



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 28, 2023 – 05:35 AM EDT

PDB ID : 3KX8
Title : Structural basis of the activity and substrate specificity of the fluoroacetyl-CoA thioesterase FLK
Authors : Chirgadze, D.Y.; Dias, M.V.B.; Huang, F.; Tosin, M.; Spitter, D.; Valentine, E.F.; Leadlay, P.F.; Spencer, J.B.; Blundell, T.L.
Deposited on : 2009-12-02
Resolution : 2.35 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 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 : 4.02b-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 : 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

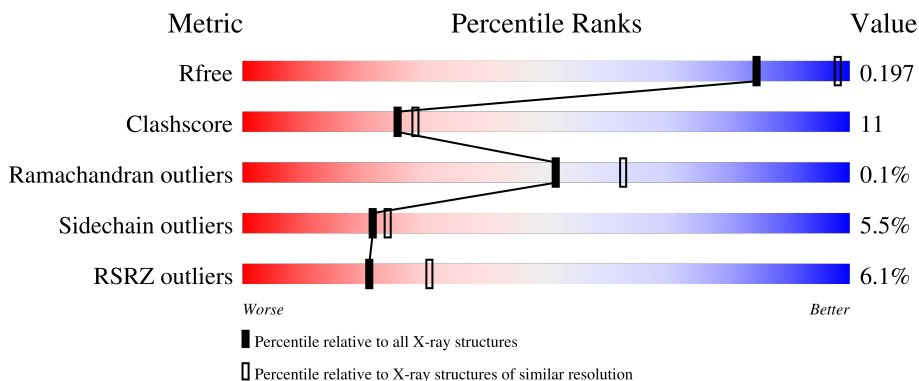
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.



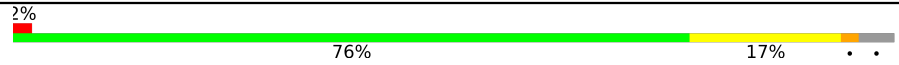


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 $\leq 5\%$. 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	139	11% (Poor fit) 71% (0 outliers) 22% (1 outlier) •• (2+ outliers)
1	B	139	6% (Poor fit) 73% (0 outliers) 22% (1 outlier) ••• (2+ outliers)
1	C	139	4% (Poor fit) 83% (0 outliers) 11% (1 outlier) • 5% (2+ outliers)
1	D	139	2% (Poor fit) 75% (0 outliers) 19% (1 outlier) •• (2+ outliers)
1	E	139	9% (Poor fit) 78% (0 outliers) 14% (1 outlier) •• (2+ outliers)

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Mol	Chain	Length	Quality of chain
1	F	139	 <p>2% 76% 17% . .</p>
1	G	139	 <p>4% 76% 19% . .</p>
1	H	139	 <p>7% 72% 22% . . .</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 8498 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 fluoroacetyl-CoA thioesterase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	133	1022	651	179	186	2	4	0	1	0
1	B	135	1061	671	191	193	2	4	0	2	0
1	C	132	1026	652	183	186	2	3	0	1	0
1	D	133	1026	653	185	182	2	4	0	1	0
1	E	133	1018	649	178	185	2	4	0	1	0
1	F	133	1030	655	184	185	2	4	0	1	0
1	G	133	1018	648	178	186	2	4	0	1	0
1	H	134	1022	651	179	186	2	4	0	1	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	37	Total 37	O 37	0	0
2	B	41	Total 41	O 41	0	0
2	C	33	Total 33	O 33	0	0
2	D	26	Total 26	O 26	0	0
2	E	30	Total 30	O 30	0	0
2	F	39	Total 39	O 39	0	0

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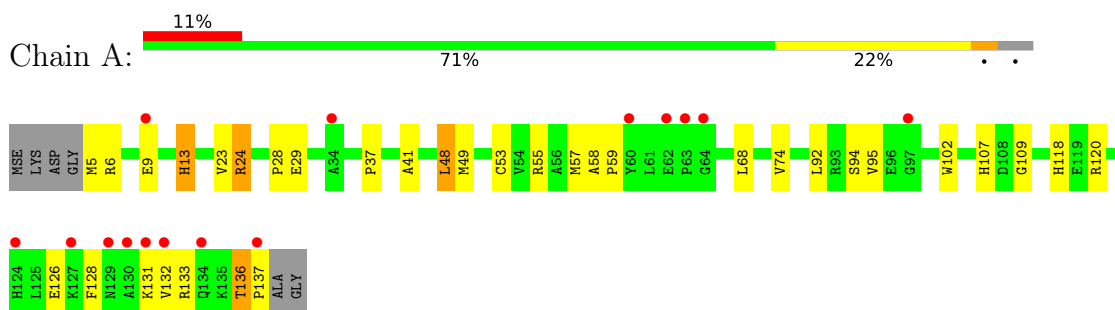
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	43	Total	O	0	0
			43	43		
2	H	26	Total	O	0	0
			26	26		

