wwPDB X-ray Structure Validation Summary Report (i)

May 17, 2020 – 03:04 am BST

PDB ID	:	1TRO
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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

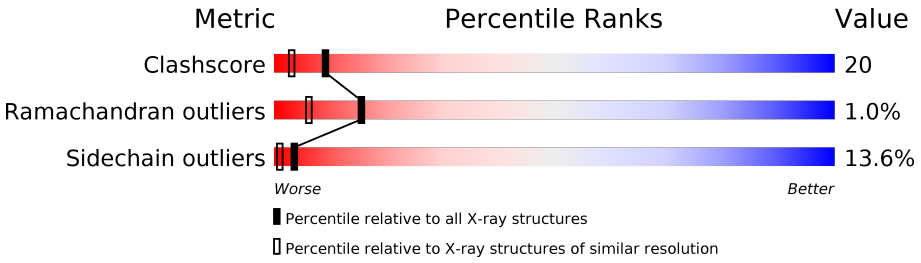
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 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	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (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 on 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	I	19	58% 32% 11%
1	J	19	58% 37% 5%
1	K	19	53% 42% 5%
1	L	19	32% 53% 16%
2	A	108	54% 31% 9% • •
2	C	108	61% 24% • • 8%
2	E	108	53% 25% 10% • 10%
2	G	108	47% 35% 8% • 6%

2 Entry composition (i)

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*T P*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			

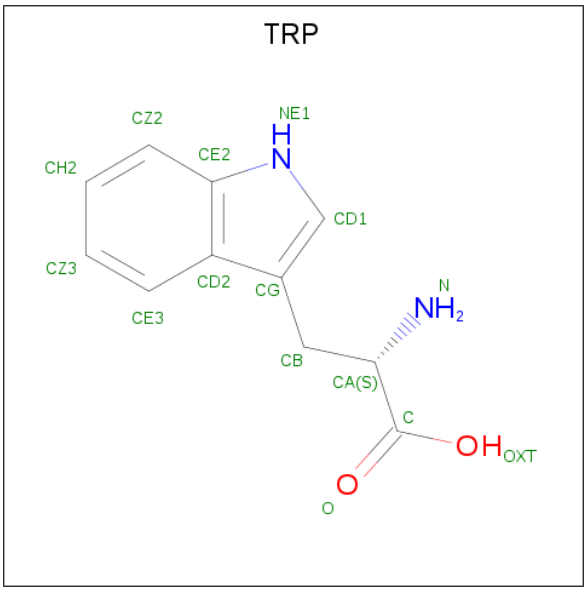
- Molecule 2 is a protein called PROTEIN (TRP REPRESSOR).

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



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

- Molecule 4 is water.

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

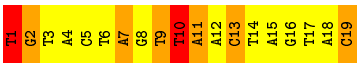
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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:

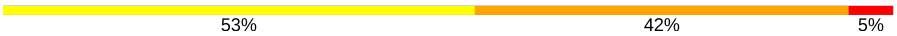


• Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP *T P*AP*C)-3')

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:

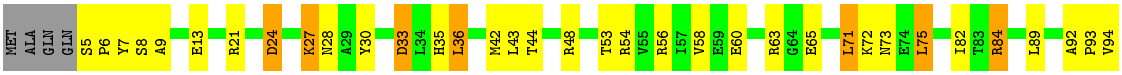


• Molecule 1: DNA (5'-D(*TP*GP*TP*AP*CP*TP*AP*GP*TP*TP*AP*AP*CP*TP*AP*GP *T P*AP*C)-3')

Chain L:

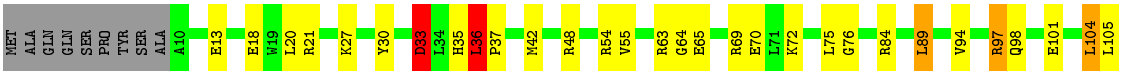
• Molecule 2: PROTEIN (TRP REPRESSOR)

