



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 08:48 AM JST

PDB ID : 6LEY  
Title : Structure of Sil1G bound FEM1C  
Authors : Chen, X.; Liao, S.; Xu, C.  
Deposited on : 2019-11-27  
Resolution : 2.39 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](mailto: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>.

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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  
Xtrriage (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

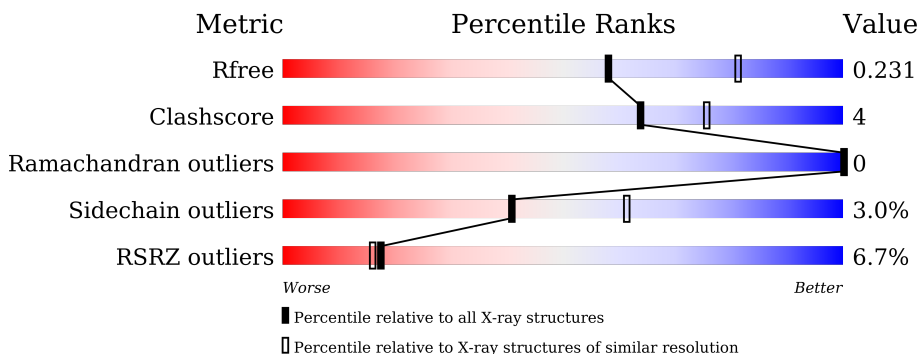
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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  $\geq 3$ , 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	419	
1	B	419	

## 2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 5752 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 Protein fem-1 homolog C, Peptide from Nucleotide exchange factor SIL1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	384	2836	1790	488	537	21	0	0	0
1	B	375	2755	1738	473	525	19	0	1	0

There are 38 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q96JP0
A	0	HIS	-	expression tag	UNP Q96JP0
A	391	GLY	-	linker	UNP Q96JP0
A	392	GLY	-	linker	UNP Q96JP0
A	393	GLY	-	linker	UNP Q96JP0
A	394	SER	-	linker	UNP Q96JP0
A	395	GLY	-	linker	UNP Q96JP0
A	396	GLY	-	linker	UNP Q96JP0
A	397	GLY	-	linker	UNP Q96JP0
A	398	SER	-	linker	UNP Q96JP0
A	399	GLY	-	linker	UNP Q96JP0
A	400	GLY	-	linker	UNP Q96JP0
A	401	GLY	-	linker	UNP Q96JP0
A	402	SER	-	linker	UNP Q96JP0
A	403	GLY	-	linker	UNP Q96JP0
A	404	GLY	-	linker	UNP Q96JP0
A	405	GLY	-	linker	UNP Q96JP0
A	406	SER	-	linker	UNP Q96JP0
A	417	GLY	-	expression tag	UNP Q9H173
B	-1	GLY	-	expression tag	UNP Q96JP0
B	0	HIS	-	expression tag	UNP Q96JP0
B	391	GLY	-	linker	UNP Q96JP0
B	392	GLY	-	linker	UNP Q96JP0
B	393	GLY	-	linker	UNP Q96JP0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	394	SER	-	linker	UNP Q96JP0
B	395	GLY	-	linker	UNP Q96JP0
B	396	GLY	-	linker	UNP Q96JP0
B	397	GLY	-	linker	UNP Q96JP0
B	398	SER	-	linker	UNP Q96JP0
B	399	GLY	-	linker	UNP Q96JP0
B	400	GLY	-	linker	UNP Q96JP0
B	401	GLY	-	linker	UNP Q96JP0
B	402	SER	-	linker	UNP Q96JP0
B	403	GLY	-	linker	UNP Q96JP0
B	404	GLY	-	linker	UNP Q96JP0
B	405	GLY	-	linker	UNP Q96JP0
B	406	SER	-	linker	UNP Q96JP0
B	417	GLY	-	expression tag	UNP Q9H173

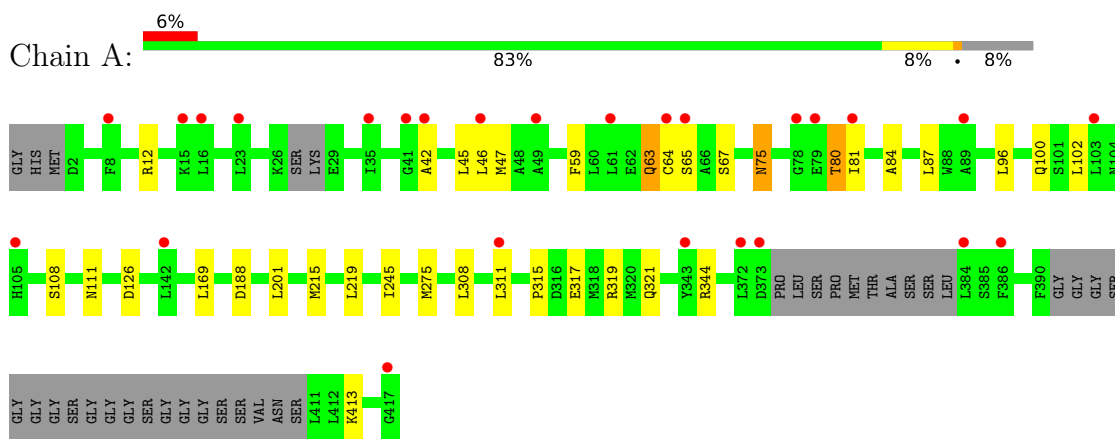
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	92	Total O 92 92	0	0
2	B	69	Total O 69 69	0	0

