



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 07:12 PM UTC

PDB ID : 7VWX / pdb_00007vwx
EMDB ID : EMD-32164
Title : CryoEM structure of football-shaped GroEL:ES2 with RuBisCO
Authors : Kim, H.; Roh, S.H.
Deposited on : 2021-11-12
Resolution : 7.60 Å(reported)
Based on initial models : 4PKO, 9RUB

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

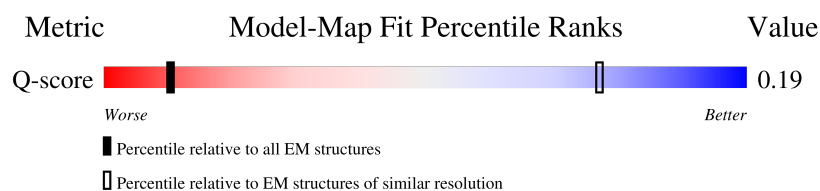
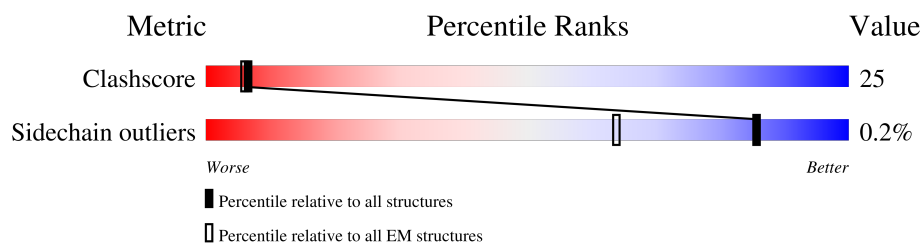
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.60 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	389 (7.10 - 8.10)

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	1	97	 44% 55% .
1	2	97	 46% 53% .
1	O	97	 51% 45% ..
1	P	97	 57% 43%
1	Q	97	 43% 54% ..

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Mol	Chain	Length	Quality of chain
1	R	97	5% 52% 48%
1	S	97	53% 46%
1	T	97	6% 54% 46%
1	U	97	57% 43%
1	V	97	60% 40%
1	W	97	44% 55%
1	X	97	51% 49%
1	Y	97	52% 46%
1	Z	97	43% 55%
2	A	548	55% 40%
2	B	548	53% 42%
2	C	548	53% 42%
2	D	548	48% 47%
2	E	548	49% 46%
2	F	548	51% 44%
2	G	548	46% 49%
2	H	548	55% 41%
2	I	548	56% 40%
2	J	548	49% 47%
2	K	548	53% 42%
2	L	548	50% 45%
2	M	548	50% 45%
2	N	548	51% 45%
3	a	466	23% 64% 34%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 67599 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 Co-chaperonin GroES.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	2	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	O	95	Total	C	N	O	S	0	0
			711	445	124	141	1		
1	P	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	Q	96	Total	C	N	O	S	0	0
			719	449	126	143	1		
1	R	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	S	96	Total	C	N	O	S	0	0
			719	449	126	143	1		
1	T	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	U	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	V	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	W	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	X	97	Total	C	N	O	S	0	0
			727	454	127	144	2		
1	Y	96	Total	C	N	O	S	0	0
			722	451	126	143	2		
1	Z	95	Total	C	N	O	S	0	0
			713	446	125	140	2		

- Molecule 2 is a protein called Chaperonin GroEL.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	C	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	D	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	E	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	F	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	G	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	H	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	I	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	J	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	K	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	L	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	M	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		
2	N	524	Total	C	N	O	S	0	0
			3855	2397	665	773	20		

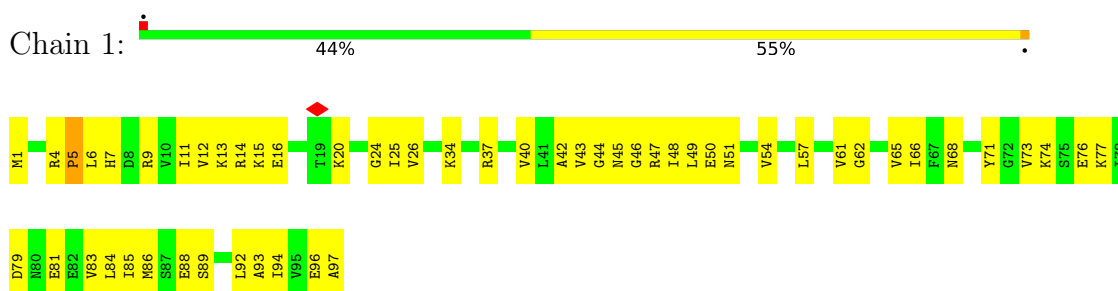
- Molecule 3 is a protein called Ribulose biphosphate carboxylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	a	459	Total	C	N	O	S	0	0
			3502	2213	613	658	18		

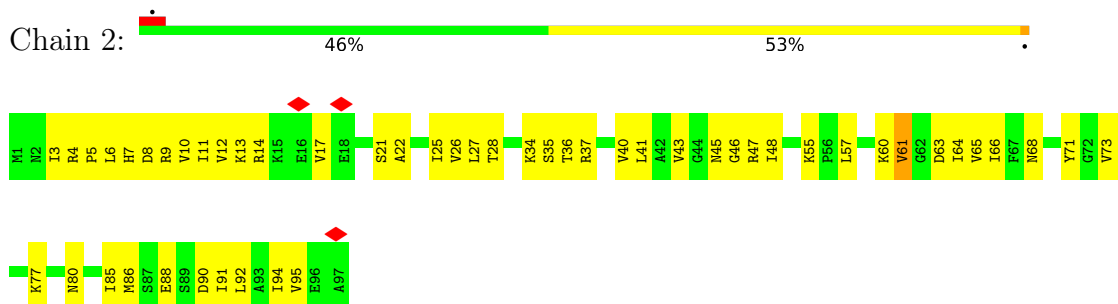
3 Residue-property plots [i](#)

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 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.

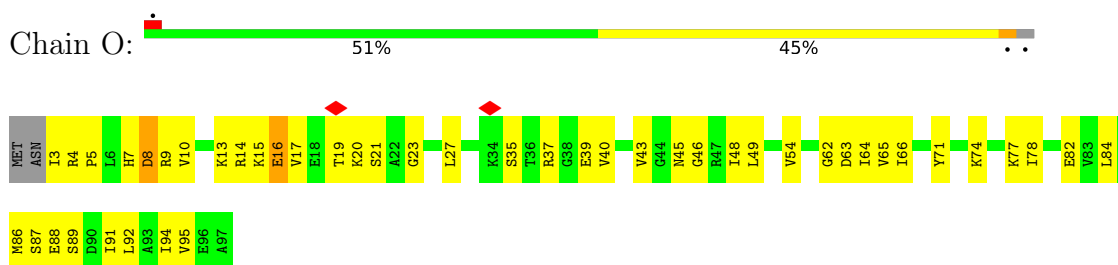
- Molecule 1: Co-chaperonin GroES



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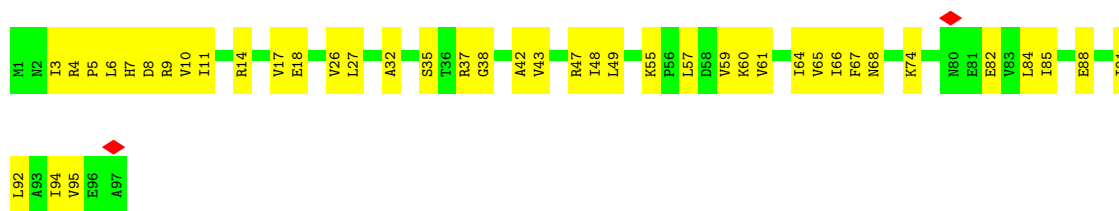


- Molecule 1: Co-chaperonin GroES

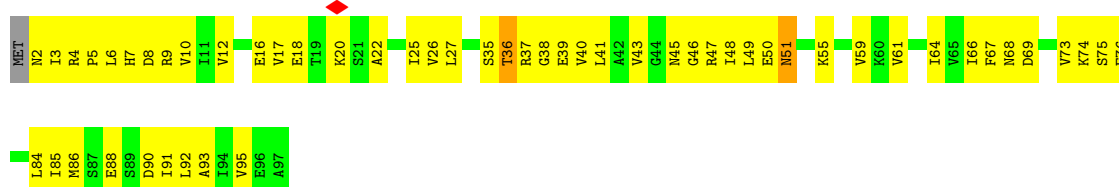


- Molecule 1: Co-chaperonin GroES

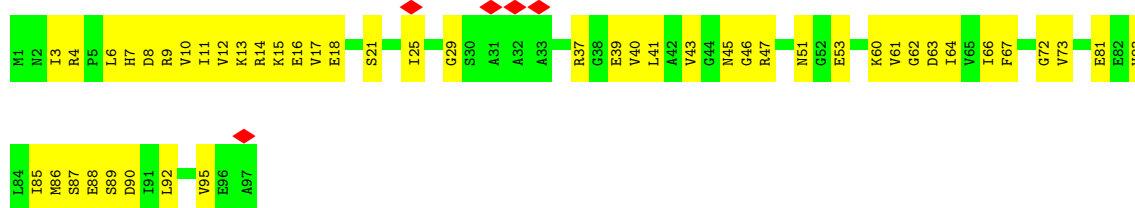




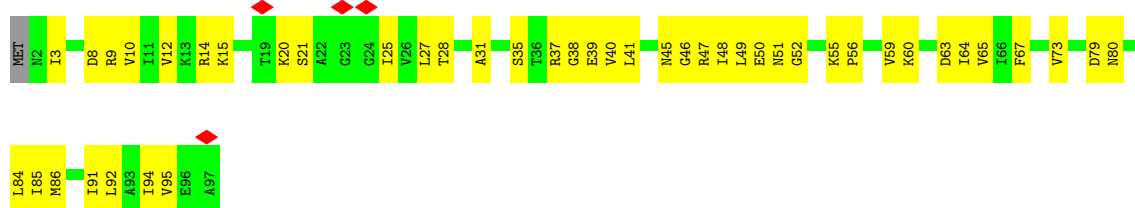
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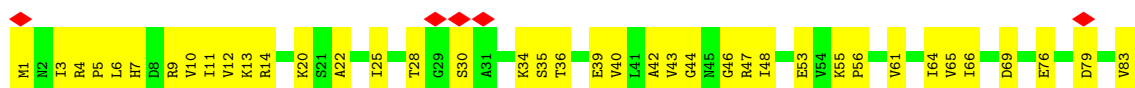
- Molecule 1: Co-chaperonin GroES

