



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:36 PM UTC

PDB ID : 1HN9 / pdb_00001hn9
Title : CRYSTAL STRUCTURE OF BETA-KETOACYL-ACP SYNTHASE III
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Deposited on : 2000-12-07
Resolution : 2.00 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

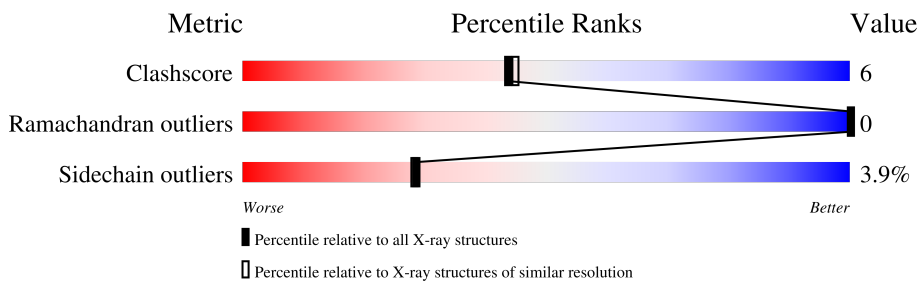
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	317	 84% 14% •
1	B	317	 82% 17% •

2 Entry composition [i](#)

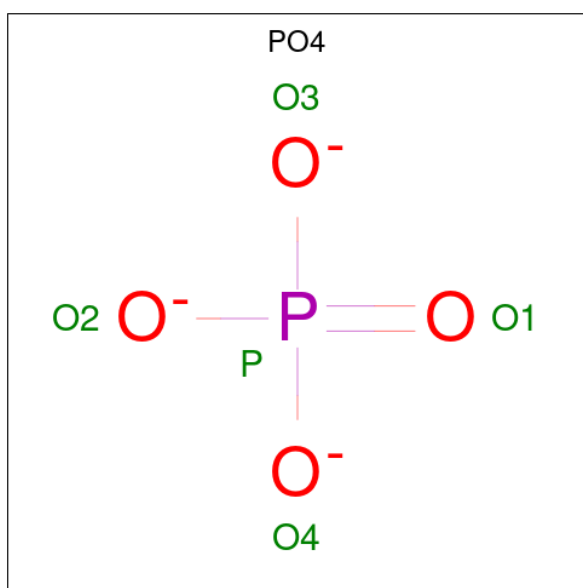
There are 3 unique types of molecules in this entry. The entry contains 5145 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BETA-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	0	0
			2331	1461	400	457	13			
1	B	317	Total	C	N	O	S	0	0	0
			2337	1463	402	459	13			

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

- Molecule 3 is water.

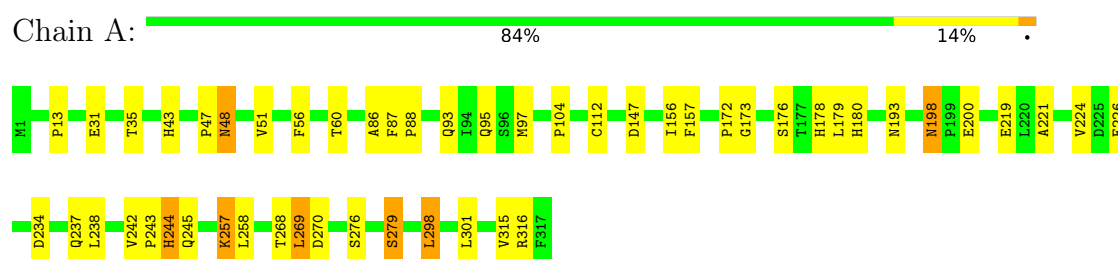
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	252	Total 252	O 252	0	0
3	B	215	Total 215	O 215	0	0

3 Residue-property plots

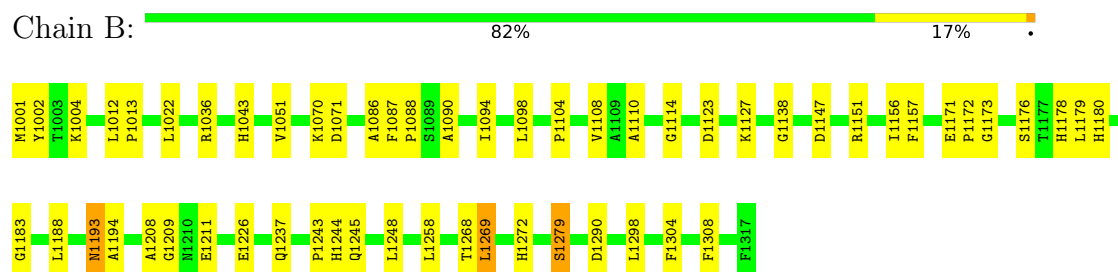
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: BETA-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III



