



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 25, 2024 – 05:39 PM EST

PDB ID : 3C2B
Title : Crystal structure of TetR transcriptional regulator from *Agrobacterium tumefaciens*
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Deposited on : 2008-01-24
Resolution : 2.10 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 ⓘ 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

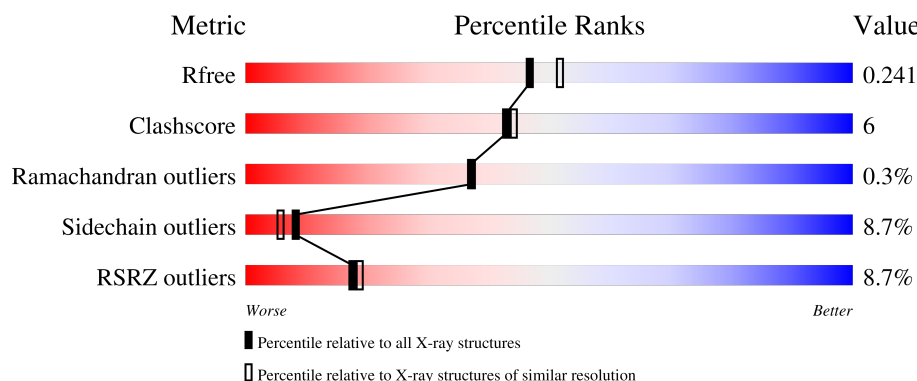
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
R_{free}	164625	6234 (2.10-2.10)
Clashscore	180529	6893 (2.10-2.10)
Ramachandran outliers	177936	6839 (2.10-2.10)
Sidechain outliers	177891	6840 (2.10-2.10)
RSRZ outliers	164620	6234 (2.10-2.10)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	221	
1	B	221	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3192 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 Transcriptional regulator, TetR family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	200	Total	C	N	O	S	Se	0	2	0
			1565	981	293	288	1	2			
1	B	194	Total	C	N	O	S	Se	0	4	0
			1529	958	281	286	2	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A9CID8
A	0	HIS	-	expression tag	UNP A9CID8
A	218	GLY	-	expression tag	UNP A9CID8
A	219	SER	-	expression tag	UNP A9CID8
B	-1	GLY	-	expression tag	UNP A9CID8
B	0	HIS	-	expression tag	UNP A9CID8
B	218	GLY	-	expression tag	UNP A9CID8
B	219	SER	-	expression tag	UNP A9CID8

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			3	1	2		
2	B	1	Total	C	O	0	0
			3	1	2		

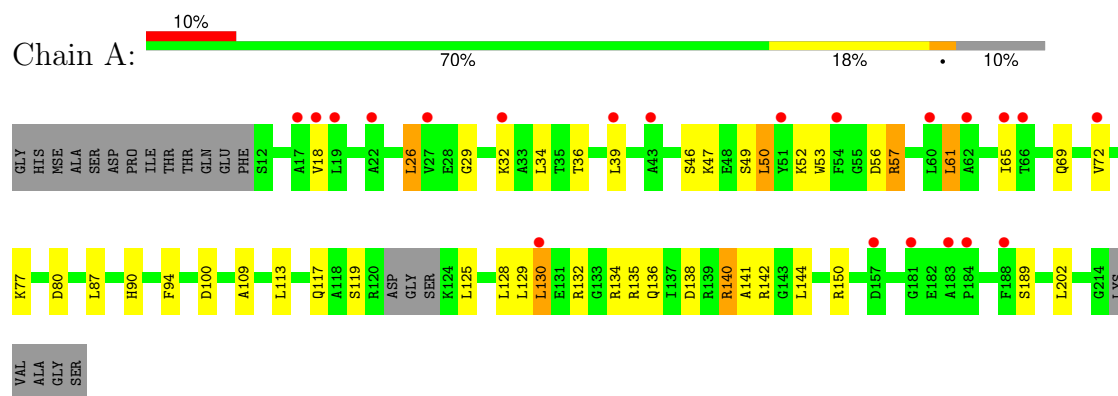
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	43	Total	O	0	0
			43	43		
3	B	49	Total	O	0	0
			49	49		

