



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 09:16 pm BST

PDB ID : 4WSC
Title : Crystal structure of a GroELK105A mutant
Authors : Lorimer, G.H.; Ye, X.; Fei, X.; Yang, D.; Corsepilus, N.; LaRonde, N.A.
Deposited on : 2014-10-26
Resolution : 3.04 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	:	2.11
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)	:	2.11

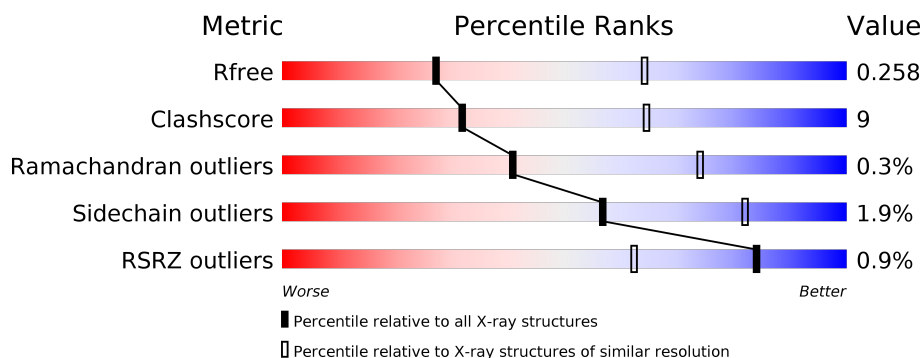
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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	2752 (3.08-3.00)
Clashscore	141614	3096 (3.08-3.00)
Ramachandran outliers	138981	2986 (3.08-3.00)
Sidechain outliers	138945	2988 (3.08-3.00)
RSRZ outliers	127900	2636 (3.08-3.00)

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 on 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	548	<div> <div>3%</div> <div> <div></div> <div>74%</div> <div>20%</div> <div>• •</div> </div> </div>
1	B	548	<div> <div>77%</div> <div>17%</div> <div>• •</div> </div>
1	C	548	<div> <div>77%</div> <div>18%</div> <div>• •</div> </div>
1	D	548	<div> <div>77%</div> <div>17%</div> <div>• •</div> </div>
1	E	548	<div> <div>%</div> <div> <div></div> <div>74%</div> <div>20%</div> <div>• •</div> </div> </div>
1	F	548	<div> <div>72%</div> <div>22%</div> <div>• •</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	548	<div><div></div><div>74%21%</div><div></div><div></div></div>
1	H	548	<div><div></div><div>73%21%</div><div></div><div></div></div>
1	I	548	<div><div></div><div>74%20%</div><div></div><div></div></div>
1	J	548	<div><div></div><div>73%22%</div><div></div><div></div></div>
1	K	548	<div><div></div><div>76%19%</div><div></div><div></div></div>
1	L	548	<div><div>7%</div><div></div><div>76%18%</div><div></div><div></div></div>
1	M	548	<div><div></div><div>73%22%</div><div></div><div></div></div>
1	N	548	<div><div></div><div>74%20%</div><div></div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 53914 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 60 kDa chaperonin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	B	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	C	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	D	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	E	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	F	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	G	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	H	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	I	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	J	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	K	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	L	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	M	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			
1	N	524	Total	C	N	O	S	0	0	0
			3851	2394	664	773	20			

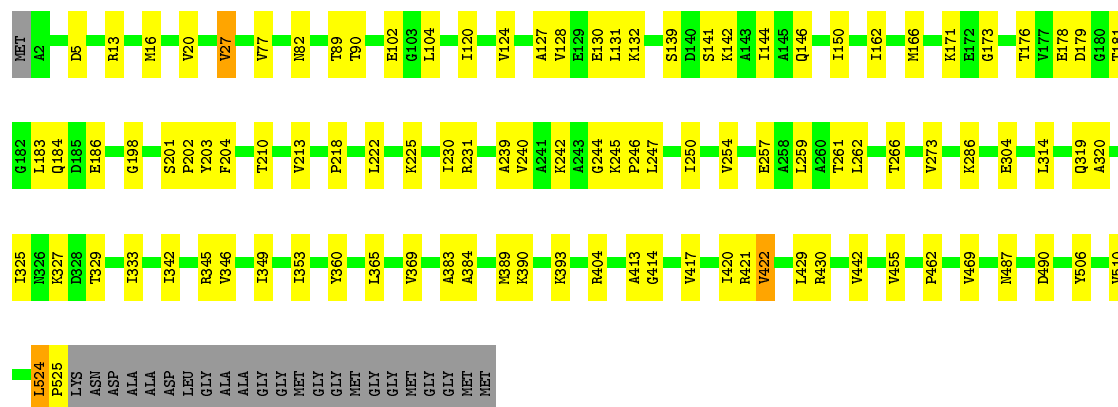
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	ALA	LYS	engineered mutation	UNP P0A6F5

