



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 03:35 AM UTC

PDB ID : 6LSY / pdb_00006lsy
EMDB ID : EMD-0965
Title : AAA+ ATPase, ClpL from Streptococcus pneumoniae - ATP bound
Authors : Kim, G.; Lee, S.G.; Han, S.; Jung, J.; Jeong, H.S.; Hyun, J.K.; Rhee, D.K.;
Kim, H.M.; Lee, S.
Deposited on : 2020-01-20
Resolution : 6.33 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>
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:

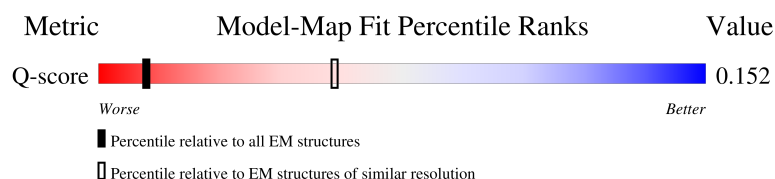
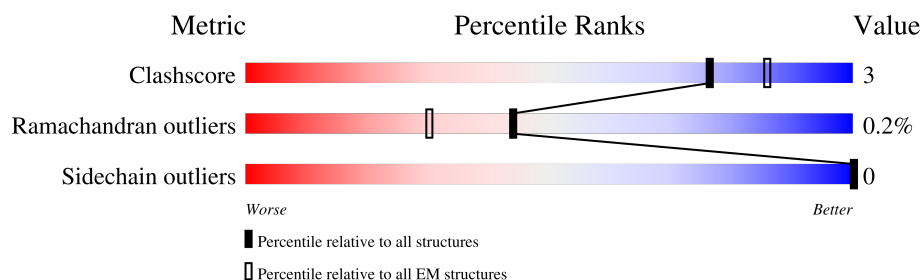
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

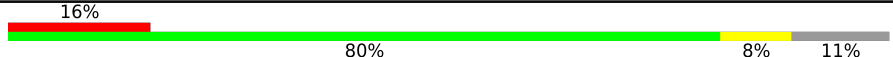
The reported resolution of this entry is 6.33 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	511 (5.84 - 6.81)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	701	
1	B	701	
1	C	701	
1	D	701	

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Mol	Chain	Length	Quality of chain
1	E	701	
1	F	701	
1	G	701	
1	H	701	
1	I	701	
1	J	701	
1	K	701	
1	L	701	
1	M	701	
1	N	701	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 135184 atoms, of which 67648 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 ATP-dependent Clp protease, ATP-binding subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	B	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	C	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	D	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	E	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	F	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	G	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	H	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	I	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	J	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	K	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	L	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	M	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		
1	N	623	Total	C	H	N	O	S	0	0
			9656	3005	4832	850	958	11		

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
A	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34

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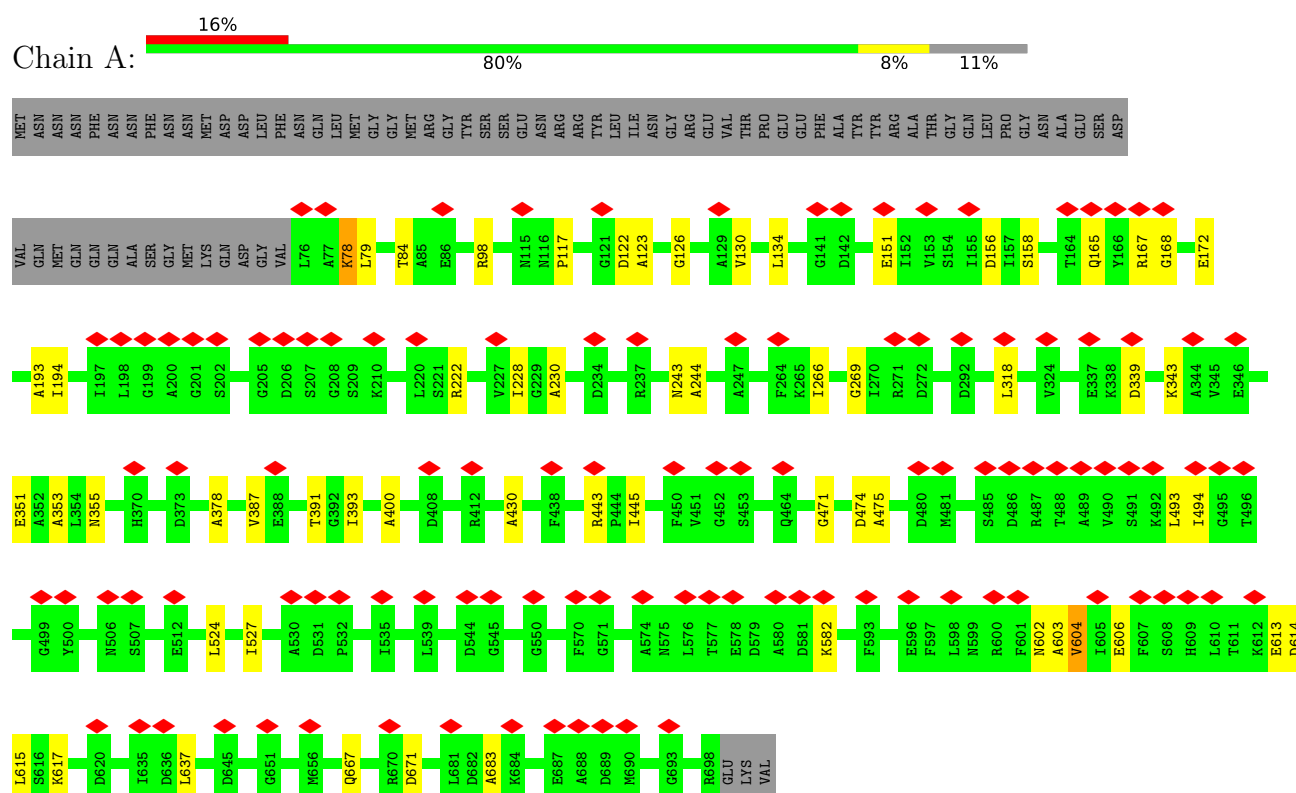
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Chain	Residue	Modelled	Actual	Comment	Reference
B	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
B	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
C	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
C	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
D	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
D	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
E	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
E	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
F	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
F	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
G	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
G	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
H	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
H	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
I	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
I	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
J	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
J	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
K	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
K	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
L	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
L	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
M	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
M	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34
N	193	ALA	GLU	engineered mutation	UNP A0A2U3RY34
N	526	ALA	GLU	engineered mutation	UNP A0A2U3RY34

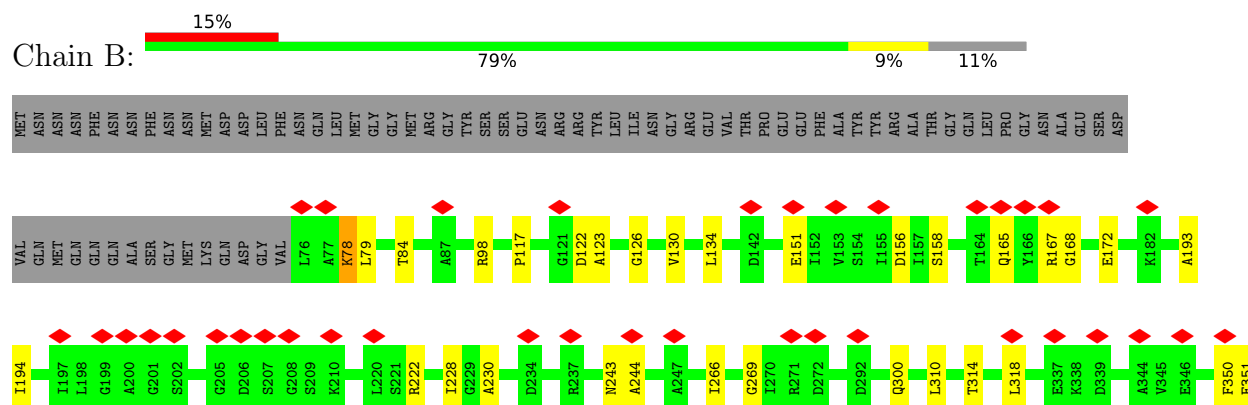
3 Residue-property plots

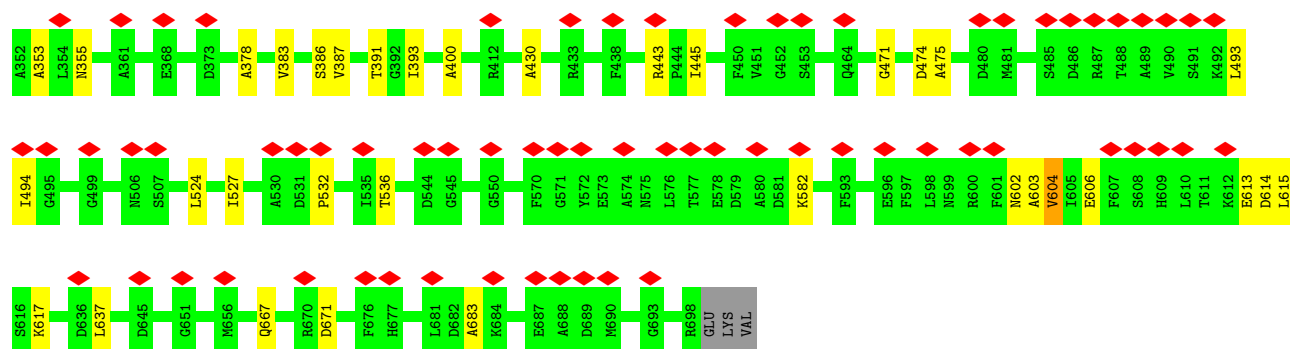
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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, ATP-binding subunit

