



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 11:50 PM UTC

PDB ID : 7LUM / pdb_00007lum
EMDB ID : EMD-23522
Title : Human TRiC in ATP/AlFx closed state
Authors : Knowlton, J.J.; Gestaut, D.; Ma, B.; Taylor, G.; Seven, A.B.; Leitner, A.;
Wilson, G.J.; Shanker, S.; Yates, N.A.; Prasad, B.V.V.; Aebersold, R.; Chiu,
W.; Frydman, J.; Dermody, T.S.
Deposited on : 2021-02-22
Resolution : 4.50 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

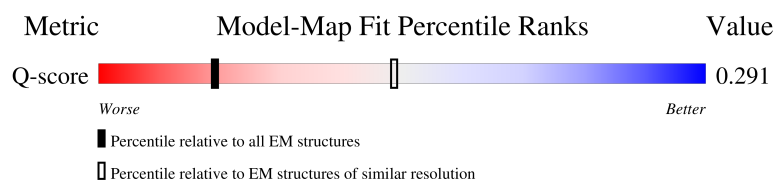
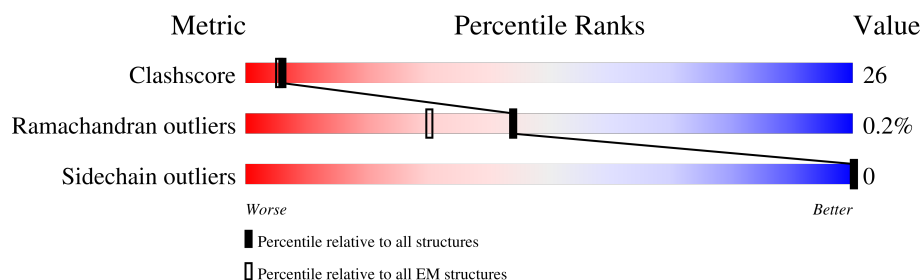
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.50 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	2937 (4.00 - 5.00)

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	D	541	12% 48% 48% ..
1	L	541	11% 49% 47% ..
2	E	535	10% 54% 42% .
2	M	535	10% 52% 44% .

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Mol	Chain	Length	Quality of chain
3	F	539	
3	N	539	
4	H	545	
4	P	545	
5	C	543	
5	K	543	
6	B	548	
6	J	548	
7	A	531	
7	I	531	
8	G	556	
8	O	556	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 63978 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 T-complex protein 1 subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L	527	Total	C	N	O	S	0	0
			4063	2544	710	779	30		
1	D	527	Total	C	N	O	S	0	0
			4063	2544	710	779	30		

- Molecule 2 is a protein called T-complex protein 1 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	M	518	Total	C	N	O	S	0	0
			3898	2438	687	754	19		
2	E	518	Total	C	N	O	S	0	0
			3898	2438	687	754	19		

- Molecule 3 is a protein called T-complex protein 1 subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	518	Total	C	N	O	S	0	0
			3911	2445	680	763	23		
3	F	518	Total	C	N	O	S	0	0
			3911	2445	680	763	23		

- Molecule 4 is a protein called T-complex protein 1 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	521	Total	C	N	O	S	0	0
			4050	2524	716	780	30		
4	P	521	Total	C	N	O	S	0	0
			4050	2524	716	780	30		

- Molecule 5 is a protein called T-complex protein 1 subunit eta.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	522	Total	C	N	O	S	0	0
			4007	2534	690	759	24		
5	C	522	Total	C	N	O	S	0	0
			4007	2534	690	759	24		

- Molecule 6 is a protein called T-complex protein 1 subunit theta.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	524	Total	C	N	O	S	0	0
			3994	2520	678	769	27		
6	B	524	Total	C	N	O	S	0	0
			3994	2520	678	769	27		

- Molecule 7 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	525	Total	C	N	O	S	0	0
			4023	2528	704	770	21		
7	A	525	Total	C	N	O	S	0	0
			4023	2528	704	770	21		