Continued on next page...

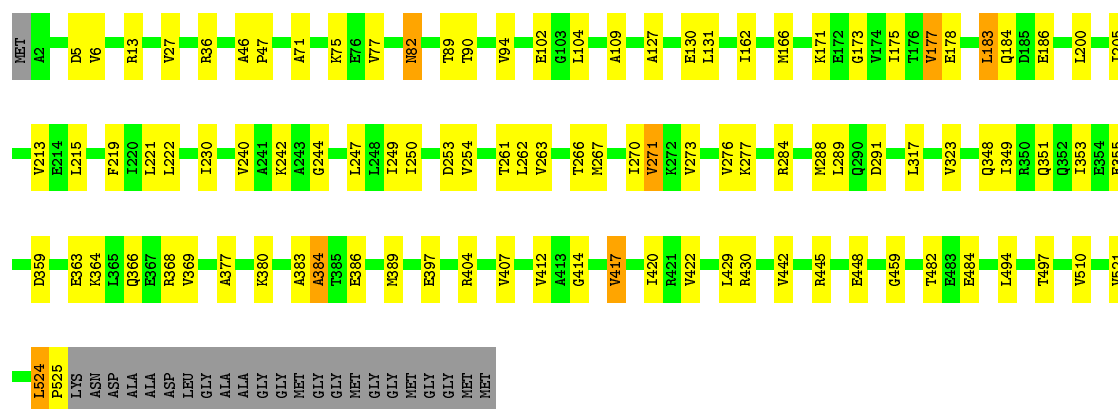
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	105	ALA	LYS	engineered mutation	UNP P0A6F5
C	105	ALA	LYS	engineered mutation	UNP P0A6F5
D	105	ALA	LYS	engineered mutation	UNP P0A6F5
E	105	ALA	LYS	engineered mutation	UNP P0A6F5
F	105	ALA	LYS	engineered mutation	UNP P0A6F5
G	105	ALA	LYS	engineered mutation	UNP P0A6F5
H	105	ALA	LYS	engineered mutation	UNP P0A6F5
I	105	ALA	LYS	engineered mutation	UNP P0A6F5
J	105	ALA	LYS	engineered mutation	UNP P0A6F5
K	105	ALA	LYS	engineered mutation	UNP P0A6F5
L	105	ALA	LYS	engineered mutation	UNP P0A6F5
M	105	ALA	LYS	engineered mutation	UNP P0A6F5
N	105	ALA	LYS	engineered mutation	UNP P0A6F5



