

Full wwPDB X-ray Structure Validation Report (i)

Oct 15, 2023 – 11:26 PM EDT

PDB ID : 7SUB

Title: 3-oxoacyl-ACP reductase FabG

Authors: Thomas, L.M.; Karr, E.A.; Dinh, D.M.

Deposited on : 2021-11-16

Resolution : 1.78 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 (i) 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 (1)) 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 : 2.36

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)

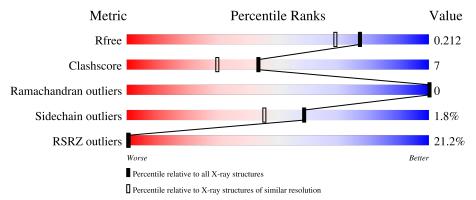
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
R_{free}	130704	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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 <=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		
			18%		
1	A	267	71%	12%	17%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

M	ol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	,	GOL	A	301	-	X	X	-



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1817 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 3-oxoacyl-reductase.

Mol	Chain	Residues		\mathbf{At}	oms			ZeroOcc	AltConf	Trace
1	٨	222	Total	С	N	О	S	0	4	0
1	A	222	1689	1073	295	310	11	0	4	

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	initiating methionine	UNP Q2LXS6
A	-7	HIS	-	expression tag	UNP Q2LXS6
A	-6	HIS	-	expression tag	UNP Q2LXS6
A	-5	HIS	-	expression tag	UNP Q2LXS6
A	-4	HIS	-	expression tag	UNP Q2LXS6
A	-3	HIS	-	expression tag	UNP Q2LXS6
A	-2	HIS	-	expression tag	UNP Q2LXS6
A	-1	GLY	-	expression tag	UNP Q2LXS6
A	0	SER	-	expression tag	UNP Q2LXS6
A	252	LEU	-	expression tag	UNP Q2LXS6
A	253	GLN	-	expression tag	UNP Q2LXS6
A	254	PRO	-	expression tag	UNP Q2LXS6
A	255	SER		expression tag	UNP Q2LXS6
A	256	LEU	-	expression tag	UNP Q2LXS6
A	257	ILE	-	expression tag	UNP Q2LXS6
A	258	SER	-	expression tag	UNP Q2LXS6

• Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total C 6 3	O 3	0	0

• Molecule 3 is water.

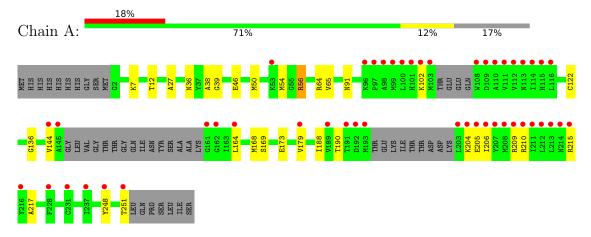
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	122	Total O 122 122	0	0



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: 3-oxoacyl-reductase





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	P 31 2 1	Depositor	
Cell constants	56.01Å 56.01Å 133.13Å	Depositor	
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor	
Resolution (Å)	39.20 - 1.78	Depositor	
resolution (A)	39.20 - 1.78	EDS	
% Data completeness	99.9 (39.20-1.78)	Depositor	
(in resolution range)	99.9 (39.20-1.78)	EDS	
R_{merge}	0.04	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	2.26 (at 1.78Å)	Xtriage	
Refinement program	PHENIX 1.20.1_4487	Depositor	
R, R_{free}	0.185 , 0.212	Depositor	
it, it free	0.183 , 0.212	DCC	
R_{free} test set	1999 reflections (8.33%)	wwPDB-VP	
Wilson B-factor (Å ²)	30.4	Xtriage	
Anisotropy	0.291	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 48.1	EDS	
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage	
Estimated twinning fraction	0.028 for -h,-k,l	Xtriage	
F_o, F_c correlation	0.96	EDS	
Total number of atoms	1817	wwPDB-VP	
Average B, all atoms (Å ²)	37.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.33% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: GOL

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).

