



wwPDB EM Map/Model Validation Report ⓘ

Apr 26, 2016 – 06:36 PM BST

PDB ID : 1GR5
EMDB ID: : EMD-1042
Title : Solution Structure of apo GroEL by Cryo-Electron microscopy
Authors : Ranson, N.A.; Farr, G.W.; Roseman, A.M.; Gowen, B.; Fenton, W.A.; Horwich, A.L.; Saibil, H.R.
Deposited on : 2001-12-14
Resolution : 7.90 Å(reported)
Based on PDB ID : 1DER

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27461

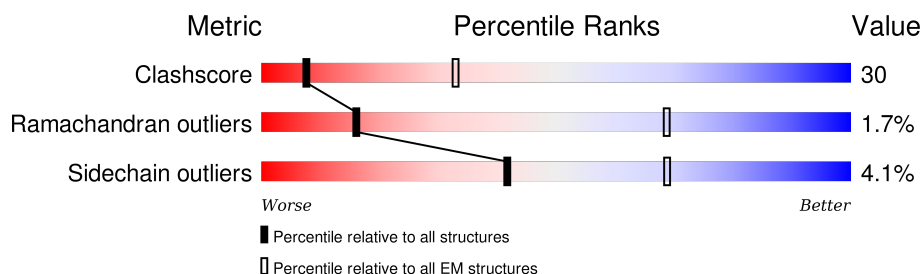
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.90 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	547	59% 33% • 5%
1	B	547	60% 33% • 5%
1	C	547	61% 32% • 5%
1	D	547	60% 33% • 5%
1	E	547	60% 33% • 5%
1	F	547	60% 33% • 5%
1	G	547	60% 33% • 5%
1	H	547	59% 34% • 5%
1	I	547	58% 34% • 5%

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Mol	Chain	Length	Quality of chain
1	J	547	<div><div></div><div>58%</div><div>35%</div><div>• 5%</div></div>
1	K	547	<div><div></div><div>58%</div><div>34%</div><div>• 5%</div></div>
1	L	547	<div><div></div><div>58%</div><div>35%</div><div>• 5%</div></div>
1	M	547	<div><div></div><div>58%</div><div>35%</div><div>• 5%</div></div>
1	N	547	<div><div></div><div>58%</div><div>35%</div><div>• 5%</div></div>

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 52668 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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					AltConf	Trace
1	A	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	B	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	C	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	D	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	E	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	F	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	G	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	H	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	I	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	J	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	K	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	L	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	M	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		
1	N	517	Total	C	N	O	S	0	0
			3762	2372	614	757	19		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
A	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6

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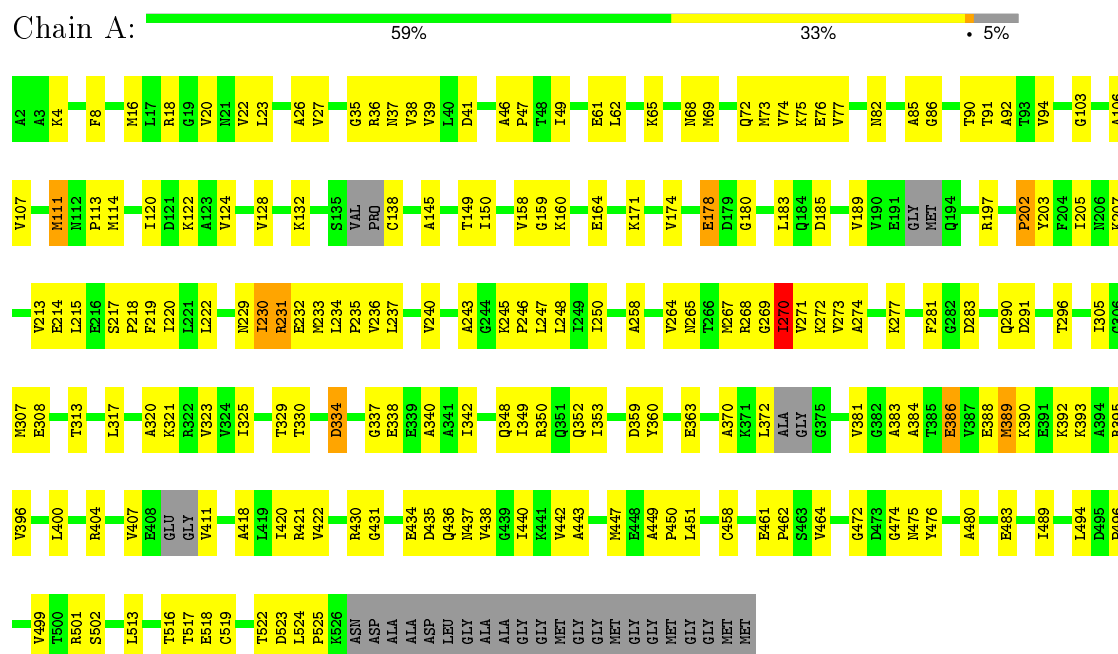
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Chain	Residue	Modelled	Actual	Comment	Reference
B	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
B	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
C	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
C	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
D	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
D	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
E	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
E	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
F	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
F	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
G	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
G	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
H	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
H	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
I	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
I	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
J	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
J	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
K	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
K	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
L	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
L	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
M	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
M	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6
N	13	GLY	ARG	ENGINEERED MUTATION	UNP P0A6F6
N	126	VAL	ALA	ENGINEERED MUTATION	UNP P0A6F6

