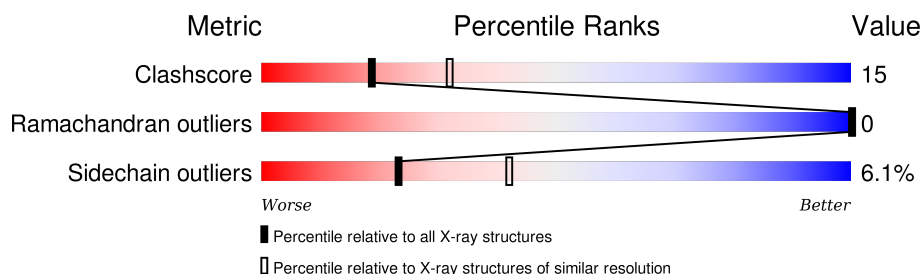
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	319	<div> <div style="width: 62%; background-color: green;"></div> <div style="width: 30%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 0%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div> <div>62% 30% 8% .</div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2634 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 TYROSYL-tRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2463	1572	428	456	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	51	PRO	THR	CONFLICT	UNP P00952

- Molecule 2 is water.

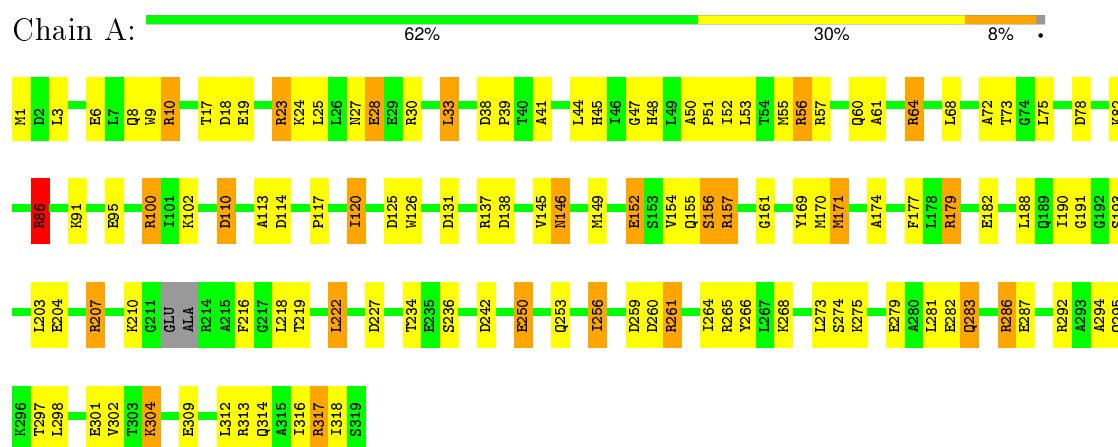
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	171	Total	O	0	0
			171	171		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: TYROSYL-tRNA SYNTHETASE



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.46 Å 64.46 Å 237.60 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.219 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2634	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	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	0.82	1/2512 (0.0%)	1.91	52/3398 (1.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	287	GLU	CB-CG	-5.84	1.41	1.52

