



# wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 13, 2020 – 10:07 AM BST

PDB ID : 1QAW  
Title : Regulatory Features of the TRP Operon and the Crystal Structure of the TRP RNA-Binding Attenuation Protein from *Bacillus Stearothermophilus*.  
Authors : Chen, X.-P.; Antson, A.A.; Yang, M.; Baumann, C.; Dodson, E.J.; Dodson, G.G.; Gollnick, P.  
Deposited on : 1999-03-31  
Resolution : 2.50 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](mailto: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.

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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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.14.4.dev1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

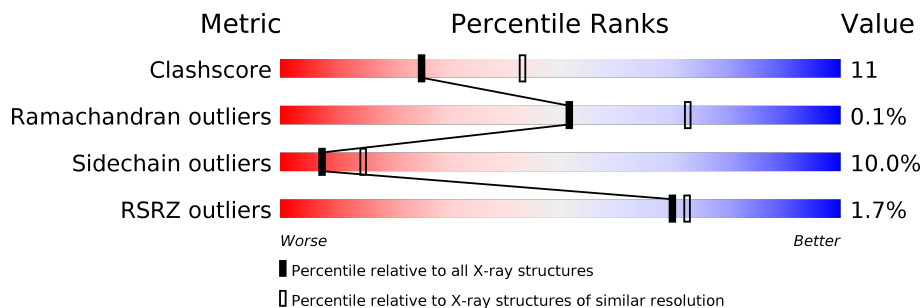
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 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  $\leq 5\%$ . 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.

Mol	Chain	Length	Quality of chain
1	A	74	
1	B	74	
1	C	74	
1	D	74	
1	E	74	
1	F	74	
1	G	74	

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Mol	Chain	Length	Quality of chain
1	H	74	
1	I	74	
1	J	74	
1	K	74	

## 2 Entry composition [i](#)

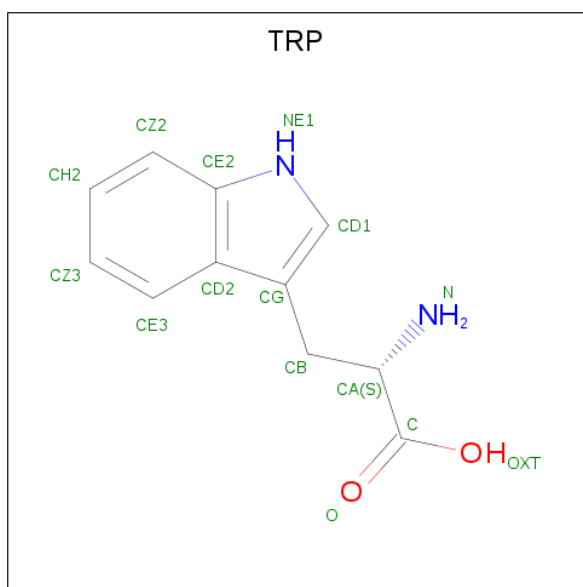
There are 3 unique types of molecules in this entry. The entry contains 6240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 TRP RNA-BINDING ATTENUATION PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	67	527	330	95	102	5	1	0
1	B	70	550	344	100	106	10	1	0
1	C	69	536	336	98	102	5	0	0
1	D	69	536	336	98	102	11	0	0
1	E	69	536	336	98	102	7	0	0
1	F	68	527	330	96	101	10	0	0
1	G	67	529	331	98	100	6	1	0
1	H	68	527	330	96	101	4	0	0
1	I	67	523	328	95	100	30	0	0
1	J	67	523	328	95	100	15	0	0
1	K	68	531	332	96	103	13	1	0

- Molecule 2 is TRYPTOPHAN (three-letter code: TRP) (formula:  $C_{11}H_{12}N_2O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			15	11	2	2		
2	B	1	Total	C	N	O	0	0
			15	11	2	2		
2	C	1	Total	C	N	O	0	0
			15	11	2	2		
2	D	1	Total	C	N	O	0	0
			15	11	2	2		
2	E	1	Total	C	N	O	0	0
			15	11	2	2		
2	G	1	Total	C	N	O	0	0
			15	11	2	2		
2	G	1	Total	C	N	O	0	0
			15	11	2	2		
2	H	1	Total	C	N	O	0	0
			15	11	2	2		
2	I	1	Total	C	N	O	0	0
			15	11	2	2		
2	J	1	Total	C	N	O	0	0
			15	11	2	2		
2	K	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	22	Total	O	0	0
			22	22		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	B	20	Total 20	O 20	0	0
3	C	28	Total 28	O 28	0	0
3	D	37	Total 37	O 37	0	0
3	E	49	Total 49	O 49	0	0
3	F	28	Total 28	O 28	0	0
3	G	19	Total 19	O 19	0	0
3	H	11	Total 11	O 11	0	0
3	I	6	Total 6	O 6	0	0
3	J	5	Total 5	O 5	0	0
3	K	5	Total 5	O 5	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 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.

