



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 15, 2026 – 01:01 AM UTC

PDB ID : 1TRO / pdb_00001tro
Title : CRYSTAL STRUCTURE OF TRP REPRESSOR OPERATOR COMPLEX
AT ATOMIC RESOLUTION
Authors : Otwinowski, Z.; Schevitz, R.W.; Zhang, R.-G.; Lawson, C.L.; Joachimiak, A.;
Marmorstein, R.; Luisi, B.F.; Sigler, P.B.
Deposited on : 1992-08-30
Resolution : 1.90 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)
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

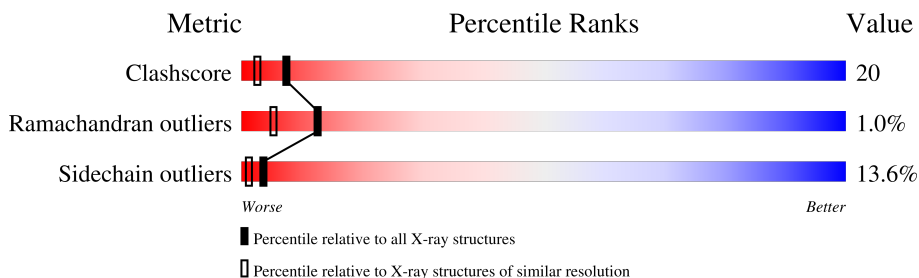
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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	I	19	
1	J	19	
1	K	19	
1	L	19	
2	A	108	
2	C	108	
2	E	108	
2	G	108	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5373 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 DNA chain called DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP*TP*AP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	I	19	Total	C	N	O	P	0	0	0
			386	187	68	113	18			
1	J	19	Total	C	N	O	P	0	0	0
			386	187	68	113	18			
1	K	19	Total	C	N	O	P	0	0	0
			386	187	68	113	18			
1	L	19	Total	C	N	O	P	0	0	0
			386	187	68	113	18			

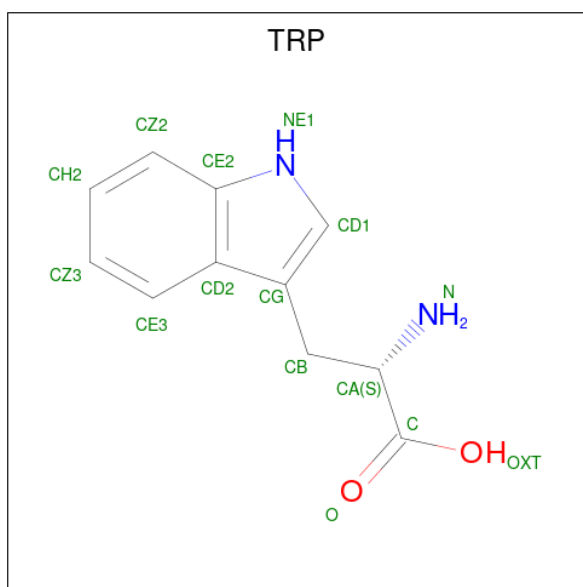
- Molecule 2 is a protein called PROTEIN (TRP REPRESSOR).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	104	Total	C	N	O	S	0	0	0
			832	520	149	160	3			
2	C	99	Total	C	N	O	S	0	0	0
			800	500	145	152	3			
2	E	97	Total	C	N	O	S	0	0	0
			769	482	139	146	2			
2	G	101	Total	C	N	O	S	0	0	0
			804	506	145	150	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	GLU	GLN	conflict	UNP P0A881
C	14	GLU	GLN	conflict	UNP P0A881
E	14	GLU	GLN	conflict	UNP P0A881
G	14	GLU	GLN	conflict	UNP P0A881

- Molecule 3 is TRYPTOPHAN (CCD ID: TRP) (formula: C₁₁H₁₂N₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			13	11	2		
3	A	1	Total	C	N	0	0
			13	11	2		
3	E	1	Total	C	N	0	0
			13	11	2		
3	G	1	Total	C	N	0	0
			13	11	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	88	Total	O	0	0
			88	88		
4	J	81	Total	O	0	0
			81	81		
4	K	56	Total	O	0	0
			56	56		
4	L	65	Total	O	0	0
			65	65		
4	A	71	Total	O	0	0
			71	71		
4	C	73	Total	O	0	0
			73	73		
4	E	68	Total	O	0	0
			68	68		
4	G	70	Total	O	0	0
			70	70		

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.