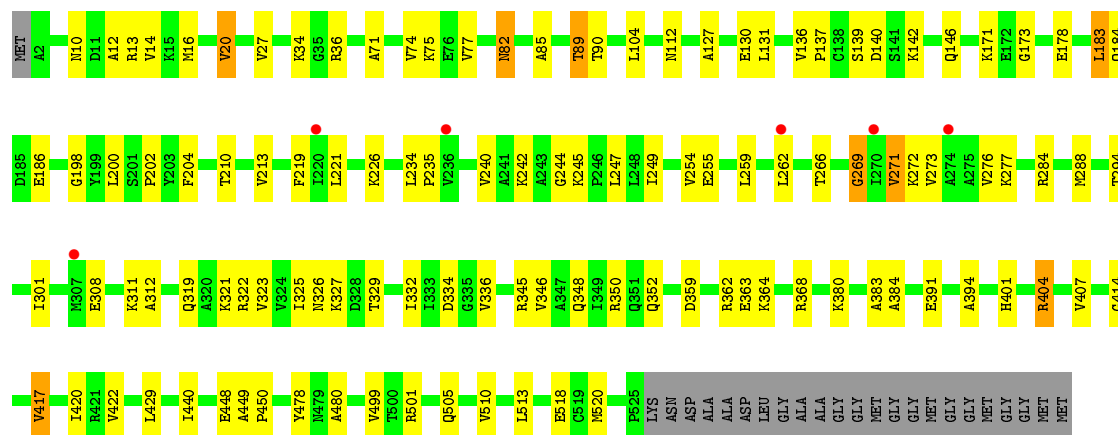
• Molecule 1: 60 kDa chaperonin

Chain D: 77% 17% . .



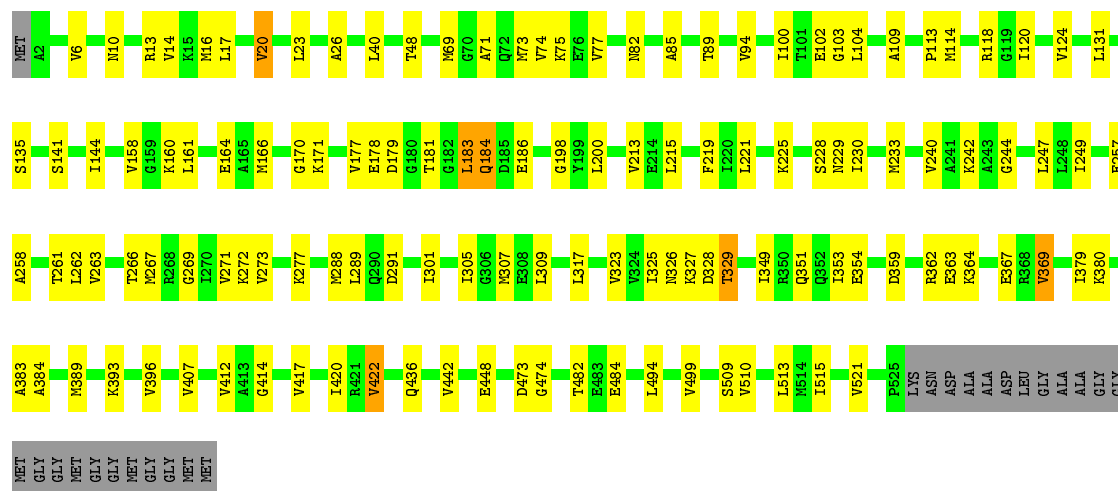
• Molecule 1: 60 kDa chaperonin

Chain E: 74% 20% . .



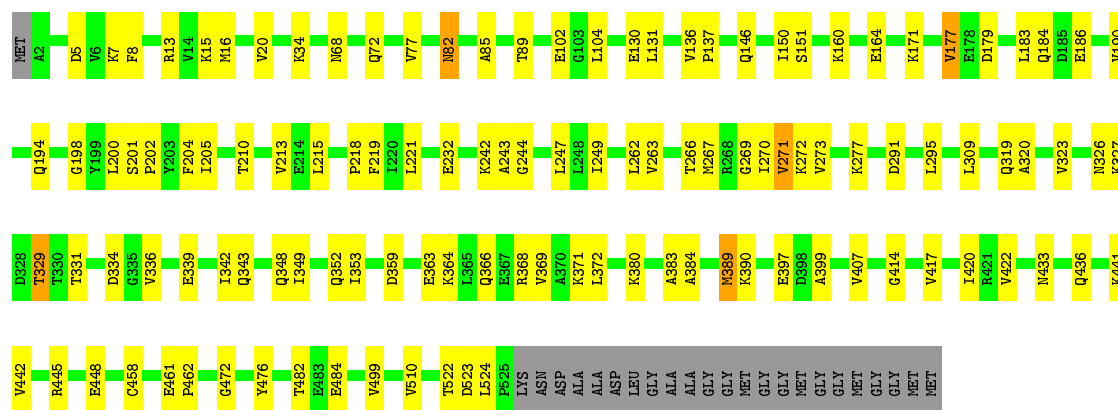
• Molecule 1: 60 kDa chaperonin

Chain F: 72% 22% . .