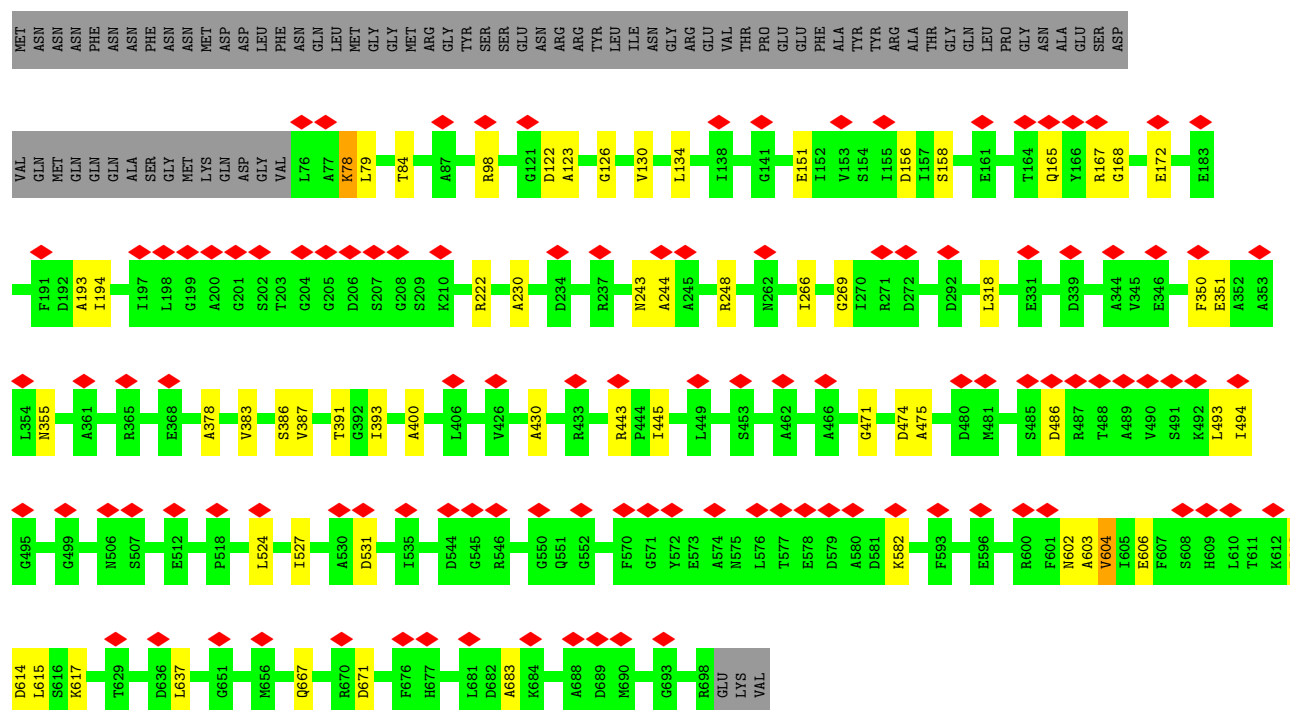
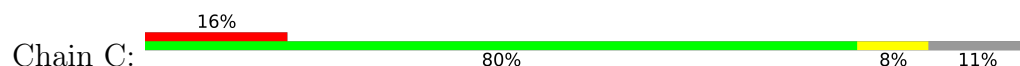


- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

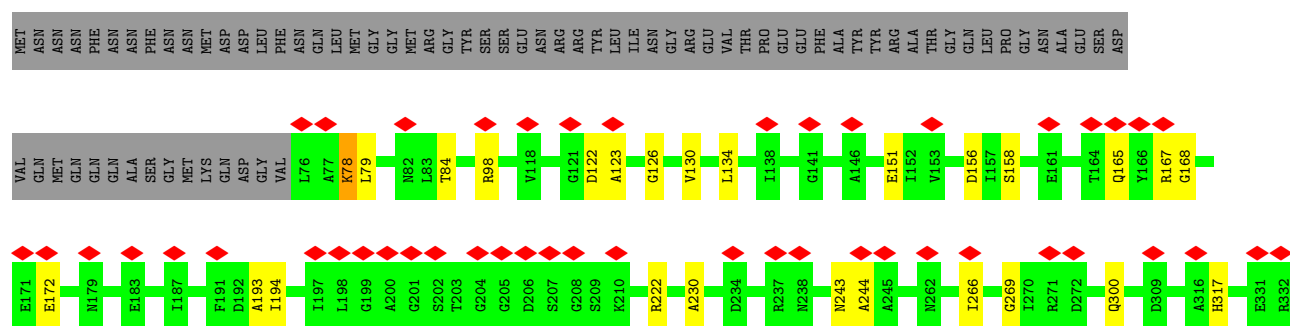
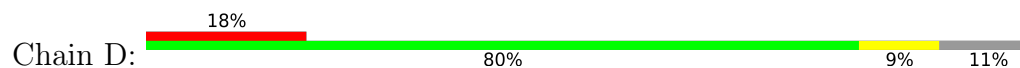


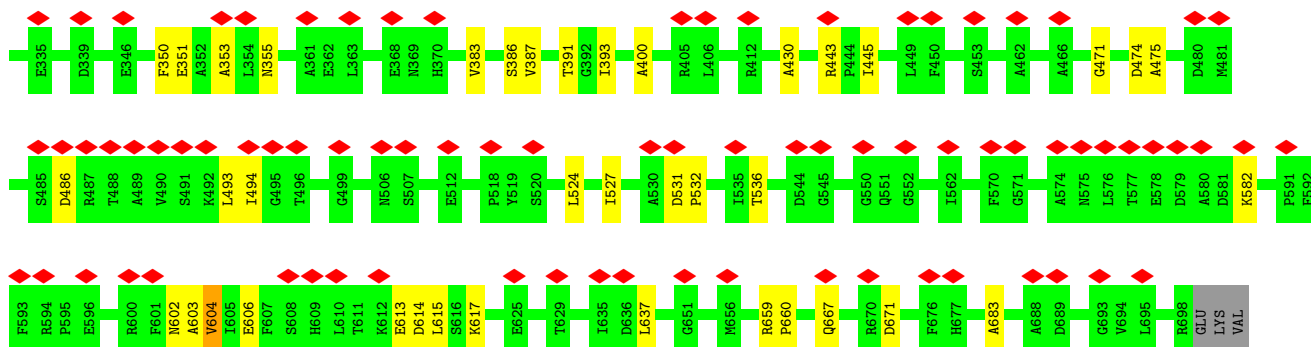


- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit



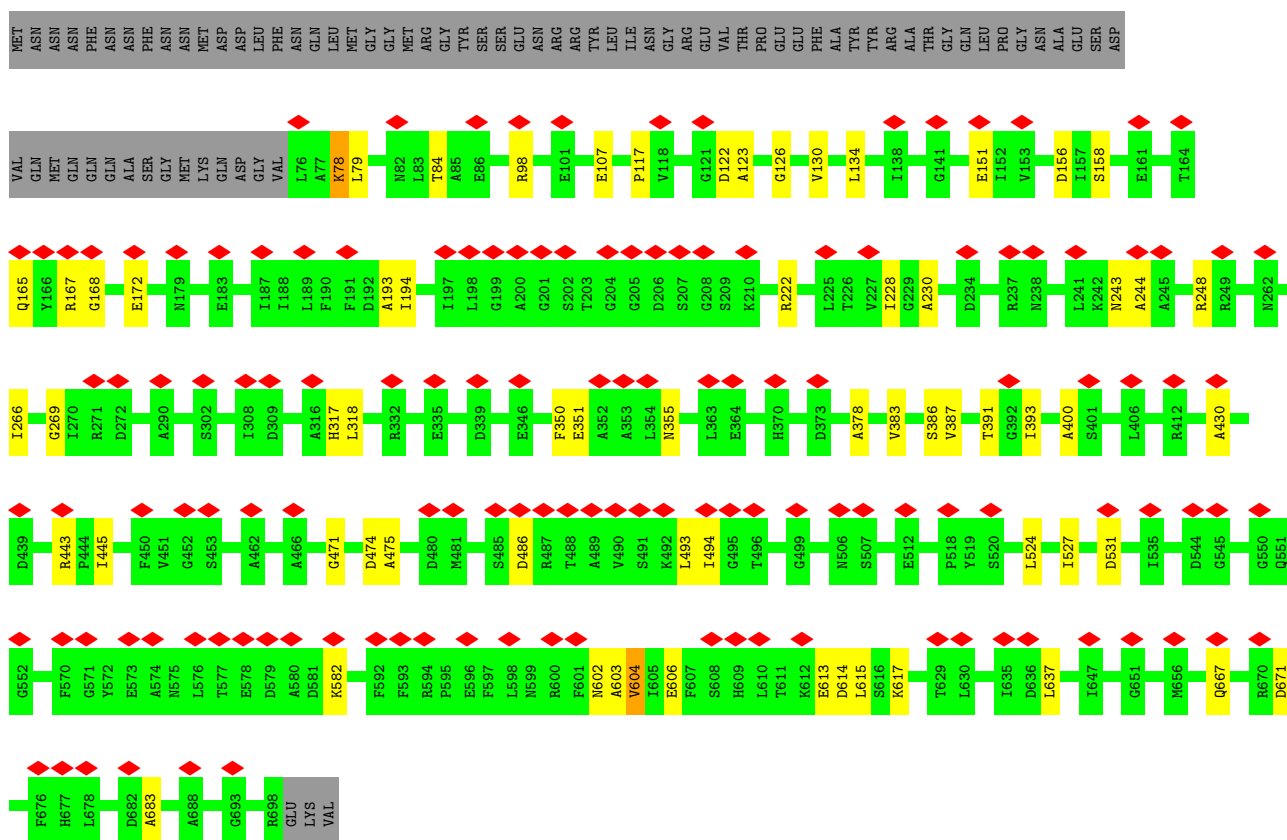
- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit





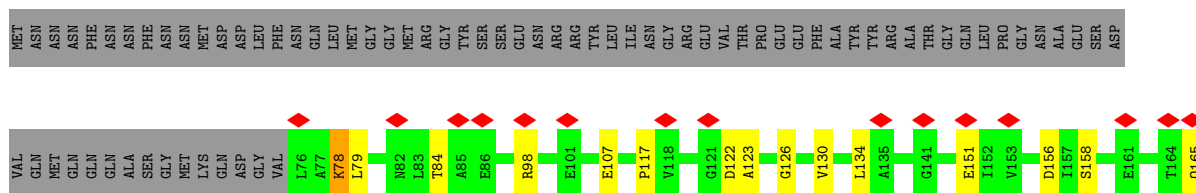
- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

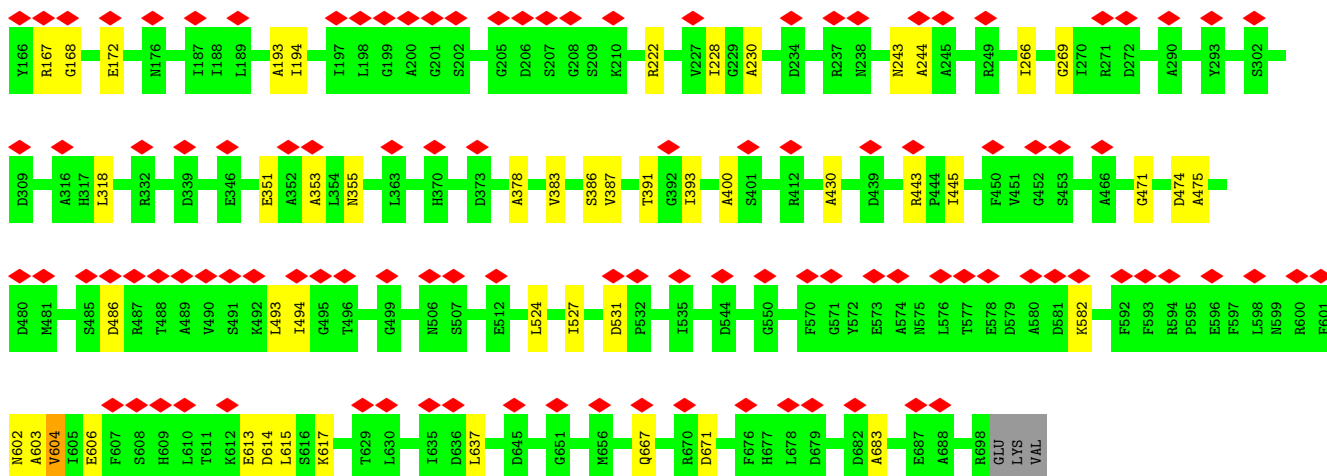
Chain E: 19% 80% 9% 11%



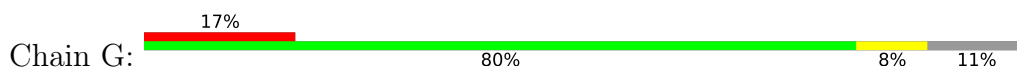
- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

Chain F: 18% 80% 9% 11%





- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit



MET ASN ASN ASN PHE ASN PHE ASN PHE ASN MET ASN MET ASP LEU PHE ASN GLN LEU MET GLY GLY MET ARG GLY TYR SER SER GLU ASN ARG ARG TYR LEU ASN ILE GLY ARG GLU VAL THR PRO GLU PHE ALA TYR ARG ALA THR GLY LEU PRO GLY ASN ALA GLU SER ASP

VAL GLN MET GLN GLN GLN ALA SER GLY LYS MET GLN ASP GLY VAL L76 A77 K78 L79 T84 A85 E86 R98 G121 D122 A123 G126 V130 L134 D142 E151 I152 V153 S154 I155 D156 I157 S158 T164 Q165 Y166 R167 G168 E172 N176 A193 I194

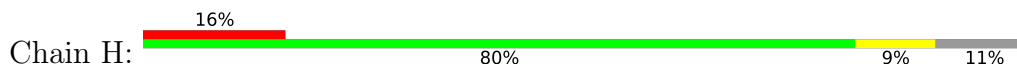
I197 L198 G199 A200 G201 S202 G205 D206 S207 G208 S209 K210 R222 V227 A230 D234 R237 N243 A244 A245 R249 I266 G269 I270 R271 D272 A290 Y293 S302 D309 A316 H317 R318 R332 D339 E346 E351 A352 A353 N355 L363 H370 D373 A378 V383 S386 V387 T391 G392 I393 A400 S401 R412 A430 D439 R443 P444 I445 F450 V451 G452 S453 A466 G471 D474 A475

N355 L363 H370 D373 V383 S386 V387 E388 R389 K390 T391 I393 A400 D408 R412 A430 R443 P444 I445 F450 V451 G452 S453 Q464 G471 D474 A475 D480 H481 S486 D487 T488 A489 V490 S491 K492 I494 F350 E351 A352 A353 G499

D504 D505 H506 S507 E512 R513 L524 I527 D531 P532 I535 L542 D543 D544 G545 G550 F570 G571 A574 N575 L576 T577 E578 D579 A580 K582 F592 F593 E596 F597 L598 N599 R600 F601 A603 V604 I605 E606 F607 S608 H609 L610 T611 K612 D614

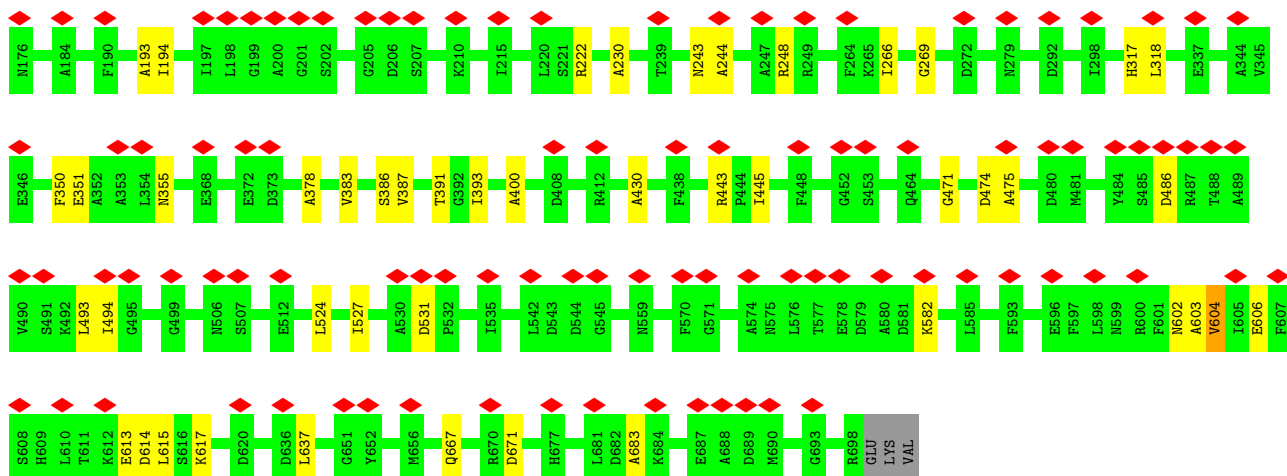
L615 S616 K617 D620 T629 T635 D636 L637 D645 G651 K656 Q667 R670 D671 D679 H680 L681 D682 A683 E687 A688 D689 R698 GLU LYS VAL

- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

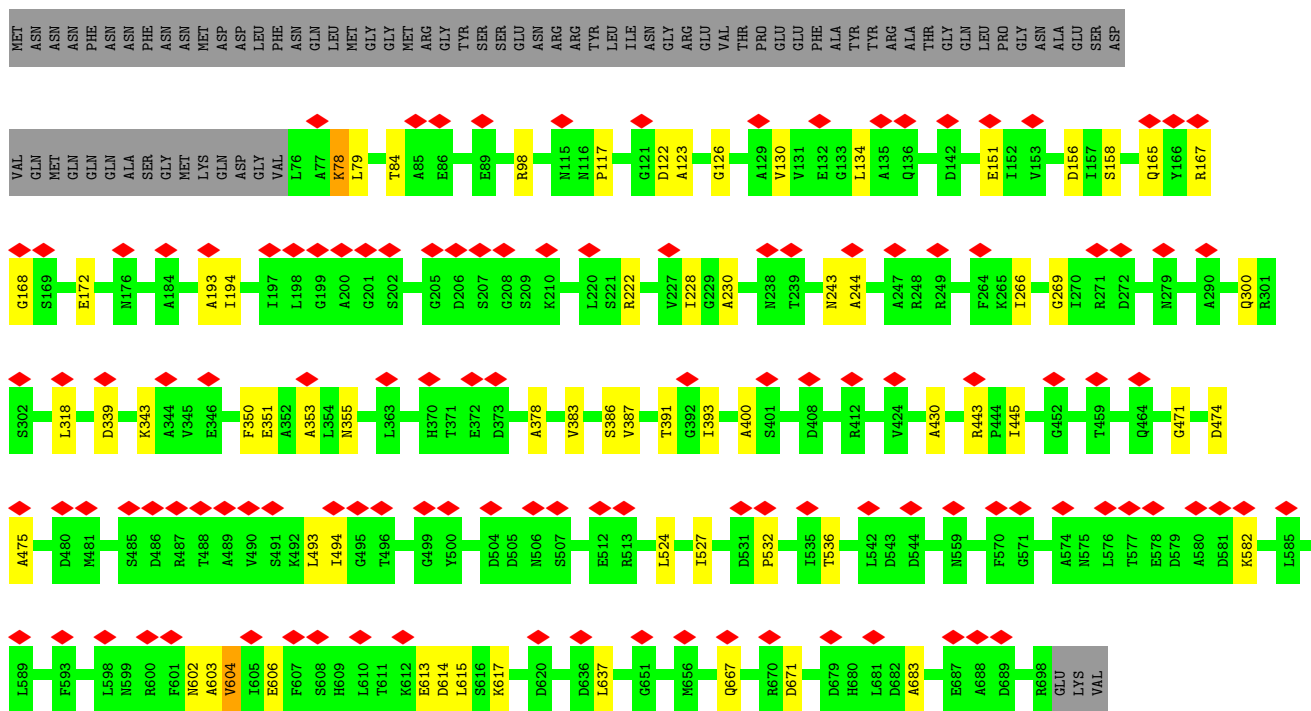
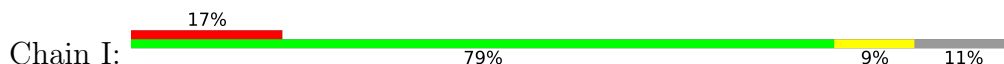


MET ASN ASN ASN PHE ASN PHE ASN PHE ASN MET ASN MET ASP LEU PHE ASN GLN LEU MET GLY GLY MET ARG GLY TYR SER SER GLU ASN ARG ARG TYR LEU ILE ASN GLY ARG GLU VAL THR PRO GLU PHE ALA TYR ARG ALA THR GLY LEU PRO GLY ASN ALA GLU SER ASP

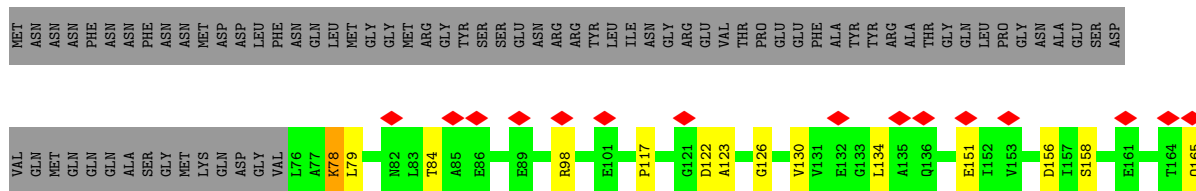
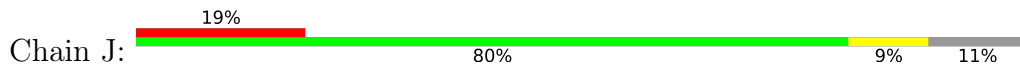
VAL GLN MET GLN GLN GLN ALA SER GLY LYS MET GLN ASP GLY VAL L76 A77 K78 L79 T84 E89 R98 S110 N115 G121 D122 A123 G126 A129 V130 L134 D142 E151 I152 V153 D156 I157 S158 T164 Q165 Y166 R167 G168 S169 E172