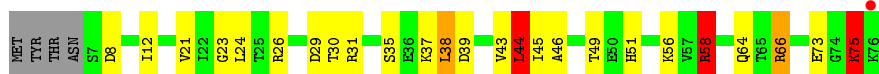
- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain A: 



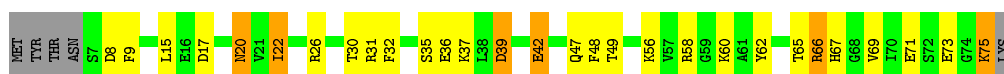
- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain B: 



- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain C: 



- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain D: 



- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain E: 



- Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN

Chain F: 



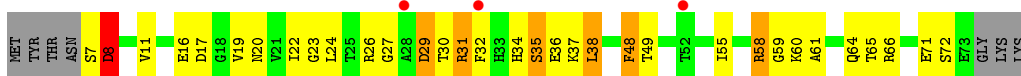
• Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN



• Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN



• Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN



• Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN



• Molecule 1: TRP RNA-BINDING ATTENUATION PROTEIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.93Å 117.96Å 147.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.50 14.96 – 2.50	Depositor EDS
% Data completeness (in resolution range)	90.4 (15.00-2.50) 90.2 (14.96-2.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 2.51Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.215 , 0.299 0.203 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.2	Xtrriage
Anisotropy	0.538	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 75.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6240	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.84	2/539 (0.4%)	1.94	16/724 (2.2%)
1	B	0.85	2/562 (0.4%)	1.99	15/751 (2.0%)
1	C	1.82	2/543 (0.4%)	2.24	28/728 (3.8%)
1	D	0.94	2/543 (0.4%)	2.12	27/728 (3.7%)
1	E	0.87	0/543	2.02	11/728 (1.5%)
1	F	0.83	0/534	1.99	15/717 (2.1%)
1	G	0.74	0/541	1.83	13/726 (1.8%)
1	H	0.58	0/534	1.64	10/717 (1.4%)
1	I	0.96	3/530 (0.6%)	1.88	13/712 (1.8%)
1	J	0.83	2/530 (0.4%)	1.57	10/712 (1.4%)
1	K	0.69	1/543 (0.2%)	1.75	10/729 (1.4%)
All	All	0.96	14/5942 (0.2%)	1.92	168/7972 (2.1%)

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	7
1	C	0	3
1	D	0	2
1	E	0	4
1	F	0	5
1	G	0	3
1	H	0	4
1	I	0	2
1	J	0	3
1	K	0	3
All	All	0	42

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	75	LYS	CE-NZ	38.06	2.44	1.49
1	I	37	LYS	CD-CE	-13.99	1.16	1.51
1	J	32	PHE	CB-CG	-11.04	1.32	1.51
1	I	38	LEU	CA-CB	10.28	1.77	1.53
1	J	40	LYS	CA-CB	-9.56	1.32	1.53

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	58	ARG	CD-NE-CZ	17.36	147.90	123.60
1	A	66	ARG	NE-CZ-NH2	16.26	128.43	120.30
1	B	75	LYS	CB-CG-CD	16.18	153.66	111.60
1	C	75	LYS	CD-CE-NZ	-15.40	76.27	111.70
1	E	8	ASP	CB-CG-OD2	-14.59	105.17	118.30

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	ARG	Mainchain
1	A	28	ALA	Mainchain
1	A	35	SER	Mainchain
1	A	37	LYS	Mainchain
1	A	56	LYS	Mainchain

## 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	527	0	527	25	0
1	B	550	0	556	15	1
1	C	536	0	541	11	0
1	D	536	0	541	4	0
1	E	536	0	541	6	0
1	F	527	0	528	9	0
1	G	529	0	534	16	0
1	H	527	0	528	10	0
1	I	523	0	525	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	523	0	525	16	0
1	K	531	0	530	23	1
2	A	15	0	9	3	0
2	B	15	0	9	1	0
2	C	15	0	9	1	0
2	D	15	0	9	1	0
2	E	15	0	9	0	0
2	G	30	0	18	1	0
2	H	15	0	9	1	0
2	I	15	0	9	1	0
2	J	15	0	9	0	0
2	K	15	0	9	3	0
3	A	22	0	0	0	0
3	B	20	0	0	1	0
3	C	28	0	0	0	0
3	D	37	0	0	0	0
3	E	49	0	0	2	0
3	F	28	0	0	0	0
3	G	19	0	0	0	0
3	H	11	0	0	0	0
3	I	6	0	0	0	0
3	J	5	0	0	0	0
3	K	5	0	0	0	0
All	All	6240	0	5975	125	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 11.