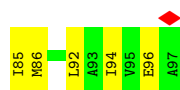


- Molecule 1: Co-chaperonin GroES

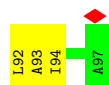


- Molecule 1: Co-chaperonin GroES





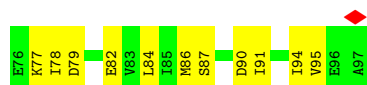
- Molecule 1: Co-chaperonin GroES



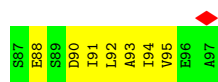
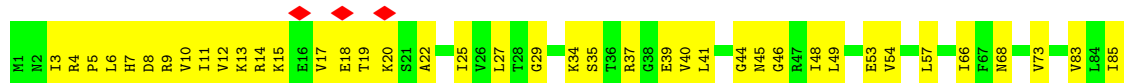
- Molecule 1: Co-chaperonin GroES



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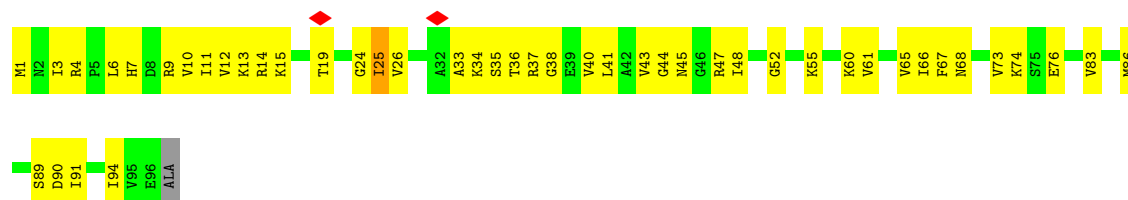


