Full wwPDB X-ray Structure Validation Report (i)

Feb 5, 2024 – 02:32 AM EST

PDB ID	:	1TYA
Title	:	STRUCTURAL ANALYSIS OF A SERIES OF MUTANTS OF TYROSYL-TRNA SYNTHETASE: ENHANCEMENT OF CATALYSIS BY HYDROPHOBIC INTERACTIONS
Authors	:	Brown, K.A.; De Meester, P.; Blow, D.M.
Deposited on	:	1992-07-06
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

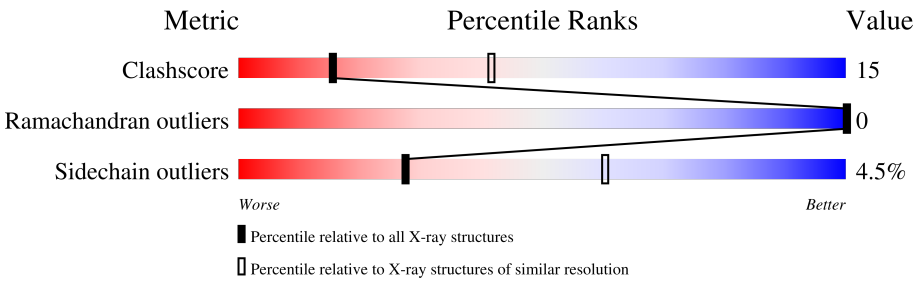
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.80 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	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	E	319	59% 34% 6% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2636 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.

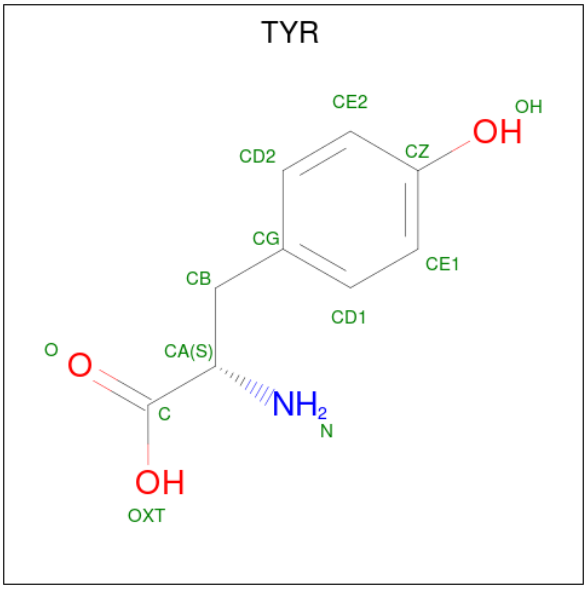
- Molecule 1 is a protein called TYROSYL-tRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	E	317	2461	1570	428	456	7	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	51	ALA	THR	conflict	UNP P00952

- Molecule 2 is TYROSINE (three-letter code: TYR) (formula: $C_9H_{11}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	E	1	13	9	1	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O			
3	E	162	162	162		0	0

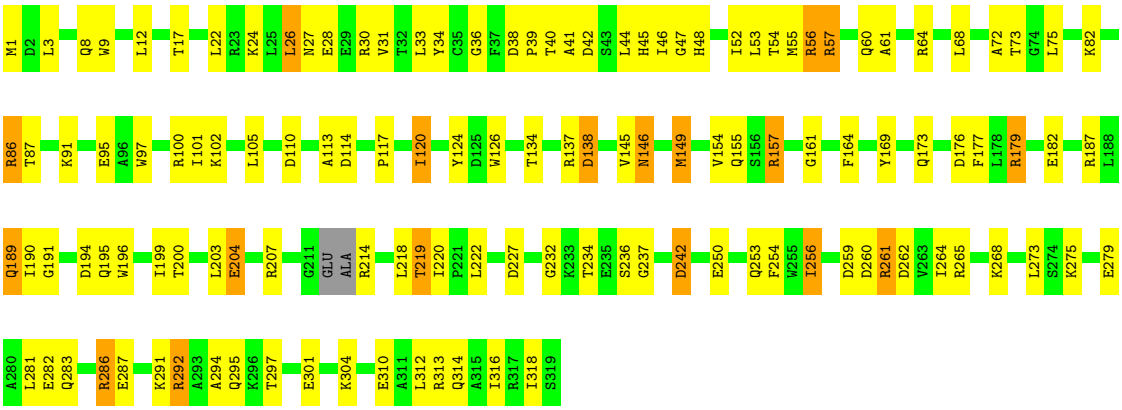
3 Residue-property plots (i)