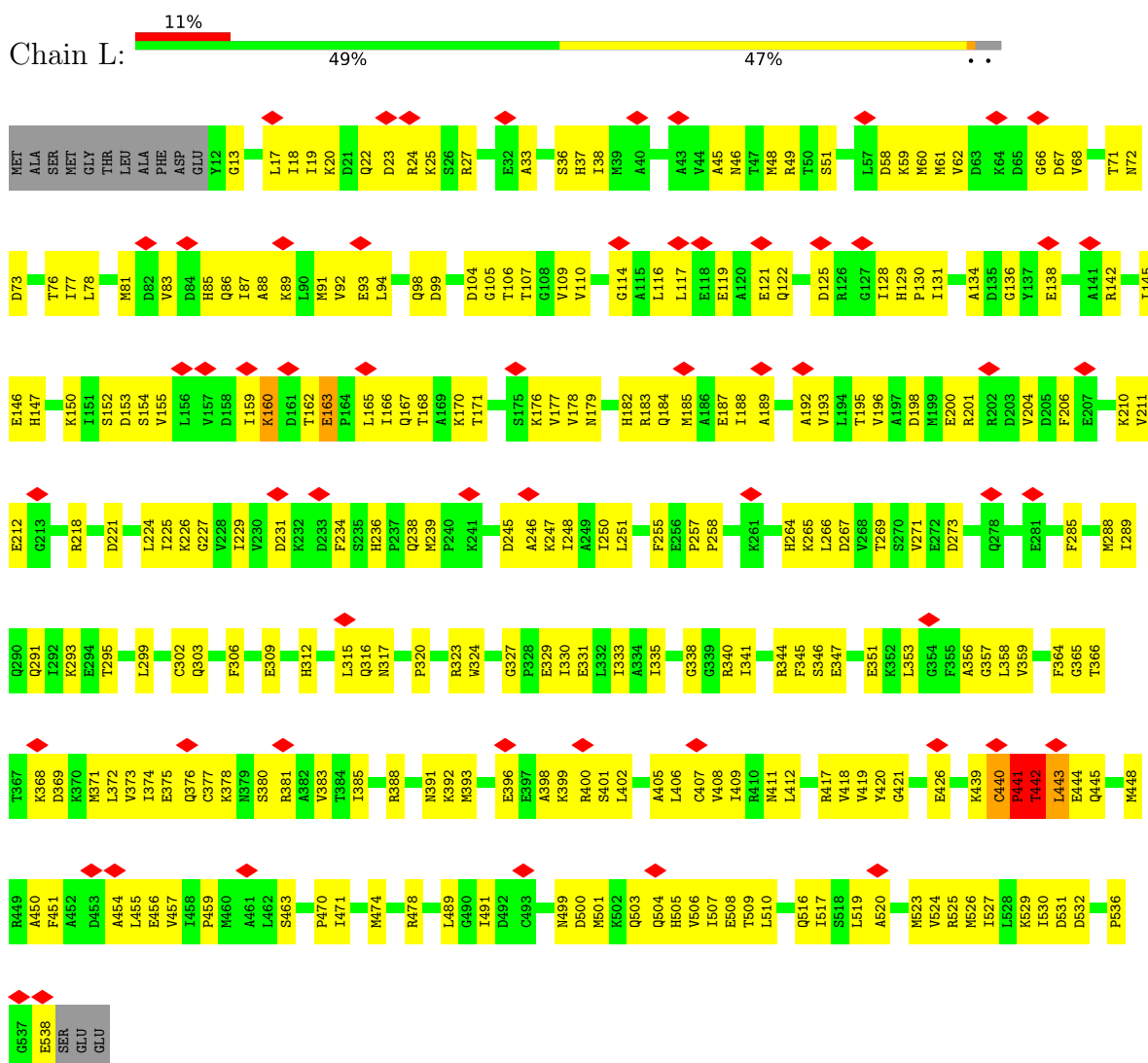
- Molecule 8 is a protein called T-complex protein 1 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	532	Total	C	N	O	S	0	0
			4043	2533	707	780	23		
8	G	532	Total	C	N	O	S	0	0
			4043	2533	707	780	23		