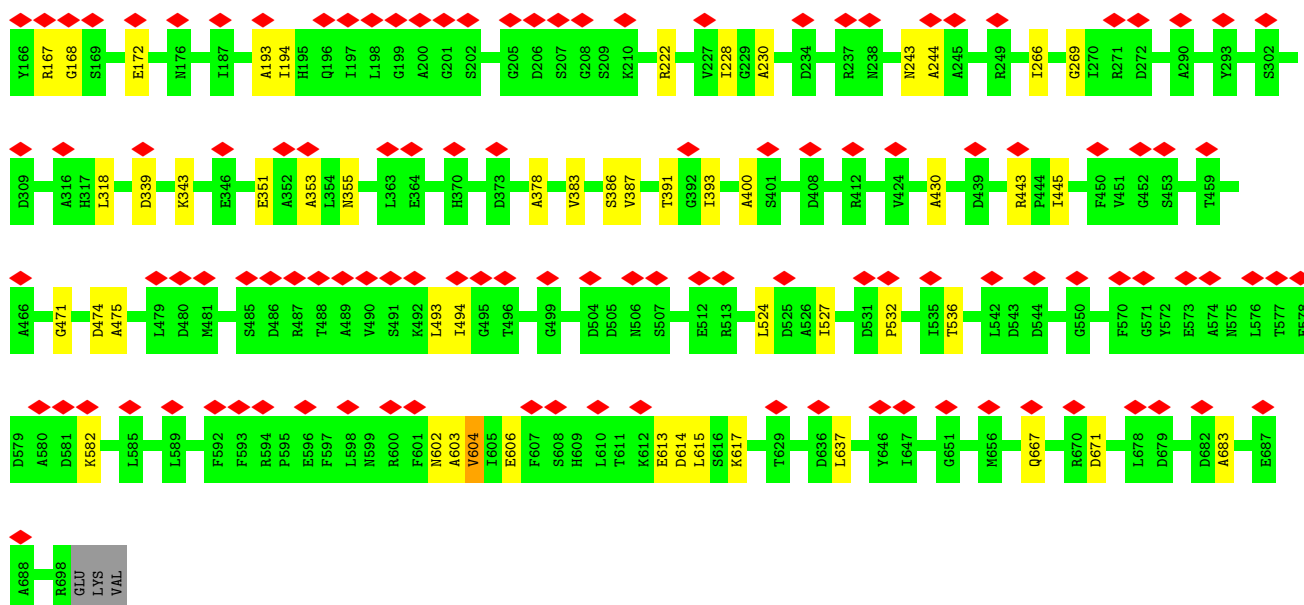


- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit



- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

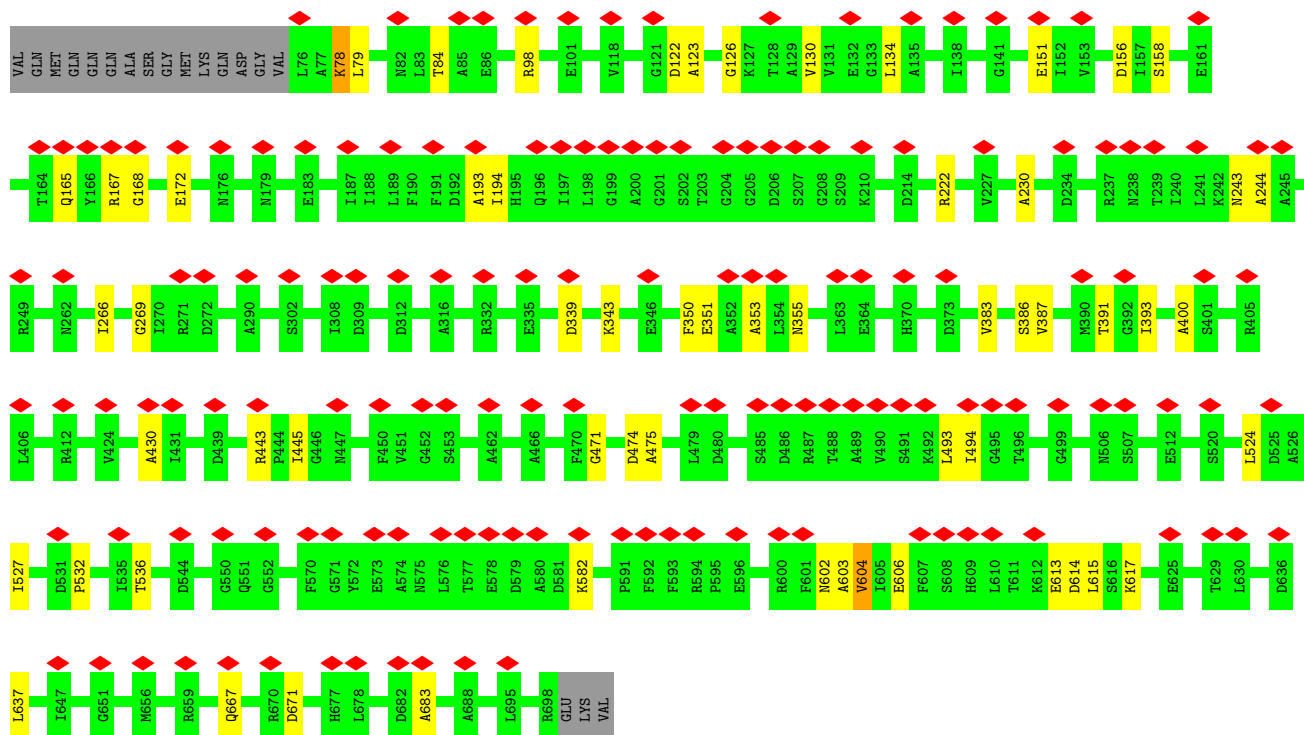




- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

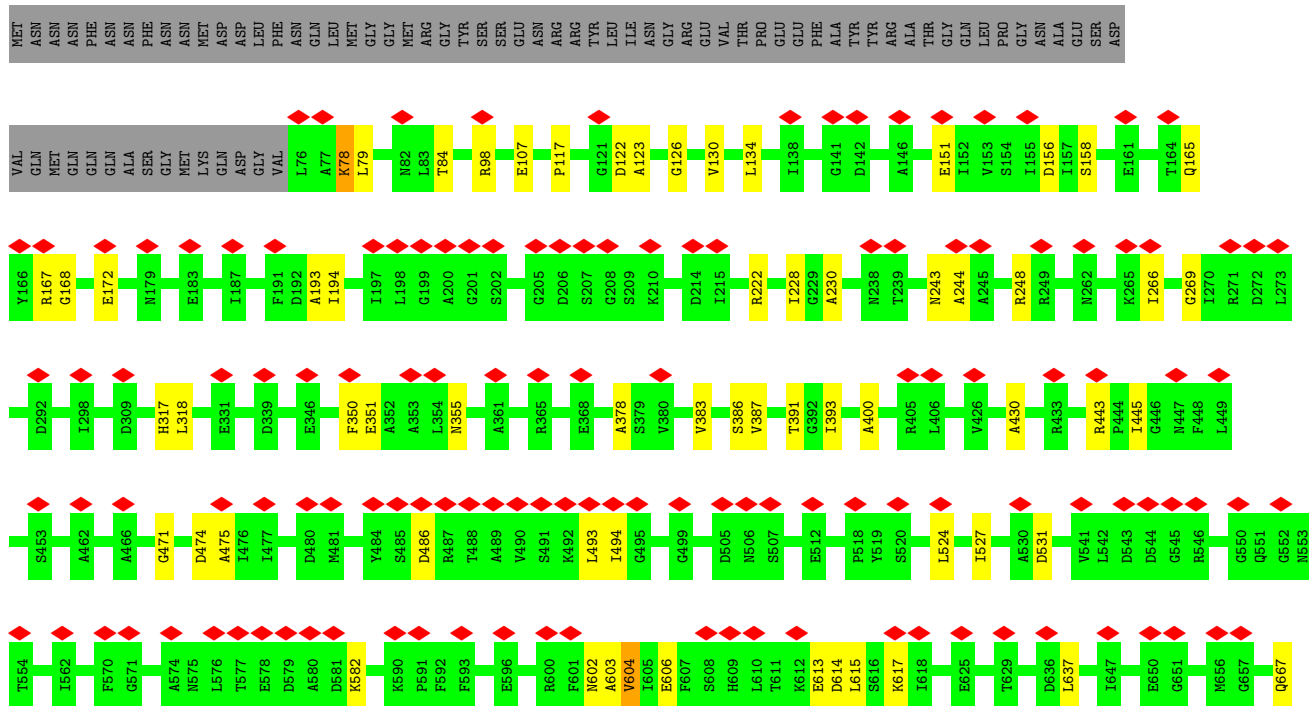
Chain K: 22% 80% 8% 11%

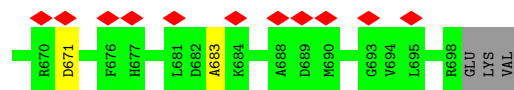
MET ASN ASN ASN PHE ASN ASN PHE ASN MET MET ASP ASP LEU PHE PHE GLN LEU MET MET GLY ARG MET F601 N602 A603 V604 I605 E606 F607 S608 H609 L610 L611 K612 E613 L614 L615 S616 K617 T629 D636 L637 Y646 I647 G651 M656 Q667 R670 D671 L678 D679 D682 A683 E687



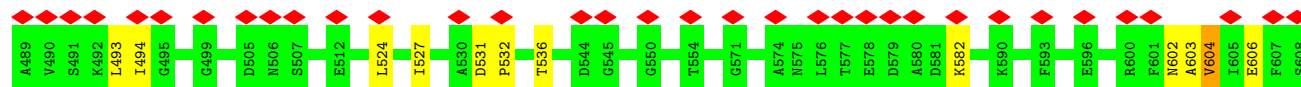
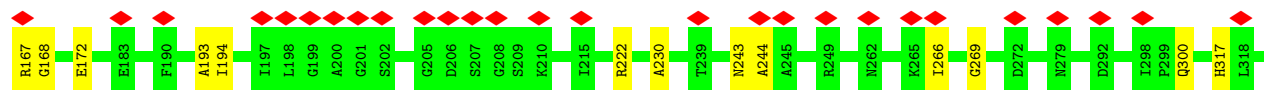
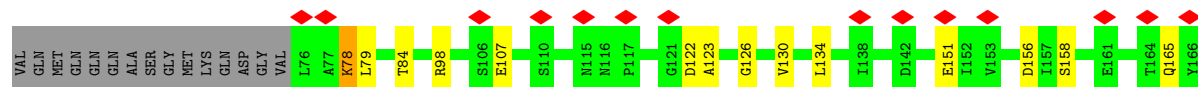
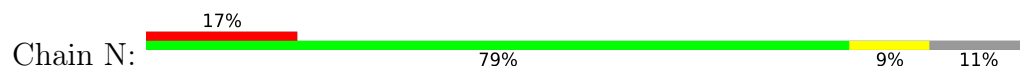
- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit

Chain L: 22% 79% 9% 11%





- Molecule 1: ATP-dependent Clp protease, ATP-binding subunit



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	52689	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.406	Depositor
Minimum map value	-1.516	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.097	Depositor
Recommended contour level	0.2	Depositor
Map size ($\text{\AA}$)	336.0, 336.0, 336.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.4, 1.4, 1.4	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	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.27	0/4883	0.59	7/6603 (0.1%)
1	B	0.27	0/4883	0.59	7/6603 (0.1%)
1	C	0.27	0/4883	0.59	7/6603 (0.1%)
1	D	0.27	0/4883	0.59	7/6603 (0.1%)
1	E	0.27	0/4883	0.59	7/6603 (0.1%)
1	F	0.27	0/4883	0.59	7/6603 (0.1%)
1	G	0.27	0/4883	0.59	8/6603 (0.1%)
1	H	0.27	0/4883	0.59	7/6603 (0.1%)
1	I	0.27	0/4883	0.59	7/6603 (0.1%)
1	J	0.27	0/4883	0.59	7/6603 (0.1%)
1	K	0.27	0/4883	0.59	7/6603 (0.1%)
1	L	0.27	0/4883	0.59	7/6603 (0.1%)
1	M	0.27	0/4883	0.59	7/6603 (0.1%)
1	N	0.27	0/4883	0.59	8/6603 (0.1%)
All	All	0.27	0/68362	0.59	100/92442 (0.1%)

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	A	0	3
1	B	0	3
1	C	0	3
1	D	0	3
1	E	0	3
1	F	0	3
1	G	0	3
1	H	0	3
1	I	0	3
1	J	0	3
1	K	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	3
1	M	0	3
1	N	0	3
All	All	0	42

There are no bond length outliers.

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	LYS	CA-C-N	8.19	136.43	121.70
1	A	78	LYS	C-N-CA	8.19	136.43	121.70
1	L	78	LYS	CA-C-N	8.17	136.41	121.70
1	L	78	LYS	C-N-CA	8.17	136.41	121.70
1	E	78	LYS	CA-C-N	8.17	136.41	121.70

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	194	ILE	Peptide
1	A	400	ALA	Peptide
1	A	603	ALA	Peptide
1	B	194	ILE	Peptide
1	B	400	ALA	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	4824	4832	4841	31	0
1	B	4824	4832	4841	35	0
1	C	4824	4832	4841	32	0
1	D	4824	4832	4841	35	0
1	E	4824	4832	4841	35	0
1	F	4824	4832	4841	33	0
1	G	4824	4832	4841	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	4824	4832	4841	33	0
1	I	4824	4832	4841	35	0
1	J	4824	4832	4841	33	0
1	K	4824	4832	4841	32	0
1	L	4824	4832	4841	35	0
1	M	4824	4832	4841	35	0
1	N	4824	4832	4841	36	0
All	All	67536	67648	67774	410	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 3.