Mal	Chain	Bond	lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.64	0/1723	0.75	1/2323 (0.0%)	

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
1	A	54	MET	CG-SD-CE	-6.28	90.15	100.20

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	1689	0	1725	23	0
2	A	6	0	7	5	0
3	A	122	0	0	1	0
All	All	1817	0	1732	23	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 7.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:7:LYS:NZ	3:A:401:HOH:O	2.31	0.64
1:A:38:ALA:H	2:A:301:GOL:H11	1.65	0.62
1:A:144:VAL:HG21	1:A:206:ILE:HD13	1.85	0.58
1:A:46:GLU:O	1:A:50:MET:HG3	2.05	0.57
1:A:27:ALA:O	1:A:56:ARG:HD3	2.05	0.56
1:A:169:SER:O	1:A:173:GLU:HG3	2.05	0.56
1:A:38:ALA:HB3	2:A:301:GOL:H11	1.87	0.55
1:A:210:ARG:HH11	1:A:215:ARG:HD2	1.72	0.54
1:A:188:ILE:HD12	1:A:217:ALA:CB	2.41	0.51
1:A:38:ALA:N	2:A:301:GOL:H11	2.26	0.50
1:A:190:THR:HA	1:A:217:ALA:O	2.14	0.47
1:A:39:GLY:H	2:A:301:GOL:H11	1.80	0.46
1:A:102:LYS:HE2	1:A:205:GLU:H	1.79	0.46
1:A:205:GLU:OE1	1:A:209:ARG:NH2	2.49	0.45
1:A:102:LYS:HE2	1:A:204:LYS:HA	1.98	0.45
1:A:205:GLU:O	1:A:209:ARG:HG2	2.17	0.45
1:A:164:LEU:O	1:A:168:MET:HG3	2.18	0.44
1:A:136:GLY:O	1:A:179:VAL:HA	2.18	0.44
1:A:248:TYR:O	1:A:251:THR:HG22	2.18	0.44
1:A:210:ARG:NH1	1:A:215:ARG:HD2	2.35	0.42
1:A:65:VAL:HB	1:A:122:CYS:SG	2.60	0.42
1:A:39:GLY:H	2:A:301:GOL:C1	2.33	0.41
1:A:12:THR:O	1:A:91:ASN:HB3	2.21	0.41

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	218/267 (82%)	213 (98%)	5 (2%)	0	100 100

There are no Ramachandran outliers to report.



5.3.2 Protein sidechains (i)

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	174/209 (83%)	171 (98%)	3 (2%)	60 48

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	56	ARG
1	A	64	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	ol Type Chain Res Link					Bond lengths			Bond angles		
IVIOI	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
2	GOL	A	301	-	5,5,5	2.08	4 (80%)	5,5,5	1.06	1 (20%)	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	301	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
2	A	301	GOL	O1-C1	-2.56	1.31	1.42
2	A	301	GOL	O2-C2	2.41	1.50	1.43
2	A	301	GOL	C3-C2	2.17	1.60	1.51
2	A	301	GOL	C1-C2	-2.07	1.43	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	301	GOL	C3-C2-C1	-2.06	103.70	111.70

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	GOL	C1-C2-C3-O3
2	A	301	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	GOL	5	0



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^{th} 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>	#RSR	$\mathbf{Z}>$	$\overline{2}$	$OWAB(A^2)$	Q<0.9
1	A	222/267 (83%)	1.25	47 (21%)	0	0	21, 30, 74, 95	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	108	TRP	13.4
1	A	111	VAL	13.3
1	A	112	VAL	12.0
1	A	109	ASP	10.7
1	A	203	LEU	10.7
1	A	206	ILE	8.3
1	A	145	ALA	8.1
1	A	213	LEU	8.0
1	A	216	TYR	7.7
1	A	144	VAL	7.3
1	A	100	LEU	7.2
1	A	211	ILE	6.4
1	A	114	ILE	6.3
1	A	103	MET	5.8
1	A	214	ASN	5.6
1	A	98	ALA	5.5
1	A	97	PRO	5.2
1	A	102	LYS	5.1
1	A	110	ALA	5.1
1	A	161	GLY	5.1
1	A	101	HIS	5.1
1	A	113	ASN	4.7
1	A	207	TYR	4.3
1	A	193	MET	4.2
1	A	189	VAL	4.1
1	A	209	ARG	4.0
1	A	212	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	99	MET	3.9
1	A	115[A]	HIS	3.8
1	A	205	GLU	3.8
1	A	162	GLY	3.6
1	A	215	ARG	3.2
1	A	208	MET	3.1
1	A	248	TYR	3.1
1	A	191	THR	2.9
1	A	96	LYS	2.9
1	A	210	ARG	2.9
1	A	192	ASP	2.8
1	A	53	LYS	2.8
1	A	228	PHE	2.7
1	A	116	LEU	2.4
1	A	164	LEU	2.4
1	A	251	THR	2.3
1	A	237	ILE	2.2
1	A	204	LYS	2.1
1	A	231	CYS	2.0
1	A	179	VAL	2.0

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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	GOL	A	301	6/6	0.84	0.19	31,41,44,48	0



6.5 Other polymers (i)

There are no such residues in this entry.