3 Residue-property plots

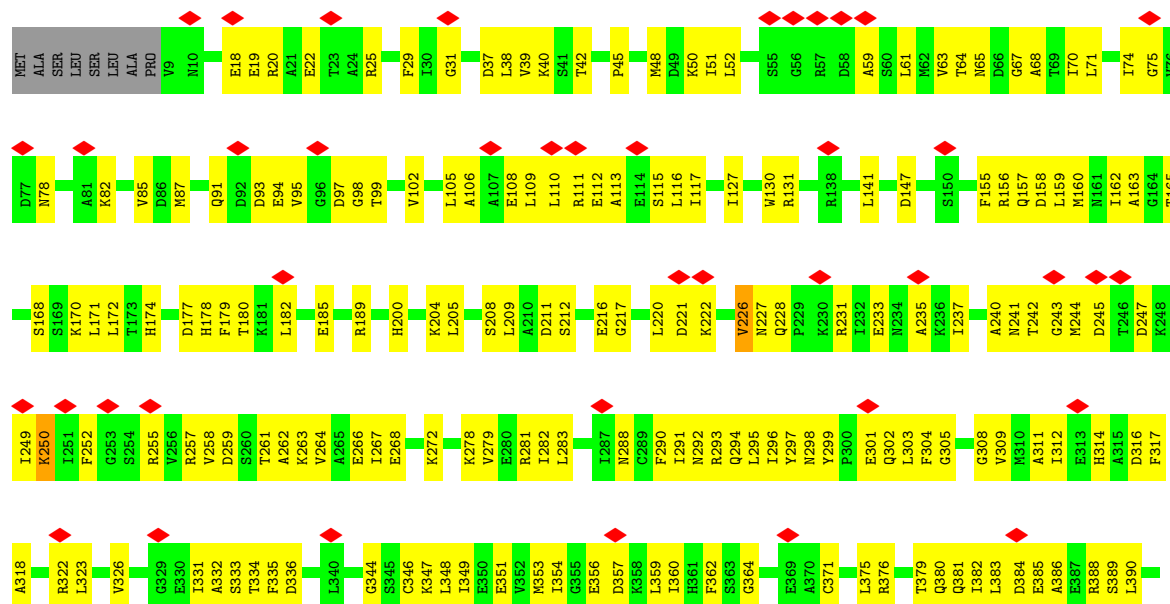
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

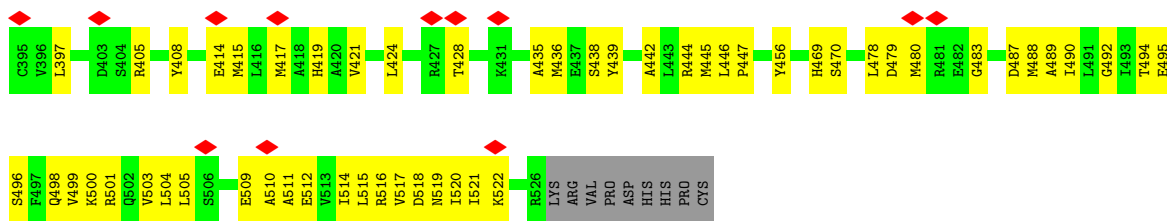
- Molecule 1: T-complex protein 1 subunit epsilon



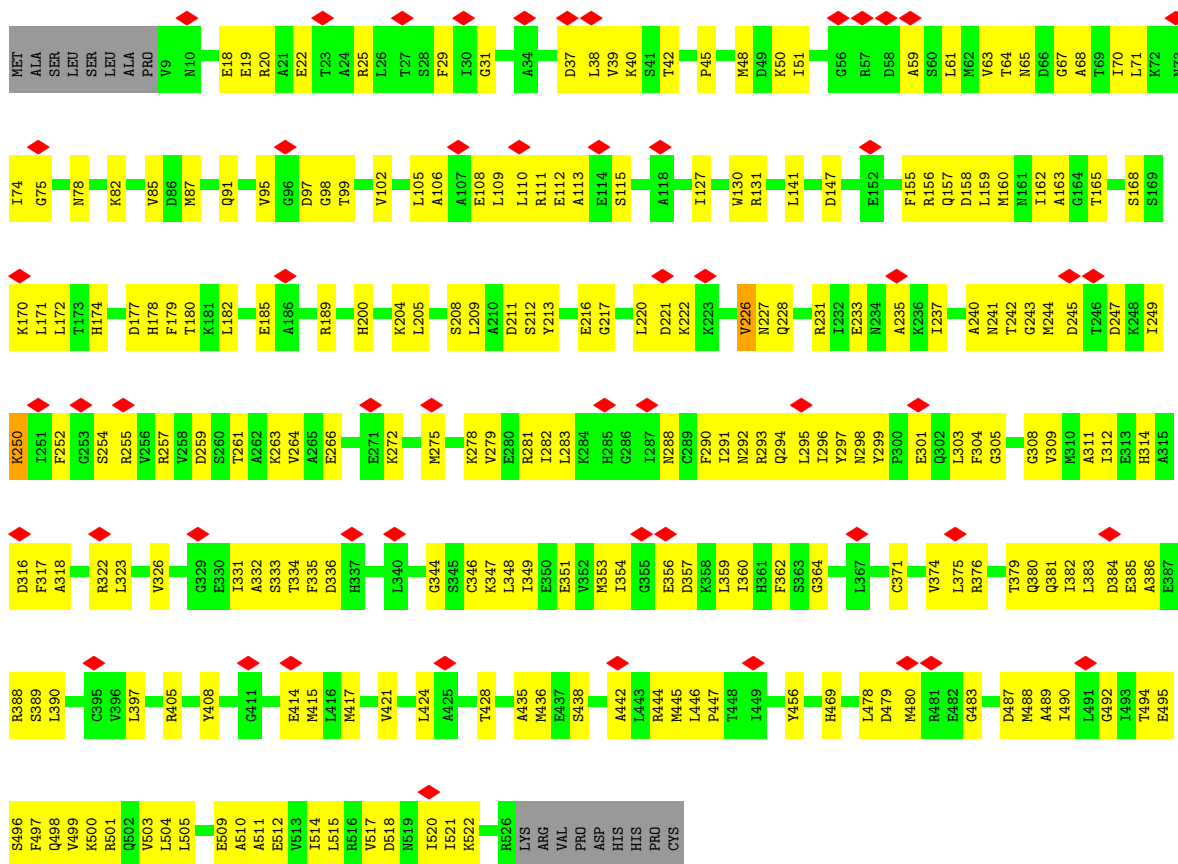
- Molecule 1: T-complex protein 1 subunit epsilon



