



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:12 PM UTC

PDB ID : 1I7S / pdb_00001i7s
Title : ANTHRANILATE SYNTHASE FROM SERRATIA MARCESCENS IN
COMPLEX WITH ITS END PRODUCT INHIBITOR L-TRYPTOPHAN
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Deposited on : 2001-03-10
Resolution : 2.40 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
Mogul : 2022.3.0, CSD as543be (2022)
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

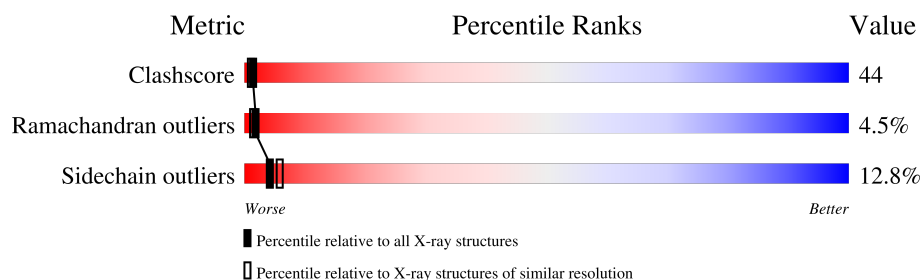
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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	519	41% 41% 14% ..
1	C	519	43% 41% 12% ..
2	B	193	39% 43% 14% ..
2	D	193	37% 45% 15% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10880 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 ANTHRANILATE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	511	Total	C	N	O	S	0	0	0
			3966	2474	721	753	18			
1	C	511	Total	C	N	O	S	0	0	0
			3966	2474	721	753	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	ARG	PRO	SEE REMARK 999	UNP P00897
A	83	LEU	VAL	see remark 999	UNP P00897
A	130	ILE	LEU	see remark 999	UNP P00897
A	164	LEU	VAL	see remark 999	UNP P00897
A	459	VAL	HIS	see remark 999	UNP P00897
A	461	ASN	HIS	see remark 999	UNP P00897
A	492	PRO	ARG	see remark 999	UNP P00897
A	493	GLU	ARG	see remark 999	UNP P00897
C	60	ARG	PRO	see remark 999	UNP P00897
C	83	LEU	VAL	see remark 999	UNP P00897
C	130	ILE	LEU	see remark 999	UNP P00897
C	164	LEU	VAL	see remark 999	UNP P00897
C	459	VAL	HIS	see remark 999	UNP P00897
C	461	ASN	HIS	see remark 999	UNP P00897
C	492	PRO	ARG	see remark 999	UNP P00897
C	493	GLU	ARG	see remark 999	UNP P00897

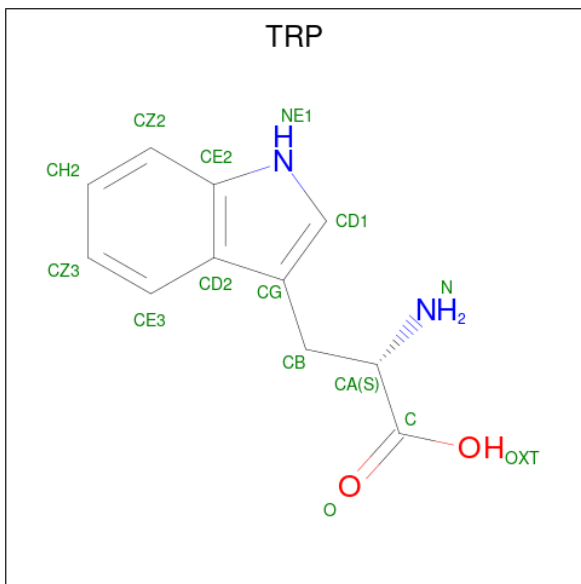
- Molecule 2 is a protein called TRPG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	192	Total	C	N	O	S	0	0	0
			1459	917	265	267	10			
2	D	192	Total	C	N	O	S	0	0	0
			1459	917	265	267	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	152	PHE	SER	see remark 999	UNP P00900
D	152	PHE	SER	see remark 999	UNP P00900

- Molecule 3 is TRYPTOPHAN (CCD ID: TRP) (formula: $C_{11}H_{12}N_2O_2$).



