



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:58 PM UTC

PDB ID : 4EMP / pdb_00004emp
Title : Crystal structure of the mutant of ClpP E137A from Staphylococcus aureus
Authors : Ye, F.; Zhang, J.; Liu, H.; Luo, C.; Yang, C.-G.
Deposited on : 2012-04-12
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 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 : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

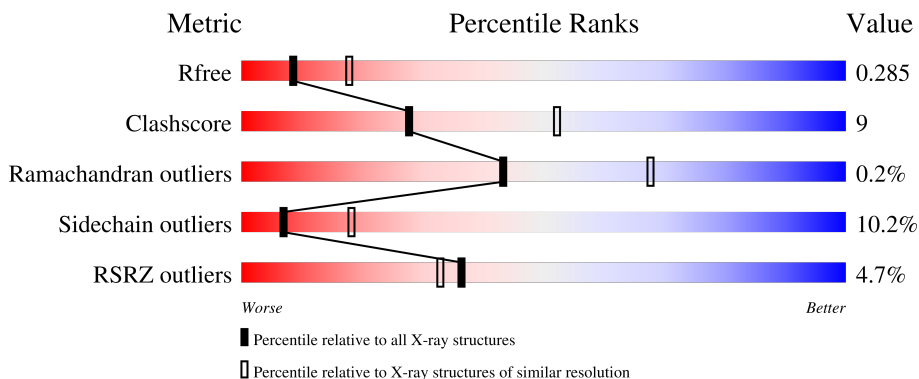
1 Overall quality at a glance

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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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	200	 4% (poor fit), 71% (0-1 outliers), 20% (2-3 outliers), 6% (not modelled)
1	B	200	 6% (poor fit), 72% (0-1 outliers), 18% (2-3 outliers), 9% (not modelled)
1	C	200	 4% (poor fit), 70% (0-1 outliers), 18% (2-3 outliers), 5% (not modelled), 8% (not modelled)
1	E	200	 6% (poor fit), 74% (0-1 outliers), 13% (2-3 outliers), 5% (not modelled), 8% (not modelled)
1	F	200	 4% (poor fit), 70% (0-1 outliers), 20% (2-3 outliers), 8% (not modelled)

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Mol	Chain	Length	Quality of chain
1	G	200	<p>4% 71% 16% 10%</p>
1	I	200	<p>2% 72% 18% 6% 6%</p>
1	K	200	<p>6% 68% 21% 7%</p>
1	L	200	<p>5% 72% 16% 8%</p>
1	M	200	<p>4% 68% 20% 8%</p>
1	N	200	<p>6% 72% 18% 8%</p>
1	S	200	<p>2% 70% 18% 8%</p>
1	T	200	<p>5% 71% 17% 5% 7%</p>
1	V	200	<p>4% 75% 16% 6%</p>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 20028 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	V	189	1462	919	251	284	8	0	2	0
1	A	189	1462	919	251	284	8	0	2	0
1	B	182	1400	884	237	272	7	0	1	0
1	C	185	1430	902	243	277	8	0	2	0
1	E	185	1432	903	243	278	8	0	2	0
1	F	185	1427	899	243	278	7	0	1	0
1	G	180	1386	876	235	268	7	0	1	0
1	I	189	1452	911	251	284	6	0	0	0
1	K	186	1431	901	244	279	7	0	1	0
1	L	184	1413	890	242	275	6	0	0	0
1	M	185	1427	899	243	278	7	0	1	0
1	N	185	1427	899	243	278	7	0	1	0
1	S	184	1425	899	242	276	8	0	2	0
1	T	186	1431	901	244	279	7	0	1	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	-4	GLY	-	expression tag	UNP P63786

