



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 10, 2021 – 08:08 AM JST

PDB ID : 7F9L
Title : Crystal structure of the variable region of Plasmodium RIFIN #6 (PF3D7_1400600) in complex with LAIR1 (with T67L, N69S and A77T mutations)
Authors : Xie, Y.; Song, H.; Li, X.; Qi, J.; Gao, G.F.
Deposited on : 2021-07-04
Resolution : 2.70 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
Xtriage (Phenix)	:	1.13
EDS	:	2.23.1
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)	:	2.23.1

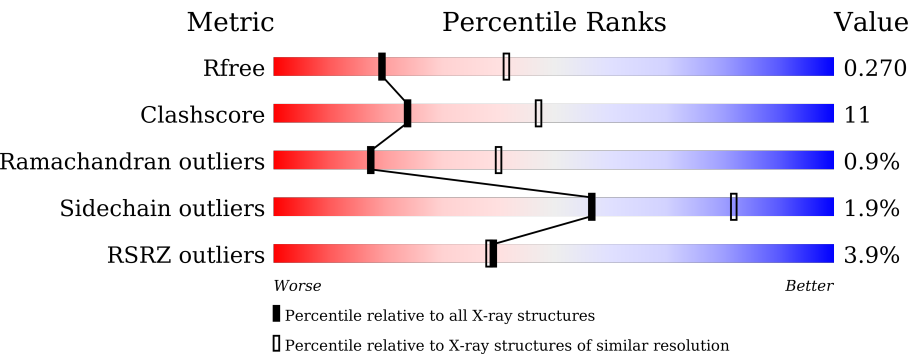
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	163	<div><div>2%</div><div><div></div><div>82%</div><div>17%</div><div>..</div></div></div>
1	B	163	<div><div>2%</div><div><div></div><div>82%</div><div>17%</div><div>.</div></div></div>
1	C	163	<div><div>3%</div><div><div></div><div>79%</div><div>17%</div><div>..</div></div></div>
1	D	163	<div><div>6%</div><div><div></div><div>74%</div><div>24%</div><div>..</div></div></div>
1	E	163	<div><div>3%</div><div><div></div><div>83%</div><div>15%</div><div>.</div></div></div>
1	F	163	<div><div>%</div><div><div></div><div>73%</div><div>20%</div><div>.. 6%</div></div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	110	<div><div>%</div><div><div></div><div>70%</div><div>19%</div><div>• 10%</div></div></div>
2	H	110	<div><div>%</div><div><div></div><div>64%</div><div>25%</div><div>• 10%</div></div></div>
2	I	110	<div><div>2%</div><div><div></div><div>70%</div><div>19%</div><div>• 10%</div></div></div>
2	J	110	<div><div>5%</div><div><div></div><div>69%</div><div>20%</div><div>• 10%</div></div></div>
2	K	110	<div><div>5%</div><div><div></div><div>63%</div><div>25%</div><div>12%</div></div></div>
2	L	110	<div><div>15%</div><div><div></div><div>47%</div><div>36%</div><div>• • 12%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11809 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 Rifin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	162	Total	C	N	O	S	0	0	0
			1184	746	198	235	5			
1	B	162	Total	C	N	O	S	0	0	0
			1184	746	198	235	5			
1	C	158	Total	C	N	O	S	0	0	0
			1158	730	194	229	5			
1	D	162	Total	C	N	O	S	0	0	0
			1184	746	198	235	5			
1	E	160	Total	C	N	O	S	0	0	0
			1171	739	196	231	5			
1	F	154	Total	C	N	O	S	0	0	0
			1127	709	188	226	4			

