



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:26 PM UTC

PDB ID : 6B02 / pdb_00006b02
Title : Crystal structure of CfFPPS2 (apo form), a lepidopteran type-II farnesyl diphosphate synthase
Authors : Picard, M.-E.; Cusson, M.; Shi, R.
Deposited on : 2017-09-13
Resolution : 2.82 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

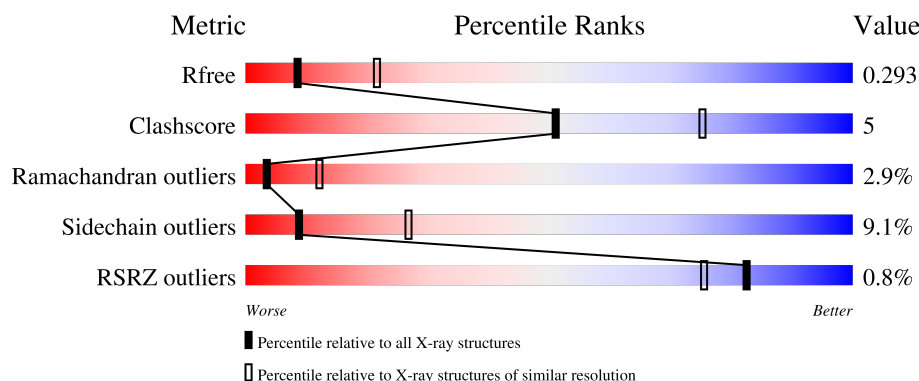
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.82 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	4591 (2.84-2.80)
Clashscore	190562	5010 (2.84-2.80)
Ramachandran outliers	187476	4916 (2.84-2.80)
Sidechain outliers	187428	4918 (2.84-2.80)
RSRZ outliers	180081	4594 (2.84-2.80)

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	341	
1	B	341	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5324 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.

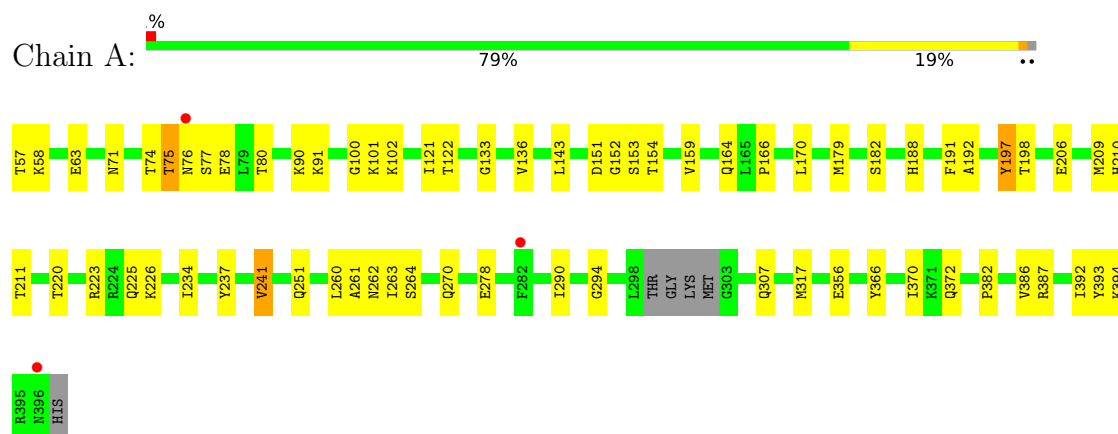
- Molecule 1 is a protein called Farnesyl diphosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2682	1724	429	510	19			
1	B	329	Total	C	N	O	S	0	0	0
			2642	1703	424	496	19			

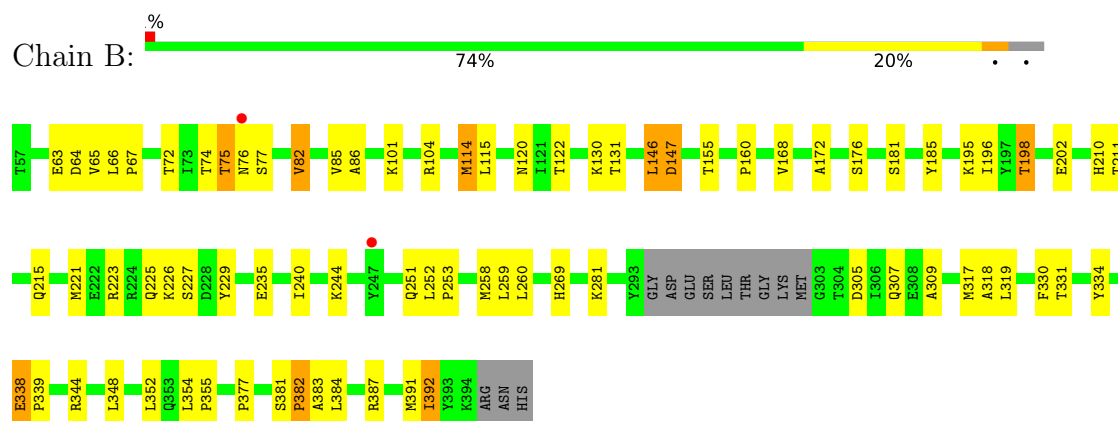
3 Residue-property plots [i](#)