- Molecule 1: Co-chaperonin GroES

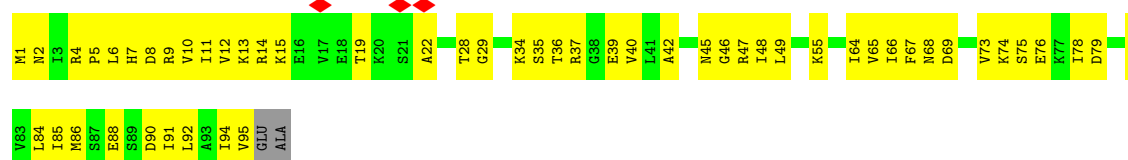


- Molecule 1: Co-chaperonin GroES

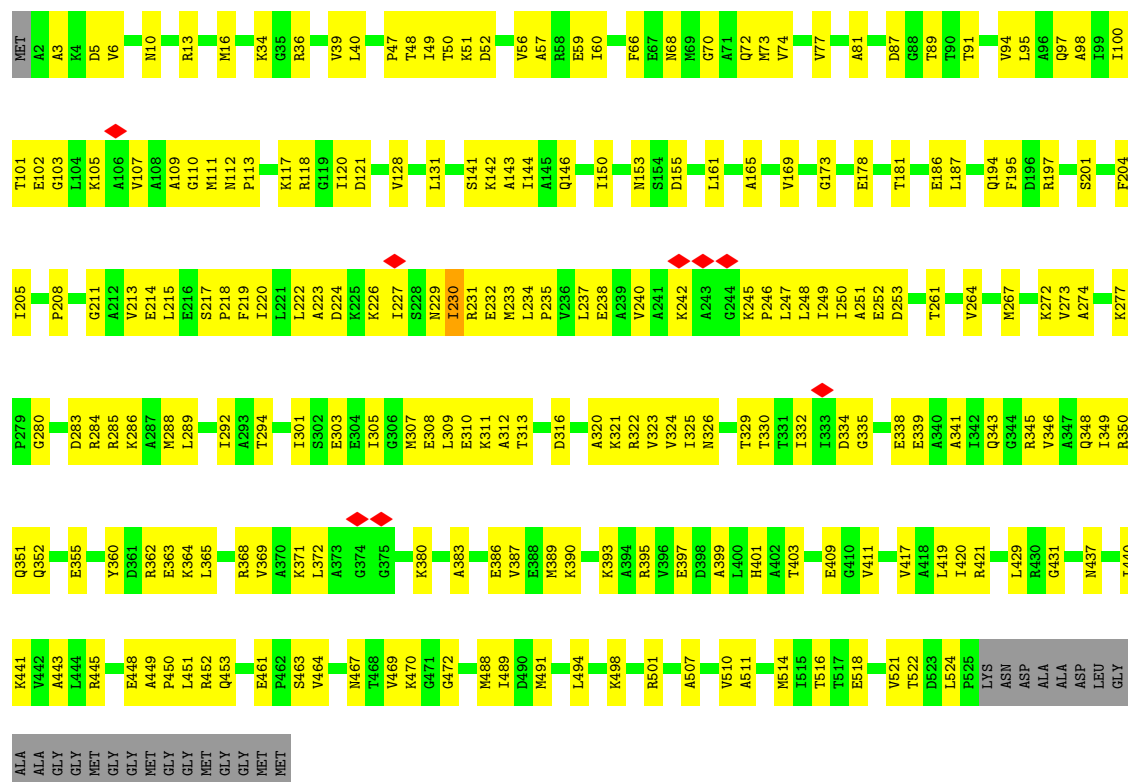




• Molecule 1: Co-chaperonin GroES



• Molecule 2: Chaperonin GroEL



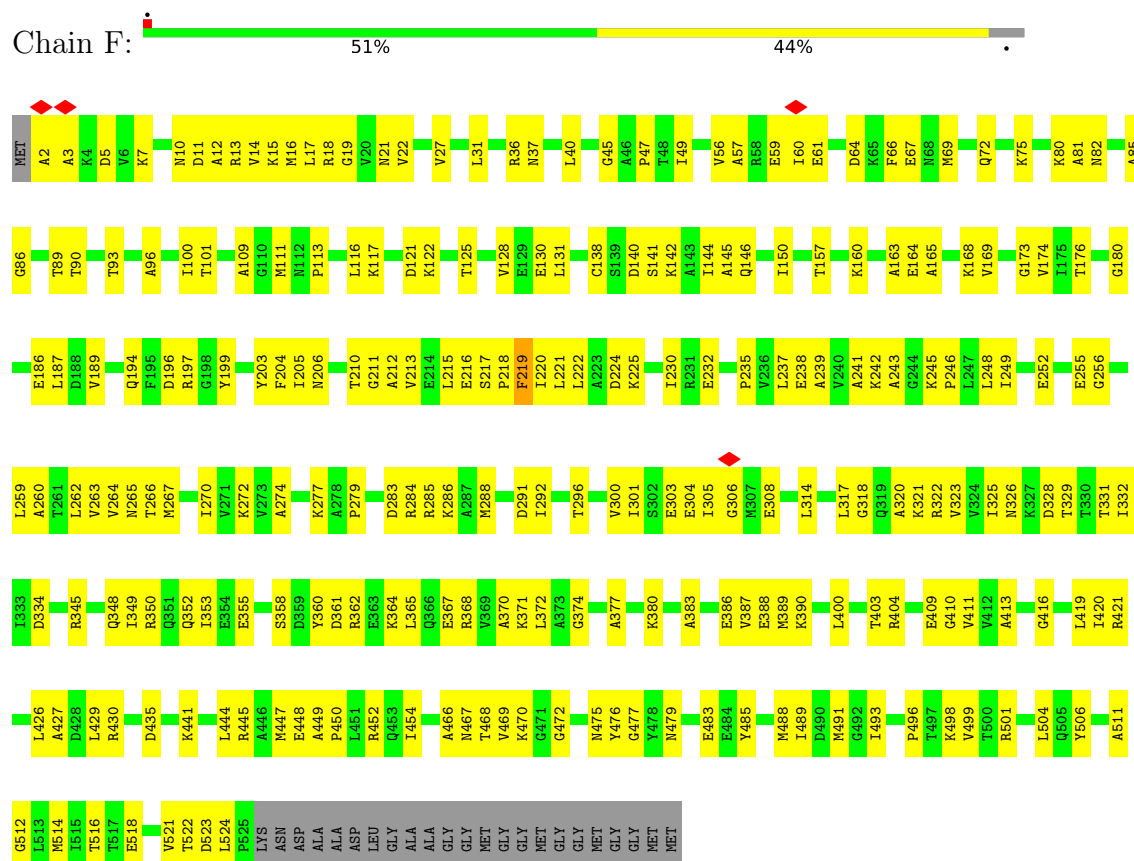
• Molecule 2: Chaperonin GroEL



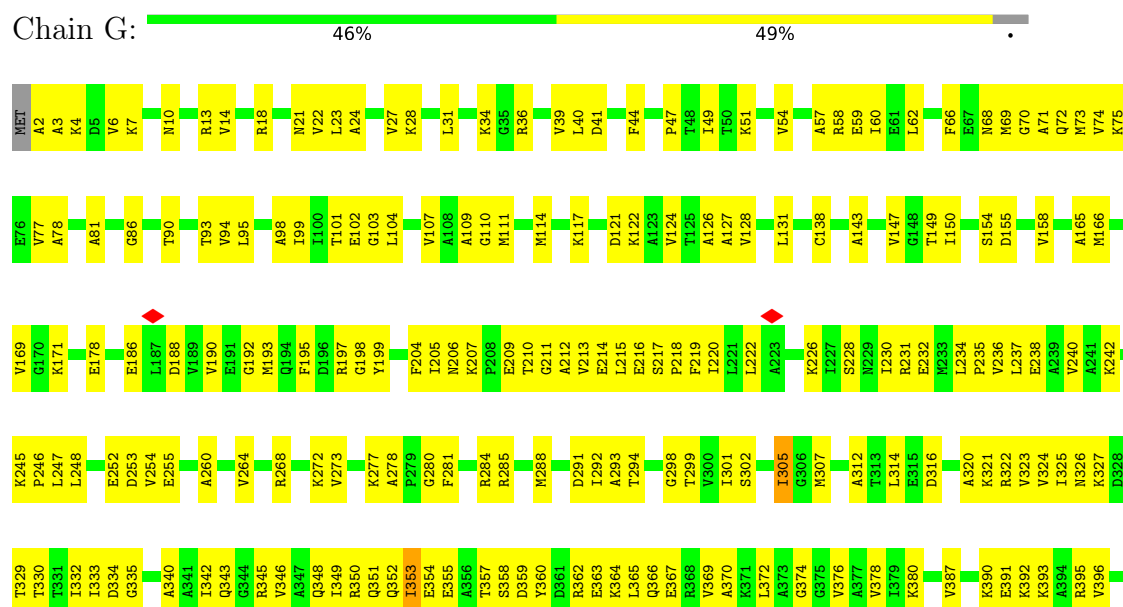


ASW	L444	L385	G289	L187	K75	MET
ASP	M447	Q366	I270	D188	A2	A2
ALA	M447	E367	V271	V189	V77	A3
ALA	E448	R368	K272	V190	K80	K4
ASP	A449		V273	E191		D5
LEU	P450	K371	A274	G192		V6
GLY	L451			M193	T90	
ALA	R452	V376	A278	Q194	T91	G9
ALA	Q453	A377	P279	F195		N10
GLY	L454	V378	G280	D196	V94	
GLY	V455	I379	F281	R197	L95	R13
MET	L456	K380	G282	G198	A86	V14
GLY	M457	V381	D283	Y199	Q97	K15
C458		G382	R284		A98	M16
MET		A383	R285		I99	L17
GLY	E461	E388		I205	N106	R18
GLY	P462	M389	M288	N206	I100	
MET	S463	K390	L289	K207	T101	
GLY		K392	A293	P208	E102	A24
GLY	M467	E391		E209	G103	
MET		K393		T210		V27
	K470	K393	G287	G211	K105	K28
	G471	A394	G288	A212	A106	V29
	D472	R395		V213	V107	T30
	D473	V396		E214		L31
		E397	I301	L215	G110	G32
	N479	L400	S302	E216	M111	P33
	A480		E303	M112	K34	
	A481	H401	F304	S217	P113	G35
	T482	A402	I305	P218		R36
	E483	T403	G306		L116	N37
		R404		L222	V38	V38
	N487	V411	L309	A223	I120	V39
	D490	V412	E310	D224	K225	L40
	M491	A413	A320	K226	D121	D41
	G492		R321	K230	A123	K42
	T493	G416	V323	R231	I227	S43
	L494	V417	V324	E232		F44
	D495	A418	I325		S141	G45
	P496	L419	K326		I144	P47
		I420	K327	E238	V147	T48
	R501	R421	D328	A239	G148	T49
		V422	T329	V240	T149	T50
	L504	A423	T330	A241	I150	K51
	Q505		T331	K242	S151	
	Y506	A427	I332		A152	S55
	A507	D428		L247	N157	V56
	A508	L429	I342		S154	A57
		R430		D253		R58
	M514		R345		V169	E59
		E434		A260		I60
	T517	D435	Q348	T261	E172	F66
	E518		I349	L262	G173	E67
	S519	V438	R350	V263		N68
	M520	G439	Q351	V264	E178	M69
	V521	I440	N265	Q352	D179	G70
		K441	I353	T266	G180	A71
	P525	V442	M267			
TVS		A443	K364	R268	E186	V74

- Molecule 2: Chaperonin GroEL

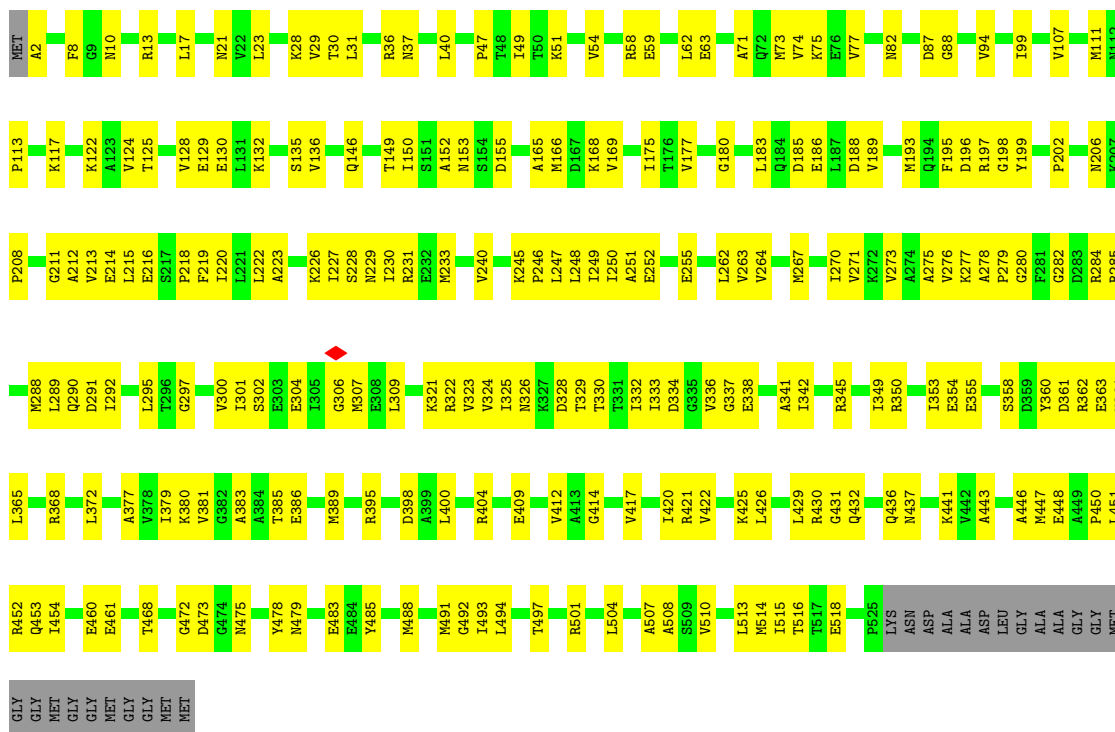


- Molecule 2: Chaperonin GroEL

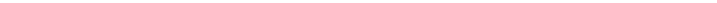


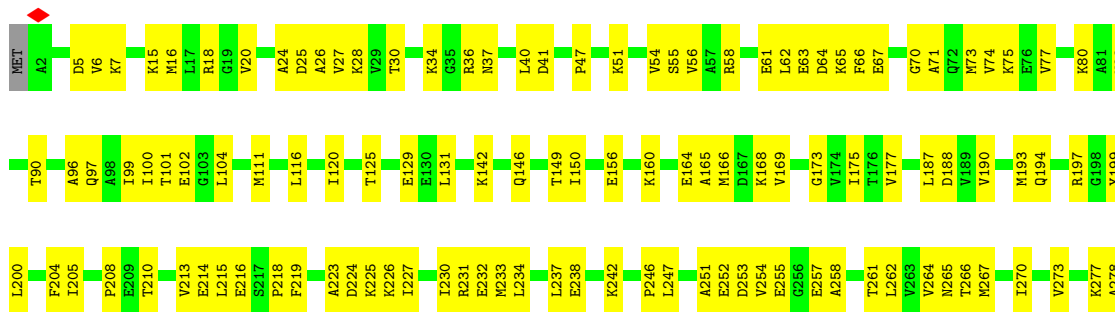
- Molecule 2: Chaperonin GroEL

Chain H: 55% 41% .

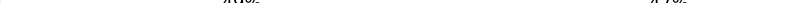


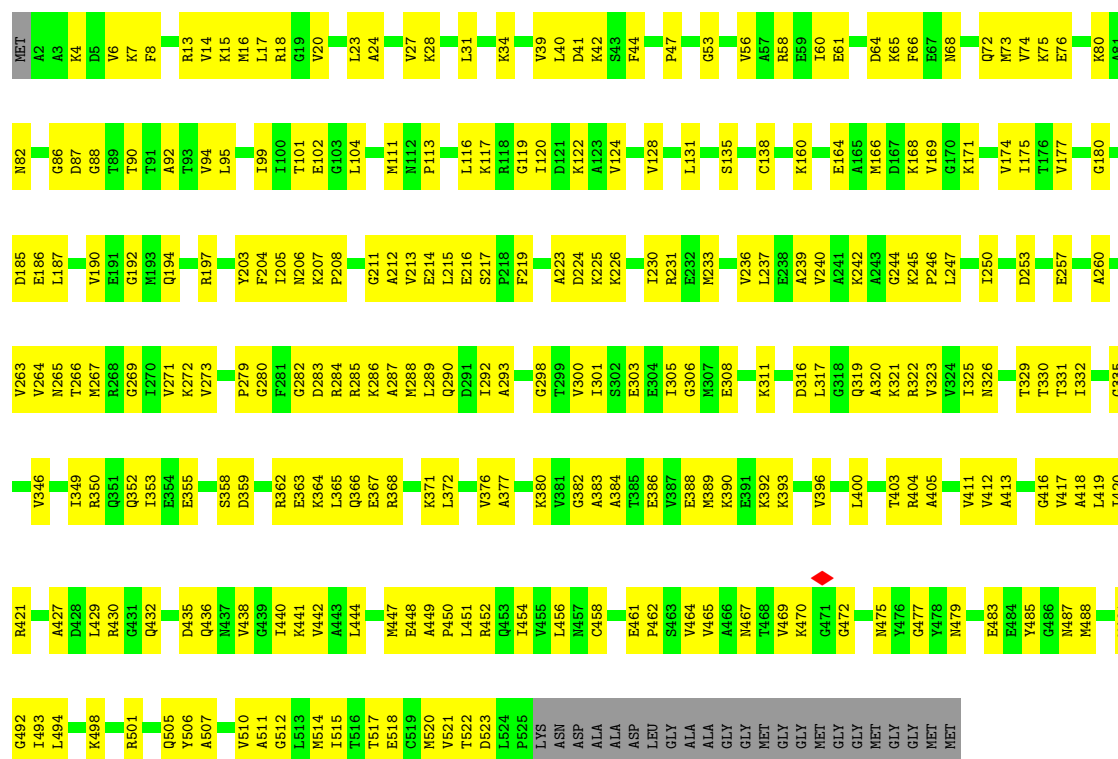
- Molecule 2: Chaperonin GroEL

Chain I:  56% 40% .