- Molecule 2 is a protein called Leukocyte-associated immunoglobulin-like receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	99	Total	C	N	O	S	0	0	0
			779	487	133	157	2			
2	H	99	Total	C	N	O	S	0	0	0
			779	487	133	157	2			
2	I	99	Total	C	N	O	S	0	0	0
			779	487	133	157	2			
2	J	99	Total	C	N	O	S	0	0	0
			779	487	133	157	2			
2	K	97	Total	C	N	O	S	0	0	0
			765	479	131	153	2			
2	L	97	Total	C	N	O	S	0	0	0
			766	480	131	153	2			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	16	HIS	-	expression tag	UNP Q6GTX8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
G	17	HIS	-	expression tag	UNP Q6GTX8
G	18	HIS	-	expression tag	UNP Q6GTX8
G	19	HIS	-	expression tag	UNP Q6GTX8
G	20	HIS	-	expression tag	UNP Q6GTX8
G	21	HIS	-	expression tag	UNP Q6GTX8
G	67	LEU	THR	engineered mutation	UNP Q6GTX8
G	69	SER	ASN	engineered mutation	UNP Q6GTX8
G	77	THR	ALA	engineered mutation	UNP Q6GTX8
G	123	ALA	-	expression tag	UNP Q6GTX8
G	124	ALA	-	expression tag	UNP Q6GTX8
G	125	ALA	-	expression tag	UNP Q6GTX8
H	16	HIS	-	expression tag	UNP Q6GTX8
H	17	HIS	-	expression tag	UNP Q6GTX8
H	18	HIS	-	expression tag	UNP Q6GTX8
H	19	HIS	-	expression tag	UNP Q6GTX8
H	20	HIS	-	expression tag	UNP Q6GTX8
H	21	HIS	-	expression tag	UNP Q6GTX8
H	67	LEU	THR	engineered mutation	UNP Q6GTX8
H	69	SER	ASN	engineered mutation	UNP Q6GTX8
H	77	THR	ALA	engineered mutation	UNP Q6GTX8
H	123	ALA	-	expression tag	UNP Q6GTX8
H	124	ALA	-	expression tag	UNP Q6GTX8
H	125	ALA	-	expression tag	UNP Q6GTX8
I	16	HIS	-	expression tag	UNP Q6GTX8
I	17	HIS	-	expression tag	UNP Q6GTX8
I	18	HIS	-	expression tag	UNP Q6GTX8
I	19	HIS	-	expression tag	UNP Q6GTX8
I	20	HIS	-	expression tag	UNP Q6GTX8
I	21	HIS	-	expression tag	UNP Q6GTX8
I	67	LEU	THR	engineered mutation	UNP Q6GTX8
I	69	SER	ASN	engineered mutation	UNP Q6GTX8
I	77	THR	ALA	engineered mutation	UNP Q6GTX8
I	123	ALA	-	expression tag	UNP Q6GTX8
I	124	ALA	-	expression tag	UNP Q6GTX8
I	125	ALA	-	expression tag	UNP Q6GTX8
J	16	HIS	-	expression tag	UNP Q6GTX8
J	17	HIS	-	expression tag	UNP Q6GTX8
J	18	HIS	-	expression tag	UNP Q6GTX8
J	19	HIS	-	expression tag	UNP Q6GTX8
J	20	HIS	-	expression tag	UNP Q6GTX8
J	21	HIS	-	expression tag	UNP Q6GTX8
J	67	LEU	THR	engineered mutation	UNP Q6GTX8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
J	69	SER	ASN	engineered mutation	UNP Q6GTX8
J	77	THR	ALA	engineered mutation	UNP Q6GTX8
J	123	ALA	-	expression tag	UNP Q6GTX8
J	124	ALA	-	expression tag	UNP Q6GTX8
J	125	ALA	-	expression tag	UNP Q6GTX8
K	16	HIS	-	expression tag	UNP Q6GTX8
K	17	HIS	-	expression tag	UNP Q6GTX8
K	18	HIS	-	expression tag	UNP Q6GTX8
K	19	HIS	-	expression tag	UNP Q6GTX8
K	20	HIS	-	expression tag	UNP Q6GTX8
K	21	HIS	-	expression tag	UNP Q6GTX8
K	67	LEU	THR	engineered mutation	UNP Q6GTX8
K	69	SER	ASN	engineered mutation	UNP Q6GTX8
K	77	THR	ALA	engineered mutation	UNP Q6GTX8
K	123	ALA	-	expression tag	UNP Q6GTX8
K	124	ALA	-	expression tag	UNP Q6GTX8
K	125	ALA	-	expression tag	UNP Q6GTX8
L	16	HIS	-	expression tag	UNP Q6GTX8
L	17	HIS	-	expression tag	UNP Q6GTX8
L	18	HIS	-	expression tag	UNP Q6GTX8
L	19	HIS	-	expression tag	UNP Q6GTX8
L	20	HIS	-	expression tag	UNP Q6GTX8
L	21	HIS	-	expression tag	UNP Q6GTX8
L	67	LEU	THR	engineered mutation	UNP Q6GTX8
L	69	SER	ASN	engineered mutation	UNP Q6GTX8
L	77	THR	ALA	engineered mutation	UNP Q6GTX8
L	123	ALA	-	expression tag	UNP Q6GTX8
L	124	ALA	-	expression tag	UNP Q6GTX8
L	125	ALA	-	expression tag	UNP Q6GTX8