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	ARG	CD-NE-CZ	36.12	174.17	123.60
1	A	10	ARG	NE-CZ-NH1	14.16	127.38	120.30
1	A	131	ASP	CB-CG-OD2	13.33	130.29	118.30
1	A	179	ARG	NE-CZ-NH1	13.26	126.93	120.30
1	A	56	ARG	NE-CZ-NH2	-12.24	114.18	120.30
1	A	179	ARG	NE-CZ-NH2	-11.47	114.56	120.30
1	A	86	ARG	NE-CZ-NH2	11.40	126.00	120.30
1	A	157	ARG	NE-CZ-NH2	-10.70	114.95	120.30
1	A	313	ARG	NE-CZ-NH1	10.52	125.56	120.30
1	A	261	ARG	NE-CZ-NH1	10.47	125.53	120.30
1	A	10	ARG	NE-CZ-NH2	-10.45	115.08	120.30
1	A	265	ARG	NE-CZ-NH1	10.08	125.34	120.30
1	A	64	ARG	NE-CZ-NH1	9.70	125.15	120.30
1	A	313	ARG	CD-NE-CZ	9.10	136.34	123.60
1	A	261	ARG	NE-CZ-NH2	-9.01	115.80	120.30
1	A	157	ARG	NE-CZ-NH1	8.77	124.68	120.30
1	A	41	ALA	N-CA-CB	8.42	121.89	110.10
1	A	137	ARG	CD-NE-CZ	7.98	134.77	123.60
1	A	286	ARG	NE-CZ-NH2	-7.58	116.51	120.30
1	A	28	GLU	CA-CB-CG	7.53	129.97	113.40
1	A	64	ARG	NE-CZ-NH2	-7.09	116.76	120.30
1	A	64	ARG	CD-NE-CZ	7.08	133.51	123.60
1	A	265	ARG	NE-CZ-NH2	-6.77	116.91	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	110	ASP	CB-CG-OD1	6.65	124.28	118.30
1	A	137	ARG	NE-CZ-NH1	6.50	123.55	120.30
1	A	179	ARG	CD-NE-CZ	6.43	132.60	123.60
1	A	261	ARG	CD-NE-CZ	6.42	132.59	123.60
1	A	286	ARG	NE-CZ-NH1	6.35	123.48	120.30
1	A	23	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	A	23	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	A	317	ARG	N-CA-CB	5.97	121.35	110.60
1	A	100	ARG	NE-CZ-NH2	-5.93	117.33	120.30
1	A	266	TYR	CB-CG-CD2	-5.89	117.47	121.00
1	A	18	ASP	CB-CG-OD1	5.87	123.58	118.30
1	A	131	ASP	OD1-CG-OD2	-5.85	112.18	123.30
1	A	30	ARG	N-CA-CB	5.76	120.97	110.60
1	A	157	ARG	N-CA-C	5.72	126.44	111.00
1	A	171	MET	CA-CB-CG	5.53	122.69	113.30
1	A	207	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	A	152	GLU	CG-CD-OE2	-5.34	107.62	118.30
1	A	125	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	317	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	A	138	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	227	ASP	CB-CG-OD1	5.27	123.05	118.30
1	A	274	SER	N-CA-CB	5.25	118.37	110.50
1	A	266	TYR	CB-CG-CD1	5.25	124.15	121.00
1	A	283	GLN	CB-CA-C	5.21	120.81	110.40
1	A	137	ARG	NH1-CZ-NH2	-5.14	113.74	119.40
1	A	283	GLN	CB-CG-CD	5.14	124.97	111.60
1	A	250	GLU	CA-CB-CG	5.11	124.64	113.40
1	A	313	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	A	120	ILE	N-CA-CB	5.09	122.51	110.80

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	2463	0	2396	75	0
2	A	171	0	0	5	0
All	All	2634	0	2396	75	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 15.