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Chain	Residue	Modelled	Actual	Comment	Reference
V	-3	PRO	-	expression tag	UNP P63786
V	-2	LEU	-	expression tag	UNP P63786
V	-1	GLY	-	expression tag	UNP P63786
V	0	SER	-	expression tag	UNP P63786
V	137	ALA	GLU	engineered mutation	UNP P63786
A	-4	GLY	-	expression tag	UNP P63786
A	-3	PRO	-	expression tag	UNP P63786
A	-2	LEU	-	expression tag	UNP P63786
A	-1	GLY	-	expression tag	UNP P63786
A	0	SER	-	expression tag	UNP P63786
A	137	ALA	GLU	engineered mutation	UNP P63786
B	-4	GLY	-	expression tag	UNP P63786
B	-3	PRO	-	expression tag	UNP P63786
B	-2	LEU	-	expression tag	UNP P63786
B	-1	GLY	-	expression tag	UNP P63786
B	0	SER	-	expression tag	UNP P63786
B	137	ALA	GLU	engineered mutation	UNP P63786
C	-4	GLY	-	expression tag	UNP P63786
C	-3	PRO	-	expression tag	UNP P63786
C	-2	LEU	-	expression tag	UNP P63786
C	-1	GLY	-	expression tag	UNP P63786
C	0	SER	-	expression tag	UNP P63786
C	137	ALA	GLU	engineered mutation	UNP P63786
E	-4	GLY	-	expression tag	UNP P63786
E	-3	PRO	-	expression tag	UNP P63786
E	-2	LEU	-	expression tag	UNP P63786
E	-1	GLY	-	expression tag	UNP P63786
E	0	SER	-	expression tag	UNP P63786
E	137	ALA	GLU	engineered mutation	UNP P63786
F	-4	GLY	-	expression tag	UNP P63786
F	-3	PRO	-	expression tag	UNP P63786
F	-2	LEU	-	expression tag	UNP P63786
F	-1	GLY	-	expression tag	UNP P63786
F	0	SER	-	expression tag	UNP P63786
F	137	ALA	GLU	engineered mutation	UNP P63786
G	-4	GLY	-	expression tag	UNP P63786
G	-3	PRO	-	expression tag	UNP P63786
G	-2	LEU	-	expression tag	UNP P63786
G	-1	GLY	-	expression tag	UNP P63786
G	0	SER	-	expression tag	UNP P63786
G	137	ALA	GLU	engineered mutation	UNP P63786
I	-4	GLY	-	expression tag	UNP P63786

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	PRO	-	expression tag	UNP P63786
I	-2	LEU	-	expression tag	UNP P63786
I	-1	GLY	-	expression tag	UNP P63786
I	0	SER	-	expression tag	UNP P63786
I	137	ALA	GLU	engineered mutation	UNP P63786
K	-4	GLY	-	expression tag	UNP P63786
K	-3	PRO	-	expression tag	UNP P63786
K	-2	LEU	-	expression tag	UNP P63786
K	-1	GLY	-	expression tag	UNP P63786
K	0	SER	-	expression tag	UNP P63786
K	137	ALA	GLU	engineered mutation	UNP P63786
L	-4	GLY	-	expression tag	UNP P63786
L	-3	PRO	-	expression tag	UNP P63786
L	-2	LEU	-	expression tag	UNP P63786
L	-1	GLY	-	expression tag	UNP P63786
L	0	SER	-	expression tag	UNP P63786
L	137	ALA	GLU	engineered mutation	UNP P63786
M	-4	GLY	-	expression tag	UNP P63786
M	-3	PRO	-	expression tag	UNP P63786
M	-2	LEU	-	expression tag	UNP P63786
M	-1	GLY	-	expression tag	UNP P63786
M	0	SER	-	expression tag	UNP P63786
M	137	ALA	GLU	engineered mutation	UNP P63786
N	-4	GLY	-	expression tag	UNP P63786
N	-3	PRO	-	expression tag	UNP P63786
N	-2	LEU	-	expression tag	UNP P63786
N	-1	GLY	-	expression tag	UNP P63786
N	0	SER	-	expression tag	UNP P63786
N	137	ALA	GLU	engineered mutation	UNP P63786
S	-4	GLY	-	expression tag	UNP P63786
S	-3	PRO	-	expression tag	UNP P63786
S	-2	LEU	-	expression tag	UNP P63786
S	-1	GLY	-	expression tag	UNP P63786
S	0	SER	-	expression tag	UNP P63786
S	137	ALA	GLU	engineered mutation	UNP P63786
T	-4	GLY	-	expression tag	UNP P63786
T	-3	PRO	-	expression tag	UNP P63786
T	-2	LEU	-	expression tag	UNP P63786
T	-1	GLY	-	expression tag	UNP P63786
T	0	SER	-	expression tag	UNP P63786
T	137	ALA	GLU	engineered mutation	UNP P63786