• Molecule 1: BETA-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.06Å 65.08Å 166.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	97.0 (20.00-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.177 , 0.218	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5145	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.68	0/2370	1.03	11/3228 (0.3%)
1	B	0.64	0/2376	1.01	11/3236 (0.3%)
All	All	0.66	0/4746	1.02	22/6464 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1086	ALA	N-CA-C	-8.41	102.07	111.07
1	B	1157	PHE	N-CA-C	8.15	122.55	110.48
1	B	1156	ILE	N-CA-C	7.72	118.63	111.45
1	A	86	ALA	N-CA-C	-7.48	103.21	111.36
1	A	157	PHE	N-CA-C	7.41	121.45	110.48
1	A	198	ASN	CA-C-N	7.28	128.94	119.84
1	A	198	ASN	C-N-CA	7.28	128.94	119.84
1	A	156	ILE	N-CA-C	7.22	118.16	111.45
1	A	193	ASN	N-CA-C	-6.73	100.83	110.59
1	B	1269	LEU	N-CA-C	6.56	119.25	111.71
1	A	244	HIS	N-CA-C	-6.32	100.92	110.28
1	B	1208	ALA	N-CA-C	-5.97	100.63	109.11
1	B	1193	ASN	N-CA-C	-5.92	102.01	110.59
1	A	279	SER	N-CA-C	5.77	117.26	110.97
1	B	1138	GLY	N-CA-C	-5.40	100.39	113.18
1	B	1279	SER	N-CA-C	5.38	116.83	110.97
1	B	1147	ASP	N-CA-C	-5.29	99.87	109.44
1	A	147	ASP	N-CA-C	-5.28	101.61	109.42
1	B	1188	LEU	N-CA-C	5.20	119.25	113.01
1	B	1209	GLY	N-CA-C	5.11	119.06	112.83
1	A	276	SER	CB-CA-C	-5.08	110.70	116.54
1	A	315	VAL	N-CA-C	5.02	115.36	108.12

There are no chirality outliers.

There are no planarity outliers.

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	2331	0	2306	35	0
1	B	2337	0	2307	26	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	252	0	0	1	0
3	B	215	0	0	0	0
All	All	5145	0	4613	57	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 6.