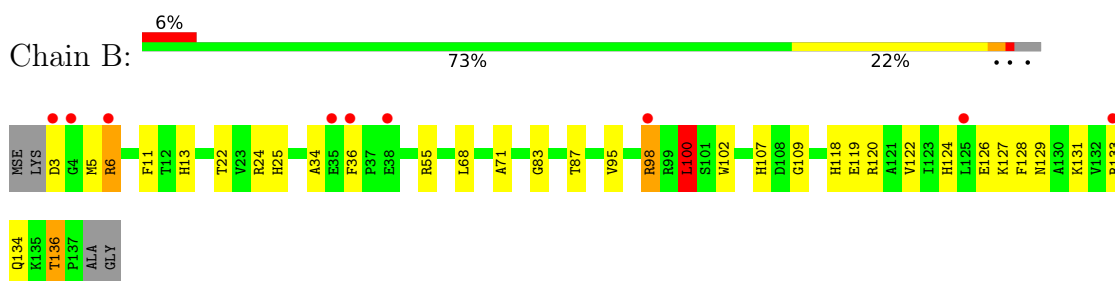
3 Residue-property plots [i](#)

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.

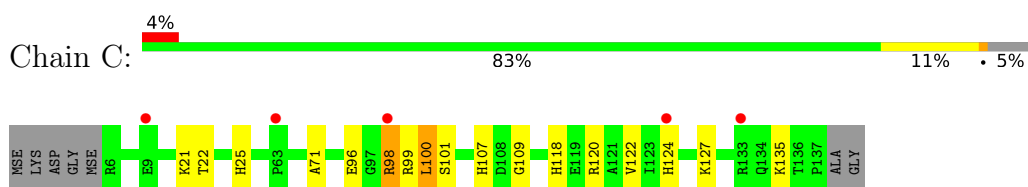
- Molecule 1: fluoroacetyl-CoA thioesterase



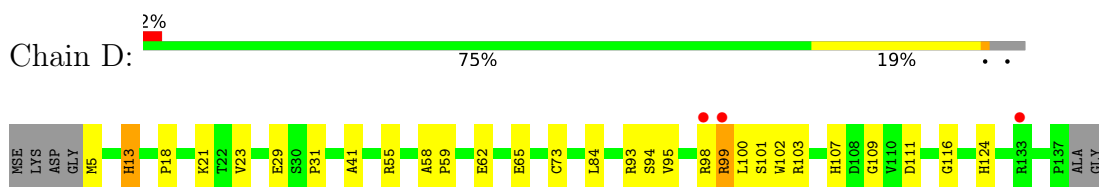
- Molecule 1: fluoroacetyl-CoA thioesterase



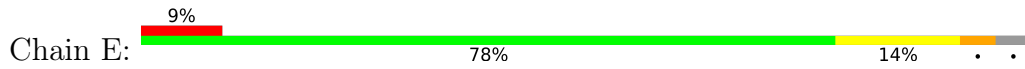
- Molecule 1: fluoroacetyl-CoA thioesterase



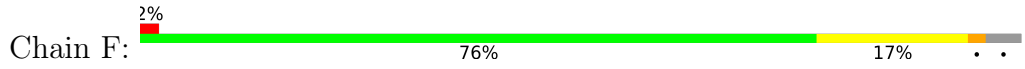
- Molecule 1: fluoroacetyl-CoA thioesterase



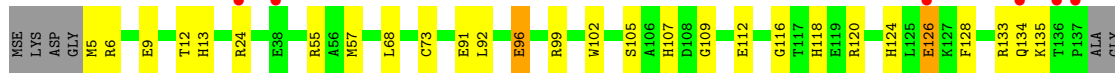
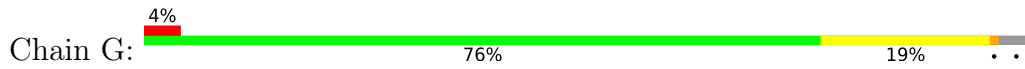
- Molecule 1: fluoroacetyl-CoA thioesterase



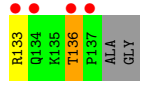
• Molecule 1: fluoroacetyl-CoA thioesterase