All (75) 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:45:HIS:H	1:A:48:HIS:HD2	1.21	0.85
1:A:234:THR:HG22	1:A:236:SER:H	1.44	0.83
1:A:1:MET:N	1:A:27:ASN:HD21	1.87	0.71
1:A:152:GLU:O	1:A:156:SER:HB3	1.89	0.71
1:A:283:GLN:HG3	1:A:286:ARG:NH1	2.08	0.68
1:A:82:LYS:HD3	1:A:86:ARG:HH11	1.58	0.67
1:A:45:HIS:H	1:A:48:HIS:CD2	2.10	0.66
1:A:9:TRP:CZ2	1:A:275:LYS:HG3	2.31	0.66
1:A:50:ALA:HB3	1:A:51:PRO:HD3	1.78	0.66
1:A:72:ALA:O	1:A:75:LEU:HB2	2.02	0.60
1:A:100:ARG:NH2	1:A:242:ASP:OD2	2.33	0.59
1:A:75:LEU:HD21	1:A:91:LYS:HA	1.84	0.57
1:A:292:ARG:NH1	1:A:295:GLN:HG2	2.20	0.57
1:A:190:ILE:HA	1:A:218:LEU:O	2.05	0.56
1:A:110:ASP:OD2	1:A:113:ALA:HB2	2.06	0.56
1:A:48:HIS:O	1:A:52:ILE:HG13	2.06	0.55
1:A:82:LYS:CD	1:A:86:ARG:HH11	2.18	0.55
1:A:234:THR:HG22	1:A:236:SER:N	2.18	0.54
1:A:145:VAL:O	1:A:149:MET:HG2	2.07	0.54
1:A:146:ASN:HB2	2:A:378:HOH:O	2.08	0.54
1:A:44:LEU:HD13	1:A:52:ILE:HD11	1.89	0.54
1:A:24:LYS:NZ	1:A:28:GLU:OE2	2.41	0.53
1:A:171:MET:O	1:A:174:ALA:HB3	2.08	0.52
1:A:222:LEU:HD23	2:A:393:HOH:O	2.09	0.52
1:A:149:MET:O	1:A:155:GLN:HG2	2.10	0.52
1:A:64:ARG:HD2	2:A:385:HOH:O	2.08	0.52
1:A:283:GLN:HG3	1:A:286:ARG:HH12	1.74	0.51
1:A:17:THR:HG21	1:A:203:LEU:CD1	2.40	0.51
1:A:157:ARG:O	1:A:161:GLY:N	2.41	0.50
1:A:314:GLN:O	1:A:318:ILE:HG13	2.11	0.50
1:A:273:LEU:HD11	1:A:297:THR:HG21	1.92	0.50
1:A:33:LEU:HA	1:A:188:LEU:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LYS:O	1:A:95:GLU:HB2	2.12	0.50
1:A:264:ILE:O	1:A:268:LYS:HG3	2.13	0.49
1:A:170:MET:HG3	1:A:171:MET:HE2	1.94	0.49
1:A:182:GLU:OE2	1:A:210:LYS:NZ	2.36	0.48
1:A:3:LEU:HD22	1:A:61:ALA:HB3	1.95	0.48
1:A:253:GLN:HA	1:A:256:ILE:HG22	1.95	0.48
1:A:45:HIS:CE1	1:A:47:GLY:HA3	2.49	0.48
1:A:25:LEU:HD22	1:A:216:PHE:HE1	1.78	0.48
1:A:82:LYS:HD3	1:A:86:ARG:NH1	2.28	0.48
1:A:292:ARG:HH11	1:A:295:GLN:HG2	1.79	0.47
1:A:126:TRP:HB2	2:A:363:HOH:O	2.14	0.47
1:A:256:ILE:O	1:A:292:ARG:NH1	2.47	0.47
1:A:10:ARG:HD3	1:A:268:LYS:O	2.13	0.47
1:A:1:MET:H1	1:A:27:ASN:HD21	1.58	0.47
1:A:297:THR:O	1:A:301:GLU:HG2	2.15	0.47
1:A:281:LEU:HD22	1:A:294:ALA:HA	1.97	0.47
1:A:82:LYS:CG	1:A:86:ARG:HH11	2.28	0.45
1:A:304:LYS:HG3	1:A:312:LEU:CD2	2.46	0.45
1:A:113:ALA:O	1:A:117:PRO:HB3	2.17	0.45
1:A:259:ASP:OD1	1:A:260:ASP:N	2.50	0.45
1:A:78:ASP:HB2	1:A:169:TYR:CZ	2.52	0.44
1:A:204:GLU:OE2	1:A:207:ARG:NH2	2.50	0.44
1:A:38:ASP:HA	1:A:39:PRO:HD3	1.84	0.44
1:A:73:THR:HB	1:A:169:TYR:CE2	2.54	0.43
1:A:309:GLU:OE1	1:A:312:LEU:HD23	2.18	0.43
1:A:53:LEU:O	1:A:56:ARG:HB3	2.19	0.43
1:A:53:LEU:O	1:A:57:ARG:HG3	2.19	0.42
1:A:9:TRP:CE2	1:A:275:LYS:HG3	2.54	0.42
1:A:56:ARG:O	1:A:60:GLN:HG3	2.20	0.42
1:A:279:GLU:O	1:A:282:GLU:HB3	2.19	0.42
1:A:19:GLU:OE2	1:A:23:ARG:NH1	2.47	0.42
1:A:82:LYS:HG2	1:A:86:ARG:NH1	2.35	0.42
1:A:3:LEU:HD22	1:A:61:ALA:CB	2.49	0.42
1:A:52:ILE:O	1:A:55:MET:HB2	2.21	0.41
1:A:191:GLY:O	1:A:219:THR:HA	2.20	0.41
1:A:283:GLN:HE21	1:A:286:ARG:HH12	1.68	0.41
1:A:154:VAL:O	1:A:155:GLN:C	2.58	0.41
1:A:6:GLU:O	1:A:10:ARG:HG3	2.19	0.41
1:A:250:GLU:HG2	2:A:472:HOH:O	2.20	0.41
1:A:312:LEU:O	1:A:316:ILE:HG13	2.20	0.41
1:A:102:LYS:HG3	1:A:120:ILE:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:LEU:O	1:A:302:VAL:HG23	2.21	0.40
1:A:82:LYS:CG	1:A:86:ARG:NH1	2.85	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	313/319 (98%)	305 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	245/269 (91%)	230 (94%)	15 (6%)	23	42

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	33	LEU
1	A	68	LEU
1	A	86	ARG

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Mol	Chain	Res	Type
1	A	114	ASP
1	A	146	ASN
1	A	156	SER
1	A	177	PHE
1	A	179	ARG
1	A	193	SER
1	A	222	LEU
1	A	256	ILE
1	A	261	ARG
1	A	304	LYS
1	A	317	ARG

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

Mol	Chain	Res	Type
1	A	27	ASN
1	A	48	HIS
1	A	60	GLN
1	A	257	ASN
1	A	283	GLN
1	A	314	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 carbohydrates 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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers

EDS was not executed - this section will therefore be empty.