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

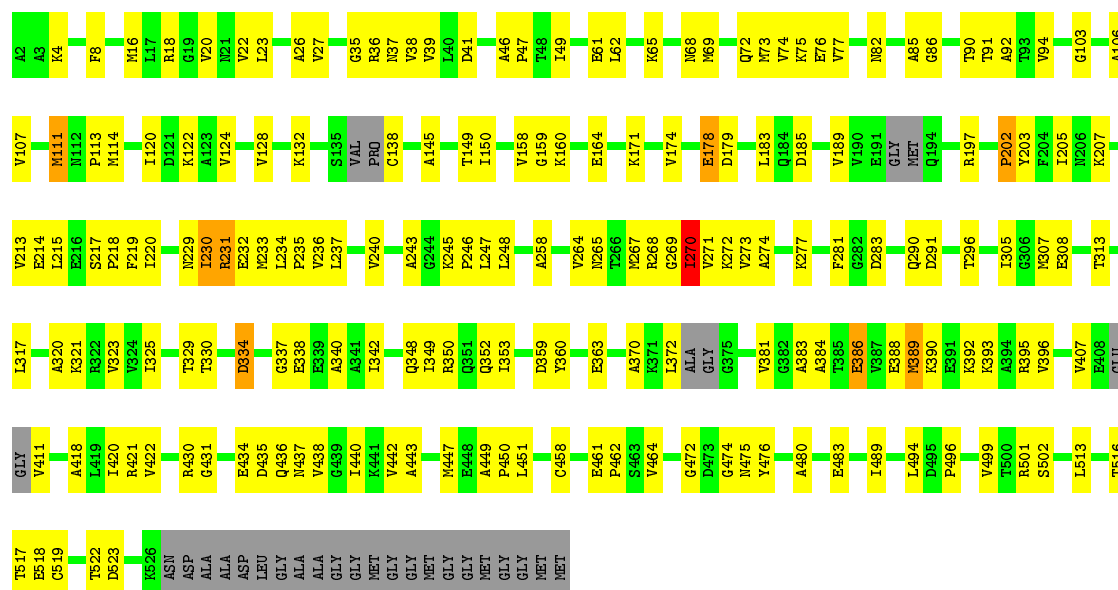
• Molecule 1: 60 KDA CHAPERONIN





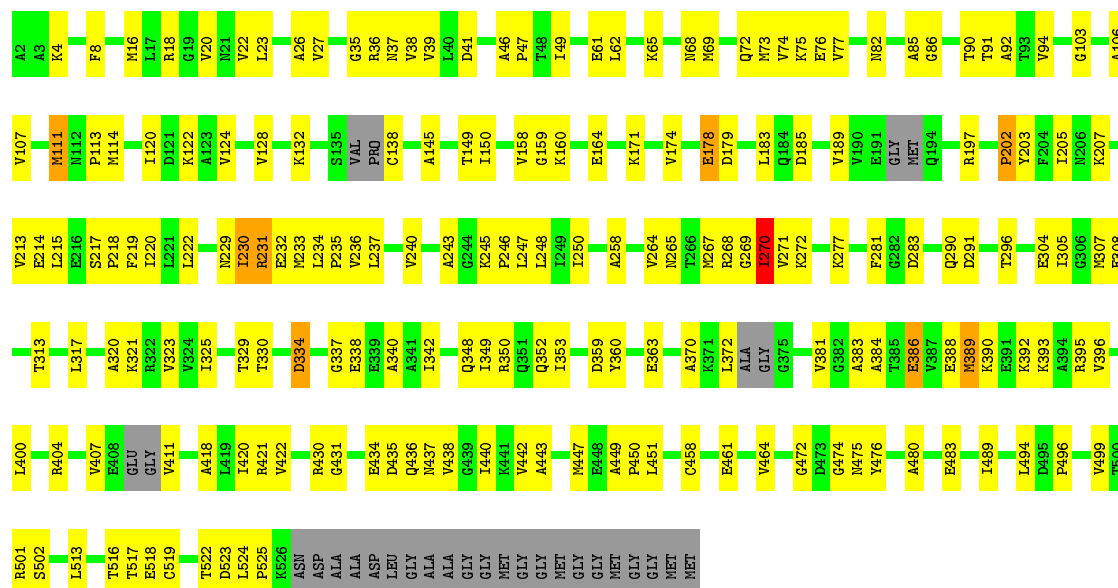