• Molecule 1: fluoroacetyl-CoA thioesterase



• Molecule 1: fluoroacetyl-CoA thioesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.91Å 71.08Å 104.35Å 90.00° 102.62° 90.00°	Depositor
Resolution (Å)	49.75 – 2.35 47.67 – 2.35	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.75-2.35) 95.2 (47.67-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.39 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.243 0.205 , 0.197	Depositor DCC
R_{free} test set	2000 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtrriage
Anisotropy	0.097	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8498	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 46.39 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1529e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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	0.49	0/1049	0.58	0/1426
1	B	0.49	0/1087	0.65	1/1472 (0.1%)
1	C	0.49	0/1053	0.65	1/1430 (0.1%)
1	D	0.48	0/1053	0.60	1/1430 (0.1%)
1	E	0.49	0/1045	0.63	0/1421
1	F	0.51	0/1057	0.62	0/1435
1	G	0.52	0/1045	0.58	0/1422
1	H	0.50	0/1048	0.59	0/1423
All	All	0.49	0/8437	0.61	3/11459 (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	C	0	1
1	H	0	2
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	100	LEU	CA-CB-CG	5.39	127.69	115.30
1	D	13	HIS	N-CA-CB	-5.28	101.09	110.60
1	B	100	LEU	CA-CB-CG	5.27	127.42	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	96	GLU	Peptide
1	H	63	PRO	Peptide
1	H	95	VAL	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 the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1022	0	982	29	0
1	B	1061	0	1027	35	2
1	C	1026	0	993	10	0
1	D	1026	0	996	23	0
1	E	1018	0	976	20	0
1	F	1030	0	998	20	0
1	G	1018	0	971	29	0
1	H	1022	0	979	22	0
2	A	37	0	0	1	3
2	B	41	0	0	3	1
2	C	33	0	0	1	0
2	D	26	0	0	1	0
2	E	30	0	0	0	0
2	F	39	0	0	2	0
2	G	43	0	0	3	0
2	H	26	0	0	1	0
All	All	8498	0	7922	171	3

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 11.

The worst 5 of 171 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:B:6:ARG:HG3	1:B:6:ARG:NH1	1.61	1.04
1:B:107[B]:HIS:HE1	1:D:99:ARG:NH1	1.60	0.98
1:B:6:ARG:HH11	1:B:6:ARG:CG	1.75	0.98
1:B:6:ARG:HG3	1:B:6:ARG:HH11	0.82	0.96
1:E:93:ARG:HG3	1:E:93:ARG:HH21	1.32	0.93

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:422:HOH:O	2:B:412:HOH:O[2_647]	0.44	1.76
1:B:13:HIS:NE2	2:A:407:HOH:O[2_657]	1.25	0.95
1:B:13:HIS:CE1	2:A:407:HOH:O[2_657]	1.95	0.25

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	132/139 (95%)	130 (98%)	2 (2%)	0	100	100
1	B	135/139 (97%)	135 (100%)	0	0	100	100
1	C	131/139 (94%)	130 (99%)	1 (1%)	0	100	100
1	D	132/139 (95%)	130 (98%)	2 (2%)	0	100	100
1	E	132/139 (95%)	130 (98%)	2 (2%)	0	100	100
1	F	132/139 (95%)	132 (100%)	0	0	100	100
1	G	132/139 (95%)	128 (97%)	4 (3%)	0	100	100
1	H	133/139 (96%)	128 (96%)	4 (3%)	1 (1%)	19	20
All	All	1059/1112 (95%)	1043 (98%)	15 (1%)	1 (0%)	51	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	96	GLU

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	107/108 (99%)	99 (92%)	8 (8%)	13	13
1	B	112/108 (104%)	106 (95%)	6 (5%)	22	25
1	C	108/108 (100%)	104 (96%)	4 (4%)	34	42
1	D	107/108 (99%)	105 (98%)	2 (2%)	57	68
1	E	106/108 (98%)	97 (92%)	9 (8%)	10	10
1	F	108/108 (100%)	101 (94%)	7 (6%)	17	18
1	G	106/108 (98%)	101 (95%)	5 (5%)	26	31
1	H	106/108 (98%)	100 (94%)	6 (6%)	20	22
All	All	860/864 (100%)	813 (94%)	47 (6%)	21	24

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	136	THR
1	F	133	ARG
1	F	12	THR
1	F	98	ARG
1	G	105	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	124	HIS
1	G	13	HIS
1	D	124	HIS
1	G	118	HIS
1	F	25	HIS

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](#)

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	129/139 (92%)	0.53	15 (11%) 4 7	13, 25, 46, 52	0
1	B	131/139 (94%)	0.51	9 (6%) 16 24	14, 24, 42, 53	0
1	C	129/139 (92%)	0.42	5 (3%) 39 52	13, 25, 45, 50	0
1	D	129/139 (92%)	0.33	3 (2%) 60 70	13, 25, 42, 46	0
1	E	129/139 (92%)	0.37	12 (9%) 8 14	12, 23, 51, 56	0
1	F	129/139 (92%)	0.35	3 (2%) 60 70	11, 22, 35, 43	0
1	G	129/139 (92%)	0.34	6 (4%) 31 44	11, 23, 40, 51	0
1	H	130/139 (93%)	0.45	10 (7%) 13 20	14, 26, 47, 51	0
All	All	1035/1112 (93%)	0.41	63 (6%) 21 31	11, 25, 45, 56	0

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	127	LYS	6.5
1	B	3	ASP	5.7
1	H	95	VAL	4.7
1	F	133	ARG	4.6
1	A	63	PRO	4.4

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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.