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: TYROSYL-tRNA SYNTHETASE

Chain E: 59% 34% 6%



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	64.46Å 64.46Å 237.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.205 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2636	wwPDB-VP
Average B, all atoms ($Å^2$)	18.0	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	E	0.95	1/2509 (0.0%)	1.90	56/3393 (1.7%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	287	GLU	CB-CG	-6.17	1.40	1.52

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	86	ARG	CD-NE-CZ	40.10	179.74	123.60
1	E	179	ARG	NE-CZ-NH1	12.45	126.53	120.30
1	E	179	ARG	CD-NE-CZ	10.73	138.62	123.60
1	E	313	ARG	CD-NE-CZ	10.28	138.00	123.60
1	E	56	ARG	NE-CZ-NH2	-10.08	115.26	120.30
1	E	157	ARG	NE-CZ-NH2	-9.99	115.30	120.30
1	E	286	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	E	157	ARG	NE-CZ-NH1	9.32	124.96	120.30
1	E	313	ARG	NE-CZ-NH1	9.00	124.80	120.30
1	E	34	TYR	CB-CG-CD2	8.78	126.27	121.00
1	E	286	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	E	261	ARG	CG-CD-NE	8.19	129.00	111.80
1	E	179	ARG	NE-CZ-NH2	-7.87	116.36	120.30
1	E	64	ARG	CD-NE-CZ	7.81	134.54	123.60
1	E	262	ASP	CB-CG-OD2	7.15	124.74	118.30
1	E	64	ARG	NE-CZ-NH1	7.12	123.86	120.30
1	E	149	MET	CA-CB-CG	7.08	125.34	113.30
1	E	34	TYR	CB-CG-CD1	-6.96	116.83	121.00
1	E	292	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	E	86	ARG	NE-CZ-NH1	6.71	123.66	120.30
1	E	57	ARG	NE-CZ-NH1	6.69	123.64	120.30
1	E	182	GLU	CG-CD-OE2	6.64	131.59	118.30
1	E	138	ASP	CB-CG-OD1	6.51	124.16	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	265	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	E	227	ASP	CB-CG-OD1	6.37	124.03	118.30
1	E	261	ARG	CD-NE-CZ	6.26	132.37	123.60
1	E	204	GLU	CG-CD-OE1	6.18	130.66	118.30
1	E	137	ARG	NE-CZ-NH2	6.16	123.38	120.30
1	E	242	ASP	CB-CG-OD2	6.06	123.75	118.30
1	E	189	GLN	N-CA-CB	6.05	121.49	110.60
1	E	40	THR	CA-CB-OG1	-5.99	96.41	109.00
1	E	219	THR	CA-CB-CG2	5.97	120.76	112.40
1	E	173	GLN	CG-CD-OE1	5.95	133.50	121.60
1	E	137	ARG	CD-NE-CZ	5.89	131.85	123.60
1	E	254	PHE	CB-CG-CD2	-5.77	116.76	120.80
1	E	30	ARG	N-CA-CB	5.69	120.84	110.60
1	E	101	ILE	CA-CB-CG2	5.64	122.17	110.90
1	E	101	ILE	CA-CB-CG1	-5.61	100.34	111.00
1	E	182	GLU	OE1-CD-OE2	-5.59	116.60	123.30
1	E	204	GLU	CG-CD-OE2	-5.56	107.17	118.30
1	E	64	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	E	261	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	E	157	ARG	CA-C-N	5.51	129.31	117.20
1	E	273	LEU	CA-CB-CG	5.43	127.80	115.30
1	E	292	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	E	41	ALA	N-CA-CB	5.40	117.66	110.10
1	E	87	THR	O-C-N	5.35	131.26	122.70
1	E	237	GLY	N-CA-C	-5.29	99.86	113.10
1	E	26	LEU	CA-CB-CG	5.27	127.43	115.30
1	E	164	PHE	CB-CG-CD1	-5.25	117.12	120.80
1	E	250	GLU	CA-CB-CG	5.23	124.91	113.40
1	E	120	ILE	N-CA-CB	5.21	122.78	110.80
1	E	313	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	E	57	ARG	CD-NE-CZ	5.15	130.80	123.60
1	E	101	ILE	CB-CA-C	5.12	121.83	111.60
1	E	157	ARG	N-CA-C	5.02	124.56	111.00