The worst 5 of 410 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:A:582:LYS:NZ	1:A:606:GLU:OE2	2.27	0.68
1:I:582:LYS:NZ	1:I:606:GLU:OE2	2.27	0.68
1:B:582:LYS:NZ	1:B:606:GLU:OE2	2.27	0.68
1:J:582:LYS:NZ	1:J:606:GLU:OE2	2.27	0.68
1:K:582:LYS:NZ	1:K:606:GLU:OE2	2.27	0.68

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 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	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43 77
1	B	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43 77
1	C	621/701 (89%)	578 (93%)	42 (7%)	1 (0%)	43 77
1	D	621/701 (89%)	578 (93%)	42 (7%)	1 (0%)	43 77

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	F	621/701 (89%)	578 (93%)	42 (7%)	1 (0%)	43	77
1	G	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	H	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	I	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	J	621/701 (89%)	578 (93%)	42 (7%)	1 (0%)	43	77
1	K	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	L	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	M	621/701 (89%)	579 (93%)	41 (7%)	1 (0%)	43	77
1	N	621/701 (89%)	578 (93%)	42 (7%)	1 (0%)	43	77
All	All	8694/9814 (89%)	8101 (93%)	579 (7%)	14 (0%)	44	77

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	604	VAL
1	B	604	VAL
1	C	604	VAL
1	D	604	VAL
1	E	604	VAL

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 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	520/586 (89%)	520 (100%)	0	100	100
1	B	520/586 (89%)	520 (100%)	0	100	100
1	C	520/586 (89%)	520 (100%)	0	100	100
1	D	520/586 (89%)	520 (100%)	0	100	100
1	E	520/586 (89%)	520 (100%)	0	100	100
1	F	520/586 (89%)	520 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	520/586 (89%)	520 (100%)	0	100	100
1	H	520/586 (89%)	520 (100%)	0	100	100
1	I	520/586 (89%)	520 (100%)	0	100	100
1	J	520/586 (89%)	520 (100%)	0	100	100
1	K	520/586 (89%)	520 (100%)	0	100	100
1	L	520/586 (89%)	520 (100%)	0	100	100
1	M	520/586 (89%)	520 (100%)	0	100	100
1	N	520/586 (89%)	520 (100%)	0	100	100
All	All	7280/8204 (89%)	7280 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	369	ASN
1	J	667	GLN
1	H	667	GLN
1	I	667	GLN
1	K	369	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

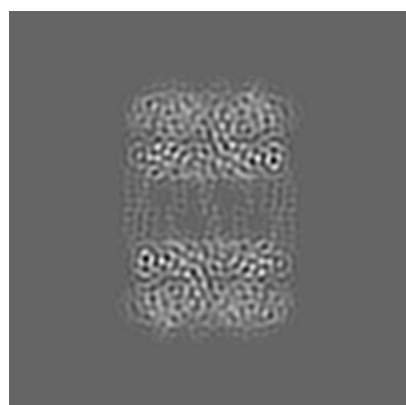
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0965. These allow visual inspection of the internal detail of the map and identification of artifacts.

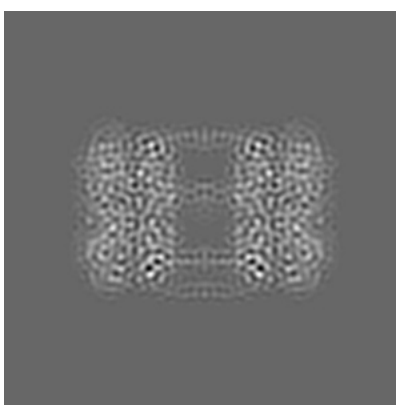
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

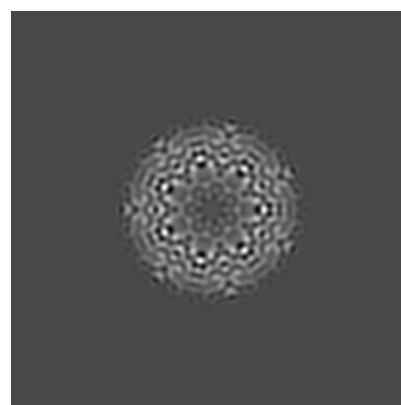
6.1.1 Primary map



X



Y



Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

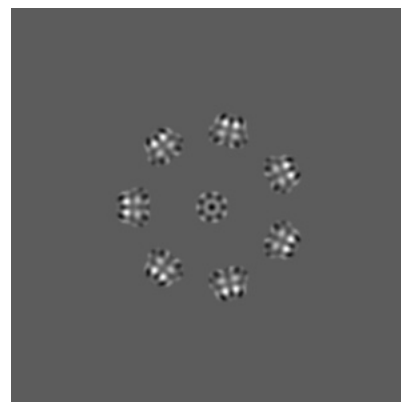
6.2.1 Primary map



X Index: 120



Y Index: 120



Z Index: 120

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 92



Y Index: 143

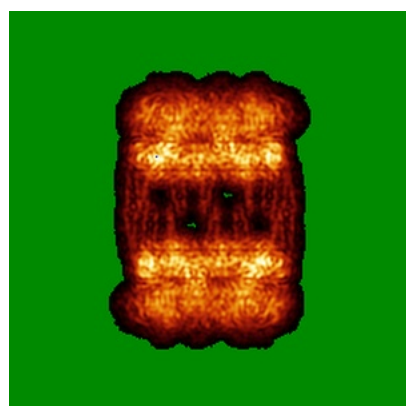


Z Index: 152

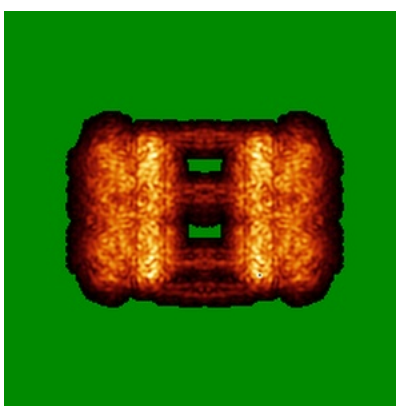
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

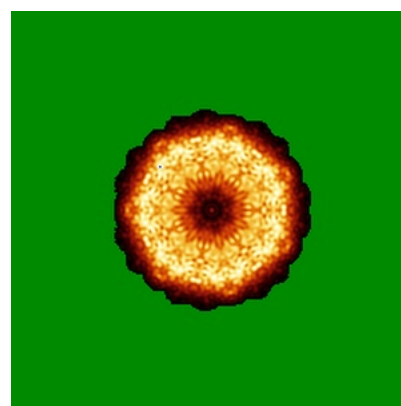
6.4.1 Primary map



X



Y

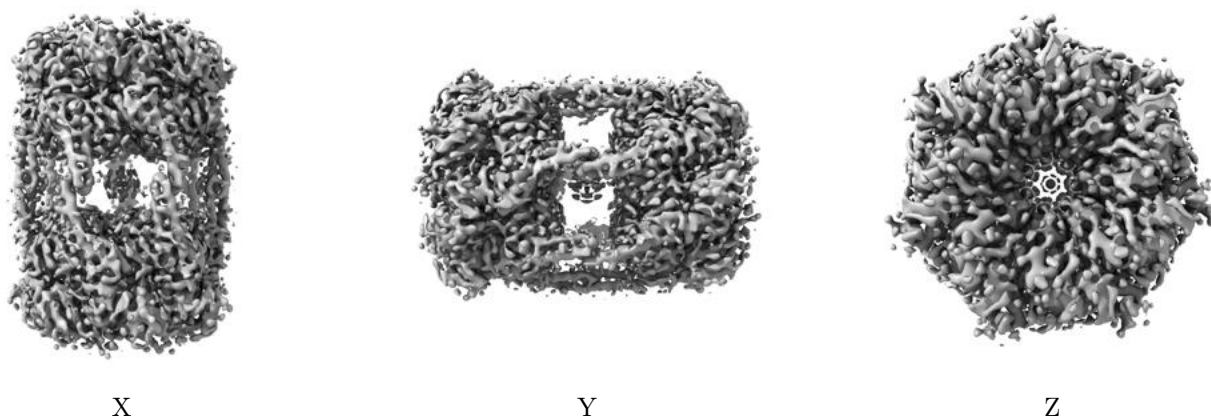


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

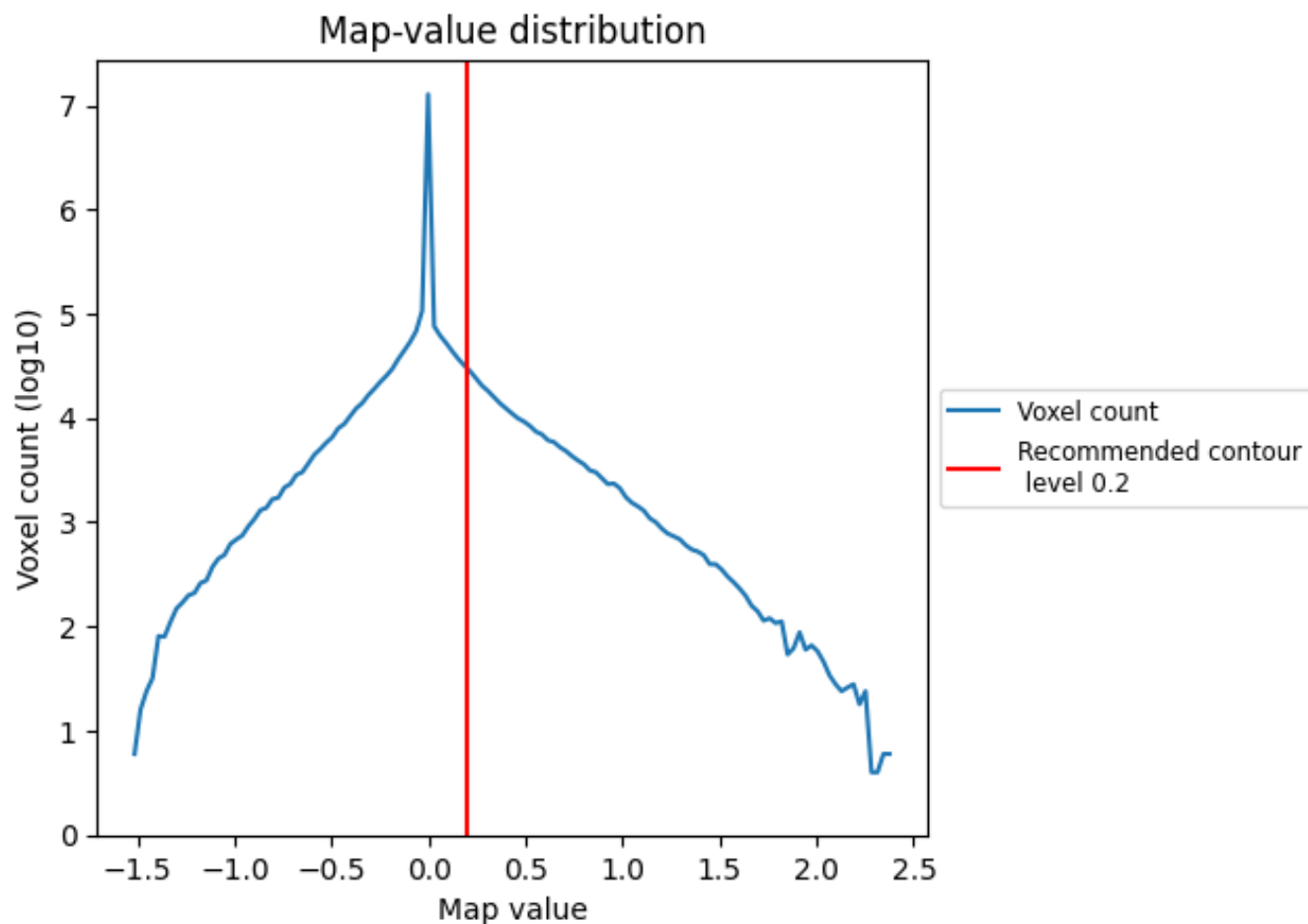
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