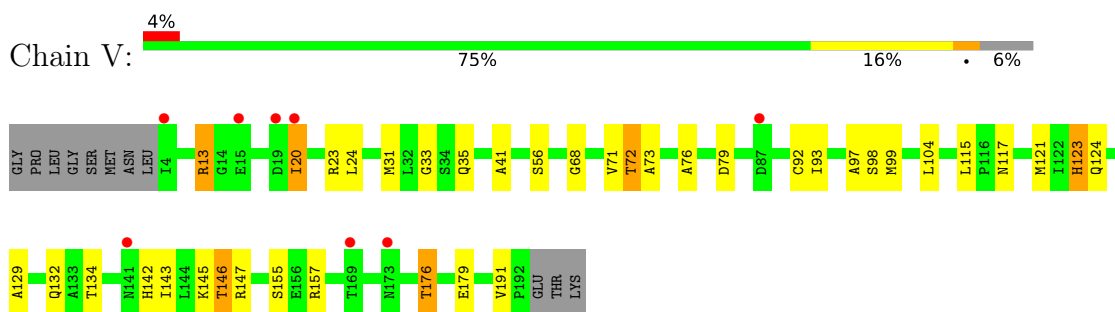
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	V	1	Total O 1 1	0	0
2	A	3	Total O 3 3	0	0
2	B	4	Total O 4 4	0	0
2	C	1	Total O 1 1	0	0
2	E	2	Total O 2 2	0	0
2	F	1	Total O 1 1	0	0
2	G	2	Total O 2 2	0	0
2	I	2	Total O 2 2	0	0
2	K	1	Total O 1 1	0	0
2	N	1	Total O 1 1	0	0
2	S	4	Total O 4 4	0	0
2	T	1	Total O 1 1	0	0

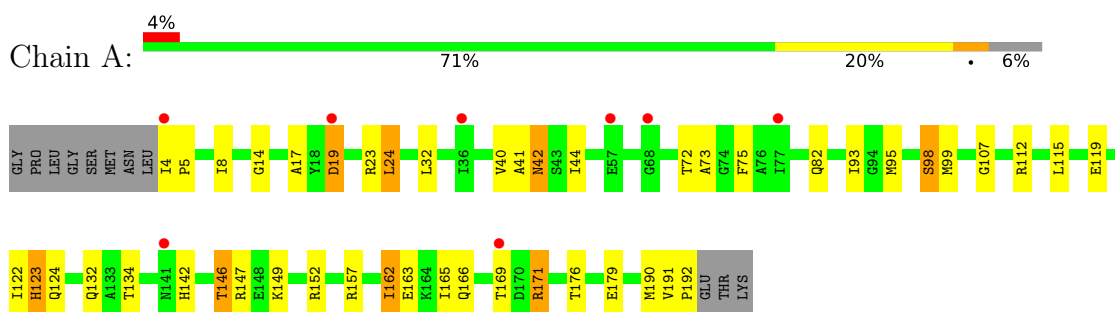
3 Residue-property plots [i](#)

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.

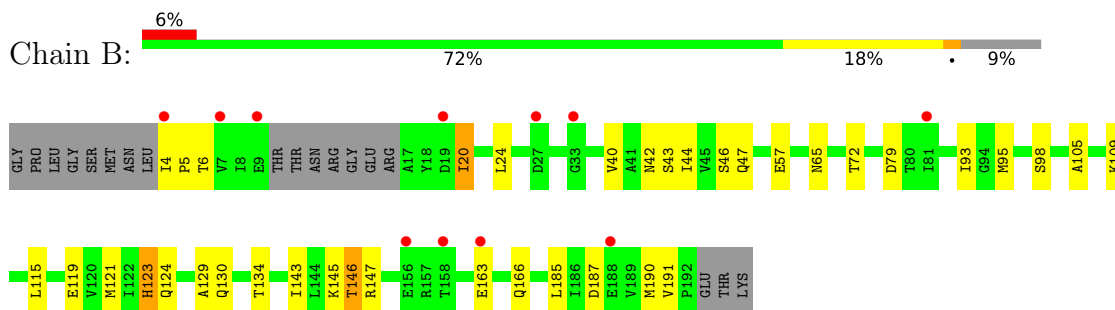
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

