



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2021 – 08:02 AM EDT

PDB ID : 7S0H
Title : Crystal structure of *Penicillium verrucosum* copalyl diphosphate synthase (PvCPS) alpha prenyltransferase domain variant, S723Y
Authors : Ronnebaum, T.A.; Christianson, D.W.
Deposited on : 2021-08-30
Resolution : 3.15 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

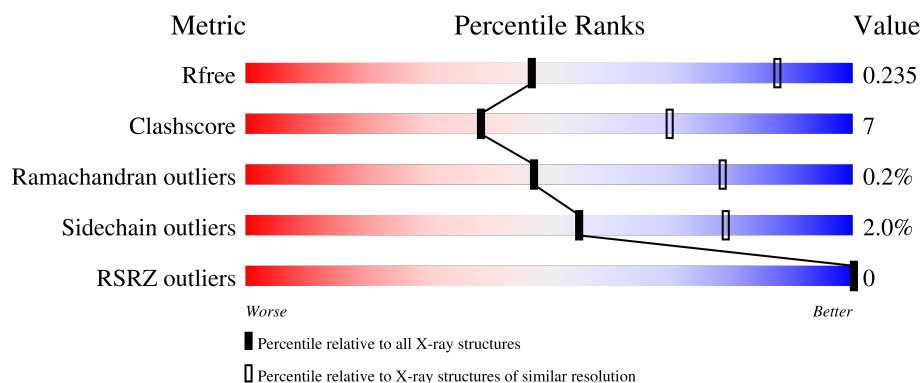
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 3.15 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}	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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	305	 82% 16% .
1	B	305	 78% 22%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4781 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
1	A	304	Total	C	N	O	S	0	1	0
			2391	1529	402	448	12			
1	B	305	Total	C	N	O	S	0	1	0
			2390	1525	396	457	12			

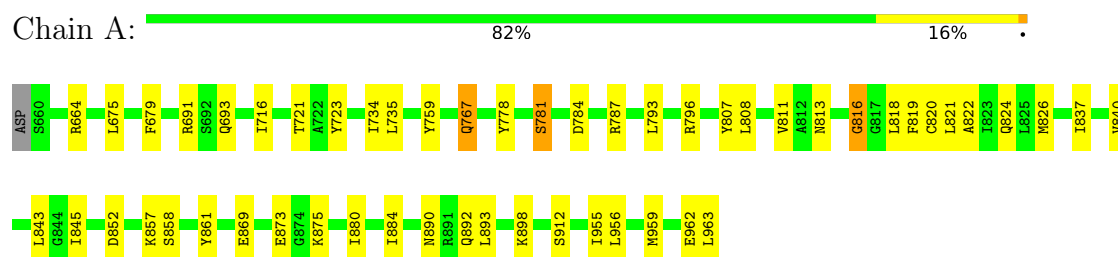
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	723	TYR	SER	engineered mutation	UNP A0A348FUE1
B	723	TYR	SER	engineered mutation	UNP A0A348FUE1

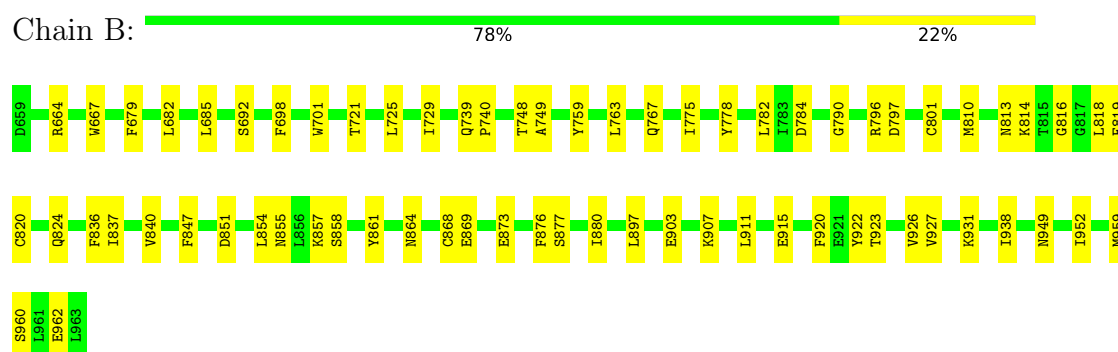
3 Residue-property plots

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 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: Terpene synthase