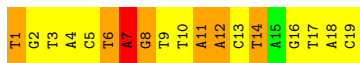
- Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP*T P*AP*C)-3')

Chain I: 

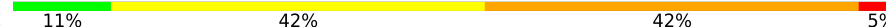


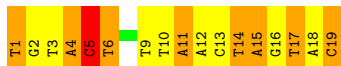
- Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP*T P*AP*C)-3')

Chain J: 



- Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP*T P*AP*C)-3')

Chain K: 



- Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP*T P*AP*C)-3')

Chain L: 



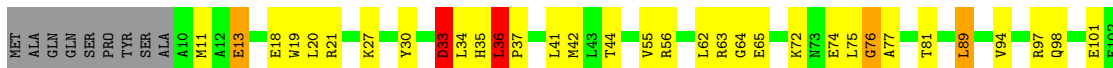
- Molecule 2: PROTEIN (TRP REPRESSOR)

Chain A: 

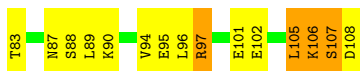
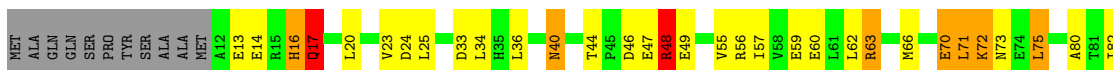




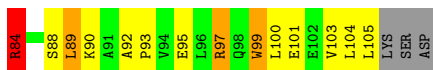
- Molecule 2: PROTEIN (TRP REPRESSOR)



- Molecule 2: PROTEIN (TRP REPRESSOR)



- Molecule 2: PROTEIN (TRP REPRESSOR)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.65Å 72.43Å 107.39Å 90.00° 94.96° 90.00°	Depositor
Resolution (Å)	10.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.167 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	5373	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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	I	2.08	13/432 (3.0%)	2.65	30/665 (4.5%)
1	J	1.94	17/432 (3.9%)	2.41	27/665 (4.1%)
1	K	1.98	13/432 (3.0%)	2.42	25/665 (3.8%)
1	L	1.67	9/432 (2.1%)	2.25	22/665 (3.3%)
2	A	1.30	4/844 (0.5%)	2.12	25/1140 (2.2%)
2	C	1.39	1/810 (0.1%)	1.87	17/1091 (1.6%)
2	E	1.30	0/779	1.94	17/1053 (1.6%)
2	G	1.09	3/816 (0.4%)	2.38	14/1104 (1.3%)
All	All	1.53	60/4977 (1.2%)	2.23	177/7048 (2.5%)

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	I	0	6
1	J	0	5
1	K	0	2
1	L	0	4
2	A	0	4
2	C	0	4
2	E	0	4
2	G	0	2
All	All	0	31

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	1	DT	O3'-P	16.53	1.85	1.61
1	I	5	DC	P-O5'	15.84	1.92	1.60
1	K	5	DC	P-OP1	11.76	1.72	1.48
1	K	15	DA	O3'-P	11.75	1.78	1.61

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	1	DT	O3'-P	10.38	1.76	1.61

The worst 5 of 177 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	54	ARG	CD-NE-CZ	39.69	179.97	124.40
2	G	84	ARG	CD-NE-CZ	32.40	169.75	124.40
2	A	84	ARG	CD-NE-CZ	17.70	149.18	124.40
1	I	3	DT	P-O3'-C3'	17.11	145.86	120.20
1	I	4	DA	O3'-P-O5'	-15.22	81.17	104.00

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	I	1	DT	Sidechain
1	I	10	DT	Sidechain
1	I	13	DC	Sidechain
1	I	7	DA	Sidechain
1	I	9	DT	Sidechain