The worst 5 of 125 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:66:ARG:HH12	1:B:66:ARG:HD2	1.23	0.99
1:B:66:ARG:HH22	1:C:66:ARG:HE	1.12	0.94
1:I:20:ASN:HD22	1:I:58:ARG:HH21	0.97	0.94
1:B:66:ARG:NH2	1:C:66:ARG:HE	1.65	0.93
1:J:22:ILE:HD12	1:J:56:LYS:HD3	1.65	0.79

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)
1:B:75:LYS:NZ	1:K:17:ASP:OD2[3_545]	1.53	0.67

### 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	66/74 (89%)	64 (97%)	2 (3%)	0	100	100
1	B	69/74 (93%)	67 (97%)	2 (3%)	0	100	100
1	C	67/74 (90%)	64 (96%)	3 (4%)	0	100	100
1	D	67/74 (90%)	67 (100%)	0	0	100	100
1	E	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
1	F	66/74 (89%)	66 (100%)	0	0	100	100
1	G	66/74 (89%)	65 (98%)	1 (2%)	0	100	100
1	H	66/74 (89%)	65 (98%)	1 (2%)	0	100	100
1	I	65/74 (88%)	62 (95%)	2 (3%)	1 (2%)	10	18
1	J	65/74 (88%)	62 (95%)	3 (5%)	0	100	100
1	K	67/74 (90%)	66 (98%)	1 (2%)	0	100	100
All	All	731/814 (90%)	713 (98%)	17 (2%)	1 (0%)	51	73

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	8	ASP

#### 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	57/62 (92%)	52 (91%)	5 (9%)	10	19
1	B	59/62 (95%)	56 (95%)	3 (5%)	24	45
1	C	57/62 (92%)	53 (93%)	4 (7%)	15	29
1	D	57/62 (92%)	53 (93%)	4 (7%)	15	29
1	E	57/62 (92%)	53 (93%)	4 (7%)	15	29
1	F	56/62 (90%)	50 (89%)	6 (11%)	6	13
1	G	57/62 (92%)	50 (88%)	7 (12%)	4	9
1	H	56/62 (90%)	48 (86%)	8 (14%)	3	6
1	I	56/62 (90%)	48 (86%)	8 (14%)	3	6
1	J	56/62 (90%)	51 (91%)	5 (9%)	9	19
1	K	57/62 (92%)	46 (81%)	11 (19%)	1	2
All	All	625/682 (92%)	560 (90%)	65 (10%)	7	13

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	35	SER
1	H	29	ASP
1	K	45	ILE
1	G	37	LYS
1	H	8	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	H	20	ASN
1	I	20	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

11 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
2	TRP	G	81	-	12,16,16	0.73	0	12,22,22	1.73	2 (16%)
2	TRP	A	81	-	12,16,16	0.86	0	12,22,22	1.42	1 (8%)
2	TRP	C	81	-	12,16,16	0.94	1 (8%)	12,22,22	0.76	0
2	TRP	B	81	-	12,16,16	0.72	0	12,22,22	1.38	2 (16%)
2	TRP	I	81	-	12,16,16	0.61	0	12,22,22	1.04	1 (8%)
2	TRP	K	81	-	12,16,16	0.62	0	12,22,22	1.14	1 (8%)
2	TRP	J	81	-	12,16,16	0.70	0	12,22,22	1.13	1 (8%)
2	TRP	D	81	-	12,16,16	0.86	0	12,22,22	1.07	0
2	TRP	G	82	-	12,16,16	0.73	0	12,22,22	1.14	1 (8%)
2	TRP	H	81	-	12,16,16	0.55	0	12,22,22	0.82	0
2	TRP	E	81	-	12,16,16	0.78	0	12,22,22	1.14	2 (16%)