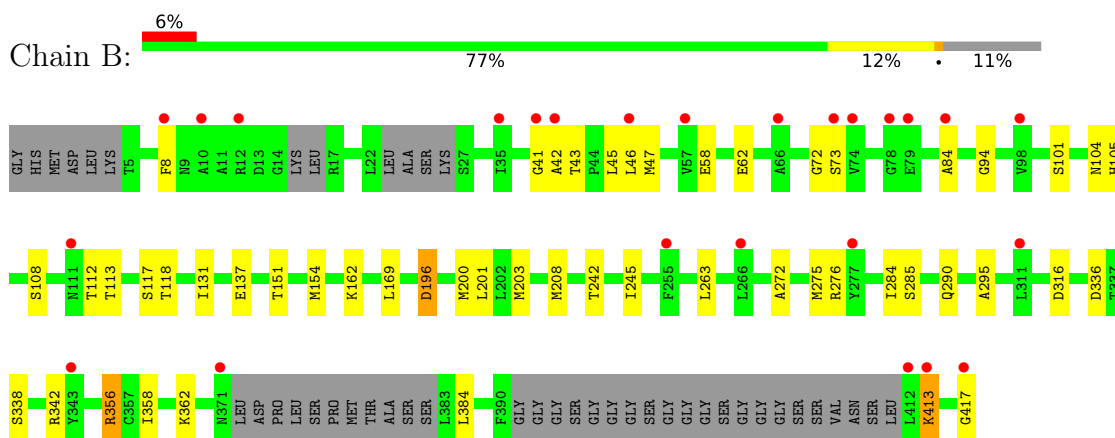
### 3 Residue-property plots [i](#)

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: Protein fem-1 homolog C,Peptide from Nucleotide exchange factor SIL1



- Molecule 1: Protein fem-1 homolog C,Peptide from Nucleotide exchange factor SIL1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.50Å 95.97Å 147.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.44 – 2.39 80.44 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.8 (80.44-2.39) 99.8 (80.44-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.20 (at 2.40Å)	Xtrriage
Refinement program	PHENIX 1.14 3260	Depositor
R, $R_{free}$	0.198 , 0.229 0.199 , 0.231	Depositor DCC
$R_{free}$ test set	2767 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.9	Xtrriage
Anisotropy	0.439	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 63.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.013 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5752	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.42	0/2884	0.54	0/3907
1	B	0.40	0/2805	0.56	0/3800
All	All	0.41	0/5689	0.55	0/7707

There are no bond length outliers.

There are no bond angle outliers.

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	2836	0	2693	20	0
1	B	2755	0	2568	26	0
2	A	92	0	0	0	0
2	B	69	0	0	0	0
All	All	5752	0	5261	46	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 4.