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: Farnesyl diphosphate synthase



- Molecule 1: Farnesyl diphosphate synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	113.68Å 113.68Å 131.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	98.45 – 2.82 98.45 – 2.82	Depositor EDS
% Data completeness (in resolution range)	98.8 (98.45-2.82) 98.8 (98.45-2.82)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.81Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.216 , 0.296 0.218 , 0.293	Depositor DCC
R_{free} test set	1221 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	89.4	Xtriage
Anisotropy	0.764	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 62.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5324	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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	0.79	0/2738	1.07	2/3711 (0.1%)
1	B	0.83	0/2698	1.07	2/3654 (0.1%)
All	All	0.81	0/5436	1.07	4/7365 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	147	ASP	N-CA-C	-5.57	105.29	111.36
1	A	392	ILE	N-CA-C	5.55	116.58	111.81
1	A	91	LYS	N-CA-C	5.21	117.63	111.33
1	B	392	ILE	CB-CA-C	5.09	118.82	111.65

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	2682	0	2648	27	0
1	B	2642	0	2635	35	0
All	All	5324	0	5283	55	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 5.

All (55) 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:74:THR:HG23	1:B:86:ALA:HB1	1.58	0.86
1:A:209:MET:HE2	1:B:181:SER:HB3	1.68	0.74
1:A:198:THR:HG22	1:B:198:THR:CG2	2.17	0.73
1:B:225:GLN:O	1:B:227:SER:N	2.23	0.71
1:A:151:ASP:O	1:A:153:SER:N	2.29	0.65
1:A:209:MET:HE3	1:B:185:TYR:CE2	2.32	0.64
1:A:234:ILE:HD13	1:A:317:MET:HE3	1.77	0.64
1:B:229:TYR:CD2	1:B:331:THR:HG22	2.36	0.61
1:B:74:THR:CG2	1:B:86:ALA:HB1	2.29	0.60
1:B:319:LEU:HD21	1:B:330:PHE:CD1	2.37	0.59
1:A:143:LEU:CD2	1:A:211:THR:HG21	2.33	0.58
1:B:381:SER:O	1:B:382:PRO:C	2.49	0.56
1:B:381:SER:O	1:B:384:LEU:N	2.40	0.55
1:B:221:MET:HE3	1:B:240:ILE:HD11	1.89	0.55
1:A:198:THR:HG22	1:B:198:THR:HG21	1.89	0.54
1:B:258:MET:HE1	1:B:269:HIS:HA	1.89	0.53
1:A:143:LEU:HD22	1:A:211:THR:HG21	1.90	0.53
1:A:382:PRO:O	1:A:386:VAL:HG23	2.10	0.51
1:A:261:ALA:O	1:A:263:ILE:HG13	2.09	0.51
1:A:154:THR:HA	1:A:164:GLN:HE21	1.76	0.50
1:B:381:SER:O	1:B:383:ALA:N	2.45	0.50
1:B:348:LEU:O	1:B:352:LEU:HG	2.14	0.48
1:A:75:THR:HG22	1:A:76:ASN:N	2.28	0.48
1:A:237:TYR:O	1:A:241:VAL:HG13	2.14	0.47
1:A:188:HIS:O	1:A:192:ALA:HB2	2.15	0.47
1:A:366:TYR:CE1	1:A:393:TYR:CD2	3.03	0.47
1:B:354:LEU:N	1:B:355:PRO:CD	2.78	0.47
1:B:66:LEU:O	1:B:67:PRO:C	2.58	0.46
1:A:290:ILE:O	1:A:294:GLY:N	2.48	0.46
1:A:209:MET:HG2	1:B:185:TYR:OH	2.16	0.46
1:B:147:ASP:OD1	1:B:215:GLN:NE2	2.49	0.46
1:B:75:THR:O	1:B:77:SER:OG	2.29	0.46
1:B:65:VAL:HG21	1:B:130:LYS:HB3	1.97	0.45
1:A:278:GLU:HG3	1:A:372:GLN:HE22	1.82	0.45
1:B:155:THR:HA	1:B:160:PRO:HA	1.98	0.45
1:A:261:ALA:O	1:A:263:ILE:N	2.50	0.45
1:A:366:TYR:CE2	1:A:370:ILE:HG13	2.52	0.44
1:A:197:TYR:OH	1:B:202:GLU:OE2	2.31	0.43
1:B:229:TYR:HD2	1:B:331:THR:HG22	1.79	0.43
1:B:114:MET:HE3	1:B:114:MET:HB3	1.95	0.43
1:B:309:ALA:HA	1:B:334:TYR:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:75:THR:O	1:B:77:SER:N	2.52	0.43
1:B:338:GLU:O	1:B:339:PRO:C	2.61	0.42
1:A:143:LEU:HD22	1:A:211:THR:CG2	2.49	0.42
1:A:191:PHE:O	1:A:197:TYR:HB2	2.20	0.42
1:B:146:LEU:N	1:B:146:LEU:HD23	2.35	0.42
1:B:146:LEU:HD21	1:B:176:SER:HB2	2.00	0.42
1:B:252:LEU:HB3	1:B:253:PRO:HD3	2.02	0.42
1:B:317:MET:O	1:B:318:ALA:C	2.63	0.42
1:A:78:GLU:OE1	1:B:210:HIS:CE1	2.72	0.41
1:A:133:GLY:O	1:A:136:VAL:HB	2.21	0.41
1:A:366:TYR:O	1:A:370:ILE:HG12	2.20	0.41
1:A:143:LEU:CD1	1:A:211:THR:HG21	2.51	0.41
1:B:82:VAL:HG12	1:B:85:VAL:HG23	2.03	0.40
1:B:196:ILE:HG21	1:B:259:LEU:O	2.21	0.40