• Molecule 1: 60 KDA CHAPERONIN

Chain C: 61% 32% 5%



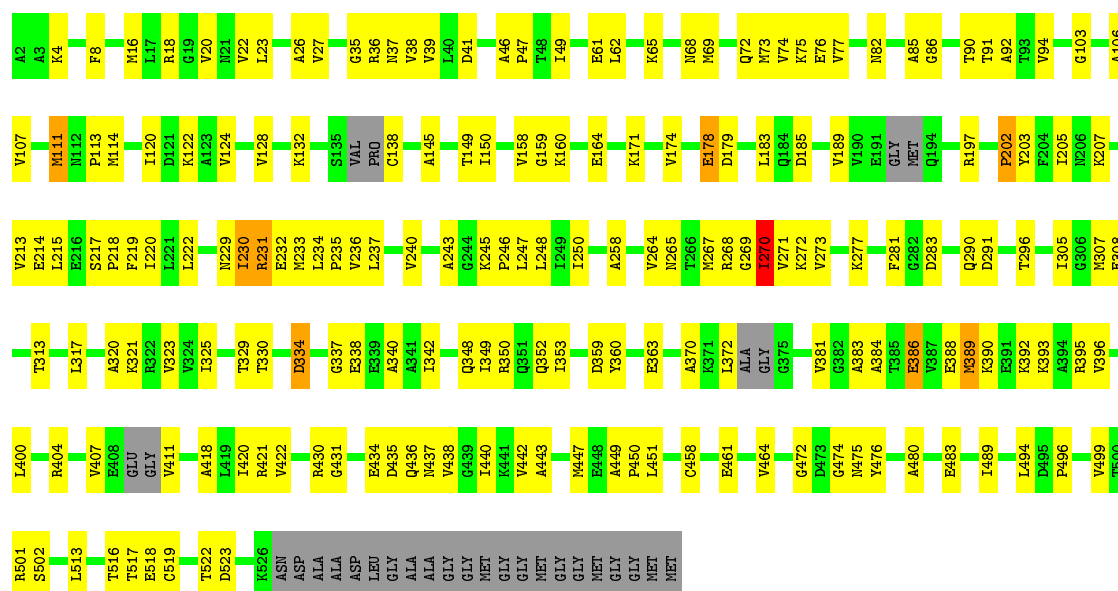
• Molecule 1: 60 KDA CHAPERONIN

Chain D: 60% 33% 5%



• Molecule 1: 60 KDA CHAPERONIN

