



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:21 PM GMT

PDB ID : 1F80  
Title : HOLO-(ACYL CARRIER PROTEIN) SYNTHASE IN COMPLEX WITH  
HOLO-(ACYL CARRIER PROTEIN)  
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Deposited on : 2000-06-28  
Resolution : 2.30 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

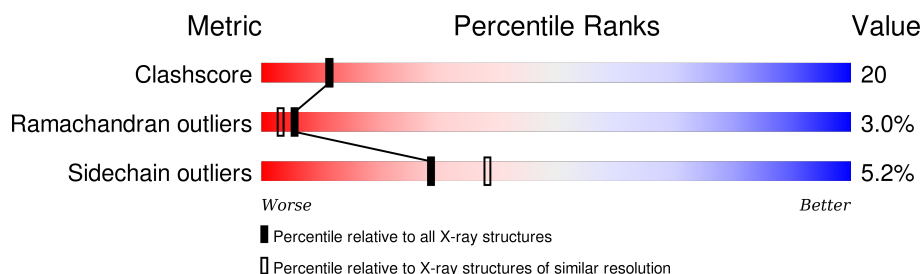
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	120	 70% 27% . .
1	B	120	 78% 18% . .
1	C	120	 67% 25% . . .
2	D	81	 46% 41% . . 9%
2	E	81	 49% 36% 5% . 9%
2	F	81	 53% 31% 6% 10%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4543 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 HOLO-(ACYL CARRIER PROTEIN) SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	118	Total	C	N	O	S	0	0	0
			908	577	159	170	2			
1	B	118	Total	C	N	O	S	0	0	0
			892	565	156	169	2			
1	C	116	Total	C	N	O	S	0	0	0
			879	559	150	168	2			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	ILE	ENGINEERED	UNP P96618
B	2	ALA	ILE	ENGINEERED	UNP P96618
C	2	ALA	ILE	ENGINEERED	UNP P96618

- Molecule 2 is a protein called ACYL CARRIER PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	74	Total	C	N	O	P	S	0	0
			584	359	87	134	1	3		
2	E	74	Total	C	N	O	P	S	0	0
			590	362	88	136	1	3		
2	F	73	Total	C	N	O	P	S	0	0
			565	347	84	131	1	2		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	GLY	-	see remark 999	UNP P80643
D	-3	PRO	-	see remark 999	UNP P80643
D	-2	LEU	-	see remark 999	UNP P80643
D	-1	GLY	-	see remark 999	UNP P80643
D	0	SER	-	see remark 999	UNP P80643

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	GLY	-	see remark 999	UNP P80643
E	-3	PRO	-	see remark 999	UNP P80643
E	-2	LEU	-	see remark 999	UNP P80643
E	-1	GLY	-	see remark 999	UNP P80643
E	0	SER	-	see remark 999	UNP P80643
F	-4	GLY	-	see remark 999	UNP P80643
F	-3	PRO	-	see remark 999	UNP P80643
F	-2	LEU	-	see remark 999	UNP P80643
F	-1	GLY	-	see remark 999	UNP P80643
F	0	SER	-	see remark 999	UNP P80643

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	47	Total O 47 47	0	0
4	B	35	Total O 35 35	0	0
4	C	26	Total O 26 26	0	0
4	D	7	Total O 7 7	0	0
4	E	2	Total O 2 2	0	0
4	F	7	Total O 7 7	0	0

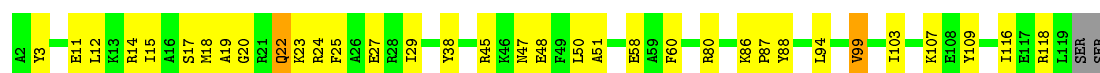
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.


Note EDS was not executed.