Chain A:



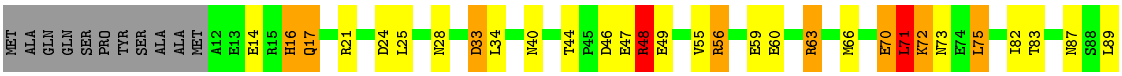
- Molecule 2: PROTEIN (TRP REPRESSOR)

Chain C:



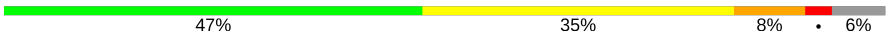
- Molecule 2: PROTEIN (TRP REPRESSOR)

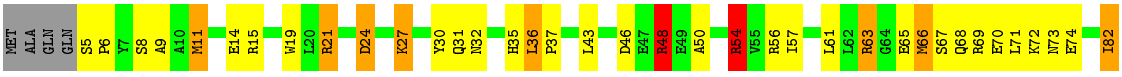
Chain E:



- Molecule 2: PROTEIN (TRP REPRESSOR)

Chain G:





4 Data and refinement statistics (i)

Xtriage (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.	Xtriage
Total number of atoms	5373	wwPDB-VP
Average B, all atoms (Å^2)	32.0	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	I	3.56	39/432 (9.0%)	3.90	111/665 (16.7%)
1	J	3.28	38/432 (8.8%)	3.79	103/665 (15.5%)
1	K	3.12	30/432 (6.9%)	3.69	108/665 (16.2%)
1	L	2.82	31/432 (7.2%)	3.42	95/665 (14.3%)
2	A	1.03	2/844 (0.2%)	1.92	13/1140 (1.1%)
2	C	1.07	0/810	1.62	11/1091 (1.0%)
2	E	1.01	0/779	1.82	13/1053 (1.2%)
2	G	0.88	0/816	2.17	8/1104 (0.7%)
All	All	2.05	140/4977 (2.8%)	2.72	462/7048 (6.6%)

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 140 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	5	DC	P-O5'	32.38	1.92	1.59
1	J	9	DT	P-O5'	21.01	1.80	1.59
1	I	1	DT	O3'-P	20.66	1.85	1.61
1	K	9	DT	P-O5'	20.02	1.79	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	16	DG	P-O5'	18.76	1.78	1.59

The worst 5 of 462 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	54	ARG	CD-NE-CZ	40.26	179.97	123.60
2	G	84	ARG	CD-NE-CZ	32.97	169.75	123.60
2	E	48	ARG	NE-CZ-NH1	-25.11	107.74	120.30
1	I	3	DT	P-O3'-C3'	21.80	145.86	119.70
2	A	84	ARG	NE-CZ-NH1	-19.34	110.63	120.30

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	48	0
2	C	800	0	814	23	1
2	E	769	0	770	36	0
2	G	804	0	813	51	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

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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	178	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 178 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%)	15 6
2	C	97/108 (90%)	94 (97%)	2 (2%)	1 (1%)	15 6
2	E	95/108 (88%)	91 (96%)	2 (2%)	2 (2%)	7 1
2	G	99/108 (92%)	96 (97%)	3 (3%)	0	100 100
All	All	393/432 (91%)	377 (96%)	12 (3%)	4 (1%)	15 6

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%)	76 (85%)	13 (15%)	3 1
2	C	86/93 (92%)	78 (91%)	8 (9%)	9 3
2	E	81/93 (87%)	71 (88%)	10 (12%)	4 1
2	G	85/93 (91%)	69 (81%)	16 (19%)	1 0
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	16	HIS
2	E	33	ASP
2	G	84	ARG
2	E	24	ASP
2	E	71	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such

sidechains are listed below:

Mol	Chain	Res	Type
2	C	73	ASN
2	C	87	ASN
2	E	87	ASN
2	C	40	ASN
2	G	35	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 ligands are modelled in this entry.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

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	L	1
1	K	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

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.