

Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 – 04:49 PM EDT

PDB ID : 3LJ7

Title : 3D-crystal structure of humanized-rat fatty acid amide hydrolase (FAAH) con-

jugated with Carbamate inhibitor URB597

Authors : Mileni, M.; Stevens, R.C.; Kamtekar, S.

Deposited on : 2010-01-25

Resolution : 2.30 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

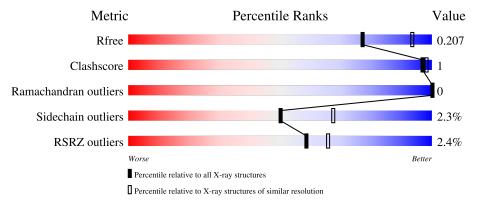
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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	
1	A	573	91%	• 5%
1	В	573	92%	• 5%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8951 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 amide hydrolase 1.

\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	545	Total 4218	C 2692	N 720	O 775	S 31	0	2	0
1	В	547	Total 4232	C 2701	N 722	O 778	S 31	0	2	0

There are 58 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	expression tag	UNP P97612
A	8	GLY	-	expression tag	UNP P97612
A	9	SER	-	expression tag	UNP P97612
A	10	SER	-	expression tag	UNP P97612
A	11	HIS	-	expression tag	UNP P97612
A	12	HIS	-	expression tag	UNP P97612
A	13	HIS	-	expression tag	UNP P97612
A	14	HIS	-	expression tag	UNP P97612
A	15	HIS	-	expression tag	UNP P97612
A	16	HIS	-	expression tag	UNP P97612
A	17	SER	-	expression tag	UNP P97612
A	18	SER	-	expression tag	UNP P97612
A	19	GLY	-	expression tag	UNP P97612
A	20	LEU	-	expression tag	UNP P97612
A	21	VAL	-	expression tag	UNP P97612
A	22	PRO	-	expression tag	UNP P97612
A	23	ARG	-	expression tag	UNP P97612
A	24	GLY	-	expression tag	UNP P97612
A	25	SER	-	expression tag	UNP P97612
A	26	HIS	-	expression tag	UNP P97612
A	27	MET	-	. ,	
A	28	ALA	-	expression tag	UNP P97612
A	29	SER	-	expression tag	UNP P97612
A	192	PHE	LEU	engineered mutation	UNP P97612
A	194	TYR	PHE	engineered mutation	UNP P97612

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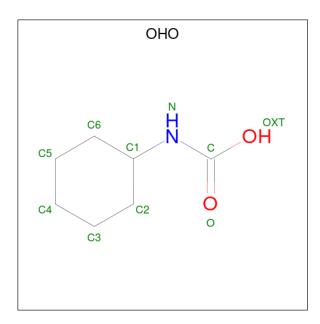


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Chain	Residue	Modelled	Actual	Comment	Reference
A	377	THR	ALA	engineered mutation	UNP P97612
A	435	ASN	SER	engineered mutation	UNP P97612
A	491	VAL	ILE	engineered mutation	UNP P97612
A	495	MET	VAL	engineered mutation	UNP P97612
В	7	MET	-	expression tag	UNP P97612
В	8	GLY	-	expression tag	UNP P97612
В	9	SER	-	expression tag	UNP P97612
В	10	SER	-	expression tag	UNP P97612
В	11	HIS	-	expression tag	UNP P97612
В	12	HIS	-	expression tag	UNP P97612
В	13	HIS	-	expression tag	UNP P97612
В	14	HIS	-	expression tag	UNP P97612
В	15	HIS	-	expression tag	UNP P97612
В	16	HIS	-	expression tag	UNP P97612
В	17	SER	-	expression tag	UNP P97612
В	18	SER	-	expression tag	UNP P97612
В	19	GLY	-	expression tag	UNP P97612
В	20	LEU	-	expression tag	UNP P97612
В	21	VAL	-	expression tag	UNP P97612
В	22	PRO	_	expression tag	UNP P97612
В	23	ARG	-	expression tag	UNP P97612
В	24	GLY	_	expression tag	UNP P97612
В	25	SER	-	expression tag	UNP P97612
В	26	HIS	-	expression tag	UNP P97612
В	27	MET	-	expression tag	UNP P97612
В	28	ALA	-	expression tag	UNP P97612
В	29	SER	-	expression tag	UNP P97612
В	192	PHE	LEU	engineered mutation	UNP P97612
В	194	TYR	PHE	engineered mutation	UNP P97612
В	377	THR	ALA	engineered mutation	UNP P97612
В	435	ASN	SER	engineered mutation	UNP P97612
В	491	VAL	ILE	engineered mutation	UNP P97612
В	495	MET	VAL	engineered mutation	UNP P97612