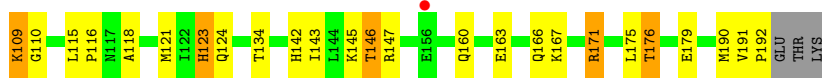


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

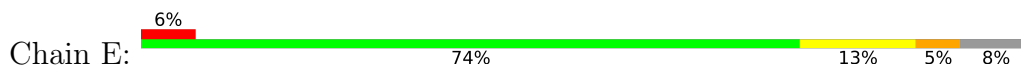


- Molecule 1: ATP-dependent Clp protease proteolytic subunit

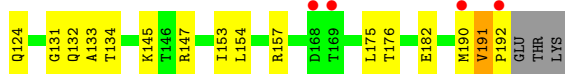
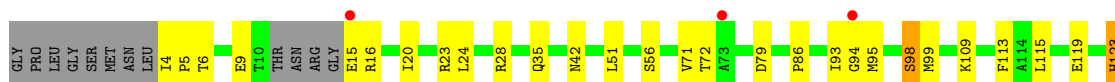




- Molecule 1: ATP-dependent Clp protease proteolytic subunit



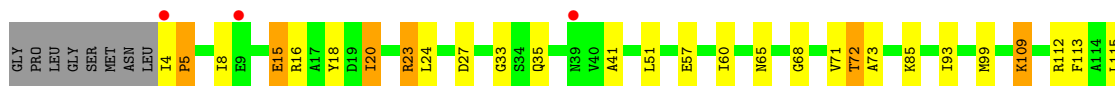
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



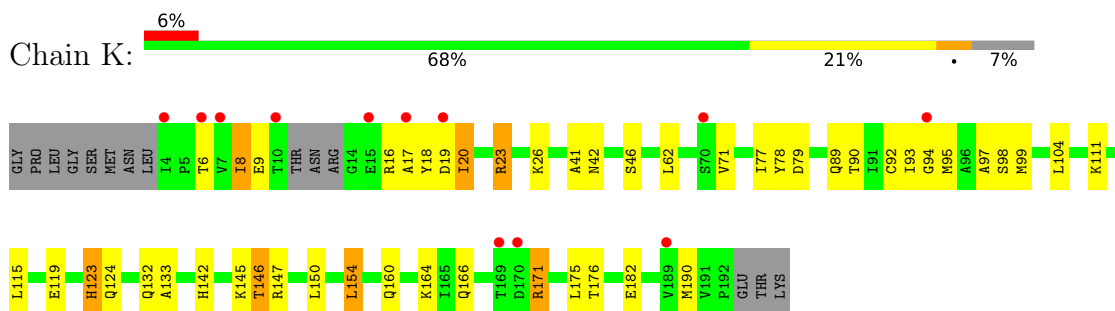
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



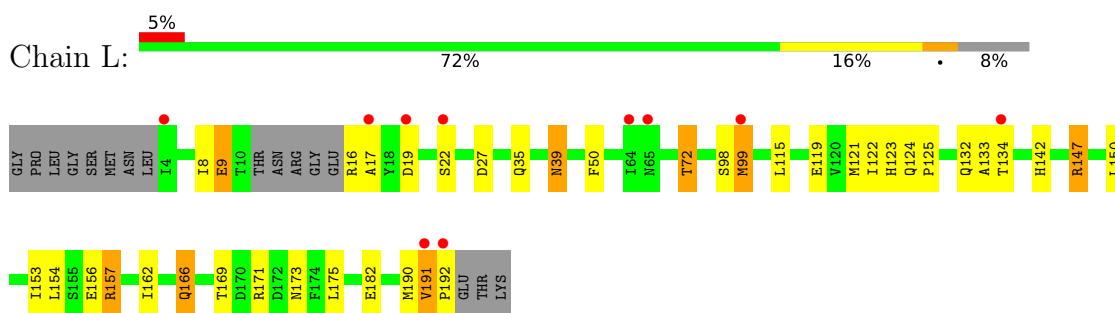
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