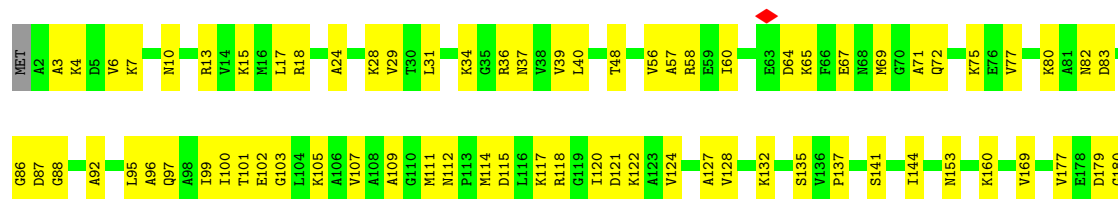
- Molecule 2: Chaperonin GroEL

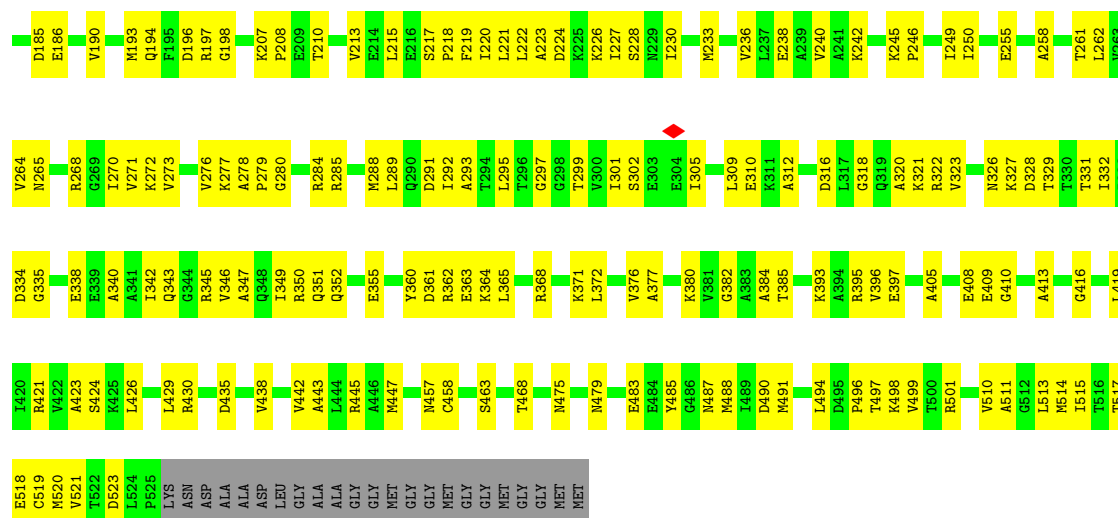
Chain J:  49% 47% .



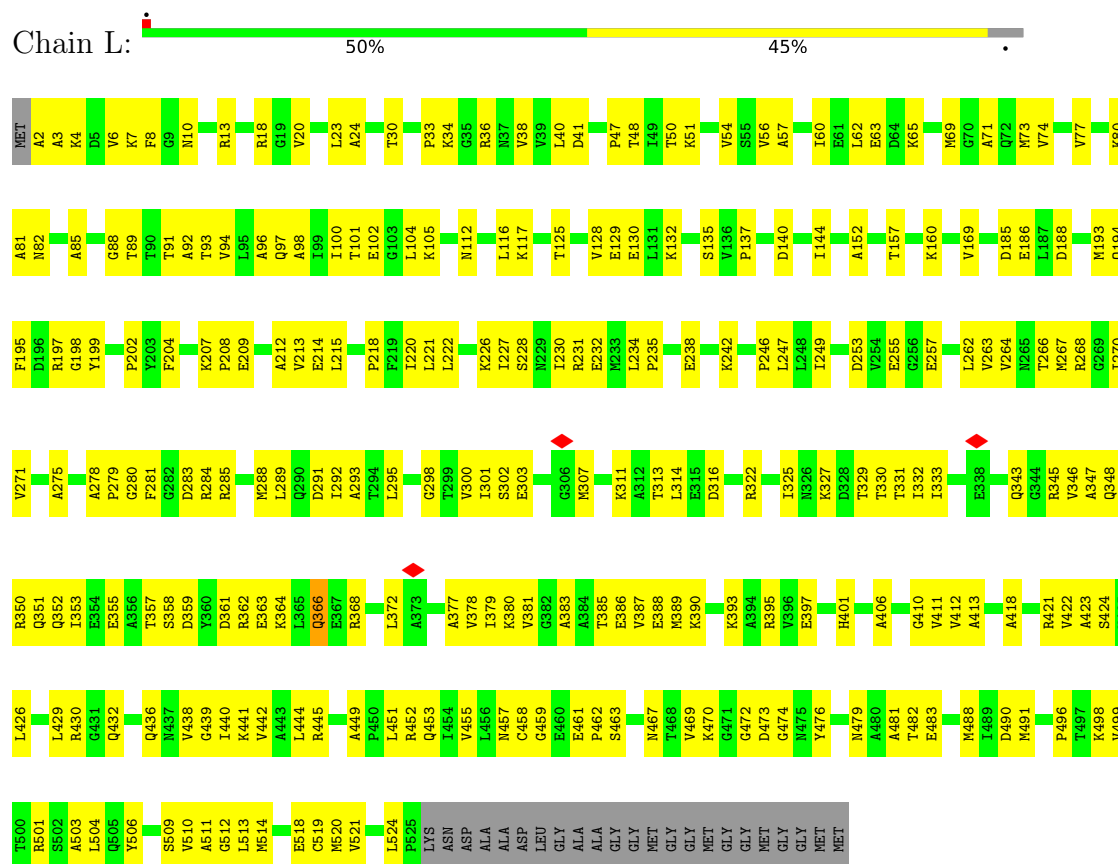
- Molecule 2: Chaperonin GroEL

Chain K: 53% 42% .