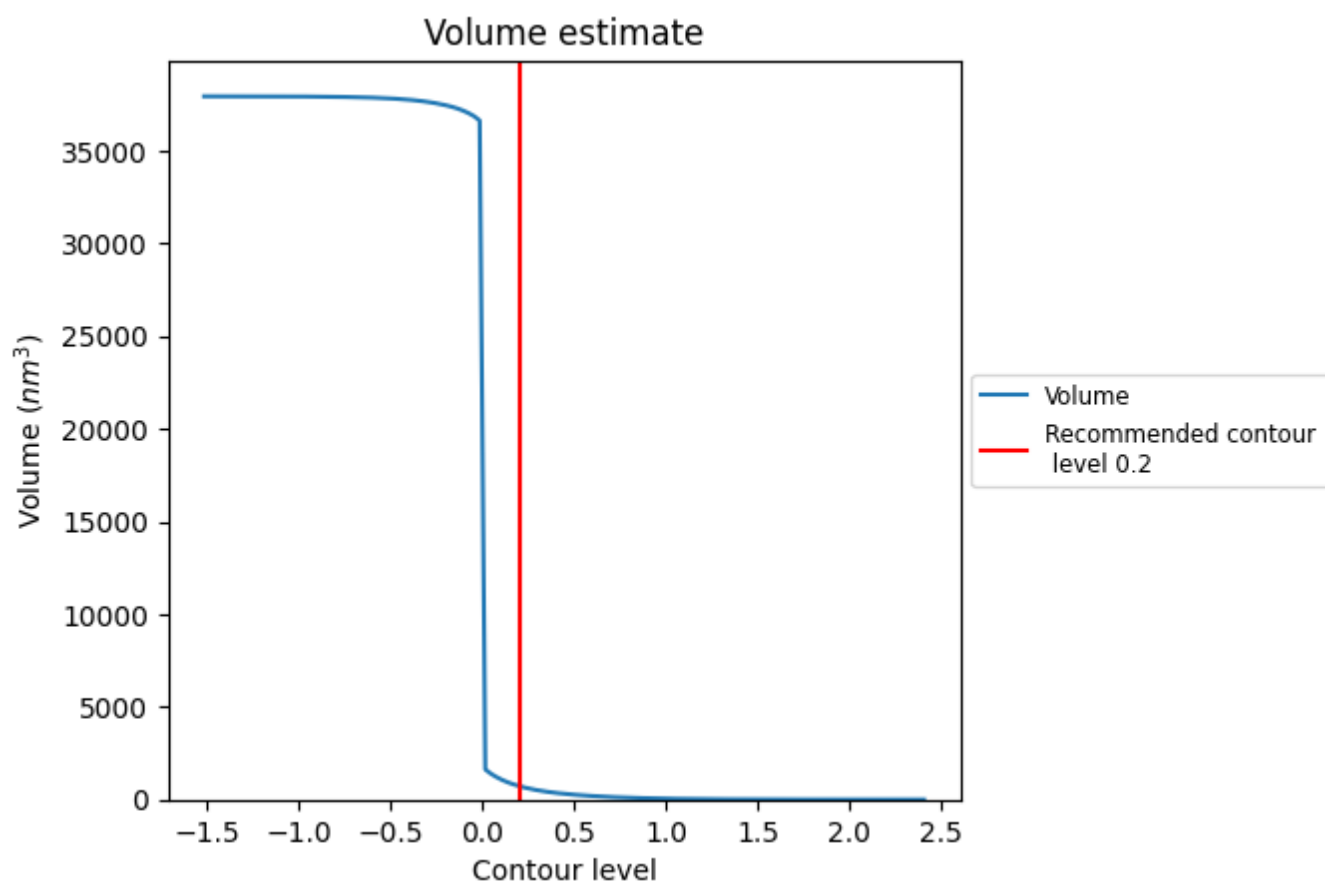
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

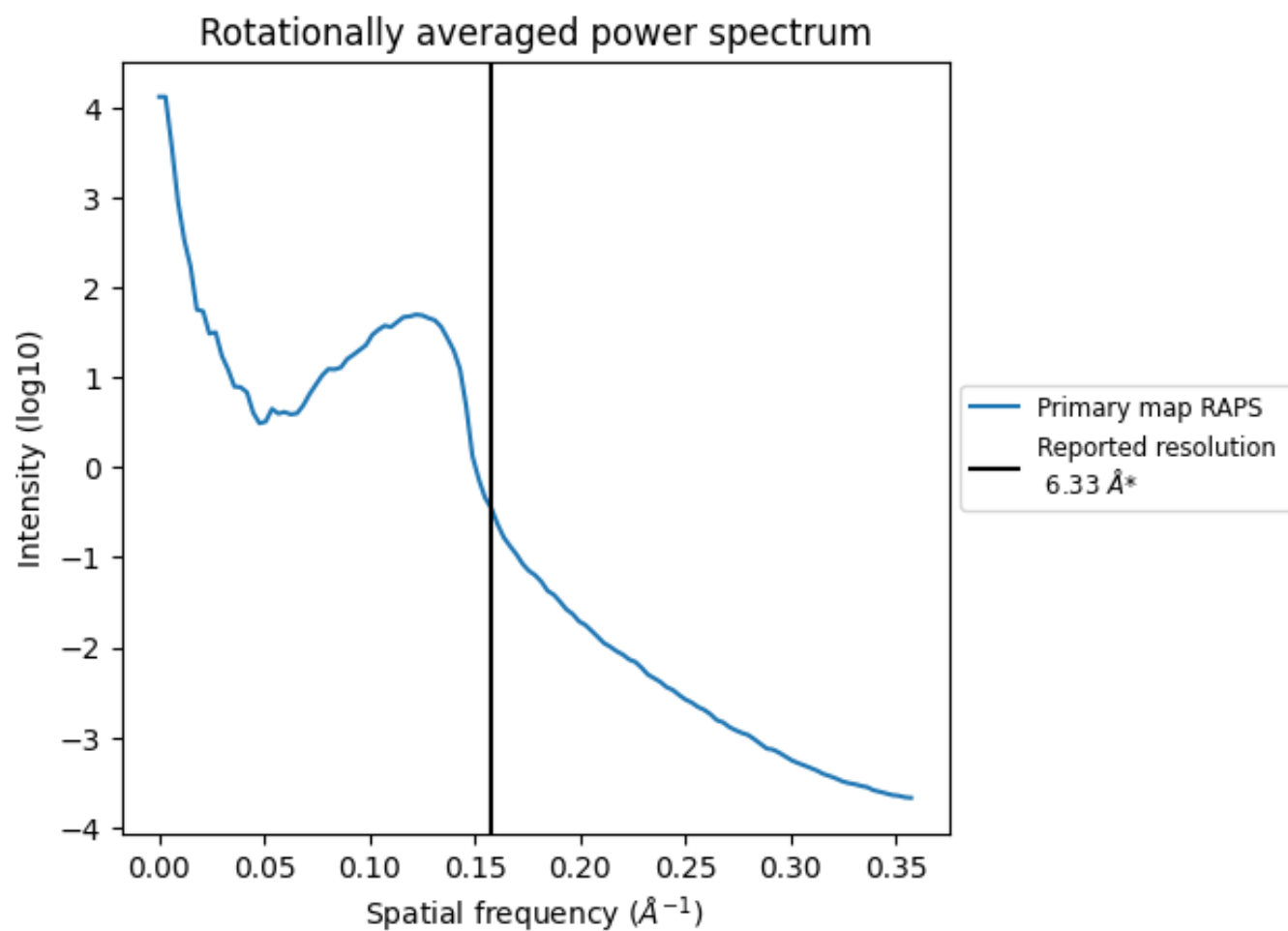
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 728 nm³; this corresponds to an approximate mass of 658 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.158 Å⁻¹