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	I	386	0	218	6	1
1	J	386	0	218	4	0
1	K	386	0	218	15	0
1	L	386	0	218	16	0
2	A	832	0	834	47	0
2	C	800	0	814	25	1
2	E	769	0	770	39	0
2	G	804	0	813	50	0
3	A	26	0	18	1	0
3	E	13	0	9	0	0
3	G	13	0	9	3	0
4	A	71	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	73	0	0	5	0
4	E	68	0	0	7	0
4	G	70	0	0	7	0
4	I	88	0	0	3	0
4	J	81	0	0	3	0
4	K	56	0	0	4	0
4	L	65	0	0	4	0
All	All	5373	0	4139	181	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 20.

The worst 5 of 181 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)
2:C:98:GLN:HG2	4:C:128:HOH:O	1.39	1.21
2:G:67:SER:OG	2:G:70:GLU:HG3	1.43	1.18
2:C:13:GLU:HG2	4:C:109:HOH:O	1.46	1.15
2:G:71:LEU:HD22	4:G:174:HOH:O	1.48	1.14
2:G:5:SER:N	2:G:8:SER:HB2	1.66	1.10

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:I:10:DT:C2'	2:C:106:LYS:NZ[1_655]	2.06	0.14

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	
2	A	102/108 (94%)	96 (94%)	5 (5%)	1 (1%)	12	5
2	C	97/108 (90%)	94 (97%)	2 (2%)	1 (1%)	12	5
2	E	95/108 (88%)	91 (96%)	2 (2%)	2 (2%)	5	1
2	G	99/108 (92%)	96 (97%)	3 (3%)	0	100	100
All	All	393/432 (91%)	377 (96%)	12 (3%)	4 (1%)	12	5

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	106	LYS
2	E	106	LYS
2	E	107	SER
2	A	107	SER

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	
2	A	89/93 (96%)	75 (84%)	14 (16%)	2	1
2	C	86/93 (92%)	78 (91%)	8 (9%)	8	3
2	E	81/93 (87%)	70 (86%)	11 (14%)	3	1
2	G	85/93 (91%)	71 (84%)	14 (16%)	2	1
All	All	341/372 (92%)	294 (86%)	47 (14%)	3	1

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	40	ASN
2	G	36	LEU
2	E	71	LEU
2	E	105	LEU
2	G	56	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20

such sidechains are listed below:

Mol	Chain	Res	Type
2	E	40	ASN
2	G	35	HIS
2	G	87	ASN
2	G	40	ASN
2	C	28	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](#)

4 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	G	109	-	14,14,16	0.67	0	19,19,22	1.45	2 (10%)
3	TRP	E	109	-	14,14,16	0.79	0	19,19,22	1.87	4 (21%)
3	TRP	A	109	-	14,14,16	0.95	0	19,19,22	1.17	2 (10%)
3	TRP	A	110	-	14,14,16	1.20	1 (7%)	19,19,22	1.18	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	G	109	-	-	2/4/4/8	0/2/2/2
3	TRP	E	109	-	-	2/4/4/8	0/2/2/2
3	TRP	A	109	-	-	0/4/4/8	0/2/2/2
3	TRP	A	110	-	-	0/4/4/8	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	110	TRP	C-CA	2.02	1.64	1.50

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	109	TRP	CA-CB-CG	4.61	121.72	113.55
3	G	109	TRP	C-CA-CB	4.47	117.16	111.72
3	G	109	TRP	CA-CB-CG	3.27	119.35	113.55
3	E	109	TRP	CZ2-CE2-NE1	-3.13	125.73	130.74
3	A	109	TRP	CB-CA-N	-2.86	102.94	110.72

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	109	TRP	N-CA-CB-CG
3	E	109	TRP	C-CA-CB-CG
3	G	109	TRP	N-CA-CB-CG
3	G	109	TRP	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	109	TRP	3	0
3	A	109	TRP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	I	1
1	K	1
1	L	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	1:DT	O3'	2:DG	P	1.85
1	K	15:DA	O3'	16:DG	P	1.78
1	L	1:DT	O3'	2:DG	P	1.76

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.