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	18	Total O 18 18	0	0
3	B	25	Total O 25 25	0	0
3	C	20	Total O 20 20	0	0
3	D	16	Total O 16 16	0	0
3	E	17	Total O 17 17	0	0

Continued on next page...


Continued from previous page...

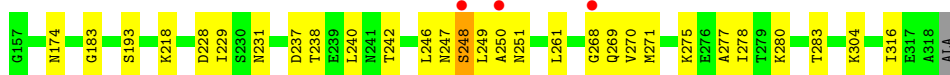
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	10	Total 10	O 10	0	0
3	G	10	Total 10	O 10	0	0
3	H	12	Total 12	O 12	0	0
3	I	2	Total 2	O 2	0	0
3	J	11	Total 11	O 11	0	0
3	K	8	Total 8	O 8	0	0
3	L	5	Total 5	O 5	0	0

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: Rifin

Chain A: 



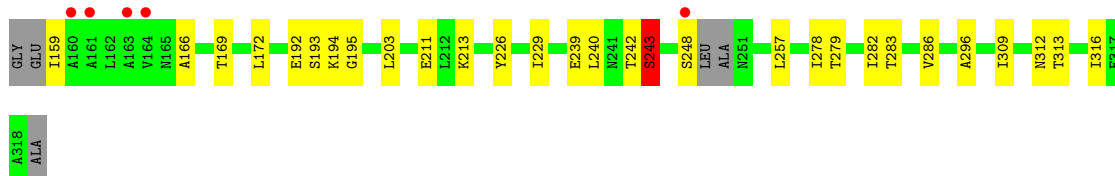
- Molecule 1: Rifin

Chain B: 



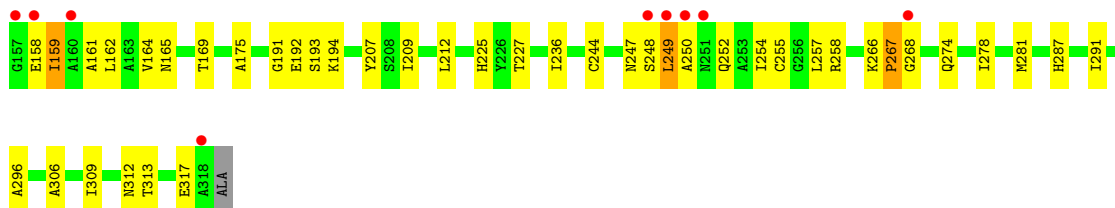
- Molecule 1: Rifin

Chain C: 