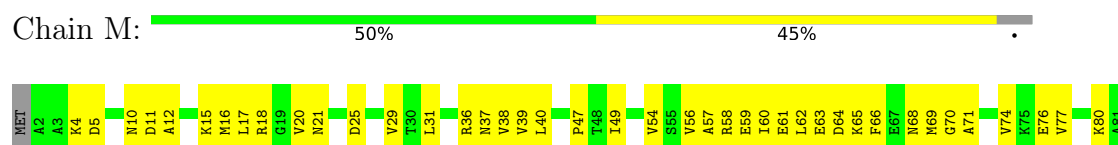


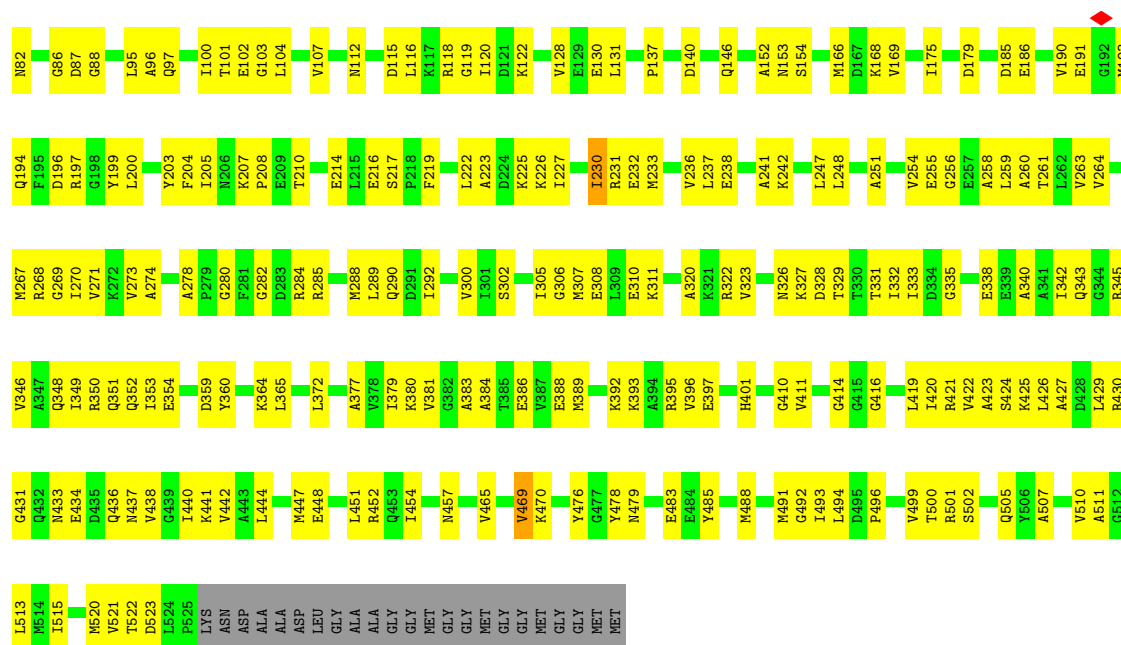


• Molecule 2: Chaperonin GroEL



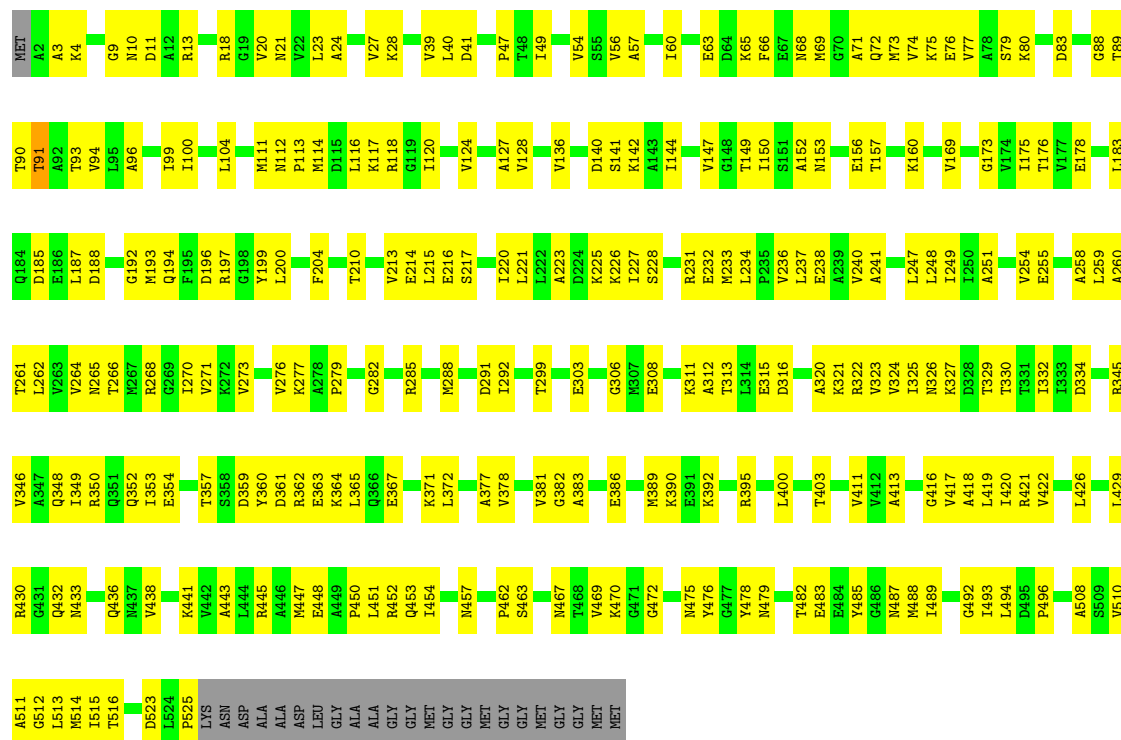
• Molecule 2: Chaperonin GroEL





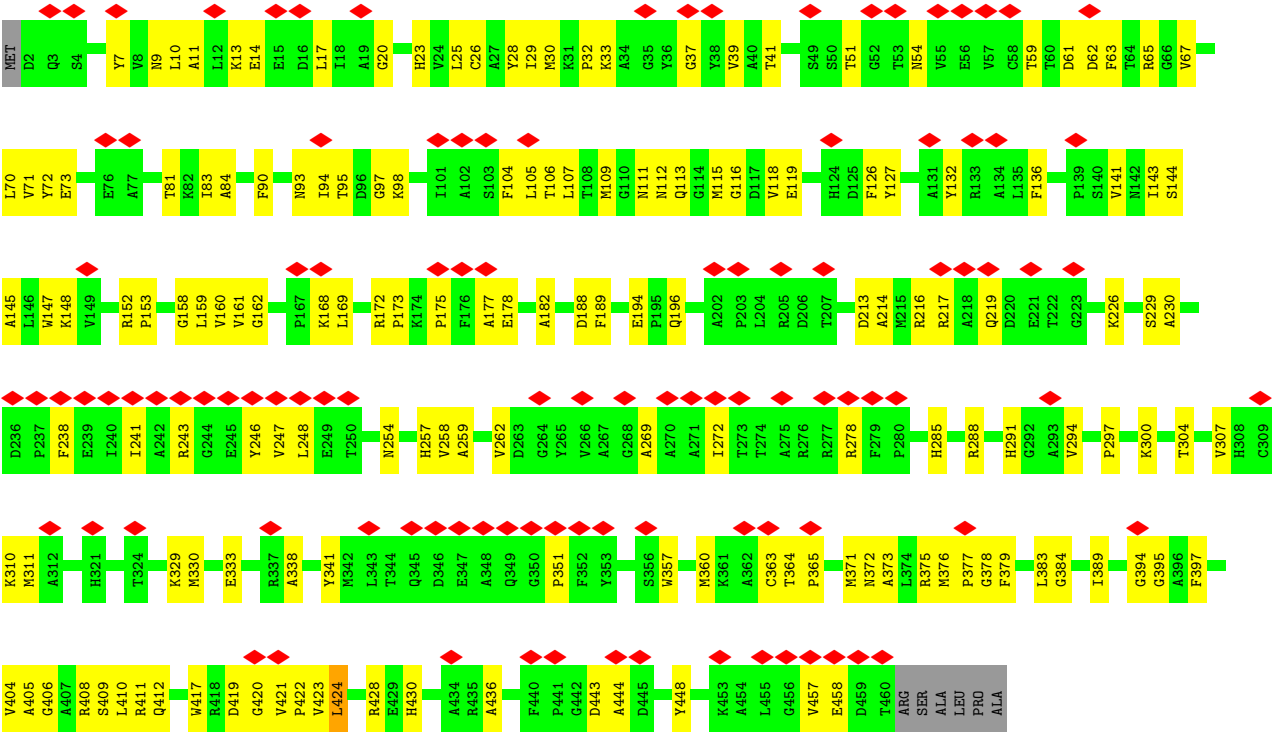
• Molecule 2: Chaperonin GroEL

Chain N: 51% 45%



• Molecule 3: Ribulose biphosphate carboxylase

Chain a: 23% 64% 34%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	35230	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor
Maximum map value	3.769	Depositor
Minimum map value	-1.623	Depositor
Average map value	0.015	Depositor
Map value standard deviation	0.204	Depositor
Recommended contour level	0.663	Depositor
Map size ($\text{\AA}$)	394.0, 394.0, 394.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.97, 1.97, 1.97	Depositor

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	1	0.46	1/731 (0.1%)	0.50	0/983
1	2	0.27	0/731	0.45	0/983
1	O	0.36	0/715	0.56	0/962
1	P	0.15	0/731	0.44	0/983
1	Q	0.22	0/723	0.54	0/973
1	R	0.17	0/731	0.48	0/983
1	S	0.23	0/723	0.50	0/973
1	T	0.24	0/731	0.44	0/983
1	U	0.16	0/731	0.43	0/983
1	V	0.22	0/731	0.51	0/983
1	W	0.26	0/731	0.47	0/983
1	X	0.17	0/731	0.47	0/983
1	Y	0.16	0/726	0.56	2/976 (0.2%)
1	Z	0.23	0/717	0.45	0/964
2	A	0.15	0/3883	0.39	1/5243 (0.0%)
2	B	0.18	0/3883	0.40	0/5243
2	C	0.16	0/3883	0.40	0/5243
2	D	0.21	0/3883	0.42	0/5243
2	E	0.17	0/3883	0.40	1/5243 (0.0%)
2	F	0.20	0/3883	0.39	0/5243
2	G	0.22	0/3883	0.43	1/5243 (0.0%)
2	H	0.21	0/3883	0.40	0/5243
2	I	0.19	0/3883	0.41	0/5243
2	J	0.20	0/3883	0.44	0/5243
2	K	0.15	0/3883	0.35	0/5243
2	L	0.21	0/3883	0.45	0/5243
2	M	0.21	0/3883	0.45	1/5243 (0.0%)
2	N	0.20	0/3883	0.42	0/5243
3	a	0.26	0/3586	0.54	1/4859 (0.0%)
All	All	0.21	1/68131 (0.0%)	0.43	7/91956 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	5	PRO	C-N	11.69	1.47	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	M	230	ILE	N-CA-C	-7.60	105.14	111.91
1	Y	25	ILE	CA-C-N	6.26	133.25	121.97
1	Y	25	ILE	C-N-CA	6.26	133.25	121.97
2	E	88	GLY	N-CA-C	-5.67	106.94	115.32
2	A	230	ILE	N-CA-C	-5.37	106.26	112.98

There are no chirality outliers.

There are no planarity outliers.

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	1	727	0	762	36	0
1	2	727	0	762	57	0
1	O	711	0	744	45	0
1	P	727	0	762	39	0
1	Q	719	0	750	54	0
1	R	727	0	762	41	0
1	S	719	0	750	52	0
1	T	727	0	762	32	0
1	U	727	0	762	38	0
1	V	727	0	762	38	0
1	W	727	0	762	47	0
1	X	727	0	762	57	0
1	Y	722	0	757	48	0
1	Z	713	0	751	56	0
2	A	3855	0	3976	184	0
2	B	3855	0	3976	175	0
2	C	3855	0	3976	190	0
2	D	3855	0	3976	213	0
2	E	3855	0	3976	209	0
2	F	3855	0	3976	198	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	3855	0	3976	215	0
2	H	3855	0	3976	198	0
2	I	3855	0	3976	181	0
2	J	3855	0	3976	221	0
2	K	3855	0	3976	182	0
2	L	3855	0	3976	237	0
2	M	3855	0	3976	210	0
2	N	3855	0	3976	218	0
3	a	3502	0	3380	145	0
All	All	67599	0	69654	3445	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 25.

The worst 5 of 3445 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:N:27:VAL:CG1	2:N:90:THR:HG23	1.50	1.42
1:S:14:ARG:NH1	1:S:67:PHE:HE1	1.34	1.23
2:L:349:ILE:O	2:L:353:ILE:HG13	1.36	1.23
2:N:27:VAL:HG13	2:N:90:THR:CG2	1.69	1.21
1:Q:36:THR:HG23	1:Q:66:ILE:HG13	1.19	1.17

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	1	68/80 (85%)	68 (100%)	0	100	100
1	2	80/80 (100%)	79 (99%)	1 (1%)	61	74
1	O	78/80 (98%)	76 (97%)	2 (3%)	40	62
1	P	80/80 (100%)	80 (100%)	0	100	100
1	Q	79/80 (99%)	77 (98%)	2 (2%)	42	63
1	R	80/80 (100%)	80 (100%)	0	100	100
1	S	79/80 (99%)	79 (100%)	0	100	100
1	T	80/80 (100%)	80 (100%)	0	100	100
1	U	80/80 (100%)	80 (100%)	0	100	100
1	V	80/80 (100%)	80 (100%)	0	100	100
1	W	80/80 (100%)	79 (99%)	1 (1%)	61	74
1	X	80/80 (100%)	80 (100%)	0	100	100
1	Y	80/80 (100%)	80 (100%)	0	100	100
1	Z	79/80 (99%)	79 (100%)	0	100	100
2	A	404/415 (97%)	404 (100%)	0	100	100
2	B	404/415 (97%)	404 (100%)	0	100	100
2	C	404/415 (97%)	404 (100%)	0	100	100
2	D	404/415 (97%)	404 (100%)	0	100	100
2	E	404/415 (97%)	404 (100%)	0	100	100
2	F	404/415 (97%)	402 (100%)	2 (0%)	81	83
2	G	404/415 (97%)	403 (100%)	1 (0%)	87	87
2	H	404/415 (97%)	404 (100%)	0	100	100
2	I	404/415 (97%)	404 (100%)	0	100	100
2	J	404/415 (97%)	404 (100%)	0	100	100
2	K	404/415 (97%)	404 (100%)	0	100	100
2	L	404/415 (97%)	403 (100%)	1 (0%)	87	87
2	M	404/415 (97%)	403 (100%)	1 (0%)	87	87
2	N	404/415 (97%)	403 (100%)	1 (0%)	87	87
3	a	348/354 (98%)	347 (100%)	1 (0%)	86	86
All	All	7107/7284 (98%)	7094 (100%)	13 (0%)	85	87

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	8	ASP
1	O	16	GLU
3	a	424	LEU
1	Q	51	ASN
1	W	25	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	82	ASN
1	Z	7	HIS
2	J	194	GLN
1	Y	51	ASN
3	a	345	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 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 [i](#)

There are no chain breaks in this entry.

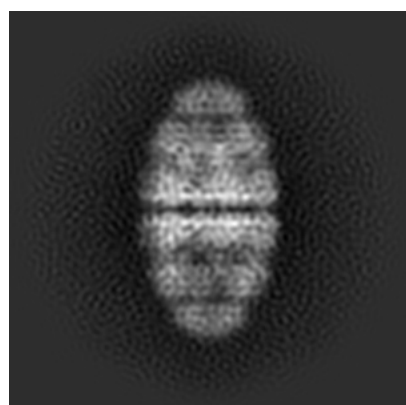
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32164. These allow visual inspection of the internal detail of the map and identification of artifacts.