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	332/341 (97%)	296 (89%)	26 (8%)	10 (3%)	3	11
1	B	325/341 (95%)	292 (90%)	24 (7%)	9 (3%)	4	13
All	All	657/682 (96%)	588 (90%)	50 (8%)	19 (3%)	3	12

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	75	THR
1	A	152	GLY
1	A	197	TYR
1	A	262	ASN

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Mol	Chain	Res	Type
1	B	172	ALA
1	B	223	ARG
1	B	226	LYS
1	B	76	ASN
1	B	305	ASP
1	A	74	THR
1	A	225	GLN
1	B	75	THR
1	A	394	LYS
1	A	100	GLY
1	B	377	PRO
1	B	382	PRO
1	A	166	PRO
1	A	121	ILE
1	B	168	VAL

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	294/304 (97%)	267 (91%)	27 (9%)	8	26
1	B	291/304 (96%)	265 (91%)	26 (9%)	9	27
All	All	585/608 (96%)	532 (91%)	53 (9%)	9	27

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	THR
1	A	58	LYS
1	A	63	GLU
1	A	71	ASN
1	A	77	SER
1	A	80	THR
1	A	90	LYS
1	A	101	LYS

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Mol	Chain	Res	Type
1	A	102	LYS
1	A	122	THR
1	A	159	VAL
1	A	170	LEU
1	A	179	MET
1	A	182	SER
1	A	206	GLU
1	A	210	HIS
1	A	220	THR
1	A	223	ARG
1	A	226	LYS
1	A	241	VAL
1	A	251	GLN
1	A	260	LEU
1	A	264	SER
1	A	270	GLN
1	A	307	GLN
1	A	356	GLU
1	A	387	ARG
1	B	63	GLU
1	B	64	ASP
1	B	72	THR
1	B	82	VAL
1	B	101	LYS
1	B	104	ARG
1	B	114	MET
1	B	115	LEU
1	B	120	ASN
1	B	122	THR
1	B	131	THR
1	B	146	LEU
1	B	195	LYS
1	B	198	THR
1	B	211	THR
1	B	235	GLU
1	B	244	LYS
1	B	251	GLN
1	B	260	LEU
1	B	281	LYS
1	B	307	GLN
1	B	338	GLU
1	B	344	ARG

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Mol	Chain	Res	Type
1	B	387	ARG
1	B	391	MET
1	B	392	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	216	HIS
1	A	320	GLN
1	A	351	GLN
1	A	372	GLN
1	A	374	HIS
1	B	96	ASN
1	B	174	ASN
1	B	205	ASN
1	B	225	GLN
1	B	320	GLN
1	B	353	GLN
1	B	390	HIS

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, 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	336/341 (98%)	-0.13	3 (0%) 81 74	76, 107, 143, 177	0
1	B	329/341 (96%)	-0.16	2 (0%) 85 80	69, 101, 135, 183	0
All	All	665/682 (97%)	-0.15	5 (0%) 82 75	69, 105, 142, 183	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	396	ASN	3.7
1	A	282	PHE	3.3
1	B	247	TYR	3.1
1	A	76	ASN	2.8
1	B	76	ASN	2.1

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.