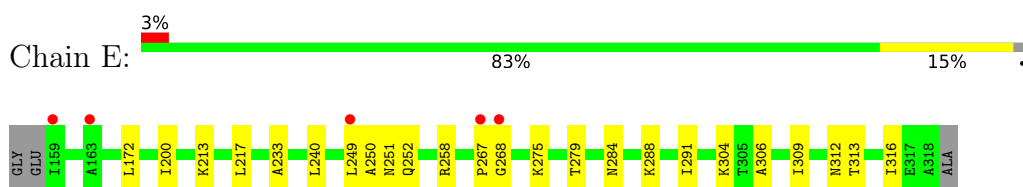


- Molecule 1: Rifin

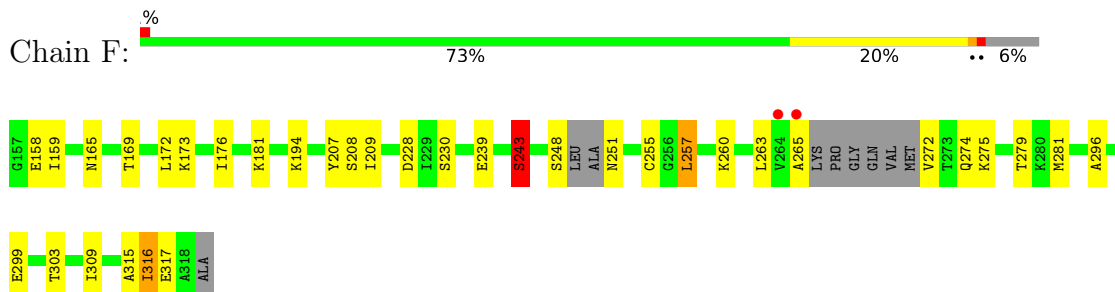
Chain D: 



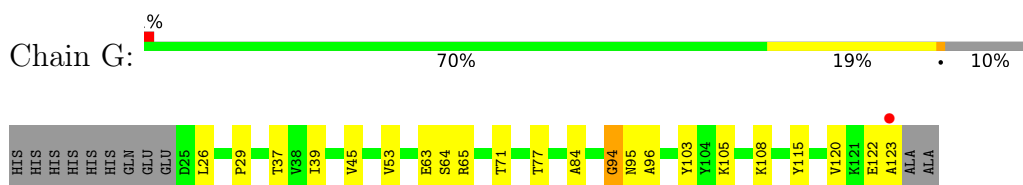
- Molecule 1: Rifin



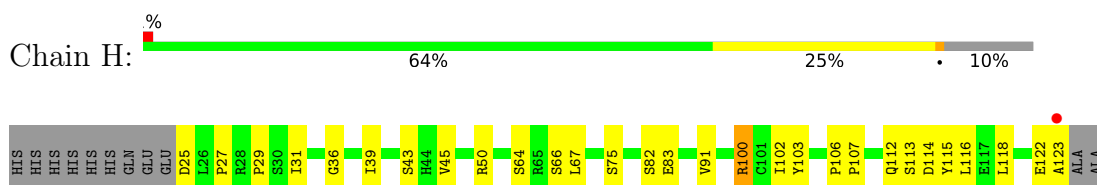
- Molecule 1: Rifin



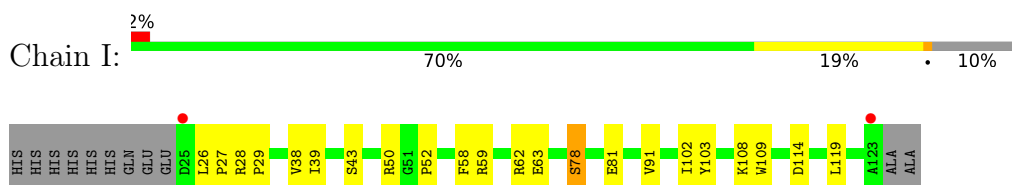
- Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1



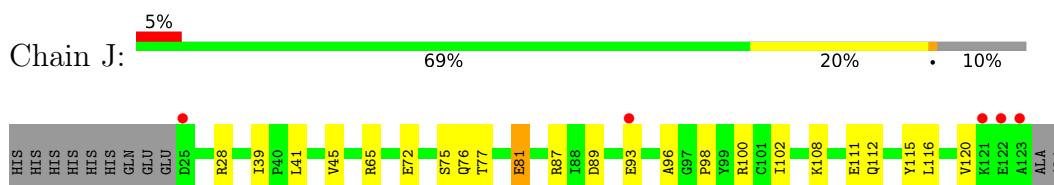
- Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1



- Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1

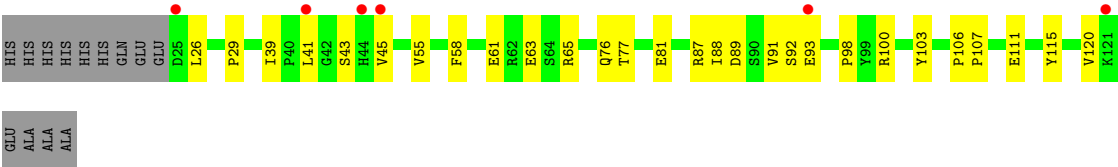


- Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1

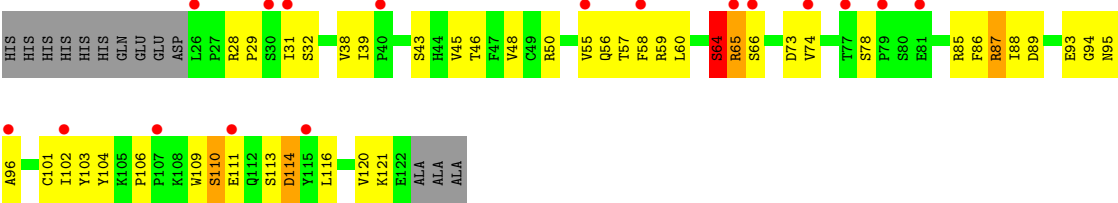


- Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1





● Molecule 2: Leukocyte-associated immunoglobulin-like receptor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	120.13Å 94.12Å 126.03Å 90.00° 117.94° 90.00°	Depositor
Resolution (Å)	41.88 – 2.70 41.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	84.9 (41.88-2.70) 84.9 (41.88-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.213 , 0.270 0.213 , 0.270	Depositor DCC
R_{free} test set	2585 reflections (4.43%)	wwPDB-VP
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.014 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11809	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.57% 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	0.50	0/1195	0.64	1/1619 (0.1%)
1	B	0.51	0/1195	0.61	0/1619
1	C	0.49	0/1168	0.62	0/1581
1	D	0.50	0/1195	0.60	1/1619 (0.1%)
1	E	0.46	0/1182	0.63	3/1602 (0.2%)
1	F	0.44	0/1135	0.57	0/1535
2	G	0.56	0/798	0.65	0/1085
2	H	0.54	0/798	0.67	0/1085
2	I	0.44	0/798	0.66	0/1085
2	J	0.57	0/798	0.68	0/1085
2	K	0.54	0/784	0.68	0/1066
2	L	0.55	0/785	0.66	0/1067
All	All	0.50	0/11831	0.63	5/16048 (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	D	0	1
2	G	0	1
All	All	0	2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	LEU	CB-CG-CD1	-7.06	99.00	111.00
1	D	249	LEU	CA-CB-CG	-6.93	99.37	115.30
1	E	249	LEU	CA-CB-CG	6.11	129.34	115.30
1	E	249	LEU	CB-CG-CD1	6.06	121.30	111.00
1	E	249	LEU	CB-CG-CD2	-5.80	101.13	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	159	ILE	Peptide
2	G	94	GLY	Peptide

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	1184	0	1230	20	0
1	B	1184	0	1230	19	0
1	C	1158	0	1204	19	0
1	D	1184	0	1230	35	0
1	E	1171	0	1221	15	0
1	F	1127	0	1163	29	0
2	G	779	0	748	18	0
2	H	779	0	748	26	0
2	I	779	0	748	17	0
2	J	779	0	748	21	0
2	K	765	0	737	25	0
2	L	766	0	739	38	0
3	A	18	0	0	6	0
3	B	25	0	0	1	0
3	C	20	0	0	0	0
3	D	16	0	0	1	0
3	E	17	0	0	2	0
3	F	10	0	0	1	0
3	G	10	0	0	0	0
3	H	12	0	0	4	0
3	I	2	0	0	0	0
3	J	11	0	0	0	0
3	K	8	0	0	1	0
3	L	5	0	0	2	0
All	All	11809	0	11746	260	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 11.