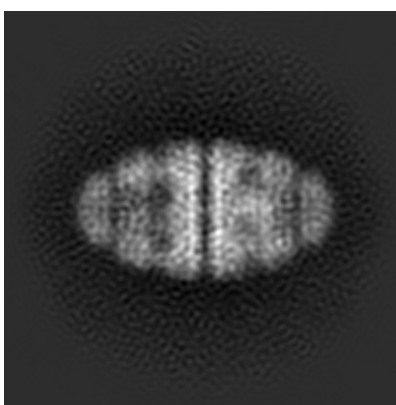
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

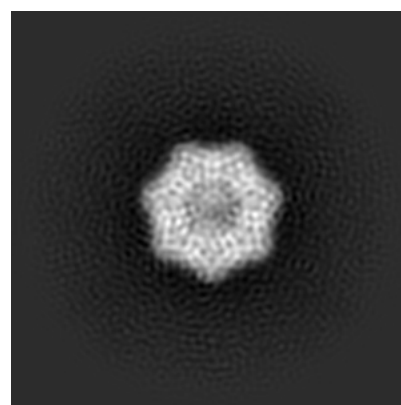
6.1.1 Primary map



X



Y

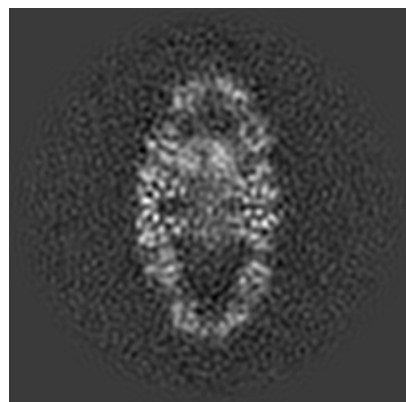


Z

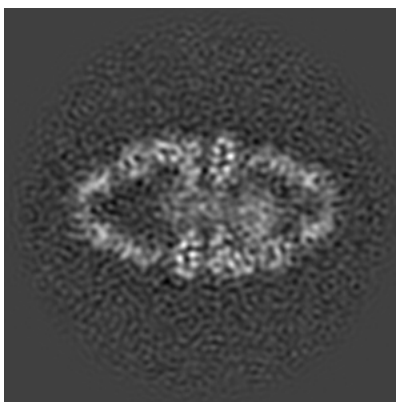
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

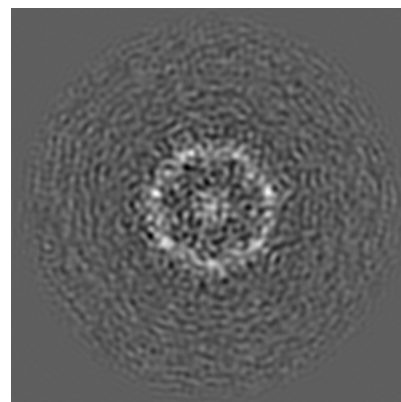
6.2.1 Primary map



X Index: 100



Y Index: 100

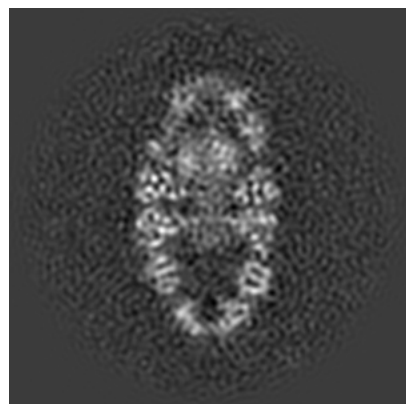


Z Index: 100

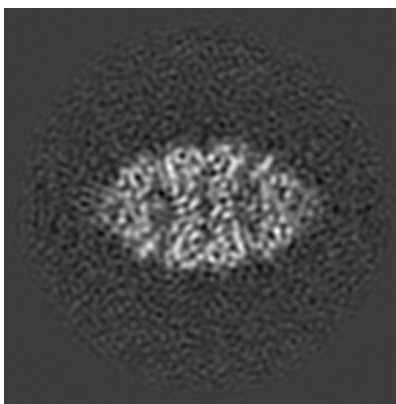
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

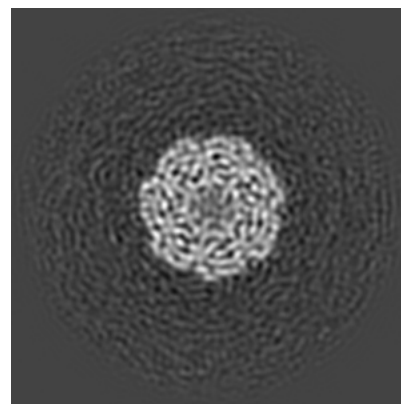
6.3.1 Primary map



X Index: 98



Y Index: 81

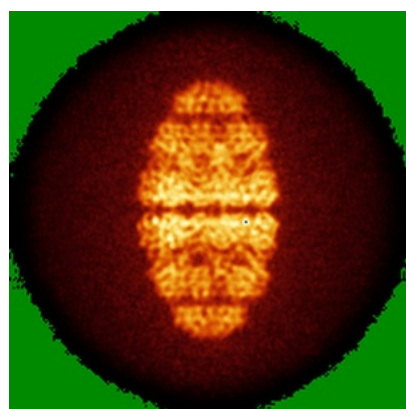


Z Index: 93

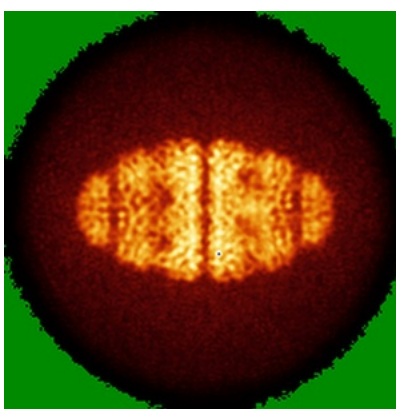
The images above show the largest variance slices of the map in three orthogonal directions.

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

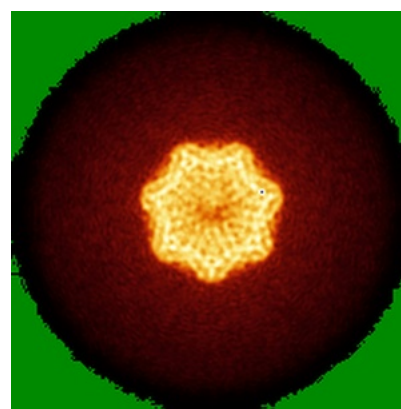
6.4.1 Primary map



X



Y



Z

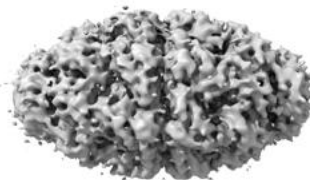
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

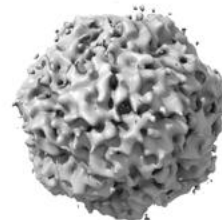
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.663. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

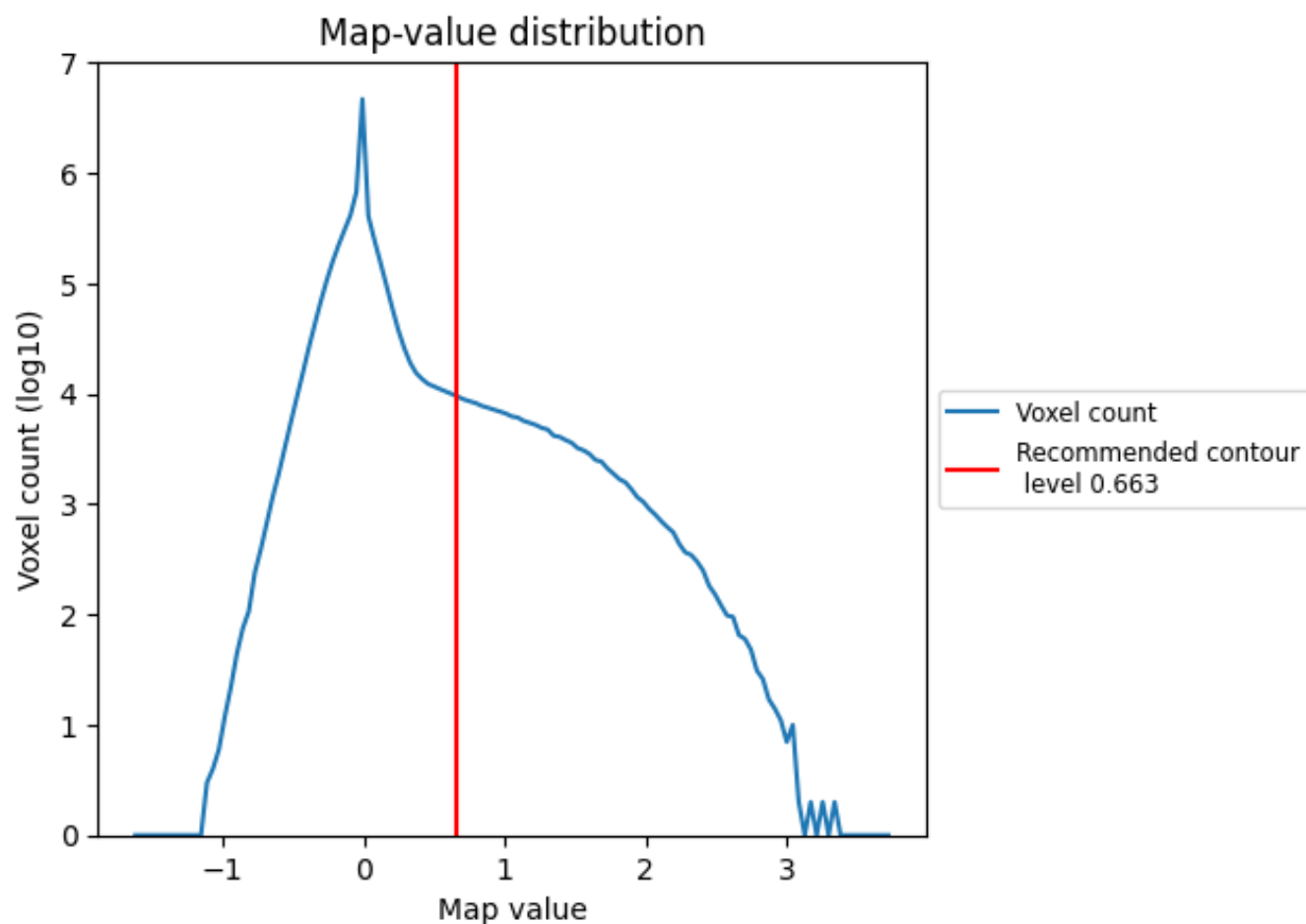
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

