



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:40 PM UTC

PDB ID : 9B99 / pdb_00009b99
Title : Crystal structure of Grindelia robusta 7,13-copalyl diphosphate synthase
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Deposited on : 2024-04-01
Resolution : 2.12 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

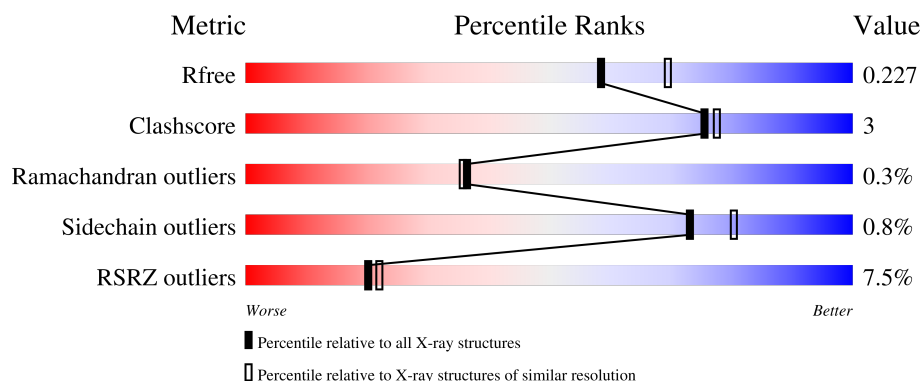
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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}	180053	8290 (2.14-2.10)
Clashscore	190562	8817 (2.14-2.10)
Ramachandran outliers	187476	8738 (2.14-2.10)
Sidechain outliers	187428	8739 (2.14-2.10)
RSRZ outliers	180081	8294 (2.14-2.10)

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 $\leq 5\%$. 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	733	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11822 atoms, of which 5719 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 Labda-7,13E-dienyl diphosphate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	711	Total	C	H	N	O	S	0	1	0
			11518	3740	5719	950	1080	29			

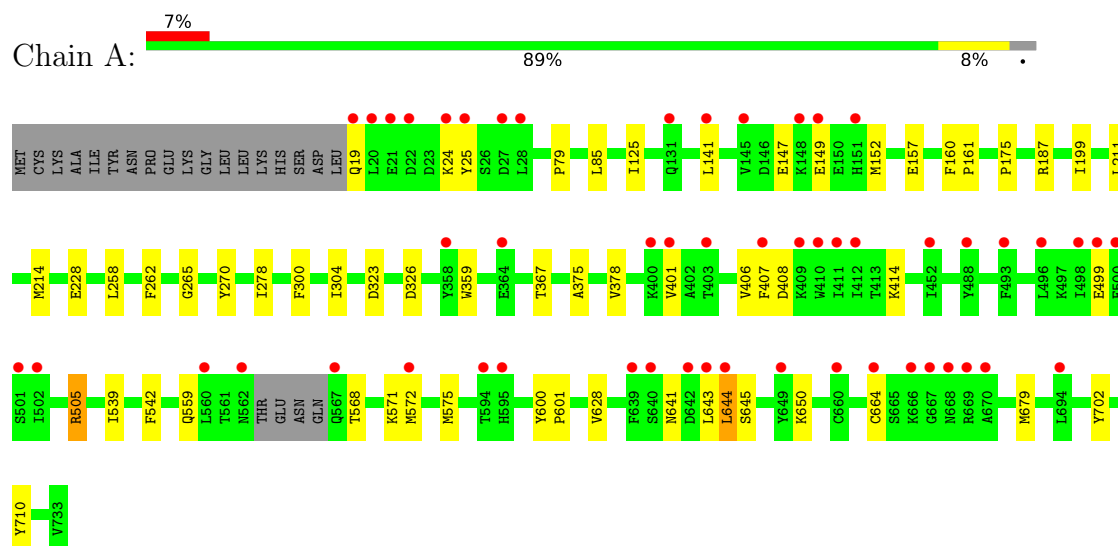
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	304	Total	O	0	0
			304	304		

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: Labda-7,13E-dienyl diphosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	56.07Å 79.11Å 88.44Å 90.00° 97.59° 90.00°	Depositor
Resolution (Å)	58.73 – 2.12 58.73 – 2.12	Depositor EDS
% Data completeness (in resolution range)	99.4 (58.73-2.12) 99.4 (58.73-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.12Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.185 , 0.229 0.184 , 0.227	Depositor DCC
R_{free} test set	2178 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.531	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11822	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% 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](#)

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	0.17	2/5945 (0.0%)	0.30	0/8056

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	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	505	ARG	C-O	-5.51	1.17	1.24
1	A	175	PRO	C-O	-5.14	1.14	1.23

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	505	ARG	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	A	5799	5719	5719	34	0
2	A	304	0	0	2	0
All	All	6103	5719	5719	34	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 3.