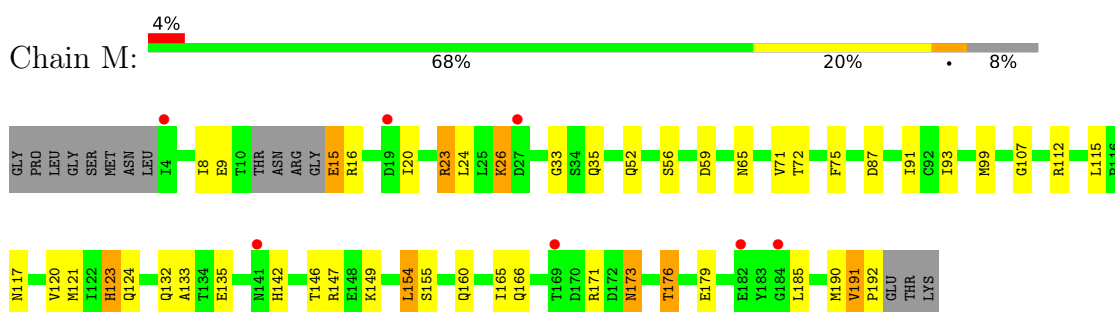
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



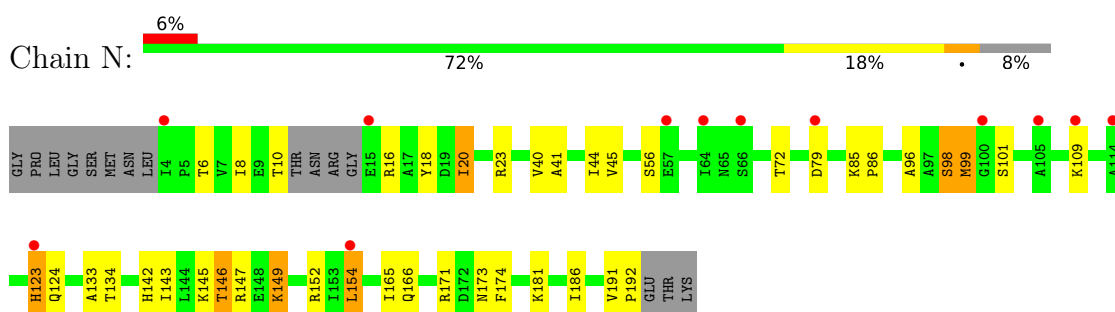
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



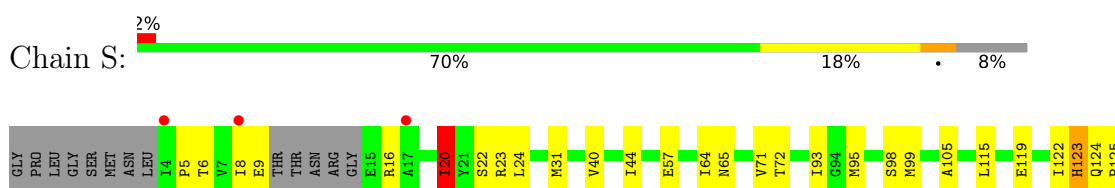
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