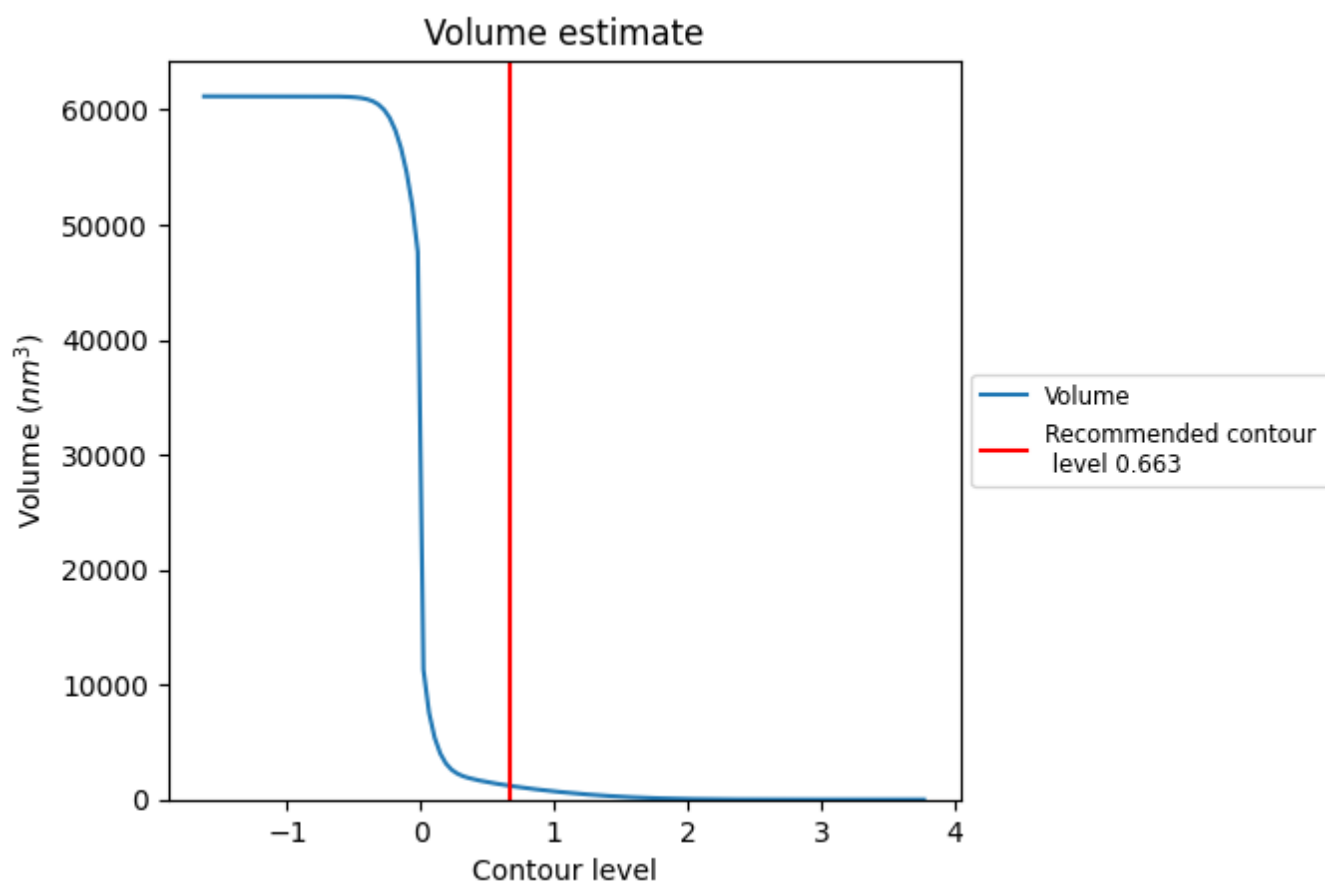
This section contains the results of statistical analysis of the map.

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.

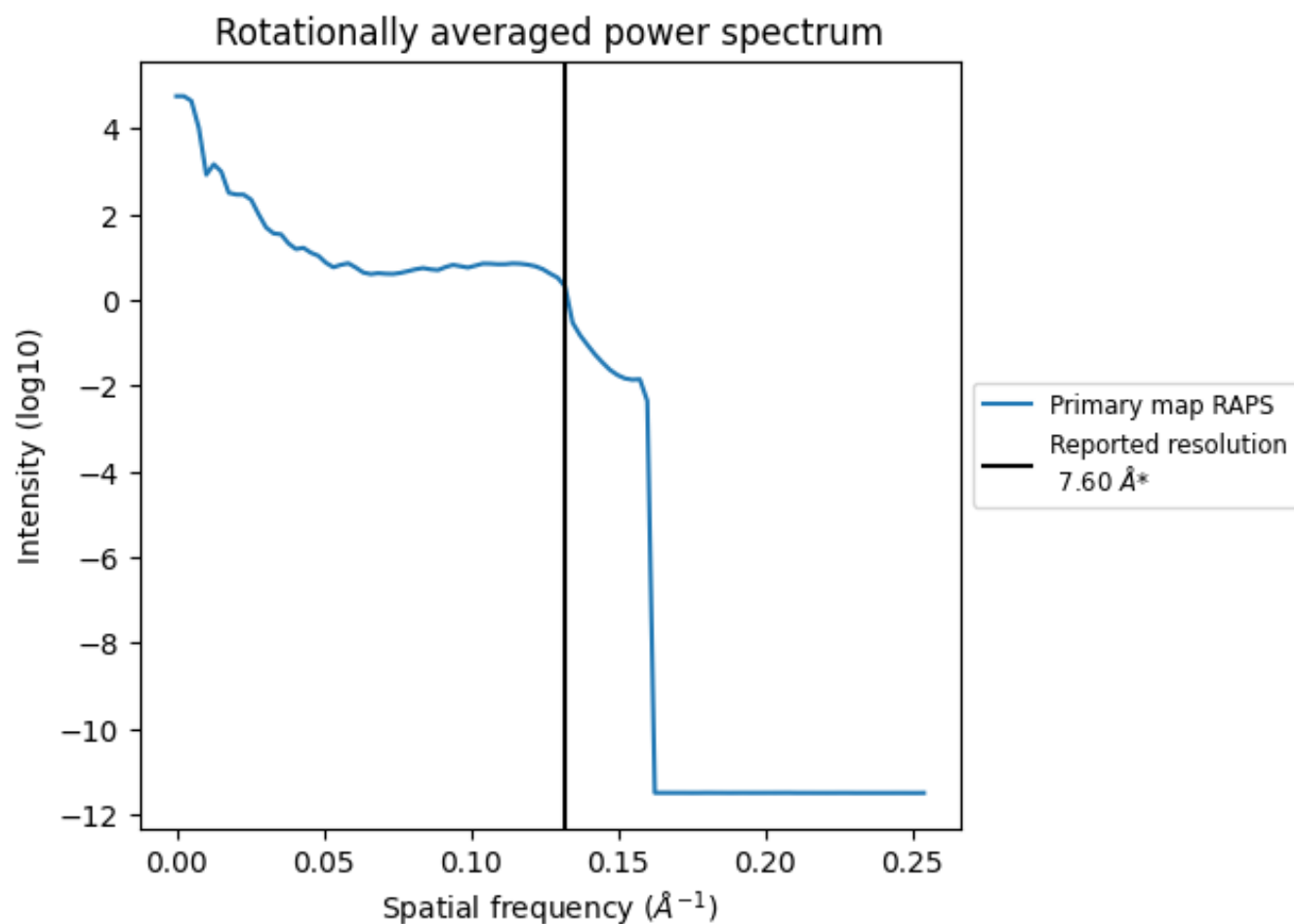
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1203 nm³; this corresponds to an approximate mass of 1086 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 ⓘ

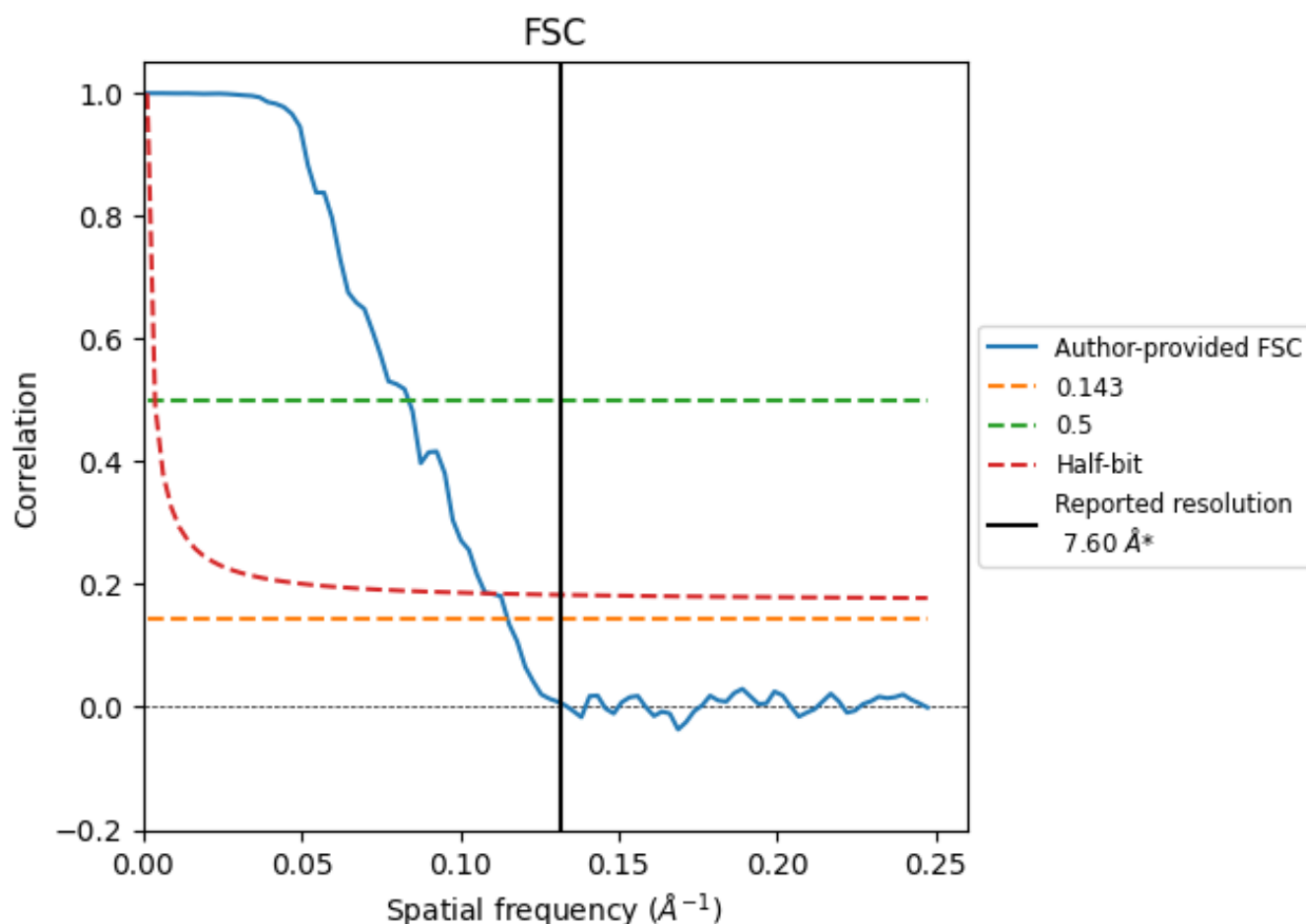


*Reported resolution corresponds to spatial frequency of 0.132 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.132 Å⁻¹