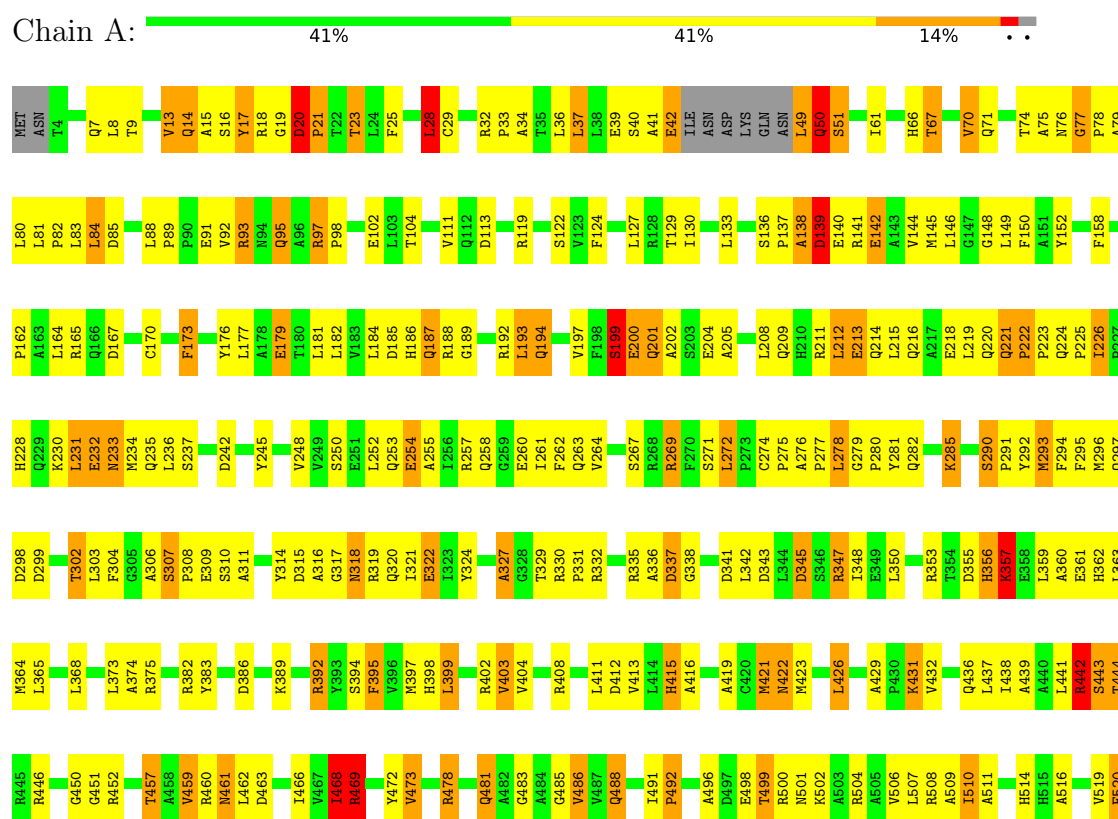
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			15	11	2	2		
3	C	1	Total	C	N	O	0	0
			15	11	2	2		

3 Residue-property plots

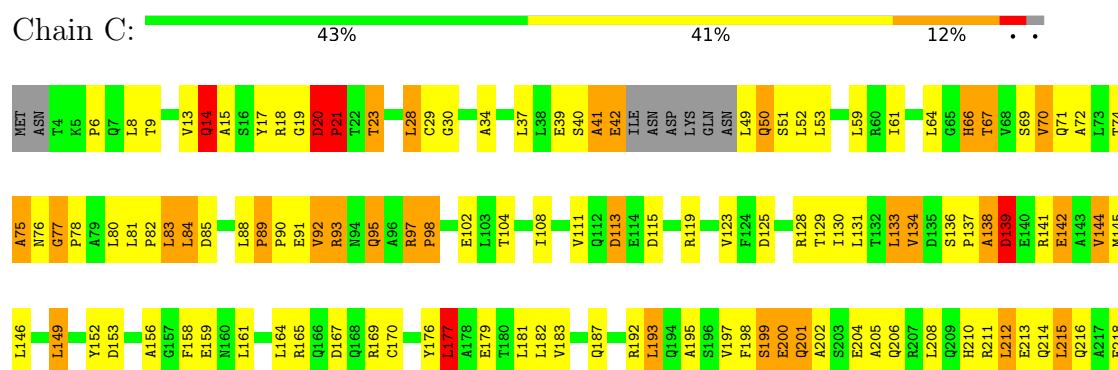
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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.