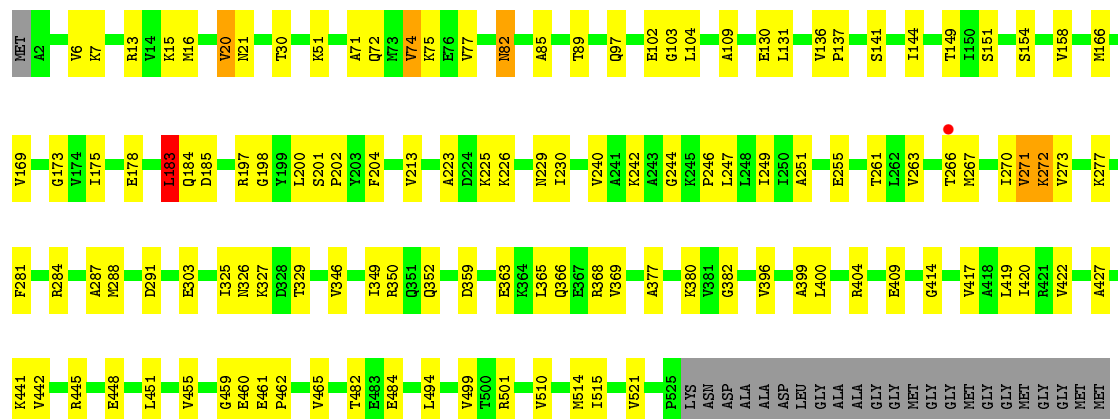
- Molecule 1: 60 kDa chaperonin

Chain G: 74% 21%



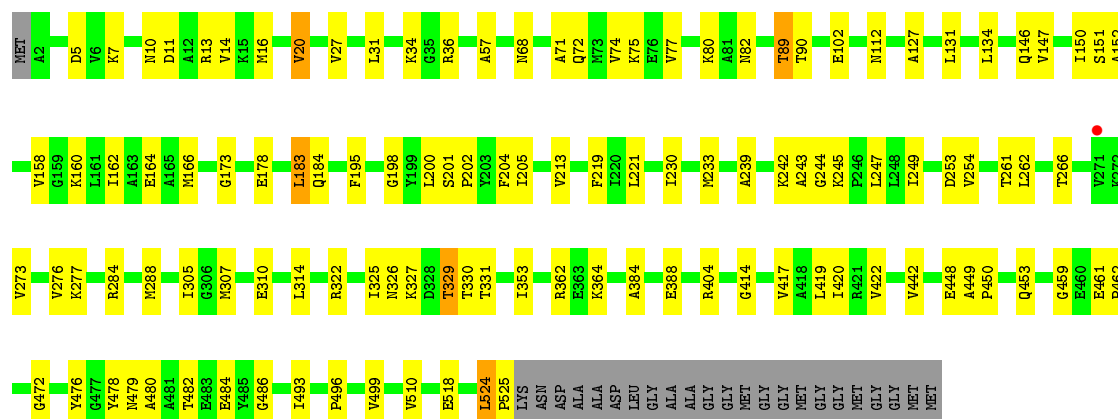
- Molecule 1: 60 kDa chaperonin

Chain H: 73% 21%



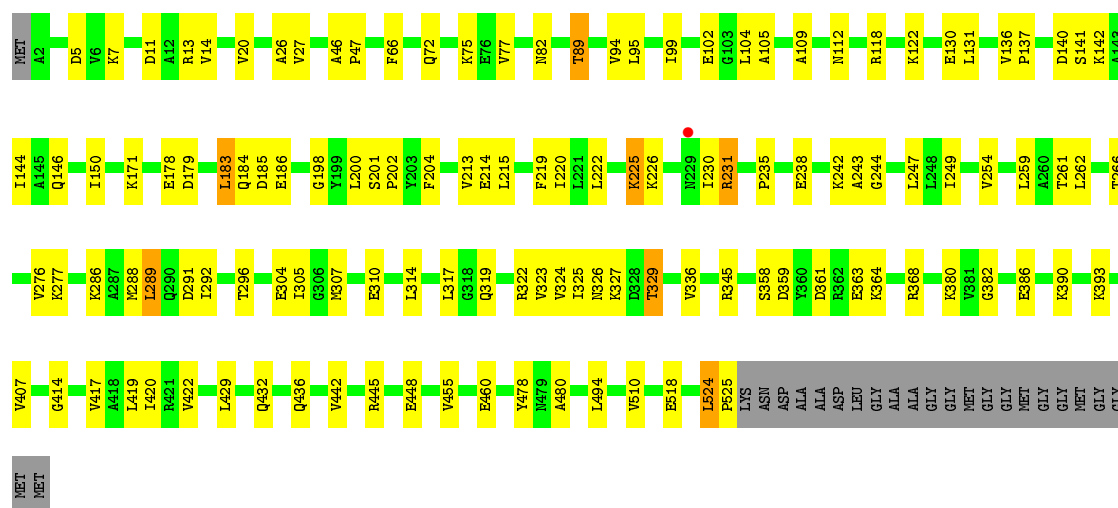
- Molecule 1: 60 kDa chaperonin

Category	Percentage
Very bad	74%
Bad	20%
Good	6%



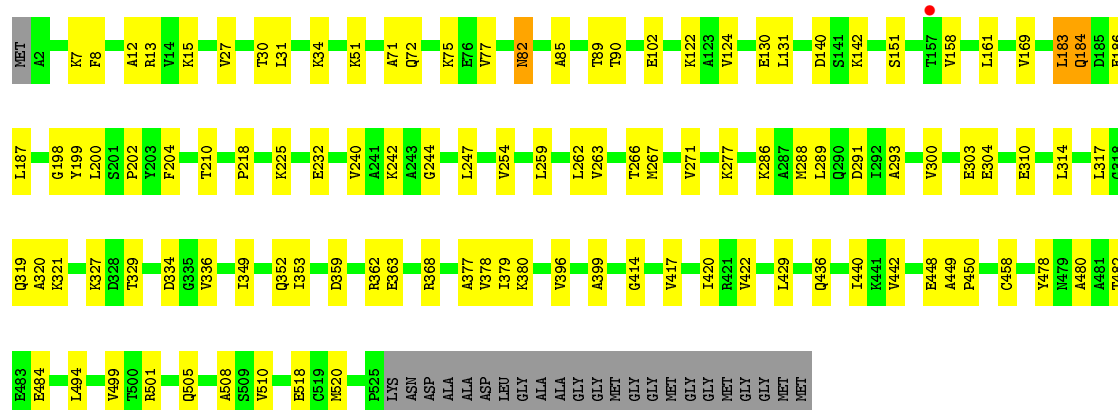
- Molecule 1: 60 kDa chaperonin

Category	Percentage
Very bad	73%
Bad	22%

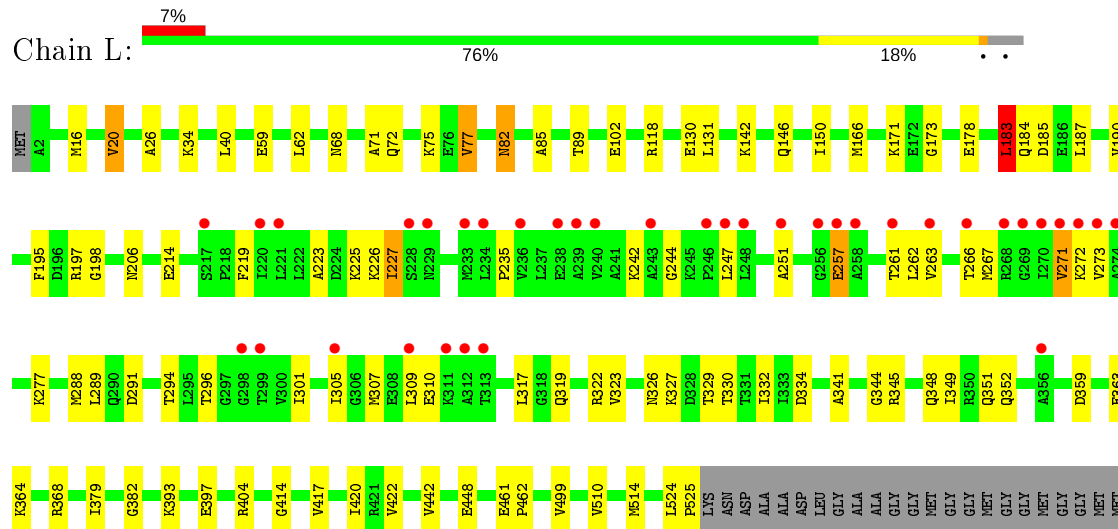


- Molecule 1: 60 kDa chaperonin

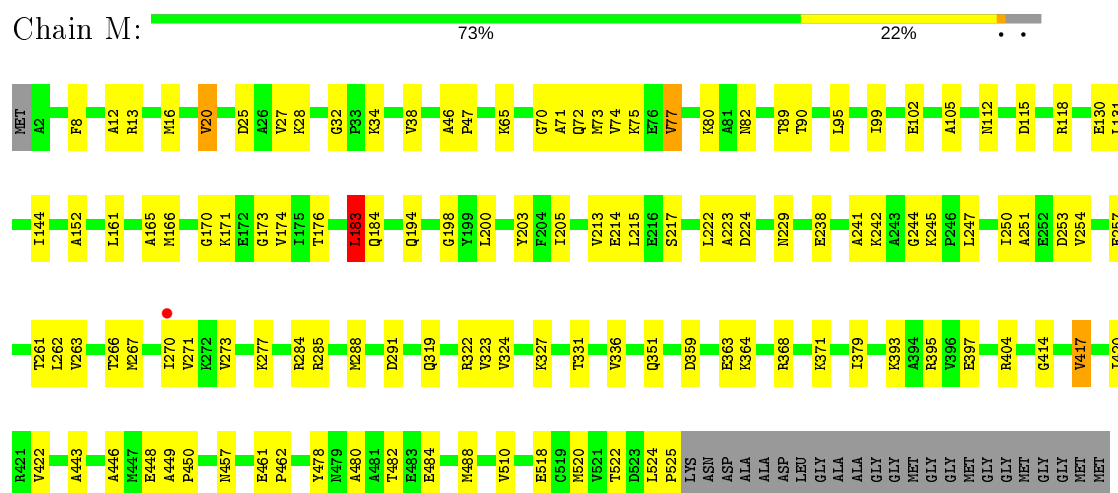
76% 19%



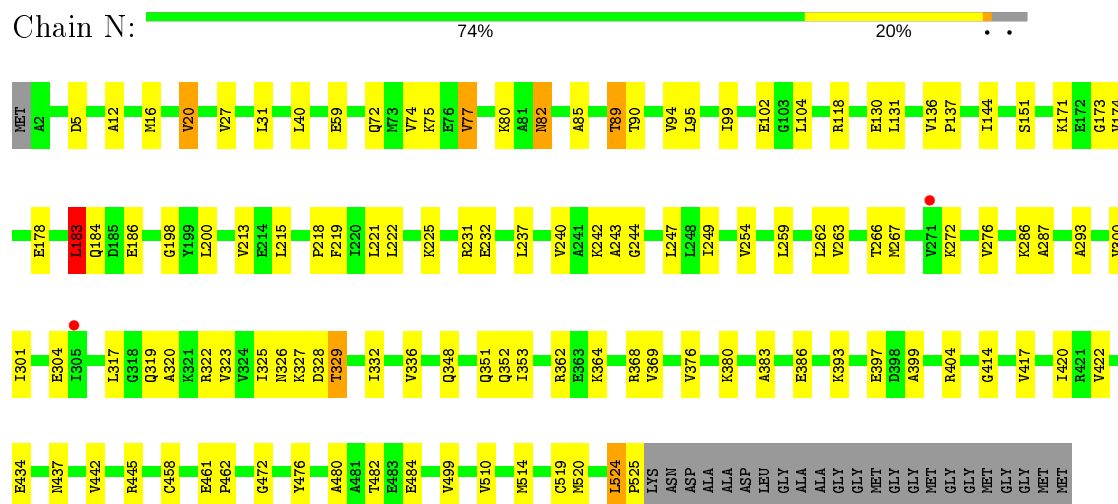
- Molecule 1: 60 kDa chaperonin



- Molecule 1: 60 kDa chaperonin