• Molecule 1: Terpene synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	188.53Å 188.53Å 56.44Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	81.64 – 3.15 94.27 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.7 (81.64-3.15) 93.0 (94.27-3.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.186 , 0.234 0.188 , 0.235	Depositor DCC
R_{free} test set	2012 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.058 for -h,-k,l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	4781	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.54% 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	0.54	0/2438	0.83	3/3306 (0.1%)
1	B	0.56	0/2437	0.68	0/3306
All	All	0.55	0/4875	0.76	3/6612 (0.0%)

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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	767	GLN	CG-CD-NE2	-16.12	78.02	116.70
1	A	767	GLN	CG-CD-OE1	14.34	150.28	121.60
1	A	767	GLN	OE1-CD-NE2	-7.30	105.11	121.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	767	GLN	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	2391	0	2359	31	1
1	B	2390	0	2338	43	1
All	All	4781	0	4697	71	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 7.

All (71) 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:858:SER:HB3	1:A:861:TYR:HB2	1.65	0.77
1:B:857:LYS:HE2	1:B:920:PHE:CD2	2.32	0.65
1:A:880:ILE:O	1:A:884:ILE:HG13	1.98	0.62
1:A:884:ILE:HG12	1:A:893:LEU:HD23	1.80	0.62
1:A:807:TYR:OH	1:A:852:ASP:OD2	2.13	0.61
1:B:763:LEU:HD13	1:B:778:TYR:CD1	2.36	0.60
1:A:716:ILE:HG23	1:A:818:LEU:HD22	1.83	0.60
1:B:685:LEU:HD22	1:B:739:GLN:HG3	1.83	0.60
1:A:824:GLN:HG3	1:A:837:ILE:HD11	1.83	0.59
1:B:816:GLY:HA2	1:B:820:CYS:HB2	1.85	0.58
1:B:857:LYS:HE2	1:B:920:PHE:CG	2.40	0.56
1:A:784:ASP:O	1:A:813:ASN:HB3	2.06	0.56
1:B:837:ILE:HA	1:B:840:VAL:HG12	1.88	0.55
1:B:819:PHE:HB3	1:B:840:VAL:HG22	1.87	0.55
1:A:787:ARG:HB3	1:B:667:TRP:CH2	2.42	0.54
1:A:759:TYR:O	1:A:778:TYR:OH	2.26	0.54
1:A:734:ILE:HD12	1:A:869:GLU:OE2	2.09	0.53
1:B:858:SER:HB3	1:B:861:TYR:HB2	1.91	0.53
1:B:796:ARG:HD2	1:B:873:GLU:O	2.09	0.53
1:A:793:LEU:HD22	1:B:749:ALA:HB1	1.91	0.52
1:A:822:ALA:O	1:A:826:MET:HG3	2.10	0.52
1:A:716:ILE:HG13	1:A:822:ALA:HB2	1.92	0.52
1:B:739:GLN:HB3	1:B:740:PRO:HD2	1.92	0.51
1:B:810:MET:SD	1:B:814:LYS:HE2	2.49	0.51
1:B:679:PHE:CE1	1:B:721:THR:HB	2.45	0.51
1:A:962:GLU:O	1:A:963:LEU:HB2	2.13	0.49
1:B:868:CYS:SG	1:B:911:LEU:HD22	2.52	0.49
1:B:931:LYS:HD2	1:B:960:SER:OG	2.13	0.48
1:A:675:LEU:HD21	1:B:790:GLY:HA3	1.96	0.48
1:A:890:ASN:OD1	1:A:892:GLN:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:701:TRP:HH2	1:B:938:ILE:HG23	1.79	0.47
1:B:903:GLU:O	1:B:907:LYS:HG3	2.14	0.47
1:B:880:ILE:HG21	1:B:897:LEU:HD11	1.97	0.47
1:A:811:VAL:HG12	1:A:845:ILE:HG12	1.97	0.47