8.2 Resolution estimates [i](#)

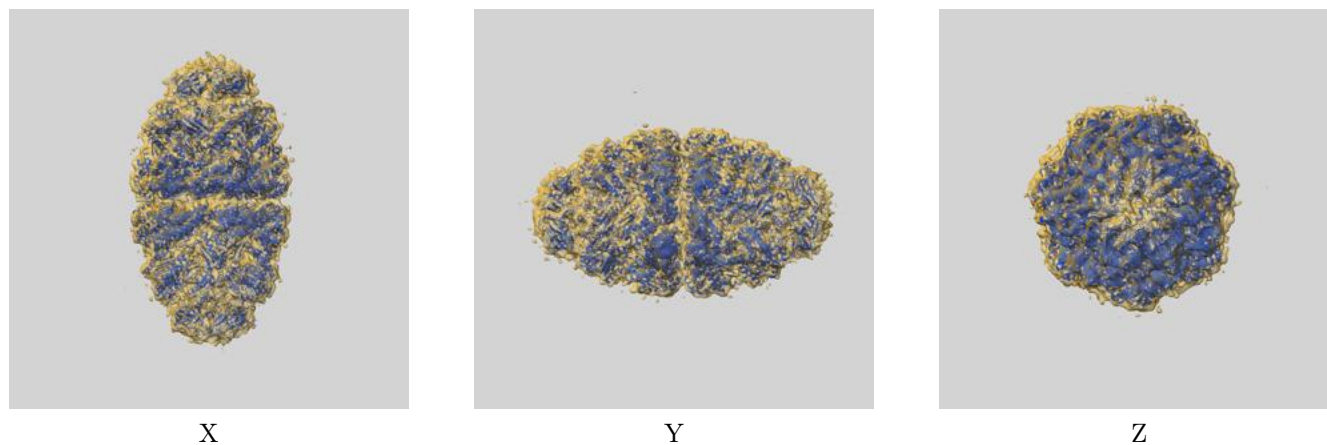
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.60	-	-
Author-provided FSC curve	8.70	11.93	9.14
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 8.70 differs from the reported value 7.6 by more than 10 %

9 Map-model fit [i](#)

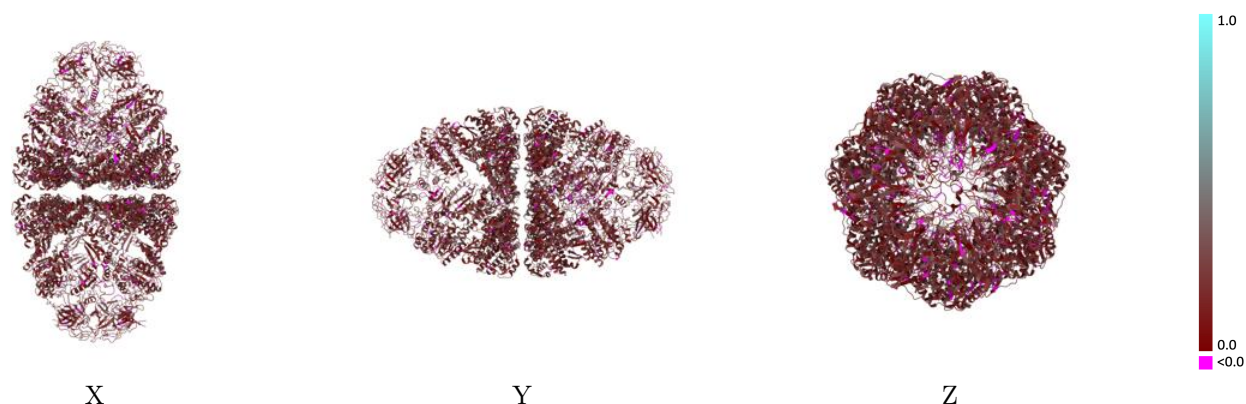
This section contains information regarding the fit between EMDB map EMD-32164 and PDB model 7VWX. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



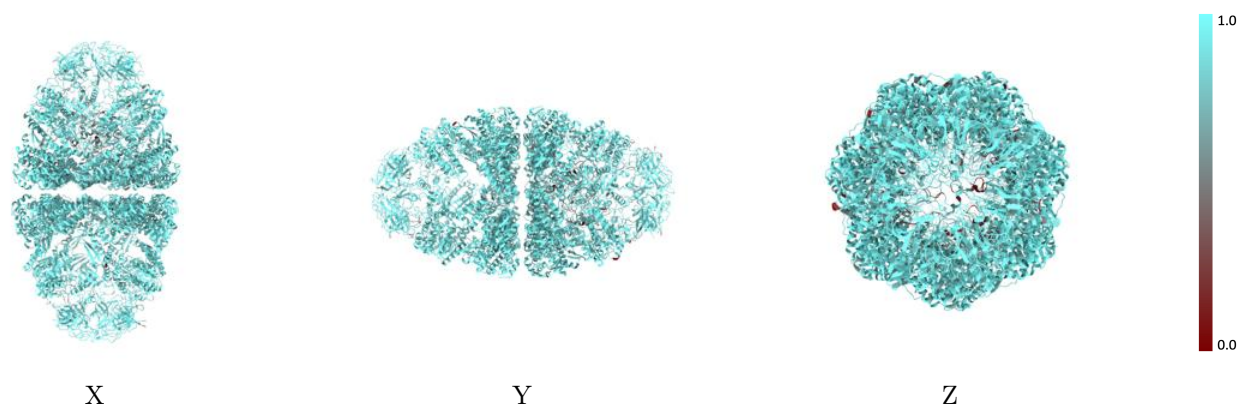
The images above show the 3D surface view of the map at the recommended contour level 0.663 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



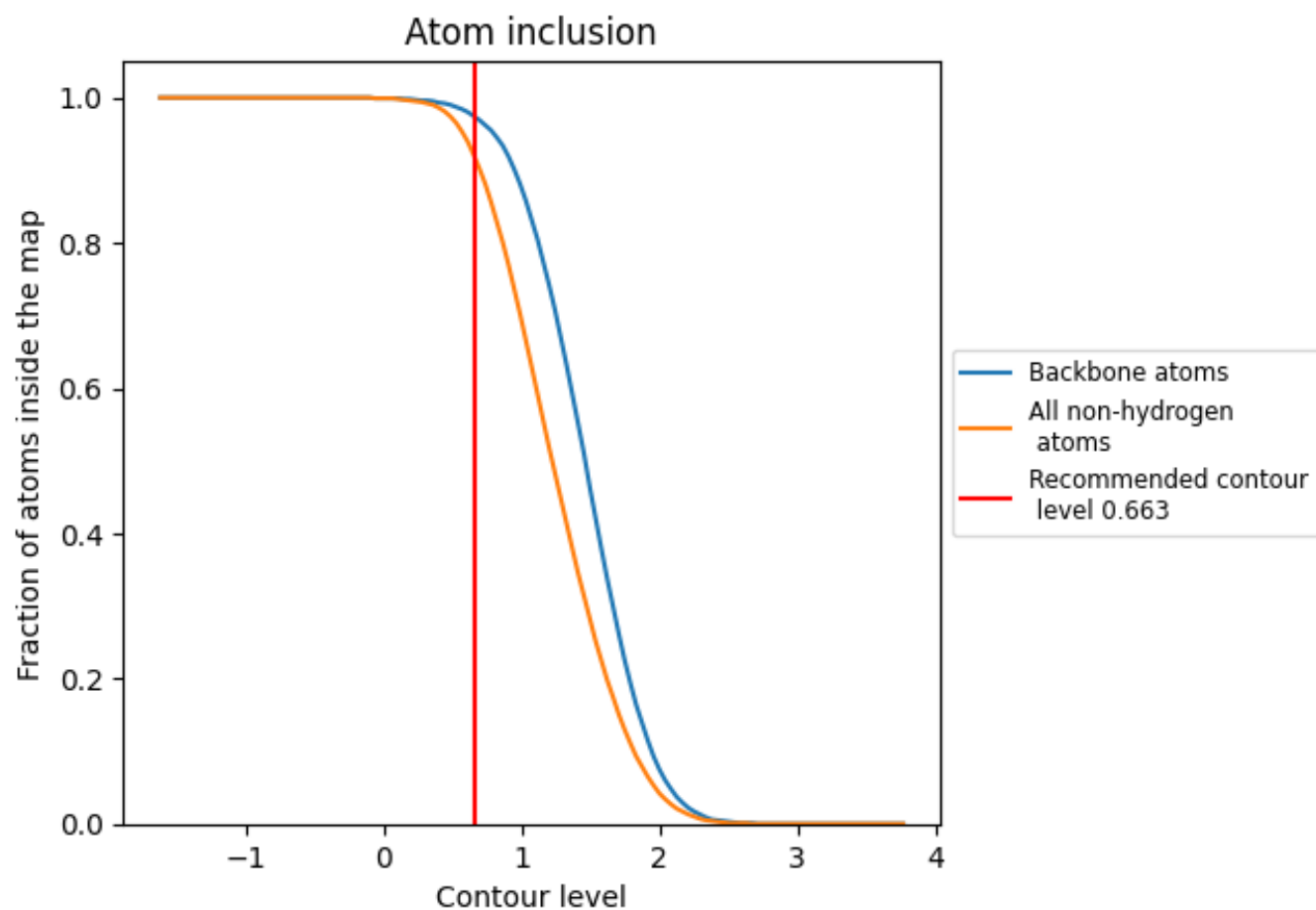
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.663).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 92% 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 (0.663) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.1900
1	 0.9540	 0.1950
2	 0.9080	 0.1890
A	 0.9140	 0.1950
B	 0.9120	 0.1900
C	 0.9270	 0.1960
D	 0.9300	 0.1940
E	 0.9260	 0.1910
F	 0.9170	 0.1930
G	 0.9260	 0.1950
H	 0.9320	 0.1960
I	 0.9290	 0.1950
J	 0.9330	 0.2000
K	 0.9320	 0.1990
L	 0.9380	 0.1840
M	 0.9390	 0.2010
N	 0.9370	 0.1980
O	 0.9240	 0.1930
P	 0.9060	 0.1970
Q	 0.9290	 0.1910
R	 0.9190	 0.1680
S	 0.8940	 0.2010
T	 0.9010	 0.1880
U	 0.9270	 0.1850
V	 0.9250	 0.1960
W	 0.9360	 0.2150
X	 0.9110	 0.1870
Y	 0.9240	 0.1980
Z	 0.9340	 0.1930
a	 0.7180	 0.1200