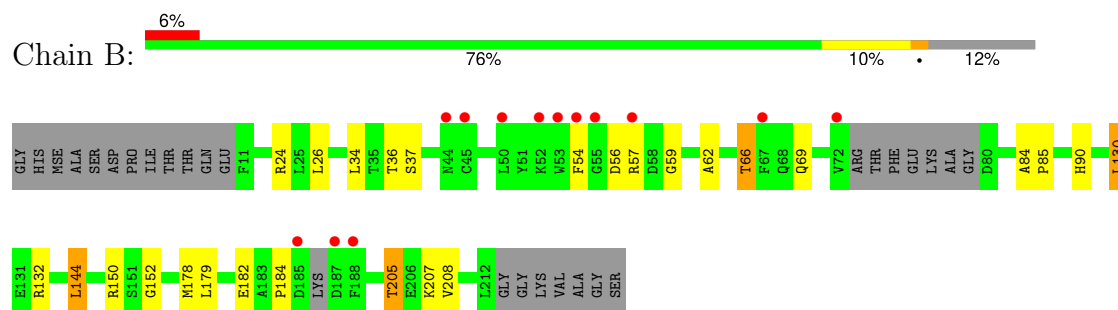
3 Residue-property plots [i](#)

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.

- Molecule 1: Transcriptional regulator, TetR family



- Molecule 1: Transcriptional regulator, TetR family



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.13Å 72.79Å 127.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.80 – 2.10 37.80 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.5 (37.80-2.10) 93.5 (37.80-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.10Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.198 , 0.241 0.197 , 0.241	Depositor DCC
R_{free} test set	1190 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	41.8	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 67.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3192	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FMT

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	0.73	1/1589 (0.1%)	0.77	0/2128
1	B	0.76	0/1558	0.80	2/2089 (0.1%)
All	All	0.74	1/3147 (0.0%)	0.78	2/4217 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	77	LYS	CE-NZ	6.06	1.64	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	130	LEU	CA-CB-CG	5.10	127.03	115.30
1	B	144	LEU	CA-CB-CG	5.00	126.80	115.30

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	A	1565	0	1598	22	0
1	B	1529	0	1545	17	0
2	A	3	0	1	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3	0	1	0	0
3	A	43	0	0	1	0
3	B	49	0	0	1	0
All	All	3192	0	3145	38	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 6.

All (38) 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:B:152:GLY:O	1:B:205:THR:HG21	1.73	0.87
1:A:46:SER:HB3	1:A:49:SER:HB3	1.66	0.77
1:A:140:ARG:NH2	3:A:306:HOH:O	2.22	0.73
1:A:117:GLN:HG3	1:A:125:LEU:HD22	1.79	0.65
1:B:90:HIS:HB3	1:B:144:LEU:HD11	1.81	0.62
1:B:150:ARG:HD2	3:B:345:HOH:O	2.02	0.59
1:A:26:LEU:HD13	1:A:109:ALA:HB1	1.86	0.58
1:A:57:ARG:NH2	1:A:61:LEU:HD21	2.19	0.57
1:A:134:ARG:NH2	2:A:302:FMT:O1	2.37	0.57
1:B:205:THR:HG22	1:B:208:VAL:H	1.70	0.57
1:B:178:MSE:SE	1:B:184:PRO:HG3	2.56	0.56
1:B:205:THR:HG23	1:B:207:LYS:H	1.69	0.56
1:B:90:HIS:CB	1:B:144:LEU:HD11	2.36	0.55
1:A:57:ARG:HH21	1:A:61:LEU:HD21	1.73	0.53
1:B:54:PHE:O	1:B:59:GLY:HA3	2.08	0.53
1:B:62:ALA:O	1:B:132:ARG:NH2	2.42	0.53
1:A:46:SER:HB3	1:A:49:SER:CB	2.36	0.53
1:A:80:ASP:O	1:A:150:ARG:NH1	2.41	0.52
1:A:69:GLN:OE1	1:A:132[B]:ARG:HG2	2.08	0.52
1:B:34:LEU:O	1:B:57:ARG:NH2	2.24	0.52
1:B:205:THR:HG23	1:B:207:LYS:N	2.25	0.51
1:A:94:PHE:CZ	1:A:141:ALA:HB2	2.45	0.50
1:A:90:HIS:HB3	1:A:144:LEU:HD11	1.92	0.50
1:A:65:ILE:HD13	1:A:129:LEU:CD2	2.42	0.50
1:A:29:GLY:O	1:A:32[A]:LYS:HG2	2.13	0.49
1:B:66:THR:HG22	1:B:132:ARG:NH2	2.28	0.49
1:A:130:LEU:HD21	1:B:182:GLU:HB2	1.94	0.48
1:B:66:THR:CG2	1:B:132:ARG:NH2	2.77	0.47
1:B:84:ALA:HB3	1:B:85:PRO:HD3	1.97	0.47
1:A:39:LEU:HD12	1:A:50:LEU:HD21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:ARG:HD3	1:A:140:ARG:C	2.38	0.44
1:A:138:ASP:O	1:A:142:ARG:HG3	2.19	0.42
1:A:18:VAL:HG21	1:A:53:TRP:CZ3	2.55	0.42
1:B:205:THR:CG2	1:B:207:LYS:HB3	2.50	0.42
1:A:61:LEU:HG	1:A:113:LEU:HD21	2.01	0.41
1:A:69:GLN:O	1:A:72:VAL:HG22	2.21	0.41
1:B:66:THR:O	1:B:69:GLN:HB2	2.21	0.40

