



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 31, 2025 – 12:26 PM JST

PDB ID : 9KGB
Title : Crystal structure of tolypothrichol synthase
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Deposited on : 2024-11-08
Resolution : 1.76 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

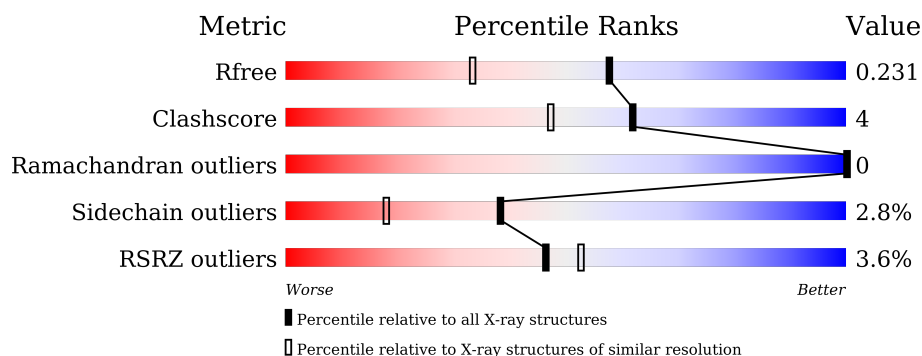
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.76 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	2888 (1.76-1.76)
Clashscore	180529	3097 (1.76-1.76)
Ramachandran outliers	177936	3072 (1.76-1.76)
Sidechain outliers	177891	3072 (1.76-1.76)
RSRZ outliers	164620	2887 (1.76-1.76)

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 $\leq 5\%$. 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	377	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2731 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 terpene synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	336	2641	1697	428	499	17	0	1	0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

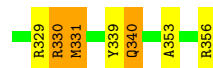


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	85	Total	O	0	0
			85	85		

- Molecule 1: terpene synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.16Å 55.77Å 57.66Å 90.00° 90.75° 90.00°	Depositor
Resolution (Å)	49.20 – 1.76 49.20 – 1.76	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.20-1.76) 99.2 (49.20-1.76)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
R, R_{free}	0.179 , 0.224 0.190 , 0.231	Depositor DCC
R_{free} test set	1559 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 31.7	EDS
L-test for twinning ¹	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k 0.024 for -h,-l,-k 0.028 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	2731	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.77	0/2701	1.21	17/3683 (0.5%)

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	A	0	3

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	NE-CZ-NH2	-7.96	116.32	120.30
1	A	81	GLU	CG-CD-OE2	-7.82	102.66	118.30
1	A	81	GLU	CG-CD-OE1	7.62	133.53	118.30
1	A	118	LYS	CD-CE-NZ	-7.29	94.93	111.70
1	A	331	MET	CG-SD-CE	-7.22	88.65	100.20
1	A	143	GLU	CB-CA-C	7.19	124.77	110.40
1	A	251	GLU	OE1-CD-OE2	6.97	131.66	123.30
1	A	218	PRO	N-CA-CB	-6.67	95.27	102.60
1	A	330	ARG	CD-NE-CZ	6.49	132.69	123.60
1	A	330	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	A	219	LEU	N-CA-CB	6.34	123.07	110.40
1	A	198	MET	CG-SD-CE	5.68	109.29	100.20
1	A	323	THR	CA-CB-OG1	-5.49	97.48	109.00
1	A	59	ARG	CD-NE-CZ	5.41	131.17	123.60
1	A	309	LYS	N-CA-CB	-5.30	101.06	110.60
1	A	339	TYR	CB-CG-CD1	5.06	124.04	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	N-CA-CB	-5.01	101.58	110.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	182	ARG	Sidechain
1	A	31	ARG	Sidechain
1	A	330	ARG	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	2641	0	2615	21	0
2	A	5	0	0	0	0
3	A	85	0	0	1	0
All	All	2731	0	2615	21	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 4.

All (21) 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:177[B]:HIS:HE1	1:A:218:PRO:HB3	1.16	1.06
1:A:177[B]:HIS:CE1	1:A:218:PRO:HB3	1.95	1.01
1:A:217:ALA:HB1	1:A:331:MET:SD	2.33	0.68
1:A:235:GLU:HG2	1:A:236:PHE:CZ	2.35	0.62
1:A:49:VAL:HG21	1:A:60:MET:CE	2.32	0.60
1:A:49:VAL:HG21	1:A:60:MET:HE2	1.84	0.59
1:A:235:GLU:HG2	1:A:236:PHE:CE2	2.39	0.57
1:A:314:ILE:HD11	1:A:329:ARG:HD3	1.90	0.53
1:A:112:MET:SD	1:A:147:TRP:HB2	2.49	0.52
1:A:112:MET:HE1	1:A:150:LEU:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ALA:HB3	1:A:218:PRO:CD	2.43	0.49
1:A:230:GLU:HB2	1:A:320:SER:HB2	1.96	0.48
1:A:85:MET:HB2	1:A:157:PHE:CZ	2.50	0.47
1:A:353:ALA:HA	1:A:356:ARG:CZ	2.45	0.47
1:A:156:LYS:HE2	3:A:514:HOH:O	2.17	0.43
1:A:141:ILE:HG22	1:A:147:TRP:CZ2	2.53	0.43
1:A:132:PRO:HA	1:A:135:ILE:HG12	2.01	0.42
1:A:340:GLN:CD	1:A:340:GLN:H	2.23	0.41
1:A:177[B]:HIS:HE1	1:A:218:PRO:CB	2.07	0.41
1:A:141:ILE:HD13	1:A:141:ILE:HG21	1.85	0.40
1:A:97:GLU:O	1:A:98:ASP:CB	2.70	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	333/377 (88%)	329 (99%)	4 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	289/327 (88%)	281 (97%)	8 (3%)	38	18

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	MET
1	A	94	ASP
1	A	140	THR
1	A	178	PHE
1	A	218	PRO
1	A	241	PRO
1	A	281	LEU
1	A	340	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	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](#)

1 ligand is 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	SO4	A	401	-	4,4,4	0.29	0	6,6,6	0.53	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.

No monomer is involved in short contacts.

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, 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	336/377 (89%)	0.37	12 (3%)	46 53	12, 35, 57, 75	1 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	98	ASP	3.5
1	A	103	THR	3.4
1	A	287	THR	2.9
1	A	198	MET	2.9
1	A	218	PRO	2.7
1	A	73	TYR	2.6
1	A	199	GLY	2.6
1	A	17	THR	2.5
1	A	195	VAL	2.5
1	A	200	SER	2.1
1	A	192	THR	2.1
1	A	197	GLU	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(\AA^2)	Q<0.9
2	SO4	A	401	5/5	0.93	0.10	35,37,38,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.