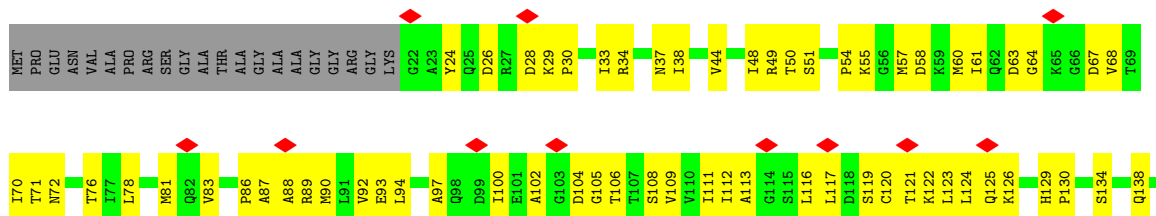




• Molecule 2: T-complex protein 1 subunit beta



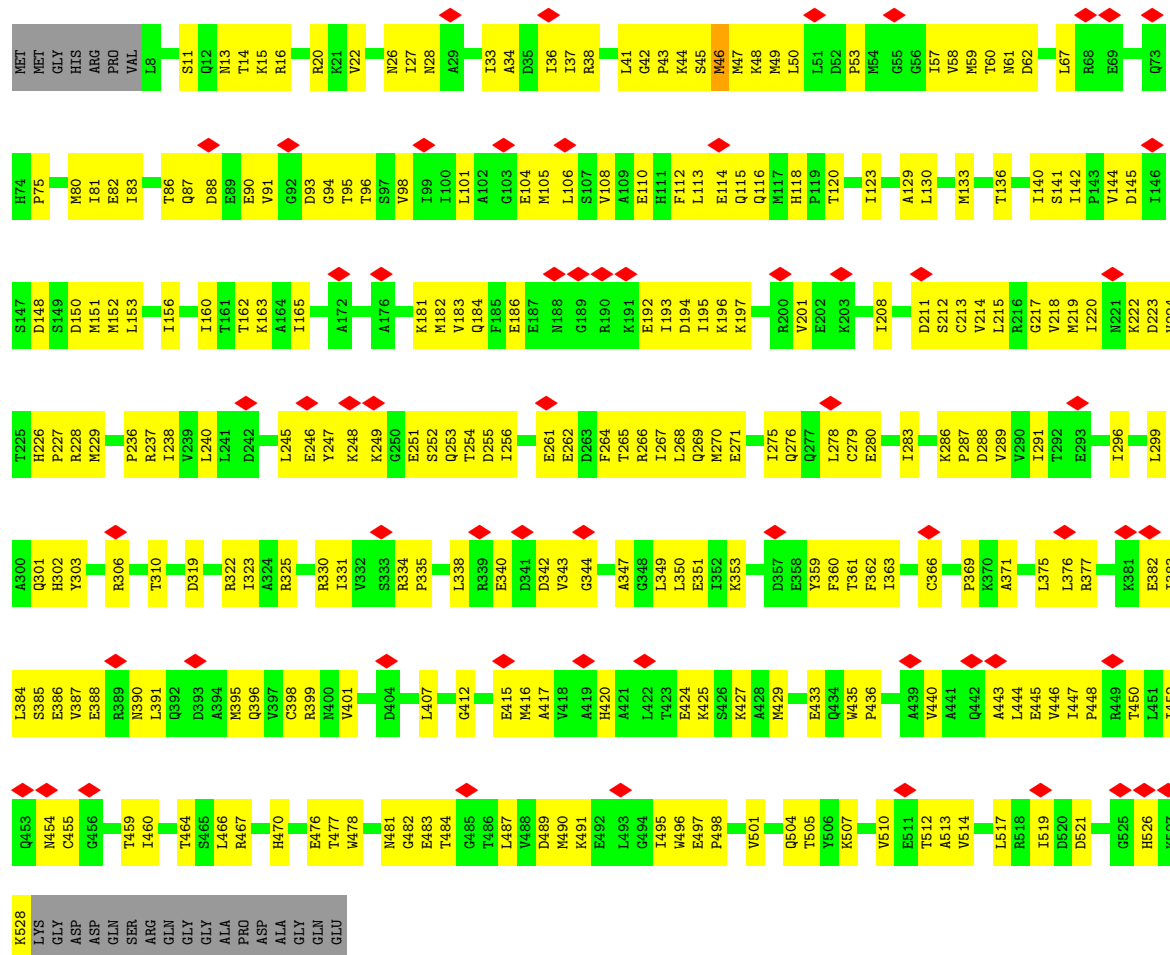
• Molecule 3: T-complex protein 1 subunit delta