- Molecule 1: 60 kDa chaperonin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	135.64Å 259.39Å 143.31Å 90.00° 105.12° 90.00°	Depositor
Resolution (Å)	80.52 – 3.04 84.15 – 3.04	Depositor EDS
% Data completeness (in resolution range)	98.4 (80.52-3.04) 96.2 (84.15-3.04)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.190 , 0.256 0.194 , 0.258	Depositor DCC
R_{free} test set	2001 reflections (1.11%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.870	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	53914	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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	0/3879	0.73	2/5239 (0.0%)
1	B	0.52	0/3879	0.71	0/5239
1	C	0.53	0/3879	0.75	0/5239
1	D	0.51	0/3879	0.72	0/5239
1	E	0.46	0/3879	0.69	1/5239 (0.0%)
1	F	0.52	0/3879	0.73	0/5239
1	G	0.48	0/3879	0.71	0/5239
1	H	0.45	0/3879	0.67	1/5239 (0.0%)
1	I	0.49	0/3879	0.70	1/5239 (0.0%)
1	J	0.48	0/3879	0.71	0/5239
1	K	0.47	0/3879	0.67	0/5239
1	L	0.45	0/3879	0.67	1/5239 (0.0%)
1	M	0.47	0/3879	0.68	1/5239 (0.0%)
1	N	0.47	0/3879	0.67	1/5239 (0.0%)
All	All	0.49	0/54306	0.70	8/73346 (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	E	0	1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	183	LEU	CA-CB-CG	5.81	128.65	115.30
1	L	183	LEU	CA-CB-CG	5.78	128.59	115.30
1	M	183	LEU	CA-CB-CG	5.46	127.85	115.30
1	H	183	LEU	CA-CB-CG	5.30	127.50	115.30
1	A	182	GLY	N-CA-C	5.29	126.32	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	183	LEU	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	3851	0	3968	69	0
1	B	3851	0	3968	60	0
1	C	3851	0	3968	66	0
1	D	3851	0	3968	65	0
1	E	3851	0	3968	77	0
1	F	3851	0	3968	79	0
1	G	3851	0	3968	66	0
1	H	3851	0	3968	77	0
1	I	3851	0	3968	72	0
1	J	3851	0	3968	83	0
1	K	3851	0	3968	64	0
1	L	3851	0	3968	66	0
1	M	3851	0	3968	81	0
1	N	3851	0	3968	76	0
All	All	53914	0	55552	970	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 970 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:34:LYS:HE2	1:M:118:ARG:HH22	1.31	0.95
1:M:173:GLY:O	1:M:404:ARG:NH2	2.07	0.87
1:H:200:LEU:HD21	1:H:277:LYS:HG3	1.56	0.85
1:A:183:LEU:HG	1:A:384:ALA:HB2	1.60	0.83
1:N:524:LEU:HD12	1:N:525:PRO:HD2	1.61	0.82