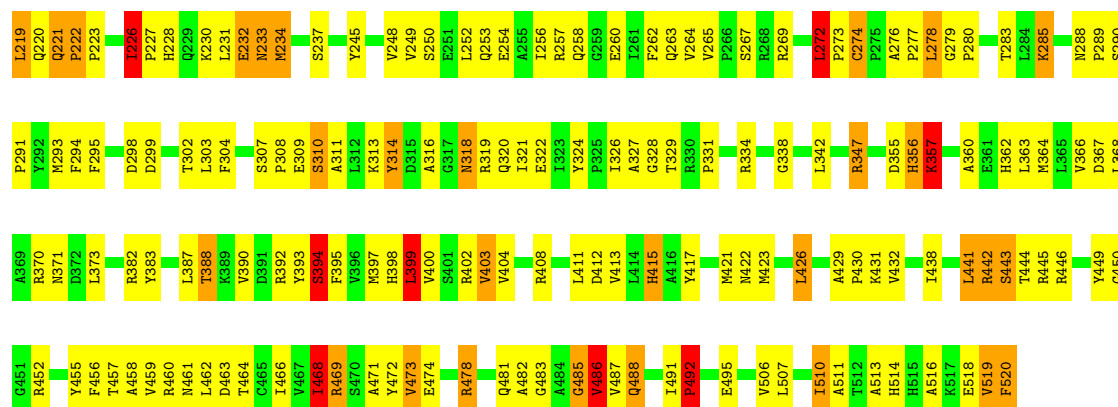
Note EDS was not executed.

• Molecule 1: ANTHRANILATE SYNTHASE

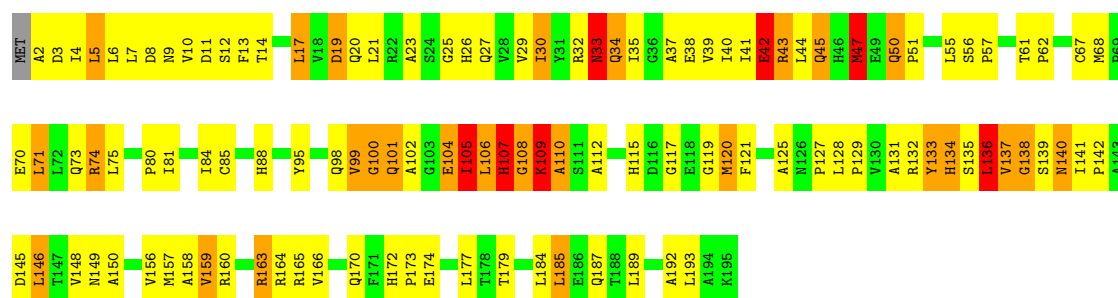


• Molecule 1: ANTHRANILATE SYNTHASE

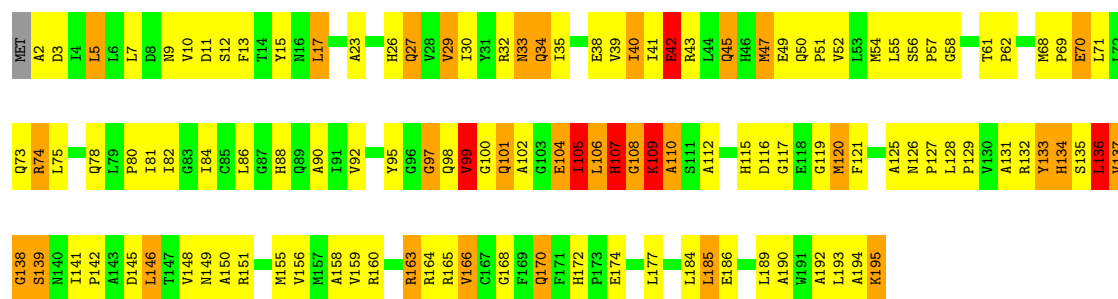




• Molecule 2: TRPG



• Molecule 2: TRPG



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.27Å 123.56Å 179.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.90 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (44.90-2.40)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0 REFMAC, REFMAC	Depositor
R, R_{free}	0.247 , 0.318	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	10880	wwPDB-VP
Average B, all atoms (Å ²)	60.0	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	1.05	4/4035 (0.1%)	1.39	50/5474 (0.9%)
1	C	1.06	6/4035 (0.1%)	1.37	42/5474 (0.8%)
2	B	1.31	7/1487 (0.5%)	1.50	23/2015 (1.1%)
2	D	1.09	5/1487 (0.3%)	1.42	19/2015 (0.9%)
All	All	1.10	22/11044 (0.2%)	1.40	134/14978 (0.9%)