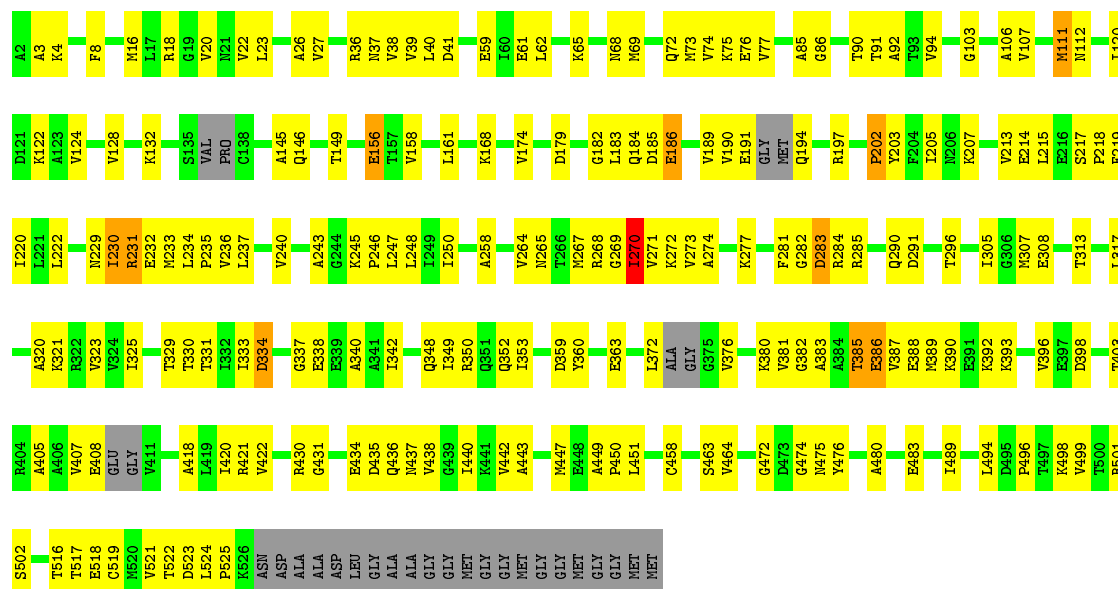
Chain E: 60% 33% 5%

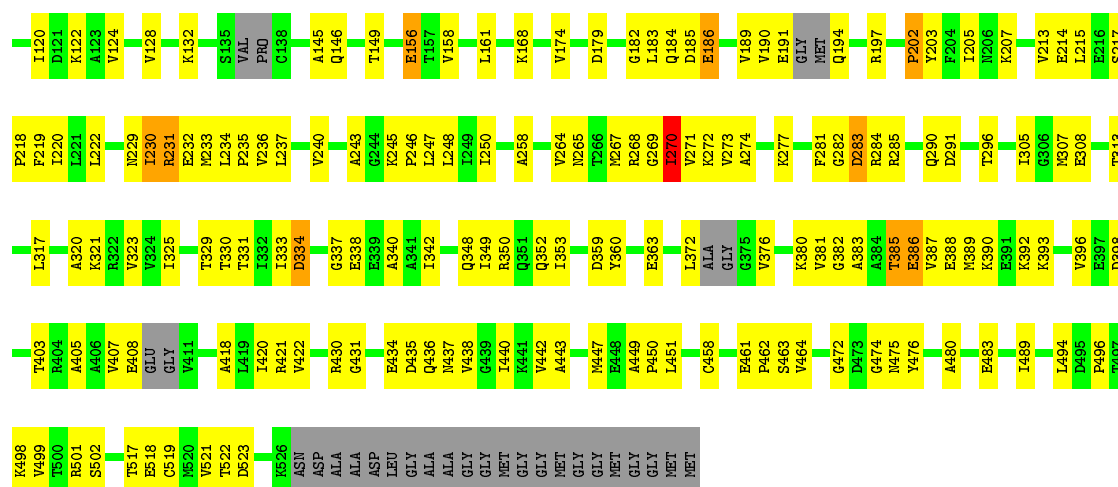




- Molecule 1: 60 KDA CHAPERONIN

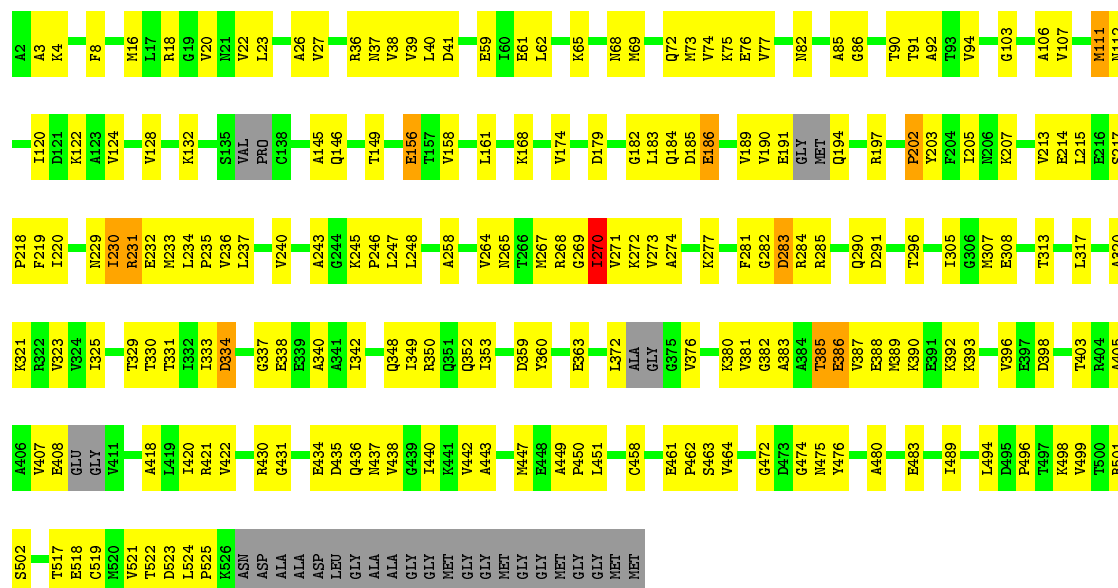