#### • Molecule 1: HOLO-(ACYL CARRIER PROTEIN) SYNTHASE

Chain A: 



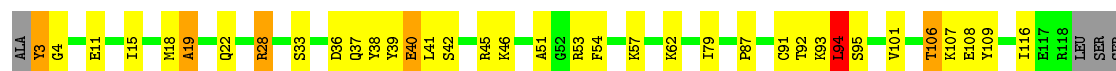
#### • Molecule 1: HOLO-(ACYL CARRIER PROTEIN) SYNTHASE

Chain B: 



#### • Molecule 1: HOLO-(ACYL CARRIER PROTEIN) SYNTHASE

Chain C: 



#### • Molecule 2: ACYL CARRIER PROTEIN

Chain D: 



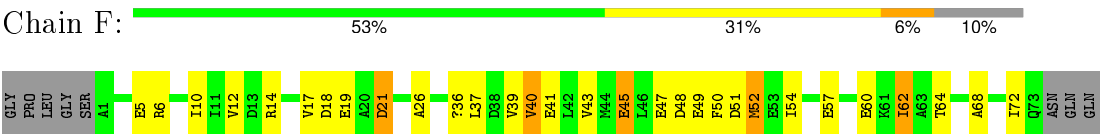
ASN  
GLN  
GLN

#### • Molecule 2: ACYL CARRIER PROTEIN

Chain E: 



● Molecule 2: ACYL CARRIER PROTEIN



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.46 Å   122.03 Å   136.77 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	50.00 – 2.30	Depositor
% Data completeness (in resolution range)	95.4 (50.00-2.30)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.222 , 0.279	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4543	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, PN2

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	0.83	0/921	0.95	1/1238 (0.1%)
1	B	0.80	0/905	0.91	0/1222
1	C	0.67	0/892	0.84	0/1202
2	D	0.57	0/558	0.84	0/754
2	E	0.57	0/564	0.77	0/762
2	F	0.47	0/556	0.63	0/751
All	All	0.69	0/4396	0.85	1/5929 (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
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	GLN	O-C-N	-6.96	111.57	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	88	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	B	111	ALA	Mainchain

## 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	908	0	902	34	0
1	B	892	0	860	19	0
1	C	879	0	853	36	0
2	D	584	0	554	49	0
2	E	590	0	559	28	0
2	F	565	0	532	27	0
3	A	1	0	0	0	0
4	A	47	0	0	0	0
4	B	35	0	0	1	0
4	C	26	0	0	0	0
4	D	7	0	0	1	0
4	E	2	0	0	1	0
4	F	7	0	0	0	0
All	All	4543	0	4260	177	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 20.

The worst 5 of 177 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)
2:E:62:ILE:HG22	2:E:67:ASP:HB3	1.45	0.98
1:C:106:THR:HG22	1:C:109:TYR:H	1.24	0.96
2:D:72:ILE:O	2:D:73:GLN:HG3	1.66	0.94
1:A:86:LYS:HD2	1:A:87:PRO:HD2	1.51	0.91
2:D:14:ARG:HD2	2:D:41:GLU:HG2	1.52	0.91

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	116/120 (97%)	113 (97%)	1 (1%)	2 (2%)	11	10
1	B	116/120 (97%)	109 (94%)	6 (5%)	1 (1%)	21	24
1	C	114/120 (95%)	106 (93%)	3 (3%)	5 (4%)	3	1
2	D	71/81 (88%)	58 (82%)	10 (14%)	3 (4%)	3	1
2	E	71/81 (88%)	60 (84%)	8 (11%)	3 (4%)	3	1
2	F	70/81 (86%)	61 (87%)	6 (9%)	3 (4%)	3	1
All	All	558/603 (92%)	507 (91%)	34 (6%)	17 (3%)	5	3

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	19	ALA
1	C	95	SER
2	D	17	VAL
2	E	19	GLU
2	F	17	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	89/97 (92%)	88 (99%)	1 (1%)	80	90
1	B	85/97 (88%)	82 (96%)	3 (4%)	43	58
1	C	85/97 (88%)	80 (94%)	5 (6%)	24	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	61/68 (90%)	57 (93%)	4 (7%)	21	27
2	E	62/68 (91%)	58 (94%)	4 (6%)	21	27
2	F	61/68 (90%)	55 (90%)	6 (10%)	10	11
All	All	443/495 (90%)	420 (95%)	23 (5%)	29	38

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	21	ASP
2	D	42	LEU
2	F	48	ASP
2	D	39	VAL
2	E	19	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	113	GLN
1	C	22	GLN
2	D	70	ASN
1	B	96	GLN
2	D	73	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

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](#)

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.