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	TRP	G	81	-	-	0/3/8/8	0/2/2/2
2	TRP	A	81	-	-	0/3/8/8	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TRP	C	81	-	-	0/3/8/8	0/2/2/2
2	TRP	B	81	-	-	0/3/8/8	0/2/2/2
2	TRP	I	81	-	-	1/3/8/8	0/2/2/2
2	TRP	K	81	-	-	0/3/8/8	0/2/2/2
2	TRP	J	81	-	-	0/3/8/8	0/2/2/2
2	TRP	D	81	-	-	1/3/8/8	0/2/2/2
2	TRP	G	82	-	-	0/3/8/8	0/2/2/2
2	TRP	H	81	-	-	0/3/8/8	0/2/2/2
2	TRP	E	81	-	-	0/3/8/8	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	81	TRP	CZ3-CE3	2.02	1.41	1.36

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	81	TRP	CB-CA-C	4.34	117.71	110.69
2	A	81	TRP	CB-CG-CD1	-3.44	123.71	127.97
2	E	81	TRP	CB-CA-C	2.78	115.19	110.69
2	G	82	TRP	CZ3-CE3-CD2	-2.62	117.26	120.89
2	B	81	TRP	CZ3-CE3-CD2	-2.60	117.28	120.89

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	81	TRP	C-CA-CB-CG
2	I	81	TRP	C-CA-CB-CG

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	81	TRP	3	0
2	C	81	TRP	1	0
2	B	81	TRP	1	0
2	I	81	TRP	1	0
2	K	81	TRP	3	0
2	D	81	TRP	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	82	TRP	1	0
2	H	81	TRP	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](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	67/74 (90%)	-0.33	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	42, 59, 74, 80	2 (2%)
1	B	70/74 (94%)	-0.44	1 (1%) <span style="border: 1px solid blue; padding: 2px;">75</span> <span style="border: 1px solid blue; padding: 2px;">77</span>	36, 51, 65, 85	3 (4%)
1	C	69/74 (93%)	-0.68	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	31, 43, 63, 75	2 (2%)
1	D	69/74 (93%)	-0.79	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	30, 37, 52, 65	3 (4%)
1	E	69/74 (93%)	-0.70	1 (1%) <span style="border: 1px solid blue; padding: 2px;">75</span> <span style="border: 1px solid blue; padding: 2px;">77</span>	29, 37, 52, 75	2 (2%)
1	F	68/74 (91%)	-0.64	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	33, 44, 58, 69	2 (2%)
1	G	67/74 (90%)	-0.48	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	41, 54, 67, 78	1 (1%)
1	H	68/74 (91%)	0.16	2 (2%) <span style="border: 1px solid blue; padding: 2px;">51</span> <span style="border: 1px solid blue; padding: 2px;">55</span>	54, 71, 88, 92	1 (1%)
1	I	67/74 (90%)	0.31	3 (4%) <span style="border: 1px solid red; padding: 2px;">33</span> <span style="border: 1px solid red; padding: 2px;">36</span>	65, 80, 90, 96	7 (10%)
1	J	67/74 (90%)	0.33	4 (5%) <span style="border: 1px solid red; padding: 2px;">21</span> <span style="border: 1px solid red; padding: 2px;">22</span>	63, 77, 90, 93	3 (4%)
1	K	68/74 (91%)	0.04	2 (2%) <span style="border: 1px solid blue; padding: 2px;">51</span> <span style="border: 1px solid blue; padding: 2px;">55</span>	52, 69, 82, 88	3 (4%)
All	All	749/814 (92%)	-0.30	13 (1%) <span style="border: 1px solid blue; padding: 2px;">70</span> <span style="border: 1px solid blue; padding: 2px;">72</span>	29, 57, 85, 96	29 (3%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	75	LYS	3.9
1	I	28	ALA	3.7
1	J	28	ALA	3.6
1	J	15	LEU	3.5
1	K	74	GLY	3.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	TRP	I	81	15/15	0.91	0.22	70,74,82,83	0
2	TRP	J	81	15/15	0.91	0.20	67,69,74,75	0
2	TRP	H	81	15/15	0.91	0.23	74,79,88,90	0
2	TRP	K	81	15/15	0.93	0.16	41,52,61,62	0
2	TRP	G	82	15/15	0.94	0.16	53,59,66,69	0
2	TRP	A	81	15/15	0.96	0.13	38,45,50,51	0
2	TRP	G	81	15/15	0.96	0.13	29,44,51,53	0
2	TRP	E	81	15/15	0.97	0.17	28,39,43,44	0
2	TRP	B	81	15/15	0.98	0.14	24,37,46,47	0
2	TRP	D	81	15/15	0.99	0.10	25,30,36,36	0
2	TRP	C	81	15/15	0.99	0.10	20,32,39,40	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.