Chain J: 





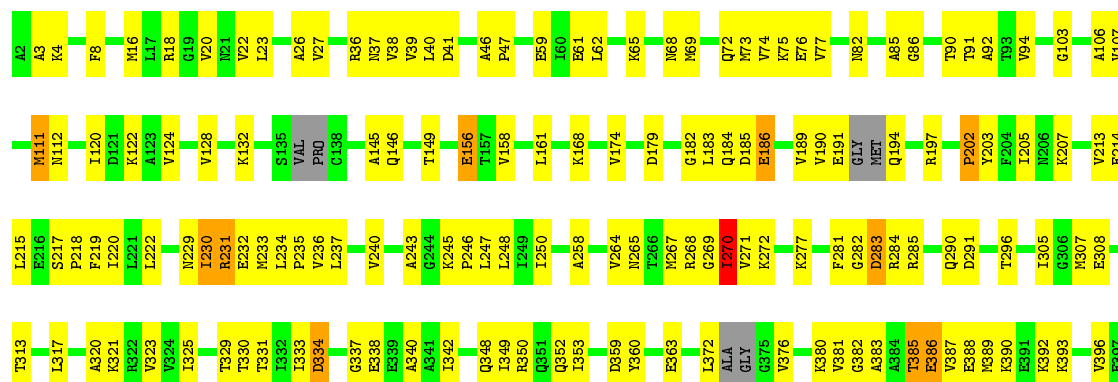
• Molecule 1: 60 KDA CHAPERONIN

Chain M: 58% 35% • 5%



• Molecule 1: 60 KDA CHAPERONIN

Chain N: 58% 35% • 5%



[illegible]