There are no chirality outliers.

There are no planarity outliers.

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	E	2461	0	2394	72	0
2	E	13	0	8	1	0
3	E	162	0	0	3	1
All	All	2636	0	2402	72	1

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 (72) 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:E:45:HIS:H	1:E:48:HIS:HD2	1.21	0.86
1:E:82:LYS:HD3	1:E:86:ARG:HH11	1.45	0.80
1:E:110:ASP:OD2	1:E:113:ALA:HB2	1.91	0.71
1:E:45:HIS:H	1:E:48:HIS:CD2	2.07	0.69
1:E:36:GLY:HA3	2:E:320:TYR:CD1	2.31	0.66
1:E:82:LYS:CD	1:E:86:ARG:HH11	2.11	0.64
1:E:234:THR:HG22	1:E:236:SER:H	1.63	0.64
1:E:292:ARG:NH1	1:E:295:GLN:HG2	2.15	0.61
1:E:253:GLN:HA	1:E:256:ILE:HG22	1.83	0.60
1:E:291:LYS:O	1:E:292:ARG:HB2	2.01	0.59
1:E:292:ARG:HH11	1:E:295:GLN:HG2	1.67	0.59
1:E:72:ALA:O	1:E:75:LEU:HB2	2.03	0.59
1:E:314:GLN:O	1:E:318:ILE:HG13	2.02	0.58
1:E:44:LEU:HD13	1:E:52:ILE:HD11	1.85	0.58
1:E:1:MET:N	1:E:27:ASN:HD21	2.01	0.57
1:E:9:TRP:CZ2	1:E:275:LYS:HG3	2.39	0.57
1:E:146:ASN:HB2	3:E:377:HOH:O	2.04	0.57
1:E:102:LYS:HG3	1:E:120:ILE:HG21	1.86	0.56
1:E:187:ARG:HD3	1:E:214:ARG:O	2.06	0.56
1:E:196:TRP:HE3	1:E:219:THR:HG23	1.69	0.56
1:E:3:LEU:HD22	1:E:61:ALA:HB3	1.88	0.55
1:E:82:LYS:CG	1:E:86:ARG:HH11	2.19	0.55
1:E:54:THR:HG21	1:E:220:ILE:HD11	1.87	0.55
1:E:82:LYS:HD3	1:E:86:ARG:NH1	2.20	0.55
1:E:149:MET:O	1:E:155:GLN:HG2	2.08	0.54
1:E:48:HIS:O	1:E:52:ILE:HG13	2.09	0.53
1:E:3:LEU:HD22	1:E:61:ALA:CB	2.38	0.53
1:E:195:GLN:O	1:E:199:ILE:HG13	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:145:VAL:O	1:E:149:MET:HG2	2.09	0.52
1:E:275:LYS:NZ	1:E:279:GLU:OE2	2.35	0.52
1:E:310:GLU:O	1:E:314:GLN:HG3	2.10	0.52
1:E:45:HIS:CE1	1:E:47:GLY:HA3	2.45	0.51
1:E:264:ILE:O	1:E:268:LYS:HG3	2.10	0.51
1:E:194:ASP:OD1	1:E:195:GLN:HG2	2.10	0.51
1:E:100:ARG:NH2	1:E:242:ASP:OD2	2.40	0.51
1:E:187:ARG:HG3	3:E:321:HOH:O	2.11	0.50
1:E:17:THR:HG21	1:E:203:LEU:CD1	2.42	0.49
1:E:256:ILE:O	1:E:292:ARG:NH1	2.45	0.49
1:E:283:GLN:HG3	1:E:286:ARG:NH1	2.28	0.48
1:E:157:ARG:O	1:E:161:GLY:N	2.44	0.47
1:E:312:LEU:O	1:E:316:ILE:HG13	2.15	0.46
1:E:46:ILE:HD11	1:E:232:GLY:HA2	1.98	0.46
1:E:126:TRP:HB2	3:E:364:HOH:O	2.16	0.46
1:E:264:ILE:HG22	1:E:268:LYS:HE3	1.98	0.46
1:E:53:LEU:O	1:E:57:ARG:HG3	2.17	0.45
1:E:27:ASN:HD22	1:E:27:ASN:N	2.15	0.44
1:E:12:LEU:O	1:E:220:ILE:HD13	2.17	0.44