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	1
1	C	0	1
2	D	0	1
All	All	0	3

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	157	MET	SD-CE	-10.12	1.54	1.79
1	C	468	ILE	C-O	6.99	1.31	1.23
2	B	45	GLN	CD-OE1	6.62	1.36	1.23
1	A	70	VAL	CA-CB	6.60	1.62	1.54
2	D	47	MET	SD-CE	6.53	1.95	1.79

The worst 5 of 134 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	146	LEU	N-CA-C	-12.15	84.62	107.71
1	C	20	ASP	CA-C-N	10.88	133.44	119.84
1	C	20	ASP	C-N-CA	10.88	133.44	119.84
2	D	146	LEU	N-CA-C	-10.84	82.66	107.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	222	PRO	N-CA-C	9.79	122.64	110.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	PHE	Sidechain
1	C	314	TYR	Sidechain
2	D	15	TYR	Sidechain

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	3966	0	3940	350	0
1	C	3966	0	3940	331	0
2	B	1459	0	1459	148	0
2	D	1459	0	1459	152	0
3	A	15	0	9	1	0
3	C	15	0	9	2	0
All	All	10880	0	10816	959	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 44.

The worst 5 of 959 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:263:GLN:NE2	1:A:364:MET:HG2	1.42	1.32
1:C:263:GLN:NE2	1:C:364:MET:HG2	1.44	1.28
2:D:41:ILE:HG22	2:D:45:GLN:HE21	1.15	1.09
1:C:263:GLN:HE22	1:C:364:MET:HG2	0.92	1.06
2:B:163:ARG:NH1	2:B:163:ARG:H	1.54	1.05

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	507/519 (98%)	449 (89%)	36 (7%)	22 (4%)	2	1
1	C	507/519 (98%)	449 (89%)	39 (8%)	19 (4%)	2	2
2	B	190/193 (98%)	162 (85%)	18 (10%)	10 (5%)	1	1
2	D	190/193 (98%)	158 (83%)	20 (10%)	12 (6%)	1	0
All	All	1394/1424 (98%)	1218 (87%)	113 (8%)	63 (4%)	2	1

5 of 63 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	ASP
1	A	21	PRO
1	A	139	ASP
1	A	201	GLN
1	A	221	GLN

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	422/434 (97%)	371 (88%)	51 (12%)	5	7
1	C	422/434 (97%)	370 (88%)	52 (12%)	4	6
2	B	152/153 (99%)	130 (86%)	22 (14%)	3	4
2	D	152/153 (99%)	130 (86%)	22 (14%)	3	4
All	All	1148/1174 (98%)	1001 (87%)	147 (13%)	4	6

5 of 147 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	441	LEU
2	D	170	GLN
1	C	478	ARG
2	D	42	GLU
1	A	488	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 57 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	140	ASN
2	D	170	GLN
1	C	228	HIS
2	D	115	HIS
2	D	27	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are 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
3	TRP	A	601	-	15,16,16	1.30	3 (20%)	18,22,22	0.40	0
3	TRP	C	701	-	15,16,16	1.38	3 (20%)	18,22,22	0.43	0

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
3	TRP	A	601	-	-	0/8/8/8	0/2/2/2
3	TRP	C	701	-	-	1/8/8/8	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	TRP	CB-CG	-2.62	1.45	1.50
3	C	701	TRP	OXT-C	-2.37	1.23	1.30
3	C	701	TRP	CD1-NE1	2.29	1.40	1.37
3	A	601	TRP	CZ3-CE3	2.29	1.42	1.38
3	A	601	TRP	O-C	2.07	1.28	1.22

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	701	TRP	OXT-C-CA-N

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	TRP	1	0
3	C	701	TRP	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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.