 \bullet Molecule 2 is CYCLOHEXANE AMINOCARBOXYLIC ACID (three-letter code: OHO) (formula: $\mathrm{C_7H_{13}NO_2}).$





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 9		N 1	O 1	0	0
2	В	1	Total 9	C 7	N 1	O 1	0	0

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cl 2 2	0	0

• Molecule 4 is water.

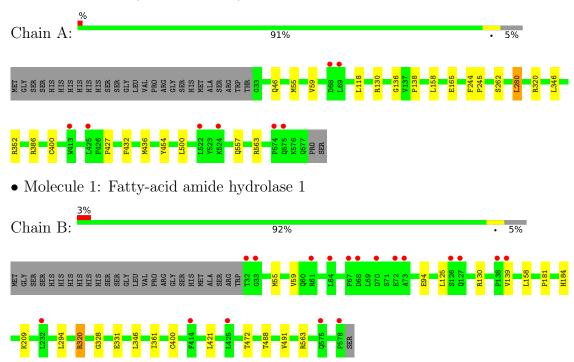
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	229	Total O 229 229	0	0
4	В	252	Total O 252 252	0	0



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: Fatty-acid amide hydrolase 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	102.73Å 105.08Å 147.80Å	Danagitan
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.80 - 2.30	Depositor
Resolution (A)	29.80 - 2.30	EDS
% Data completeness	97.7 (29.80-2.30)	Depositor
(in resolution range)	97.7 (29.80-2.30)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.23 (at 2.31Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
D.D.	0.176 , 0.214	Depositor
R, R_{free}	0.170 , 0.207	DCC
R_{free} test set	3549 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	40.3	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31 , 34.1	EDS
L-test for twinning ²	$< L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	0.020 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8951	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.16% 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: CL, OHO

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		
IVIOI		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.57	0/4318	0.64	0/5856	
1	В	0.58	0/4333	0.65	1/5878~(0.0%)	
All	All	0.58	0/8651	0.65	1/11734 (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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	320	ARG	NE-CZ-NH1	5.45	123.03	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	118	LEU	Peptide

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



All

All

8951

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4218	0	4278	7	0
1	В	4232	0	4292	9	0
2	A	9	0	12	0	0
2	В	9	0	12	0	0
3	A	2	0	0	0	0
4	A	229	0	0	0	0
4	В	252	0	0	2	0

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

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 1.

16

0

8594

All (16) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
		$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)
1:B:331:GLU:HG2	1:B:346:LEU:HD12	1.85	0.57
1:B:55:MET:O	1:B:59:VAL:HG23	2.09	0.53
1:B:488:THR:O	1:B:491:VAL:HG22	2.12	0.50
1:A:432:PHE:CZ	1:A:436:MET:HE1	2.47	0.49
1:A:55:MET:O	1:A:59:VAL:HG23	2.14	0.48
1:A:454:TYR:CE1	1:A:500:LEU:HD21	2.50	0.47
1:B:125:LEU:CD1	4:B:816:HOH:O	2.64	0.45
1:B:328:GLY:HA2	1:B:361:ILE:O	2.17	0.45
1:A:262:SER:O	1:A:280:LEU:HD21	2.17	0.45
1:A:346:LEU:C	1:A:346:LEU:HD13	2.37	0.44
1:B:139:VAL:O	1:B:181:PRO:HA	2.18	0.43
1:B:346:LEU:C	1:B:346:LEU:HD13	2.39	0.42
1:B:94:GLU:HA	1:B:125:LEU:HD21	2.01	0.42
1:A:136:GLY:O	1:A:138:PRO:HD3	2.20	0.41
1:B:209:LYS:NZ	4:B:794:HOH:O	2.52	0.41
1:A:244:PHE:HB2	1:A:245:PRO:HD3	2.04	0.40

