



wwPDB X-ray Structure Validation Summary Report ⓘ

May 22, 2020 – 10:41 am BST

PDB ID : 1VI1
Title : Crystal structure of a fatty acid/phospholipid synthesis protein
Authors : Structural GenomiX
Deposited on : 2003-12-01
Resolution : 2.95 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

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
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

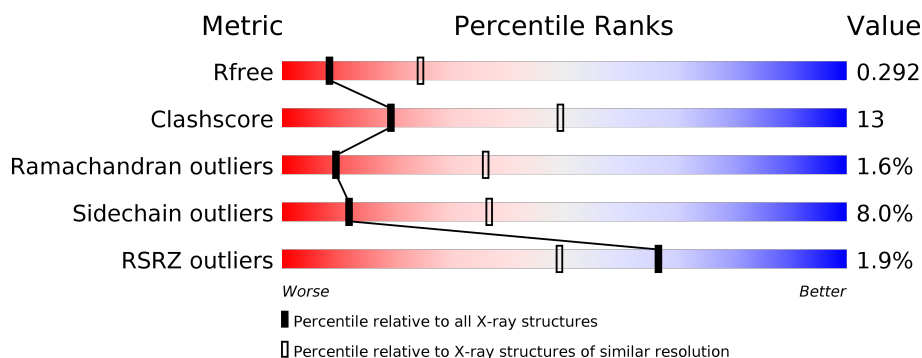
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 ≥ 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	345	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>24%</div> <div>• 5%</div> </div> </div>
1	B	345	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>27%</div> <div>5%</div> <div>7%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4784 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 Fatty acid/phospholipid synthesis protein plsX.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	Se	0	3	0
			2412	1501	419	476	1	15			
1	B	321	Total	C	N	O	S	Se	0	3	0
			2368	1476	410	466	1	15			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	cloning artifact	UNP P71018
A	0	SER	-	cloning artifact	UNP P71018
A	1	LEU	-	cloning artifact	UNP P71018
A	8	MSE	MET	modified residue	UNP P71018
A	80	MSE	MET	modified residue	UNP P71018
A	83	MSE	MET	modified residue	UNP P71018
A	105	MSE	MET	modified residue	UNP P71018
A	157	MSE	MET	modified residue	UNP P71018
A	245	MSE	MET	modified residue	UNP P71018
A	246	MSE	MET	modified residue	UNP P71018
A	250	MSE	MET	modified residue	UNP P71018
A	270	MSE	MET	modified residue	UNP P71018
A	272	MSE	MET	modified residue	UNP P71018
A	274	MSE	MET	modified residue	UNP P71018
A	305	ARG	HIS	modified residue	UNP P71018
A	313	MSE	MET	modified residue	UNP P71018
A	334	GLU	-	cloning artifact	UNP P71018
A	335	GLY	-	cloning artifact	UNP P71018
A	336	GLY	-	cloning artifact	UNP P71018
A	337	SER	-	cloning artifact	UNP P71018
A	338	HIS	-	cloning artifact	UNP P71018
A	339	HIS	-	cloning artifact	UNP P71018
A	340	HIS	-	cloning artifact	UNP P71018
A	341	HIS	-	cloning artifact	UNP P71018
A	342	HIS	-	cloning artifact	UNP P71018

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	343	HIS	-	cloning artifact	UNP P71018
B	-1	MSE	-	cloning artifact	UNP P71018
B	0	SER	-	cloning artifact	UNP P71018
B	1	LEU	-	cloning artifact	UNP P71018
B	8	MSE	MET	modified residue	UNP P71018
B	80	MSE	MET	modified residue	UNP P71018
B	83	MSE	MET	modified residue	UNP P71018
B	105	MSE	MET	modified residue	UNP P71018
B	157	MSE	MET	modified residue	UNP P71018
B	245	MSE	MET	modified residue	UNP P71018
B	246	MSE	MET	modified residue	UNP P71018
B	250	MSE	MET	modified residue	UNP P71018
B	270	MSE	MET	modified residue	UNP P71018
B	272	MSE	MET	modified residue	UNP P71018
B	274	MSE	MET	modified residue	UNP P71018
B	305	ARG	HIS	modified residue	UNP P71018
B	313	MSE	MET	modified residue	UNP P71018
B	334	GLU	-	cloning artifact	UNP P71018
B	335	GLY	-	cloning artifact	UNP P71018
B	336	GLY	-	cloning artifact	UNP P71018
B	337	SER	-	cloning artifact	UNP P71018
B	338	HIS	-	cloning artifact	UNP P71018
B	339	HIS	-	cloning artifact	UNP P71018
B	340	HIS	-	cloning artifact	UNP P71018
B	341	HIS	-	cloning artifact	UNP P71018
B	342	HIS	-	cloning artifact	UNP P71018
B	343	HIS	-	cloning artifact	UNP P71018