- Molecule 1: ATP-dependent Clp protease proteolytic subunit

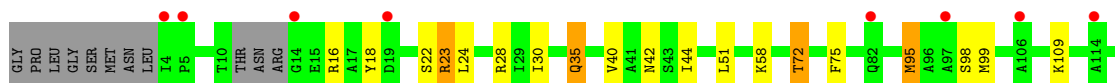


- Molecule 1: ATP-dependent Clp protease proteolytic subunit





- Molecule 1: ATP-dependent Clp protease proteolytic subunit



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.73Å 96.06Å 192.43Å 90.00° 91.17° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 30.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	95.2 (30.00-2.70) 95.1 (30.00-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.235 , 0.290 0.231 , 0.285	Depositor DCC
R_{free} test set	4444 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	52.9	Xtrriage
Anisotropy	0.245	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 13.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.012 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.010 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.014 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.015 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.016 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	20028	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.46% 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 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	0.62	0/1487	0.87	0/2007
1	B	0.65	0/1421	0.91	0/1918
1	C	0.61	0/1454	0.90	0/1962
1	E	0.60	0/1456	0.91	2/1964 (0.1%)
1	F	0.58	0/1448	0.92	1/1954 (0.1%)
1	G	0.59	0/1407	0.89	0/1899
1	I	0.61	0/1471	0.91	1/1987 (0.1%)
1	K	0.57	0/1452	0.91	1/1959 (0.1%)
1	L	0.58	0/1431	0.90	0/1932
1	M	0.57	0/1448	0.89	0/1954
1	N	0.59	0/1448	0.89	2/1954 (0.1%)
1	S	0.62	0/1449	0.92	2/1954 (0.1%)
1	T	0.60	0/1452	0.90	0/1959
1	V	0.62	0/1487	0.90	0/2007
All	All	0.60	0/20311	0.90	9/27410 (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	B	0	2

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	20	ILE	N-CA-C	6.62	117.38	110.62
1	E	4	ILE	CA-C-N	5.95	127.27	119.84
1	E	4	ILE	C-N-CA	5.95	127.27	119.84
1	F	131	GLY	N-CA-C	5.60	117.21	111.56
1	S	20	ILE	N-CA-C	5.51	116.90	110.62

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	4	ILE	Peptide
1	B	5	PRO	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	1462	0	1482	46	0
1	B	1400	0	1417	27	0
1	C	1430	0	1453	34	0
1	E	1432	0	1452	29	0
1	F	1427	0	1443	26	0
1	G	1386	0	1406	32	0
1	I	1452	0	1464	34	0
1	K	1431	0	1446	41	0
1	L	1413	0	1428	33	0
1	M	1427	0	1443	34	0
1	N	1427	0	1443	28	0
1	S	1425	0	1445	35	0
1	T	1431	0	1446	33	0
1	V	1462	0	1482	29	0
2	A	3	0	0	0	0
2	B	4	0	0	0	0
2	C	1	0	0	0	0
2	E	2	0	0	0	0
2	F	1	0	0	0	0
2	G	2	0	0	0	0
2	I	2	0	0	0	0
2	K	1	0	0	0	0
2	N	1	0	0	0	0
2	S	4	0	0	0	0
2	T	1	0	0	0	0
2	V	1	0	0	0	0
All	All	20028	0	20250	361	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 9.

The worst 5 of 361 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:L:191:VAL:HG22	1:L:192:PRO:HA	1.27	1.14
1:E:93:ILE:HG22	1:E:115:LEU:CD1	1.83	1.09
1:M:191:VAL:HG22	1:M:192:PRO:HA	1.34	1.08
1:E:93:ILE:HG22	1:E:115:LEU:HD12	1.37	1.04
1:F:191:VAL:HG22	1:F:192:PRO:HA	1.37	1.02

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	189/200 (94%)	182 (96%)	6 (3%)	1 (0%)	24	48
1	B	179/200 (90%)	173 (97%)	6 (3%)	0	100	100
1	C	183/200 (92%)	178 (97%)	4 (2%)	1 (0%)	24	48
1	E	183/200 (92%)	181 (99%)	2 (1%)	0	100	100
1	F	182/200 (91%)	177 (97%)	4 (2%)	1 (0%)	24	48
1	G	177/200 (88%)	169 (96%)	7 (4%)	1 (1%)	21	44
1	I	187/200 (94%)	181 (97%)	6 (3%)	0	100	100
1	K	183/200 (92%)	175 (96%)	7 (4%)	1 (0%)	24	48
1	L	180/200 (90%)	172 (96%)	8 (4%)	0	100	100
1	M	182/200 (91%)	174 (96%)	7 (4%)	1 (0%)	24	48
1	N	182/200 (91%)	172 (94%)	10 (6%)	0	100	100
1	S	182/200 (91%)	177 (97%)	5 (3%)	0	100	100
1	T	183/200 (92%)	179 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	V	189/200 (94%)	185 (98%)	4 (2%)	0	100	100
All	All	2561/2800 (92%)	2475 (97%)	80 (3%)	6 (0%)	43	68

