



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 21, 2026 – 07:02 AM JST

PDB ID : 9K9B / pdb\_00009k9b  
Title : Apo form of Solanum tuberosum solanesyl diphosphate synthase  
Authors : Xiao, H.; Li, M.; Yang, G.-F.  
Deposited on : 2024-10-26  
Resolution : 2.19 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](mailto: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>.

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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

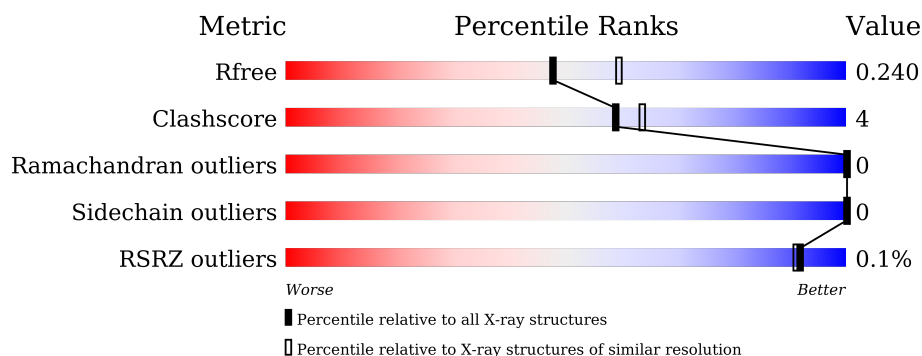
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.19 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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  $\geq 3$ , 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	325	<div> <div>82%</div> <div>7%</div> <div>11%</div> </div>
1	B	325	<div> <div>84%</div> <div>6%</div> <div>10%</div> </div>
1	C	325	<div> <div>82%</div> <div>7%</div> <div>10%</div> </div>
1	D	325	<div> <div>83%</div> <div>11%</div> <div>6%</div> </div>
1	E	325	<div> <div>82%</div> <div>12%</div> <div>6%</div> </div>
1	F	325	<div> <div>78%</div> <div>14%</div> <div>8%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14201 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 Solanesyl diphosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	0	0	0
			2236	1419	376	433	8			
1	B	292	Total	C	N	O	S	0	0	0
			2253	1428	378	439	8			
1	C	291	Total	C	N	O	S	0	0	0
			2240	1420	376	436	8			
1	D	305	Total	C	N	O	S	0	0	0
			2345	1488	393	456	8			
1	E	305	Total	C	N	O	S	0	0	0
			2343	1487	392	456	8			
1	F	300	Total	C	N	O	S	0	0	0
			2312	1469	387	448	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	MET	-	initiating methionine	UNP M1AAA6
B	74	MET	-	initiating methionine	UNP M1AAA6
C	74	MET	-	initiating methionine	UNP M1AAA6
D	74	MET	-	initiating methionine	UNP M1AAA6
E	74	MET	-	initiating methionine	UNP M1AAA6
F	74	MET	-	initiating methionine	UNP M1AAA6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	84	Total	O	0	0
			84	84		
2	B	86	Total	O	0	0
			86	86		
2	C	90	Total	O	0	0
			90	90		

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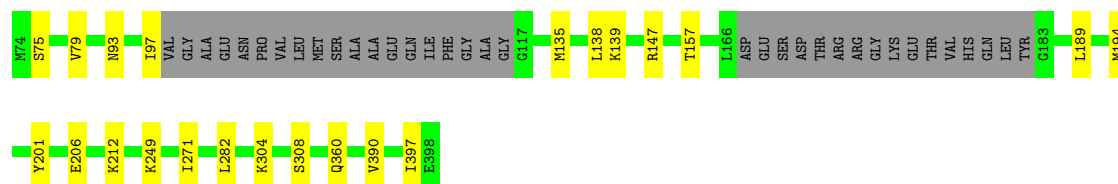
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	64	Total 64	O 64	0	0
2	E	76	Total 76	O 76	0	0
2	F	72	Total 72	O 72	0	0

### 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.

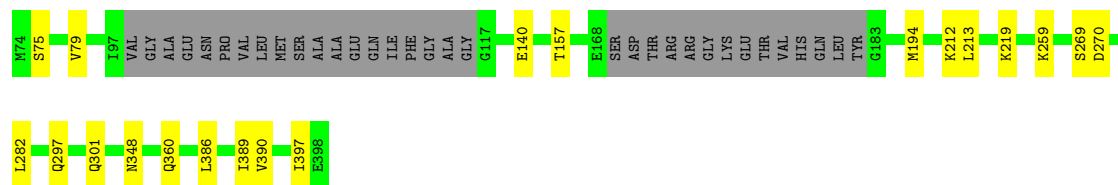
- Molecule 1: Solanesyl diphosphate synthase

Chain A: 




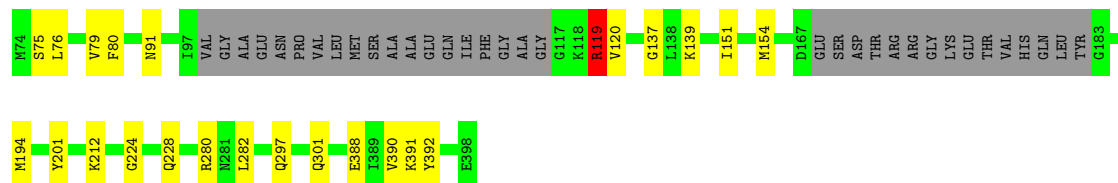
- Molecule 1: Solanesyl diphosphate synthase

Chain B: 




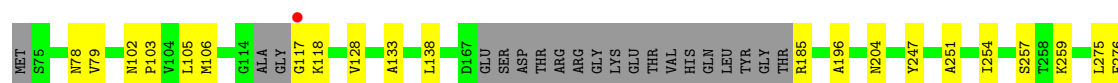
- Molecule 1: Solanesyl diphosphate synthase