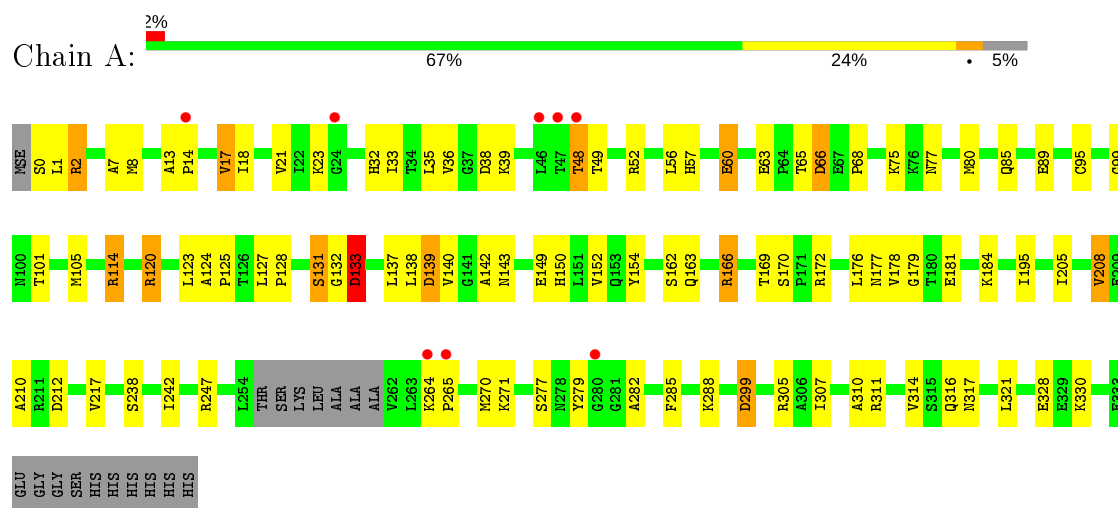
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total O 3 3	0	0
2	B	1	Total O 1 1	0	0

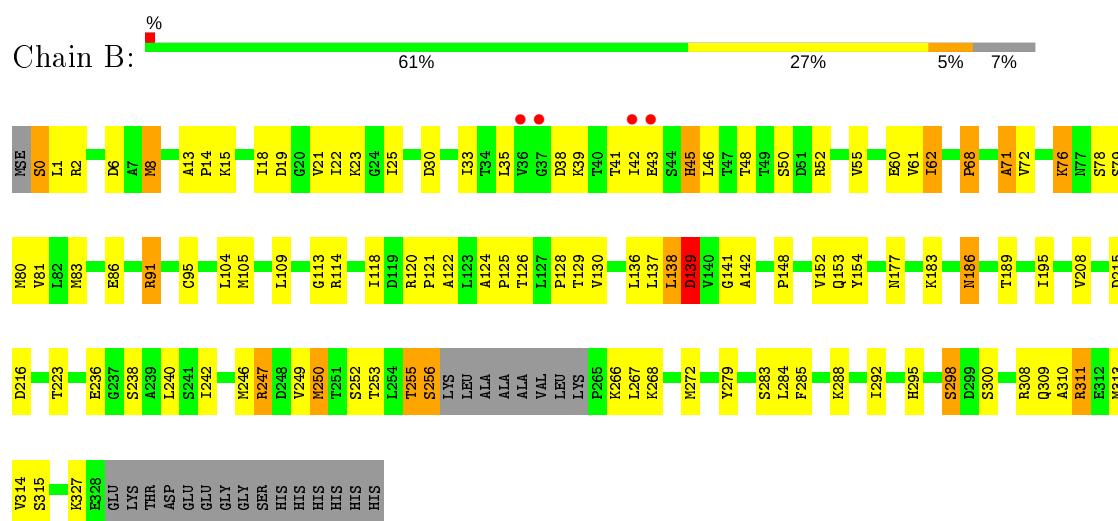
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Fatty acid/phospholipid synthesis protein plsX