The worst 5 of 260 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)
2:K:63:GLU:HG2	2:K:98:PRO:HD2	1.32	1.07
2:K:77:THR:HG22	2:K:81:GLU:OE2	1.61	0.99
1:D:249:LEU:HD23	1:D:249:LEU:H	1.27	0.96
1:C:229:ILE:HG21	1:C:283:THR:HG22	1.52	0.91
1:D:247:ASN:HB2	1:D:249:LEU:HD21	1.52	0.90

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	160/163 (98%)	153 (96%)	6 (4%)	1 (1%)	25	50
1	B	160/163 (98%)	152 (95%)	8 (5%)	0	100	100
1	C	154/163 (94%)	147 (96%)	5 (3%)	2 (1%)	12	30
1	D	160/163 (98%)	148 (92%)	11 (7%)	1 (1%)	25	50
1	E	158/163 (97%)	151 (96%)	4 (2%)	3 (2%)	8	20
1	F	148/163 (91%)	137 (93%)	8 (5%)	3 (2%)	7	19
2	G	97/110 (88%)	95 (98%)	2 (2%)	0	100	100
2	H	97/110 (88%)	91 (94%)	6 (6%)	0	100	100
2	I	97/110 (88%)	90 (93%)	7 (7%)	0	100	100
2	J	97/110 (88%)	96 (99%)	1 (1%)	0	100	100
2	K	95/110 (86%)	92 (97%)	3 (3%)	0	100	100
2	L	95/110 (86%)	83 (87%)	9 (10%)	3 (3%)	4	9
All	All	1518/1638 (93%)	1435 (94%)	70 (5%)	13 (1%)	17	40

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	243	SER
1	E	251	ASN
2	L	64	SER
1	A	250	ALA
1	F	243	SER

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	122/122 (100%)	119 (98%)	3 (2%)	47	76
1	B	122/122 (100%)	120 (98%)	2 (2%)	62	85
1	C	120/122 (98%)	117 (98%)	3 (2%)	47	76
1	D	122/122 (100%)	121 (99%)	1 (1%)	81	93
1	E	121/122 (99%)	121 (100%)	0	100	100
1	F	116/122 (95%)	112 (97%)	4 (3%)	37	66
2	G	89/98 (91%)	89 (100%)	0	100	100
2	H	89/98 (91%)	88 (99%)	1 (1%)	73	90
2	I	89/98 (91%)	87 (98%)	2 (2%)	52	79
2	J	89/98 (91%)	86 (97%)	3 (3%)	37	66
2	K	88/98 (90%)	88 (100%)	0	100	100
2	L	88/98 (90%)	83 (94%)	5 (6%)	20	44
All	All	1255/1320 (95%)	1231 (98%)	24 (2%)	57	82

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	I	58	PHE
2	J	81	GLU
2	J	75	SER
2	J	108	LYS
1	C	211	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	269	GLN
1	D	231	ASN

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 ⓘ

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, 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	162/163 (99%)	-0.13	3 (1%) 66 69	23, 36, 65, 120	0
1	B	162/163 (99%)	-0.09	4 (2%) 57 59	18, 32, 85, 147	0
1	C	158/163 (96%)	-0.10	5 (3%) 47 48	19, 35, 89, 139	0
1	D	162/163 (99%)	0.01	9 (5%) 24 23	24, 40, 101, 182	0
1	E	160/163 (98%)	-0.14	5 (3%) 49 49	21, 37, 88, 122	0
1	F	154/163 (94%)	-0.07	2 (1%) 77 78	23, 42, 84, 104	0
2	G	99/110 (90%)	-0.31	1 (1%) 82 83	21, 37, 56, 87	0
2	H	99/110 (90%)	-0.17	1 (1%) 82 83	24, 37, 54, 107	0
2	I	99/110 (90%)	0.09	2 (2%) 65 67	31, 50, 84, 117	0
2	J	99/110 (90%)	-0.06	5 (5%) 28 26	22, 36, 77, 121	0
2	K	97/110 (88%)	0.31	6 (6%) 20 19	29, 48, 101, 113	0
2	L	97/110 (88%)	1.24	17 (17%) 1 1	58, 87, 111, 153	0
All	All	1548/1638 (94%)	0.02	60 (3%) 39 38	18, 39, 95, 182	0

The worst 5 of 60 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	248	SER	9.5
2	I	123	ALA	8.3
2	K	25	ASP	7.1
2	L	74	VAL	6.3
2	H	123	ALA	6.3

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.