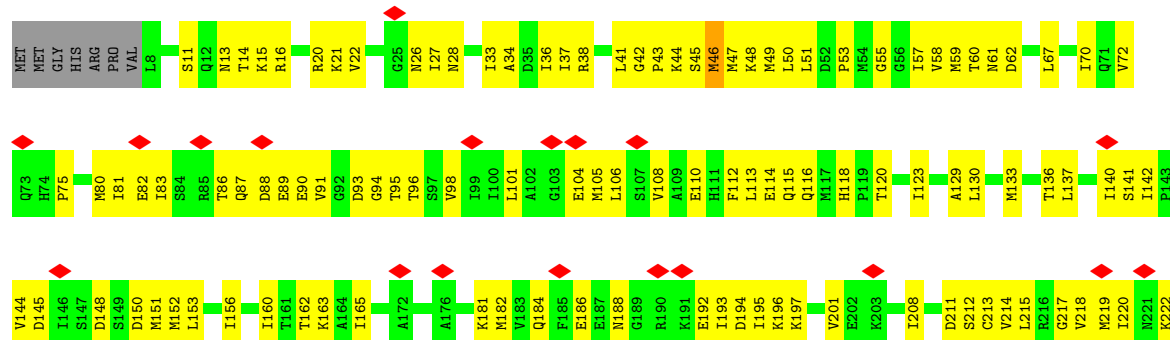


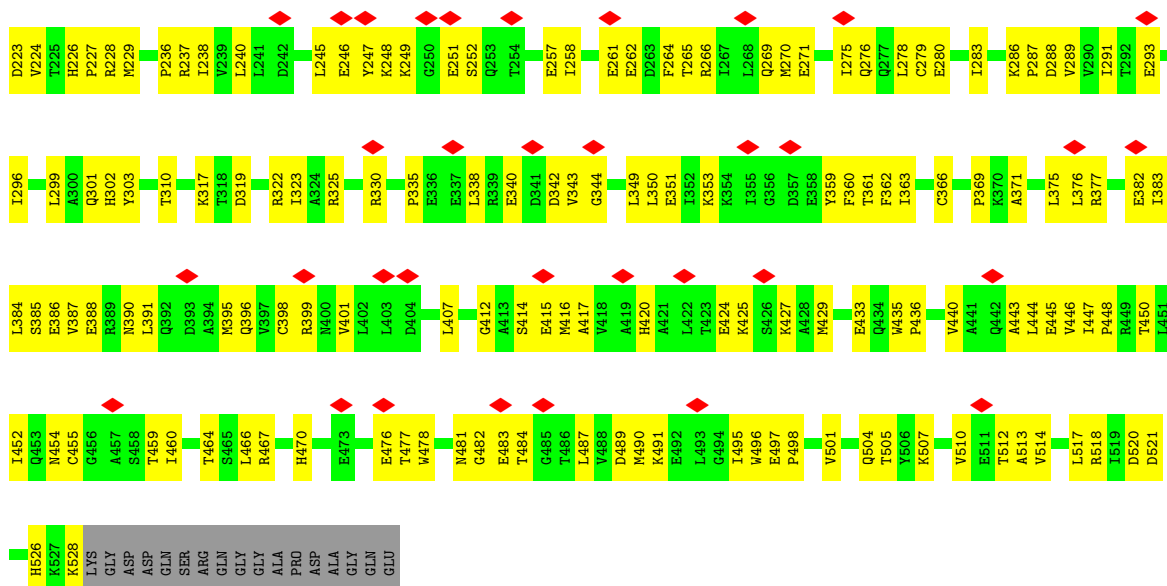


• Molecule 4: T-complex protein 