- Molecule 1: Fatty acid/phospholipid synthesis protein plsX



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	170.31Å 170.31Å 187.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.94 – 2.95 47.94 – 2.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (47.94-2.95) 100.0 (47.94-2.95)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.95 (at 2.96Å)	Xtriage
Refinement program	REFMAC 4.0	Depositor
R, R_{free}	0.285 , 0.334 0.241 , 0.292	Depositor DCC
R_{free} test set	1116 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	69.2	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 56.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4784	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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

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	0.68	0/2439	1.26	14/3283 (0.4%)
1	B	0.67	0/2395	1.19	12/3223 (0.4%)
All	All	0.67	0/4834	1.23	26/6506 (0.4%)

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	5
1	B	0	9
All	All	0	14

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	ARG	NE-CZ-NH1	-10.95	114.82	120.30
1	A	52	ARG	CD-NE-CZ	9.38	136.74	123.60
1	A	52	ARG	NE-CZ-NH2	9.04	124.82	120.30
1	A	114	ARG	NE-CZ-NH2	8.80	124.70	120.30
1	B	139	ASP	CB-CG-OD2	-7.61	111.46	118.30

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	149	GLU	Mainchain
1	A	17	VAL	Mainchain
1	A	299	ASP	Mainchain
1	A	32	HIS	Mainchain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	A	95	CYS	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	2412	0	2373	55	0
1	B	2368	0	2358	68	0
2	A	3	0	0	0	0
2	B	1	0	0	0	0
All	All	4784	0	4731	123	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 13.

The worst 5 of 123 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:13:ALA:HB1	1:A:14:PRO:HA	1.33	1.04
1:B:309:GLN:HG2	1:B:313:MSE:HE2	1.46	0.98
1:B:13:ALA:HB1	1:B:14:PRO:HA	1.49	0.95
1:A:138:LEU:HD23	1:A:154:TYR:HB3	1.63	0.80
1:A:1:LEU:HD12	1:A:2:ARG:H	1.45	0.79

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	326/345 (94%)	296 (91%)	27 (8%)	3 (1%)	17	51
1	B	320/345 (93%)	284 (89%)	29 (9%)	7 (2%)	6	28
All	All	646/690 (94%)	580 (90%)	56 (9%)	10 (2%)	9	38

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	327	LYS
1	B	139	ASP
1	B	141	GLY
1	B	142	ALA
1	B	186	ASN

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	252/270 (93%)	231 (92%)	21 (8%)	11	35
1	B	252/270 (93%)	232 (92%)	20 (8%)	12	37
All	All	504/540 (93%)	463 (92%)	41 (8%)	12	36

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	316	GLN
1	B	8	MSE
1	B	256	SER
1	A	328	GLU
1	A	330	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	45	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	323	GLN
1	B	164	GLN
1	A	323	GLN
1	B	85	GLN

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 carbohydrates 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	315/345 (91%)	0.16	8 (2%) 57 40	30, 64, 86, 93	0
1	B	309/345 (89%)	0.09	4 (1%) 77 61	35, 66, 86, 93	0
All	All	624/690 (90%)	0.12	12 (1%) 66 49	30, 65, 86, 93	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	42	ILE	3.8
1	A	265	PRO	3.6
1	B	43	GLU	2.7
1	A	47	THR	2.7
1	A	280	GLY	2.6

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 carbohydrates 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.