There are no symmetry-related clashes.

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	198/221 (90%)	192 (97%)	6 (3%)	0	100	100
1	B	192/221 (87%)	188 (98%)	3 (2%)	1 (0%)	25	23
All	All	390/442 (88%)	380 (97%)	9 (2%)	1 (0%)	37	37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	56	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	159/170 (94%)	140 (88%)	19 (12%)	4	2
1	B	158/170 (93%)	150 (95%)	8 (5%)	20	19
All	All	317/340 (93%)	290 (92%)	27 (8%)	8	6

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	34	LEU
1	A	36	THR
1	A	47	LYS
1	A	50	LEU
1	A	52	LYS
1	A	56	ASP
1	A	57	ARG
1	A	61	LEU
1	A	87	LEU
1	A	100	ASP
1	A	119	SER
1	A	128	LEU
1	A	130	LEU
1	A	135	ARG
1	A	136	GLN
1	A	140	ARG
1	A	189	SER
1	A	202	LEU
1	B	24	ARG
1	B	26	LEU
1	B	36	THR
1	B	37	SER
1	B	66	THR
1	B	130	LEU
1	B	179	LEU
1	B	205	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	B	44	ASN
1	B	96	HIS

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Mol	Chain	Res	Type
1	B	117	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	$\# Z > 2$
2	FMT	A	302	-	2,2,2	0.87	0	1,1,1	0.40	0
2	FMT	B	301	-	2,2,2	0.76	0	1,1,1	0.39	0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	302	FMT	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Warning: The R factor obtained from EDS is 0.2772, which does not match the depositor's R factor of 0.1984. Please interpret the results in this section carefully.

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, 95th 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 ²)	Q < 0.9
1	A	198/221 (89%)	0.90	21 (10%)	13 13	28, 54, 82, 86	2 (1%)
1	B	192/221 (86%)	0.66	13 (6%)	25 27	28, 52, 72, 76	4 (2%)
All	All	390/442 (88%)	0.78	34 (8%)	17 19	28, 53, 77, 86	6 (1%)

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	ILE	6.5
1	B	44	ASN	4.4
1	B	50	LEU	4.0
1	B	57	ARG	4.0
1	A	39	LEU	3.9
1	A	184	PRO	3.6
1	A	181	GLY	3.5
1	B	45[A]	CYS	3.5
1	A	22	ALA	3.4
1	B	72	VAL	3.2
1	A	62	ALA	3.0
1	A	54	PHE	2.9
1	B	185	ASP	2.8
1	A	157	ASP	2.8
1	A	72	VAL	2.8
1	A	32[A]	LYS	2.6
1	B	187	ASP	2.6
1	A	183	ALA	2.5
1	A	27	VAL	2.5
1	A	66	THR	2.5
1	B	54	PHE	2.5
1	A	130	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	19	LEU	2.4
1	A	60	LEU	2.4
1	B	55	GLY	2.4
1	B	53	TRP	2.3
1	A	17	ALA	2.3
1	B	188	PHE	2.2
1	A	18	VAL	2.2
1	A	188	PHE	2.1
1	B	67	PHE	2.1
1	A	43	ALA	2.1
1	A	51	TYR	2.0
1	B	52	LYS	2.0

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, 95th 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 ²)	Q<0.9
2	FMT	A	302	3/3	0.83	0.19	51,51,54,57	0
2	FMT	B	301	3/3	0.90	0.17	60,60,61,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.