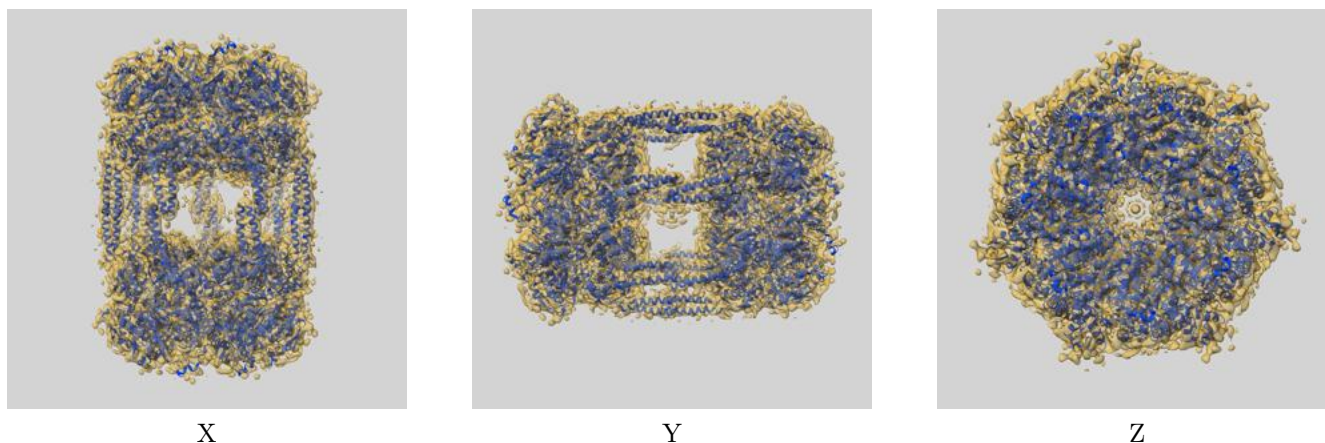
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

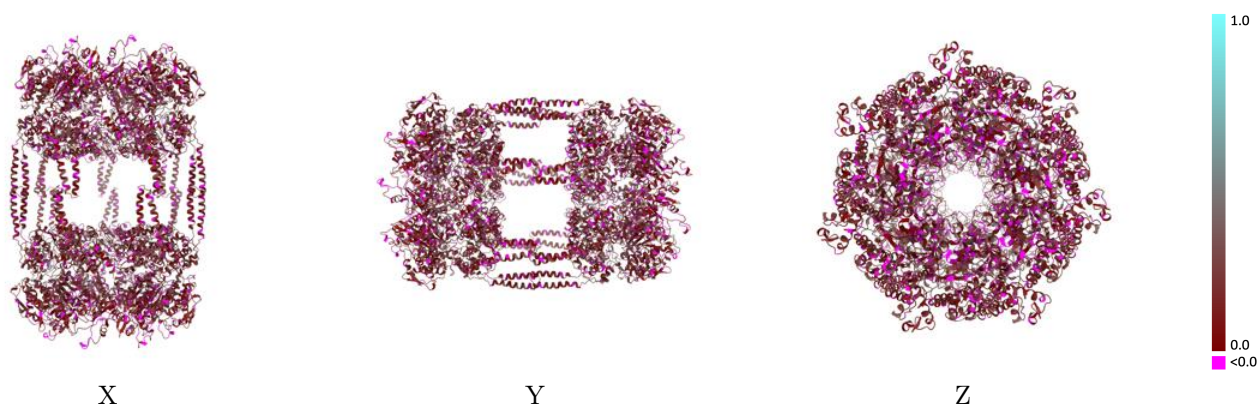
This section contains information regarding the fit between EMDB map EMD-0965 and PDB model 6LSY. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



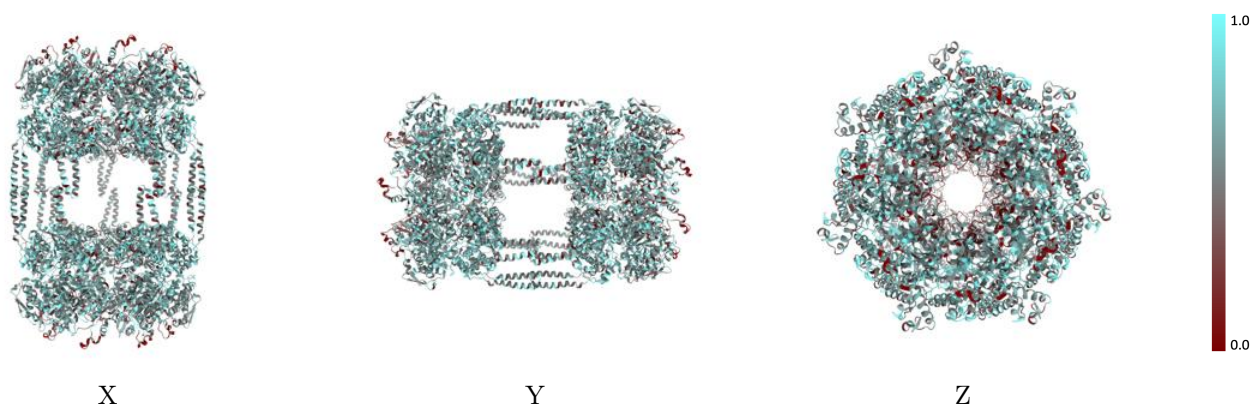
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



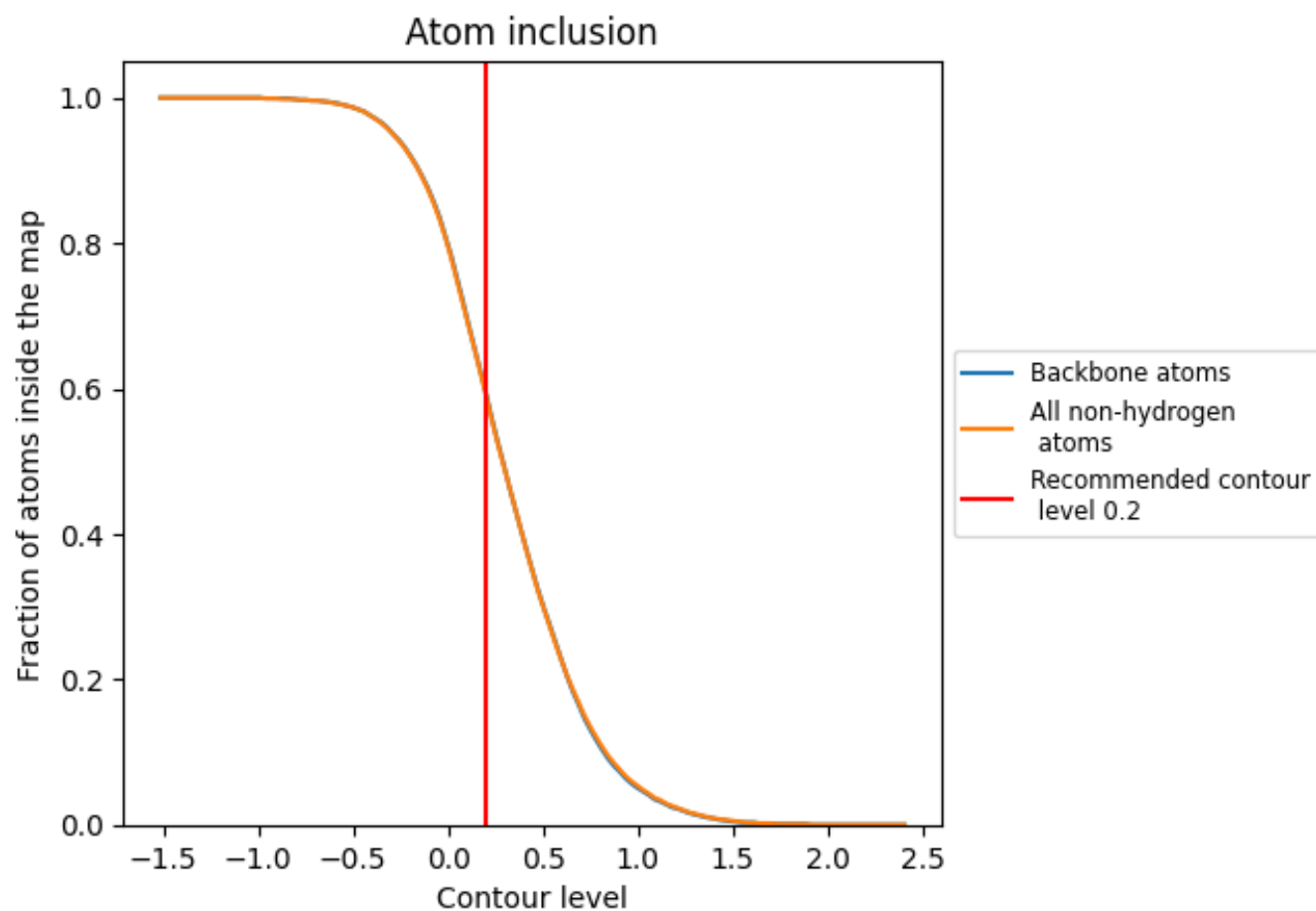
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 59% of all backbone atoms, 59% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5910	0.1520
A	0.6050	0.1580
B	0.6130	0.1580
C	0.6070	0.1530
D	0.5950	0.1520
E	0.5950	0.1520
F	0.5970	0.1550
G	0.6020	0.1590
H	0.5960	0.1550
I	0.5960	0.1530
J	0.5880	0.1500
K	0.5820	0.1460
L	0.5770	0.1440
M	0.5900	0.1460
N	0.5990	0.1510

1.0

0.0

<0.0