All (57) 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:48:ASN:HD22	1:A:48:ASN:H	1.22	0.88
1:A:234:ASP:H	1:A:237:GLN:HE21	1.22	0.85
1:A:198:ASN:HB3	1:A:200:GLU:OE1	1.78	0.82
1:A:224:VAL:CG1	1:A:258:LEU:HD21	2.18	0.74
1:B:1245:GLN:NE2	1:B:1268:THR:H	1.86	0.72
1:A:269:LEU:HD23	1:A:270:ASP:N	2.05	0.71
1:B:1012:LEU:HD21	1:B:1272:HIS:NE2	2.10	0.67
1:A:245:GLN:NE2	1:A:268:THR:H	1.93	0.65
1:B:1244:HIS:HD2	1:B:1279:SER:HB3	1.61	0.64
1:A:224:VAL:HG11	1:A:258:LEU:HD11	1.79	0.63
1:A:180:HIS:HE1	1:A:226:GLU:OE2	1.82	0.62
1:A:95:GLN:NE2	1:B:1183:GLY:H	1.99	0.60
1:A:221:ALA:HB1	1:A:257:LYS:HD2	1.83	0.60
1:B:1012:LEU:HD21	1:B:1272:HIS:CD2	2.36	0.60
1:A:234:ASP:H	1:A:237:GLN:NE2	1.97	0.59
1:A:48:ASN:HD22	1:A:48:ASN:N	2.00	0.57
1:B:1245:GLN:HB3	1:B:1269:LEU:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1245:GLN:HE21	1:B:1269:LEU:H	1.54	0.56
1:A:245:GLN:HE21	1:A:269:LEU:H	1.56	0.54
1:A:104:PRO:HB3	1:B:1179:LEU:HB2	1.90	0.53
1:A:56:PHE:O	1:A:60:THR:HG23	2.09	0.53
1:A:13:PRO:O	1:A:43:HIS:HD2	1.91	0.52
1:A:224:VAL:HG11	1:A:258:LEU:HD21	1.91	0.52
1:A:224:VAL:HG12	1:A:258:LEU:HD21	1.88	0.52
1:A:257:LYS:O	1:A:257:LYS:HG3	2.10	0.51
1:A:48:ASN:H	1:A:48:ASN:ND2	2.00	0.51
1:A:244:HIS:CD2	1:A:279:SER:HB3	2.47	0.50
1:B:1004:LYS:HE3	1:B:1171:GLU:O	2.12	0.50
1:B:1304:PHE:HZ	1:B:1308:PHE:CD2	2.30	0.49
1:A:31:GLU:O	1:A:35:THR:HG23	2.12	0.49
1:A:238:LEU:HD23	1:A:298:LEU:HD13	1.95	0.49
1:B:1180:HIS:HE1	1:B:1226:GLU:OE2	1.95	0.49
1:A:95:GLN:HE21	1:B:1183:GLY:H	1.60	0.48
1:A:93:GLN:O	1:A:97:MET:HG3	2.14	0.47
1:A:245:GLN:NE2	1:A:269:LEU:H	2.12	0.47
1:A:179:LEU:HB2	1:B:1104:PRO:HB3	1.96	0.47
1:A:245:GLN:HE21	1:A:269:LEU:HB3	1.80	0.47
1:B:1176:SER:OG	1:B:1178:HIS:HE1	1.98	0.46
1:B:1087:PHE:HA	1:B:1088:PRO:C	2.40	0.46
1:A:172:PRO:HA	1:A:173:GLY:HA3	1.77	0.45
1:A:87:PHE:HA	1:A:88:PRO:C	2.40	0.45
1:B:1070:LYS:HD3	1:B:1098:LEU:O	2.17	0.45
1:B:1002:TYR:CD2	1:B:1172:PRO:HB3	2.51	0.45
1:A:244:HIS:HD2	1:A:279:SER:HB3	1.82	0.45
1:A:112:CYS:SG	3:A:1866:HOH:O	2.48	0.43
1:B:1036:ARG:HG2	1:B:1036:ARG:HH21	1.83	0.43
1:B:1013:PRO:O	1:B:1043:HIS:HD2	2.02	0.43
1:A:219:GLU:OE2	1:A:219:GLU:HA	2.19	0.42
1:A:242:VAL:HB	1:A:301:LEU:HD23	2.02	0.42
1:A:176:SER:OG	1:A:178:HIS:HE1	2.02	0.42
1:B:1290:ASP:C	1:B:1290:ASP:OD1	2.61	0.42
1:B:1172:PRO:HA	1:B:1173:GLY:HA3	1.78	0.41
1:B:1001:MET:HB2	1:B:1127:LYS:O	2.20	0.41
1:B:1090:ALA:O	1:B:1094:ILE:HG13	2.21	0.41
1:B:1110:ALA:HB3	1:B:1114:GLY:HA2	2.03	0.41
1:B:1193:ASN:O	1:B:1194:ALA:C	2.64	0.40
1:B:1123:ASP:O	1:B:1127:LYS:HB2	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	315/317 (99%)	308 (98%)	7 (2%)	0	100	100
1	B	315/317 (99%)	305 (97%)	10 (3%)	0	100	100
All	All	630/634 (99%)	613 (97%)	17 (3%)	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	243/247 (98%)	235 (97%)	8 (3%)	33	34
1	B	244/247 (99%)	233 (96%)	11 (4%)	24	23
All	All	487/494 (99%)	468 (96%)	19 (4%)	28	28

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	PRO
1	A	48	ASN
1	A	51	VAL
1	A	243	PRO
1	A	257	LYS
1	A	269	LEU
1	A	298	LEU
1	A	316	ARG

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Mol	Chain	Res	Type
1	B	1022	LEU
1	B	1051	VAL
1	B	1071	ASP
1	B	1108	VAL
1	B	1151	ARG
1	B	1211	GLU
1	B	1237	GLN
1	B	1243	PRO
1	B	1248	LEU
1	B	1258	LEU
1	B	1298	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	48	ASN
1	A	95	GLN
1	A	178	HIS
1	A	180	HIS
1	A	193	ASN
1	A	201	ASN
1	A	237	GLN
1	A	244	HIS
1	A	245	GLN
1	B	1043	HIS
1	B	1178	HIS
1	B	1180	HIS
1	B	1245	GLN
1	B	1264	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are 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	PO4	A	350	-	4,4,4	1.13	0	6,6,6	0.47	0
2	PO4	B	1350	-	4,4,4	0.68	0	6,6,6	0.50	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.