1:E:24:LYS:NZ	1:E:28:GLU:OE2	2.50	0.44
1:E:191:GLY:O	1:E:219:THR:HA	2.17	0.44
1:E:297:THR:O	1:E:301:GLU:HG2	2.18	0.44
1:E:189:GLN:HG2	1:E:190:ILE:N	2.31	0.44
1:E:9:TRP:CH2	1:E:275:LYS:HA	2.53	0.44
1:E:52:ILE:O	1:E:55:MET:HB2	2.18	0.43
1:E:259:ASP:OD1	1:E:260:ASP:N	2.52	0.43
1:E:38:ASP:HA	1:E:39:PRO:HD3	1.84	0.43
1:E:154:VAL:O	1:E:155:GLN:C	2.56	0.43
1:E:26:LEU:HD23	1:E:31:VAL:HG21	2.01	0.43
1:E:281:LEU:HD22	1:E:294:ALA:HA	2.01	0.43
1:E:190:ILE:HA	1:E:218:LEU:O	2.19	0.42
1:E:91:LYS:O	1:E:95:GLU:HB2	2.19	0.42
1:E:282:GLU:HB3	1:E:283:GLN:NE2	2.35	0.42
1:E:56:ARG:O	1:E:60:GLN:HG3	2.20	0.41
1:E:72:ALA:HB2	1:E:124:TYR:HA	2.02	0.41
1:E:196:TRP:O	1:E:200:THR:HG23	2.20	0.41
1:E:105:LEU:HD23	1:E:105:LEU:HA	1.93	0.41
1:E:42:ASP:HB3	1:E:97:TRP:CD1	2.56	0.41
1:E:113:ALA:O	1:E:117:PRO:HB3	2.21	0.41
1:E:73:THR:HB	1:E:169:TYR:CE2	2.57	0.40
1:E:22:LEU:O	1:E:26:LEU:HG	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:134:THR:O	1:E:138:ASP:HB2	2.21	0.40
1:E:126:TRP:NE1	1:E:176:ASP:OD1	2.51	0.40
1:E:204:GLU:OE2	1:E:207:ARG:NH2	2.53	0.40

All (1) 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)
3:E:379:HOH:O	3:E:414:HOH:O[5_664]	1.74	0.46

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	E	313/319 (98%)	303 (97%)	10 (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	E	244/268 (91%)	233 (96%)	11 (4%)	27 60

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	8	GLN
1	E	33	LEU
1	E	68	LEU
1	E	114	ASP
1	E	146	ASN
1	E	177	PHE
1	E	179	ARG
1	E	222	LEU
1	E	256	ILE
1	E	261	ARG
1	E	304	LYS

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

Mol	Chain	Res	Type
1	E	27	ASN
1	E	48	HIS
1	E	60	GLN
1	E	257	ASN
1	E	283	GLN
1	E	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 monosaccharides 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	TYR	E	320	-	12,13,13	0.82	0	16,17,17	0.99	1 (6%)

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	TYR	E	320	-	-	2/8/8/8	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	320	TYR	CG-CB-CA	2.91	120.19	114.13

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	320	TYR	CA-CB-CG-CD1
2	E	320	TYR	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	320	TYR	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 (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.