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	522/548 (95%)	509 (98%)	11 (2%)	2 (0%)	34	69
1	B	522/548 (95%)	508 (97%)	12 (2%)	2 (0%)	34	69
1	C	522/548 (95%)	507 (97%)	14 (3%)	1 (0%)	47	80
1	D	522/548 (95%)	507 (97%)	11 (2%)	4 (1%)	19	54
1	E	522/548 (95%)	509 (98%)	11 (2%)	2 (0%)	34	69
1	F	522/548 (95%)	507 (97%)	13 (2%)	2 (0%)	34	69
1	G	522/548 (95%)	512 (98%)	7 (1%)	3 (1%)	25	60
1	H	522/548 (95%)	511 (98%)	10 (2%)	1 (0%)	47	80
1	I	522/548 (95%)	511 (98%)	10 (2%)	1 (0%)	47	80
1	J	522/548 (95%)	511 (98%)	10 (2%)	1 (0%)	47	80
1	K	522/548 (95%)	513 (98%)	8 (2%)	1 (0%)	47	80
1	L	522/548 (95%)	511 (98%)	10 (2%)	1 (0%)	47	80
1	M	522/548 (95%)	511 (98%)	11 (2%)	0	100	100
1	N	522/548 (95%)	510 (98%)	11 (2%)	1 (0%)	47	80
All	All	7308/7672 (95%)	7137 (98%)	149 (2%)	22 (0%)	41	74

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	184	GLN
1	B	184	GLN
1	D	184	GLN
1	F	184	GLN
1	G	243	ALA

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	403/414 (97%)	397 (98%)	6 (2%)	65	86
1	B	403/414 (97%)	395 (98%)	8 (2%)	55	81
1	C	403/414 (97%)	398 (99%)	5 (1%)	71	89
1	D	403/414 (97%)	396 (98%)	7 (2%)	60	84
1	E	403/414 (97%)	395 (98%)	8 (2%)	55	81
1	F	403/414 (97%)	394 (98%)	9 (2%)	52	79
1	G	403/414 (97%)	396 (98%)	7 (2%)	60	84
1	H	403/414 (97%)	398 (99%)	5 (1%)	71	89
1	I	403/414 (97%)	396 (98%)	7 (2%)	60	84
1	J	403/414 (97%)	393 (98%)	10 (2%)	47	77
1	K	403/414 (97%)	396 (98%)	7 (2%)	60	84
1	L	403/414 (97%)	395 (98%)	8 (2%)	55	81
1	M	403/414 (97%)	396 (98%)	7 (2%)	60	84
1	N	403/414 (97%)	392 (97%)	11 (3%)	44	75
All	All	5642/5796 (97%)	5537 (98%)	105 (2%)	57	82

5 of 105 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	329	THR
1	I	183	LEU
1	N	89	THR
1	G	331	THR
1	H	183	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	436	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	194	GLN
1	F	229	ASN
1	H	229	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 carbohydrates 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	524/548 (95%)	-0.08	19 (3%) 42 18	13, 42, 126, 158	0
1	B	524/548 (95%)	-0.44	0 100 100	14, 36, 75, 112	0
1	C	524/548 (95%)	-0.46	0 100 100	12, 32, 65, 93	0
1	D	524/548 (95%)	-0.37	0 100 100	11, 44, 93, 130	0
1	E	524/548 (95%)	-0.19	6 (1%) 80 56	18, 54, 125, 155	0
1	F	524/548 (95%)	-0.33	0 100 100	15, 40, 94, 137	0
1	G	524/548 (95%)	-0.33	0 100 100	19, 47, 86, 111	0
1	H	524/548 (95%)	-0.24	1 (0%) 95 87	18, 53, 105, 144	0
1	I	524/548 (95%)	-0.24	1 (0%) 95 87	14, 42, 83, 108	0
1	J	524/548 (95%)	-0.38	1 (0%) 95 87	18, 45, 77, 101	0
1	K	524/548 (95%)	-0.27	1 (0%) 95 87	18, 46, 86, 111	0
1	L	524/548 (95%)	0.08	37 (7%) 16 5	17, 57, 153, 189	0
1	M	524/548 (95%)	-0.37	1 (0%) 95 87	18, 49, 99, 120	0
1	N	524/548 (95%)	-0.10	2 (0%) 92 79	17, 55, 106, 140	0
All	All	7336/7672 (95%)	-0.27	69 (0%) 84 62	11, 44, 104, 189	0

The worst 5 of 69 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	240	VAL	7.2
1	L	271	VAL	7.2
1	L	299	THR	6.5
1	L	228	SER	5.5
1	A	313	THR	4.6

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 carbohydrates 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.