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	55	ASP
1	G	5	PRO
1	M	56	SER
1	A	98	SER
1	F	94	GLY

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	157/165 (95%)	144 (92%)	13 (8%)	10	26
1	B	150/165 (91%)	136 (91%)	14 (9%)	8	21
1	C	154/165 (93%)	136 (88%)	18 (12%)	5	13
1	E	154/165 (93%)	135 (88%)	19 (12%)	4	12
1	F	153/165 (93%)	138 (90%)	15 (10%)	7	19
1	G	149/165 (90%)	137 (92%)	12 (8%)	11	27
1	I	155/165 (94%)	141 (91%)	14 (9%)	9	23
1	K	153/165 (93%)	137 (90%)	16 (10%)	6	17
1	L	151/165 (92%)	134 (89%)	17 (11%)	5	14
1	M	153/165 (93%)	136 (89%)	17 (11%)	6	15
1	N	153/165 (93%)	138 (90%)	15 (10%)	7	19
1	S	153/165 (93%)	137 (90%)	16 (10%)	6	17
1	T	153/165 (93%)	132 (86%)	21 (14%)	3	9
1	V	157/165 (95%)	143 (91%)	14 (9%)	9	23
All	All	2145/2310 (93%)	1924 (90%)	221 (10%)	7	18

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	154	LEU
1	L	147	ARG
1	T	176	THR
1	S	191	VAL
1	K	8	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 157 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	39	ASN
1	S	160	GLN
1	M	124	GLN
1	N	151	ASN
1	T	123	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 oligosaccharides 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 [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	189/200 (94%)	0.44	8 (4%) 40 37	31, 54, 68, 84	2 (1%)
1	B	182/200 (91%)	0.43	11 (6%) 27 24	31, 54, 64, 72	1 (0%)
1	C	185/200 (92%)	0.40	9 (4%) 35 31	32, 56, 67, 78	2 (1%)
1	E	185/200 (92%)	0.46	11 (5%) 28 25	35, 61, 73, 81	2 (1%)
1	F	185/200 (92%)	0.48	7 (3%) 44 40	36, 62, 73, 85	1 (0%)
1	G	180/200 (90%)	0.54	8 (4%) 39 35	36, 60, 69, 75	1 (0%)
1	I	189/200 (94%)	0.43	5 (2%) 57 54	50, 60, 77, 93	0
1	K	186/200 (93%)	0.52	12 (6%) 25 22	36, 63, 81, 88	1 (0%)
1	L	184/200 (92%)	0.58	10 (5%) 31 27	58, 65, 84, 103	0
1	M	185/200 (92%)	0.56	7 (3%) 44 40	36, 63, 74, 83	1 (0%)
1	N	185/200 (92%)	0.53	12 (6%) 25 22	34, 60, 73, 85	1 (0%)
1	S	184/200 (92%)	0.38	5 (2%) 56 53	33, 55, 75, 91	2 (1%)
1	T	186/200 (93%)	0.42	10 (5%) 31 27	33, 57, 79, 89	1 (0%)
1	V	189/200 (94%)	0.38	8 (4%) 40 37	32, 55, 68, 83	2 (1%)
All	All	2594/2800 (92%)	0.47	123 (4%) 36 33	31, 59, 75, 103	17 (0%)

The worst 5 of 123 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	7	VAL	4.8
1	I	4	ILE	4.5
1	E	4	ILE	4.5
1	N	100	GLY	4.4
1	T	4	ILE	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 oligosaccharides 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.