Chain C: 



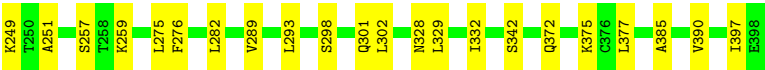
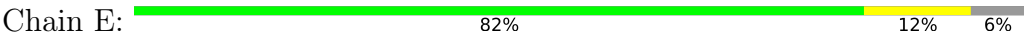
- Molecule 1: Solanesyl diphosphate synthase

Chain D: 

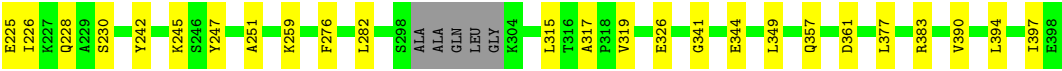
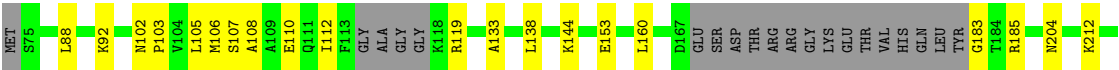
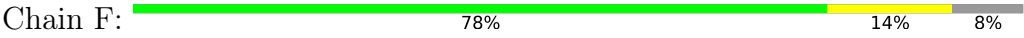




● Molecule 1: Solanesyl diphosphate synthase



● Molecule 1: Solanesyl diphosphate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.69Å 134.59Å 101.05Å 90.00° 98.69° 90.00°	Depositor
Resolution (Å)	44.73 – 2.19 44.73 – 2.19	Depositor EDS
% Data completeness (in resolution range)	99.2 (44.73-2.19) 99.1 (44.73-2.19)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.47 (at 2.18Å)	Xtriage
Refinement program	PHENIX (1.16_3549)	Depositor
R, $R_{free}$	0.201 , 0.239 0.203 , 0.240	Depositor DCC
$R_{free}$ test set	5081 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.1	Xtriage
Anisotropy	0.106	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 28.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.459 for $-1/2^*h+1/2^*k+1, 1/2^*h-1/2^*k+1, 1/2^*h+1/2^*k$ 0.467 for $-1/2^*h-1/2^*k+1, -1/2^*h-1/2^*k-1, 1/2^*h-1/2^*k$	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	14201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.04% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	0/2264	0.34	0/3054
1	B	0.18	0/2281	0.34	0/3077
1	C	0.19	0/2268	0.37	1/3061 (0.0%)
1	D	0.17	0/2375	0.35	0/3206
1	E	0.16	0/2373	0.32	0/3206
1	F	0.16	0/2341	0.34	0/3161
All	All	0.17	0/13902	0.34	1/18765 (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	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	119	ARG	N-CA-CB	-5.55	103.75	112.13

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	119	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	2236	0	2269	19	0
1	B	2253	0	2279	15	0
1	C	2240	0	2262	17	0
1	D	2345	0	2371	24	0
1	E	2343	0	2361	24	0
1	F	2312	0	2338	32	0
2	A	84	0	0	0	0
2	B	86	0	0	2	0
2	C	90	0	0	1	0
2	D	64	0	0	3	0
2	E	76	0	0	0	0
2	F	72	0	0	3	0
All	All	14201	0	13880	121	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.

The worst 5 of 121 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:157:THR:HB	1:B:194:MET:HE1	1.53	0.91
1:C:388:GLU:HA	1:C:391:LYS:HE2	1.60	0.82
1:A:157:THR:HB	1:A:194:MET:HE1	1.62	0.82
1:C:280:ARG:NH1	2:C:401:HOH:O	2.21	0.74
1:F:119:ARG:NE	1:F:153:GLU:OE1	2.23	0.72

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	284/325 (87%)	282 (99%)	2 (1%)	0	100	100
1	B	286/325 (88%)	282 (99%)	4 (1%)	0	100	100
1	C	285/325 (88%)	283 (99%)	2 (1%)	0	100	100
1	D	299/325 (92%)	290 (97%)	9 (3%)	0	100	100
1	E	299/325 (92%)	293 (98%)	6 (2%)	0	100	100
1	F	292/325 (90%)	284 (97%)	8 (3%)	0	100	100
All	All	1745/1950 (90%)	1714 (98%)	31 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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	242/270 (90%)	242 (100%)	0	100	100
1	B	244/270 (90%)	244 (100%)	0	100	100
1	C	242/270 (90%)	242 (100%)	0	100	100
1	D	253/270 (94%)	253 (100%)	0	100	100
1	E	252/270 (93%)	252 (100%)	0	100	100
1	F	251/270 (93%)	251 (100%)	0	100	100
All	All	1484/1620 (92%)	1484 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	277	GLN
1	F	216	GLN

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Mol	Chain	Res	Type
1	F	373	ASN
1	F	274	GLN
1	F	91	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	290/325 (89%)	-0.74	0	100   100	30, 42, 70, 87	0
1	B	292/325 (89%)	-0.78	0	100   100	30, 43, 71, 86	0
1	C	291/325 (89%)	-0.76	0	100   100	31, 43, 71, 82	0
1	D	305/325 (93%)	-0.77	1 (0%)	90   89	30, 46, 76, 96	0
1	E	305/325 (93%)	-0.76	0	100   100	30, 46, 76, 95	0
1	F	300/325 (92%)	-0.71	0	100   100	31, 46, 73, 82	0
All	All	1783/1950 (91%)	-0.75	1 (0%)	92   91	30, 44, 74, 96	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	117	GLY	2.4

### 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.