1:B:729:ILE:HG23	1:B:748:THR:HG22	1.97	0.46
1:B:923:THR:O	1:B:927:VAL:HG23	2.14	0.46
1:A:723:TYR:HE2	1:A:818:LEU:HG	1.80	0.46
1:B:949:ASN:HB3	1:B:952:ILE:HG22	1.96	0.46
1:B:701:TRP:CZ2	1:B:949:ASN:HB2	2.51	0.45
1:B:819:PHE:N	1:B:819:PHE:CD1	2.84	0.45
1:B:820:CYS:O	1:B:824:GLN:HB2	2.17	0.45
1:A:734:ILE:O	1:A:735:LEU:HD23	2.17	0.45
1:B:725:LEU:HD23	1:B:725:LEU:HA	1.75	0.45
1:A:818:LEU:HA	1:A:818:LEU:HD23	1.69	0.45
1:B:819:PHE:N	1:B:819:PHE:HD1	2.14	0.45
1:B:847:PHE:HD1	1:B:959:MET:CE	2.29	0.45
1:A:693:GLN:HB3	1:A:955:ILE:HD11	1.99	0.44
1:B:818:LEU:HD23	1:B:818:LEU:HA	1.85	0.44
1:A:808:LEU:HD23	1:A:808:LEU:HA	1.76	0.44
1:B:857:LYS:NZ	1:B:915:GLU:OE1	2.50	0.44
1:B:855:ASN:HD21	1:B:869:GLU:HB3	1.83	0.43
1:A:843:LEU:HD21	1:A:956:LEU:HD13	1.99	0.43
1:A:837:ILE:HA	1:A:840:VAL:HG12	2.01	0.43
1:B:922:TYR:O	1:B:926:VAL:HG23	2.19	0.42
1:B:819:PHE:HB3	1:B:840:VAL:CG2	2.50	0.42
1:B:767:GLN:HG2	1:B:775:ILE:HD11	2.01	0.42
1:A:679:PHE:CE1	1:A:721:THR:HB	2.55	0.42
1:A:819:PHE:CD1	1:A:819:PHE:N	2.87	0.42
1:B:759:TYR:O	1:B:778:TYR:OH	2.34	0.42
1:A:857:LYS:HA	1:A:857:LYS:HD2	1.93	0.42
1:B:854:LEU:HD21	1:B:962:GLU:HB2	2.02	0.41
1:B:698:PHE:HE2	1:B:836:PHE:HB3	1.85	0.41
1:A:816:GLY:HA2	1:A:820:CYS:HB2	2.03	0.41
1:A:819:PHE:N	1:A:819:PHE:HD1	2.18	0.41
1:A:796[A]:ARG:HD2	1:A:873:GLU:O	2.21	0.41
1:B:682:LEU:HD12	1:B:682:LEU:HA	1.85	0.41
1:B:801:CYS:HB2	1:B:876:PHE:CE1	2.55	0.41
1:A:781:SER:HB2	1:A:821:LEU:HD13	2.02	0.41
1:B:784:ASP:O	1:B:813:ASN:HB3	2.21	0.41
1:B:782:LEU:HD13	1:B:782:LEU:HA	1.91	0.41
1:B:877:SER:OG	1:B:880:ILE:HD12	2.21	0.40

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:A:898:LYS:NZ	1:B:797:ASP:O[2_565]	2.18	0.02

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	303/305 (99%)	285 (94%)	17 (6%)	1 (0%)	41	73
1	B	304/305 (100%)	292 (96%)	12 (4%)	0	100	100
All	All	607/610 (100%)	577 (95%)	29 (5%)	1 (0%)	47	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	816	GLY

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	256/273 (94%)	250 (98%)	6 (2%)	50	76
1	B	257/273 (94%)	253 (98%)	4 (2%)	62	83
All	All	513/546 (94%)	503 (98%)	10 (2%)	55	80

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	664	ARG
1	A	691	ARG
1	A	781	SER
1	A	875	LYS
1	A	912	SER
1	A	959	MET
1	B	664	ARG
1	B	692	SER
1	B	851	ASP
1	B	864	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

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 [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	304/305 (99%)	-0.46	0 100 100	11, 26, 55, 93	0
1	B	305/305 (100%)	-0.43	0 100 100	11, 25, 61, 86	0
All	All	609/610 (99%)	-0.44	0 100 100	11, 25, 60, 93	0

There are no RSRZ outliers to report.

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.