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CLASS AVERAGES	Depositor
Microscope	FEI CM200	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	38000	Depositor
Image detector	KODAK SO-163 FILM	Depositor

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 >2	RMSZ	# Z >2
1	A	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	B	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	C	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	D	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	E	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	F	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	G	1.43	1/3785 (0.0%)	0.56	1/5093 (0.0%)
1	H	0.27	0/3785	0.55	0/5093
1	I	0.27	0/3785	0.55	0/5093
1	J	0.27	0/3785	0.55	0/5093
1	K	0.27	0/3785	0.55	0/5093
1	L	0.27	0/3785	0.55	0/5093
1	M	0.27	0/3785	0.55	0/5093
1	N	0.27	0/3785	0.55	0/5093
All	All	1.03	7/52990 (0.0%)	0.55	7/71302 (0.0%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	386	GLU	CB-CG	86.48	3.16	1.52
1	G	386	GLU	CB-CG	86.47	3.16	1.52
1	A	386	GLU	CB-CG	86.47	3.16	1.52
1	C	386	GLU	CB-CG	86.46	3.16	1.52
1	D	386	GLU	CB-CG	86.46	3.16	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	386	GLU	CA-CB-CG	7.43	129.74	113.40
1	F	386	GLU	CA-CB-CG	7.43	129.74	113.40
1	B	386	GLU	CA-CB-CG	7.42	129.73	113.40
1	A	386	GLU	CA-CB-CG	7.42	129.73	113.40
1	C	386	GLU	CA-CB-CG	7.42	129.72	113.40

There are no chirality outliers.

There are no planarity outliers.

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	3762	0	3841	341	0
1	B	3762	0	3841	339	0
1	C	3762	0	3841	342	0
1	D	3762	0	3841	338	0
1	E	3762	0	3841	339	0
1	F	3762	0	3841	338	0
1	G	3762	0	3841	340	0
1	H	3762	0	3837	317	0
1	I	3762	0	3837	318	0
1	J	3762	0	3837	318	0
1	K	3762	0	3837	314	0
1	L	3762	0	3837	319	0
1	M	3762	0	3837	326	0
1	N	3762	0	3837	321	0
All	All	52668	0	53746	3163	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 30.

The worst 5 of 3163 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:C:47:PRO:CD	1:D:73:MET:HG2	1.20	1.64
1:D:47:PRO:CD	1:E:73:MET:HG2	1.20	1.63
1:A:150:ILE:CD1	1:A:411:VAL:HG11	1.15	1.62
1:B:150:ILE:CD1	1:B:411:VAL:HG11	1.15	1.62
1:B:47:PRO:CD	1:C:73:MET:HG2	1.20	1.62

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	B	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	C	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	D	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	E	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	F	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	G	507/547 (93%)	473 (93%)	26 (5%)	8 (2%)	12	56
1	H	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	I	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	J	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	K	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	L	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	M	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
1	N	507/547 (93%)	469 (92%)	29 (6%)	9 (2%)	11	53
All	All	7098/7658 (93%)	6594 (93%)	385 (5%)	119 (2%)	16	55

5 of 119 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	185	ASP
1	A	270	ILE
1	A	340	ALA
1	B	185	ASP
1	B	270	ILE

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 PDB entries followed by that with respect to all EM entries.

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	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	B	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	C	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	D	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	E	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	F	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	G	401/414 (97%)	384 (96%)	17 (4%)	36	70
1	H	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	I	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	J	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	K	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	L	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	M	401/414 (97%)	385 (96%)	16 (4%)	38	71
1	N	401/414 (97%)	385 (96%)	16 (4%)	38	71
All	All	5614/5796 (97%)	5383 (96%)	231 (4%)	42	71

5 of 231 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	178	GLU
1	H	307	MET
1	M	398	ASP
1	G	264	VAL
1	G	389	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 94 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	366	GLN

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Mol	Chain	Res	Type
1	I	453	GLN
1	N	146	GLN
1	H	437	ASN
1	I	146	GLN

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.