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	Perce	\mathbf{ntiles}
1	A	545/573 (95%)	535 (98%)	10 (2%)	0	100	100
1	В	547/573 (96%)	535 (98%)	12 (2%)	0	100	100
All	All	1092/1146 (95%)	1070 (98%)	22 (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	465/487 (96%)	453 (97%)	12 (3%)	46 63
1	В	467/487 (96%)	458 (98%)	9 (2%)	57 73
All	All	932/974 (96%)	911 (98%)	21 (2%)	50 67

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	130	ARG
1	A	158	LEU
1	A	165	GLU
1	A	280	LEU
1	A	320	ARG
1	A	352	ARG
1	A	386	ARG
1	A	400	CYS
1	A	427	PRO
1	A	557	GLN
1	A	563	ARG
1	В	130	ARG
1	В	158	LEU

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Mol	Chain	Res	Type
1	В	184	HIS
1	В	294	LEU
1	В	320	ARG
1	В	400	CYS
1	В	421	LEU
1	В	472	THR
1	В	563	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	334	ASN
1	A	351	GLN
1	A	466	ASN
1	В	124	GLN
1	В	334	ASN
1	В	351	GLN
1	В	449	HIS
1	В	466	ASN
1	В	575	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.



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	Dag	Link	В	ond leng	$_{ m gths}$	В	ond ang	gles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ОНО	A	1	1	9,9,10	0.89	1 (11%)	9,10,12	0.76	0
2	ОНО	В	1	1	9,9,10	0.61	0	9,10,12	0.72	0

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	ОНО	A	1	1	-	0/3/11/12	0/1/1/1
2	ОНО	В	1	1	-	0/3/11/12	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$Ideal(\AA)$
2	A	1	ОНО	C1-N	-2.25	1.45	1.47

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 (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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	545/573 (95%)	-0.27	8 (1%) 73 79	26, 41, 74, 108	0
1	В	547/573 (95%)	-0.22	18 (3%) 46 53	26, 39, 75, 104	0
All	All	1092/1146~(95%)	-0.25	26 (2%) 59 66	26, 40, 75, 108	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ
1	В	68 ASP		4.1
1	В	32	THR	3.8
1	A	575	GLN	3.7
1	A	425	LEU	3.6
1	В	575	GLN	3.4
1	В	64	LEU	3.4
1	В	578	PRO	3.3
1	A	574	PRO	3.3
1	A	522	LEU	2.9
1	A	413	TRP	2.8
1	A	69	LEU	2.7
1	В	61	ARG	2.7
1	В	139	VAL	2.6
1	В	67	PRO	2.5
1	В	127	GLN	2.5
1	В	72	GLU	2.4
1	В	126	SER	2.4
1	A	68	ASP	2.4
1	В	414	PHE	2.4
1	В	138	PRO	2.3
1	В	73	ALA	2.2
1	В	70	ASP	2.2
1	В	33	GLY	2.2
1	A	524	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	В	232	LEU	2.1
1	В	425	LEU	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
3	CL	A	2	1/1	0.94	0.08	60,60,60,60	0
2	ОНО	В	1	9/10	0.97	0.22	33,35,38,38	0
2	ОНО	A	1	9/10	0.98	0.24	30,34,39,39	0
3	CL	A	580	1/1	0.99	0.07	42,42,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.