All (46) 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:295:ALA:O	1:B:356:ARG:NH2	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:CYS:SG	1:A:65:SER:N	2.73	0.62
1:A:319:ARG:HD2	1:A:344:ARG:CZ	2.32	0.60
1:B:46:LEU:HD22	1:B:72:GLY:HA3	1.86	0.57
1:A:315:PRO:O	1:A:319:ARG:HG3	2.04	0.57
1:B:200:MET:HA	1:B:203:MET:HE2	1.86	0.56
1:B:245:ILE:HG13	1:B:275:MET:HE2	1.86	0.56
1:B:112:THR:HG22	1:B:118:THR:HG22	1.89	0.54
1:B:290:GLN:OE1	1:B:290:GLN:N	2.36	0.54
1:A:308:LEU:HD23	1:A:311:LEU:HD12	1.89	0.53
1:A:81:ILE:HD11	1:A:84:ALA:HB2	1.91	0.53
1:A:42:ALA:HA	1:A:46:LEU:HD23	1.91	0.52
1:B:272:ALA:O	1:B:276:ARG:HG3	2.10	0.51
1:B:117:SER:HB2	1:B:417:GLY:HA2	1.92	0.51
1:B:263:LEU:H	1:B:263:LEU:HD12	1.76	0.50
1:B:342:ARG:HD2	1:B:384:LEU:HD23	1.93	0.50
1:B:84:ALA:HA	1:B:113:THR:HG22	1.94	0.49
1:B:151:THR:OG1	1:B:154:MET:HG3	2.12	0.48
1:B:94:GLY:HA2	1:B:131:ILE:HD12	1.95	0.47
1:A:245:ILE:HG13	1:A:275:MET:HE2	1.98	0.46
1:A:59:PHE:O	1:A:63:GLN:HB3	2.15	0.46
1:A:75:ASN:ND2	1:A:80:THR:HG22	2.30	0.46
1:A:75:ASN:HD21	1:A:80:THR:HG22	1.82	0.44
1:A:108:SER:OG	1:A:111:ASN:HB2	2.17	0.44
1:B:42:ALA:HB3	1:B:72:GLY:HA2	1.98	0.44
1:A:169:LEU:HD11	1:A:201:LEU:HD23	2.00	0.44
1:B:169:LEU:HD11	1:B:201:LEU:HD23	1.99	0.44
1:B:413:LYS:H	1:B:413:LYS:HG2	1.63	0.43
1:A:188:ASP:OD1	1:A:413:LYS:HE3	2.18	0.43
1:B:242:THR:HG22	1:B:284:ILE:HD13	2.00	0.43
1:A:96:LEU:O	1:A:100:GLN:HG3	2.19	0.43
1:B:43:THR:HG22	1:B:45:LEU:N	2.34	0.43
1:A:87:LEU:HA	1:A:102:LEU:HD13	2.01	0.43
1:A:215:MET:HE3	1:A:215:MET:HB3	1.87	0.42
1:B:8:PHE:CZ	1:B:47:MET:HG3	2.53	0.42
1:B:43:THR:HG22	1:B:45:LEU:H	1.85	0.42
1:A:317:GLU:O	1:A:321:GLN:HG2	2.20	0.42
1:B:358:ILE:HG22	1:B:362:LYS:HD2	2.03	0.41
1:B:58:GLU:O	1:B:62:GLU:HG2	2.20	0.41
1:B:162:LYS:HE3	1:B:196:ASP:OD2	2.21	0.41
1:A:12:ARG:HA	1:A:47:MET:HB3	2.02	0.41
1:B:41:GLY:HA2	1:B:73:SER:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:338:SER:O	1:B:342:ARG:HG3	2.21	0.40
1:A:219:LEU:HD23	1:A:219:LEU:HA	1.91	0.40
1:B:101:SER:O	1:B:105:HIS:N	2.51	0.40
1:A:413:LYS:H	1:A:413:LYS:HG2	1.62	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	Percentiles	
1	A	376/419 (90%)	365 (97%)	11 (3%)	0	100	100
1	B	366/419 (87%)	343 (94%)	23 (6%)	0	100	100
All	All	742/838 (88%)	708 (95%)	34 (5%)	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	276/343 (80%)	270 (98%)	6 (2%)	52	71
1	B	261/343 (76%)	251 (96%)	10 (4%)	33	51
All	All	537/686 (78%)	521 (97%)	16 (3%)	41	61

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	LEU
1	A	63	GLN
1	A	67	SER
1	A	75	ASN
1	A	80	THR
1	A	126	ASP
1	B	104	ASN
1	B	108	SER
1	B	137	GLU
1	B	196	ASP
1	B	208	MET
1	B	285	SER
1	B	316	ASP
1	B	336	ASP
1	B	356	ARG
1	B	413	LYS

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](#)

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

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	384/419 (91%)	0.94	26 (6%) 17 15	40, 62, 133, 163	0
1	B	375/419 (89%)	0.98	25 (6%) 17 16	43, 68, 150, 182	0
All	All	759/838 (90%)	0.96	51 (6%) 17 16	40, 65, 142, 182	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	8	PHE	8.6
1	B	57	VAL	8.5
1	B	412	LEU	8.4
1	B	35	ILE	6.0
1	B	42	ALA	5.7
1	A	35	ILE	5.3
1	B	66	ALA	5.0
1	A	8	PHE	4.8
1	A	372	LEU	4.6
1	A	65	SER	4.5
1	A	384	LEU	4.5
1	B	78	GLY	4.3
1	B	46	LEU	4.3
1	B	12	ARG	4.2
1	A	417	GLY	4.1
1	A	373	ASP	4.1
1	A	23	LEU	4.0
1	A	46	LEU	3.7
1	A	311	LEU	3.6
1	A	49	ALA	3.5
1	A	16	LEU	3.3
1	B	79	GLU	3.1
1	A	41	GLY	3.1
1	A	64	CYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	79	GLU	2.9
1	B	98	VAL	2.9
1	B	74	VAL	2.9
1	B	417	GLY	2.9
1	B	371	ASN	2.9
1	A	42	ALA	2.9
1	A	15	LYS	2.8
1	B	413	LYS	2.8
1	A	61	LEU	2.8
1	A	81	ILE	2.6
1	B	41	GLY	2.5
1	A	105	HIS	2.5
1	A	343	TYR	2.5
1	B	111	ASN	2.5
1	B	84	ALA	2.3
1	A	89	ALA	2.2
1	A	386	PHE	2.1
1	A	103	LEU	2.1
1	B	10	ALA	2.1
1	B	277	TYR	2.1
1	B	255	PHE	2.1
1	A	142	LEU	2.1
1	B	266	LEU	2.1
1	B	343	TYR	2.1
1	B	73	SER	2.1
1	B	311	LEU	2.0
1	A	78	GLY	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.