All (34) 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:664:CYS:SG	2:A:875:HOH:O	2.53	0.66
1:A:571:LYS:HG2	1:A:575:MET:HE2	1.79	0.62
1:A:644:LEU:O	1:A:650:LYS:NZ	2.35	0.59
1:A:559:GLN:HB2	1:A:568:THR:HG21	1.88	0.56
1:A:375:ALA:O	1:A:378:VAL:HG22	2.06	0.56
1:A:572:MET:HE2	1:A:575:MET:HE3	1.91	0.52
1:A:24:LYS:HE3	1:A:25:TYR:CZ	2.44	0.52
1:A:401:VAL:HG22	1:A:406:VAL:HG21	1.91	0.51
1:A:85:LEU:HD13	1:A:125:ILE:CD1	2.41	0.51
1:A:628:VAL:HG11	1:A:702:TYR:CZ	2.47	0.49
1:A:258:LEU:HD13	1:A:270[B]:TYR:CD1	2.48	0.48
1:A:149:GLU:HG2	1:A:187:ARG:HH12	1.79	0.48
1:A:644:LEU:HD12	1:A:644:LEU:H	1.79	0.47
1:A:367:THR:HG23	1:A:408:ASP:OD2	2.14	0.47
1:A:600:TYR:HB3	1:A:601:PRO:HD3	1.97	0.47
1:A:643:LEU:O	1:A:644:LEU:C	2.57	0.47
1:A:160:PHE:HB3	1:A:161:PRO:HD3	1.97	0.47
1:A:407:PHE:C	1:A:407:PHE:CD1	2.93	0.46
1:A:152:MET:HE3	1:A:157:GLU:OE1	2.16	0.46
1:A:278:ILE:HG13	1:A:304:ILE:HD12	1.99	0.45
1:A:628:VAL:HG11	1:A:702:TYR:CE2	2.51	0.45
1:A:679:MET:HE3	1:A:710:TYR:CD2	2.52	0.44
1:A:211:LEU:HA	1:A:214:MET:HE2	1.98	0.44
1:A:262:PHE:HB2	1:A:265:GLY:O	2.17	0.44
1:A:542:PHE:CE1	1:A:572:MET:HG3	2.53	0.43
1:A:85:LEU:HD13	1:A:125:ILE:HD12	2.01	0.43
1:A:300:PHE:O	1:A:304:ILE:HG12	2.19	0.42
1:A:323:ASP:OD1	1:A:326:ASP:OD2	2.37	0.42
1:A:141:LEU:HD11	1:A:160:PHE:HE2	1.85	0.42
1:A:645:SER:HA	1:A:650:LYS:NZ	2.35	0.42
1:A:199:ILE:HG21	1:A:359:TRP:CZ2	2.55	0.41
1:A:79:PRO:HG3	1:A:85:LEU:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:MET:HE1	1:A:157:GLU:HB3	2.03	0.40
1:A:414:LYS:NZ	2:A:823:HOH:O	2.54	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	708/733 (97%)	686 (97%)	20 (3%)	2 (0%)	36	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	499	GLU
1	A	644	LEU

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	637/656 (97%)	632 (99%)	5 (1%)	73	80

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	147	GLU
1	A	228	GLU
1	A	539	ILE
1	A	641	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	131	GLN
1	A	277	GLN
1	A	340	GLN
1	A	347	GLN
1	A	586	HIS
1	A	595	HIS
1	A	641	ASN
1	A	668	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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	711/733 (96%)	0.26	53 (7%) 20 22	19, 45, 102, 136	1 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	644	LEU	4.2
1	A	498	ILE	4.2
1	A	411	ILE	4.1
1	A	410	TRP	3.9
1	A	412	ILE	3.8
1	A	407	PHE	3.8
1	A	643	LEU	3.7
1	A	669	ARG	3.7
1	A	496	LEU	3.7
1	A	668	ASN	3.3
1	A	640	SER	3.2
1	A	499	GLU	3.1
1	A	25	TYR	3.1
1	A	670	ALA	2.9
1	A	401	VAL	2.9
1	A	660	CYS	2.9
1	A	20	LEU	2.9
1	A	642	ASP	2.9
1	A	452	ILE	2.8
1	A	562	ASN	2.8
1	A	364	GLU	2.8
1	A	403	THR	2.7
1	A	572	MET	2.7
1	A	409	LYS	2.7
1	A	28	LEU	2.7
1	A	500	GLU	2.6
1	A	501	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	24	LYS	2.6
1	A	148	LYS	2.6
1	A	488	TYR	2.5
1	A	649	TYR	2.5
1	A	151	HIS	2.5
1	A	694	LEU	2.4
1	A	667	GLY	2.4
1	A	502	ILE	2.4
1	A	358	TYR	2.4
1	A	149	GLU	2.3
1	A	141	LEU	2.3
1	A	21	GLU	2.3
1	A	22	ASP	2.3
1	A	594	THR	2.2
1	A	27	ASP	2.2
1	A	19	GLN	2.2
1	A	664	CYS	2.2
1	A	400	LYS	2.2
1	A	560	LEU	2.2
1	A	567	GLN	2.1
1	A	639	PHE	2.1
1	A	145	VAL	2.1
1	A	595	HIS	2.1
1	A	493	PHE	2.1
1	A	131	GLN	2.1
1	A	666	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.