1 subunit gamma

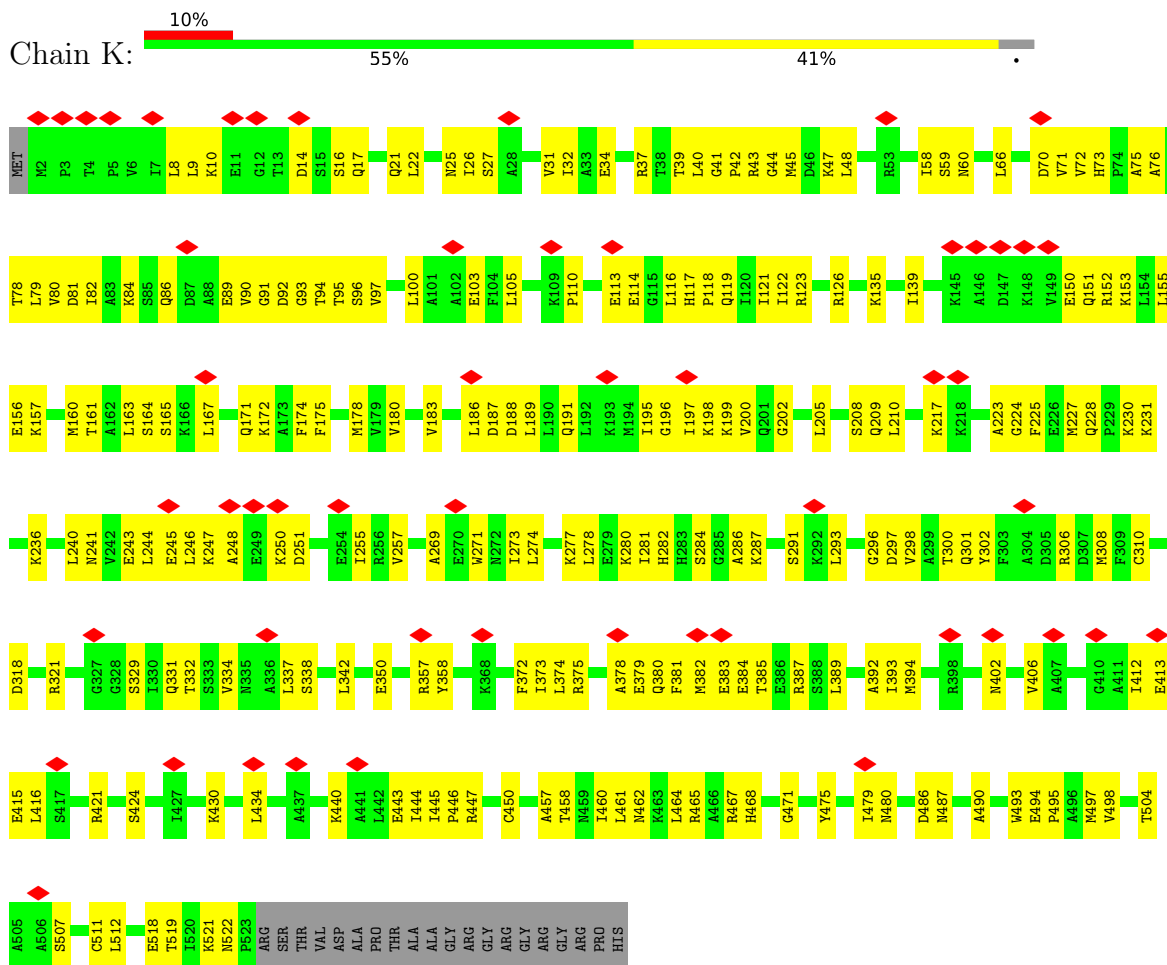


• Molecule 4: T-complex protein 1 subunit gamma



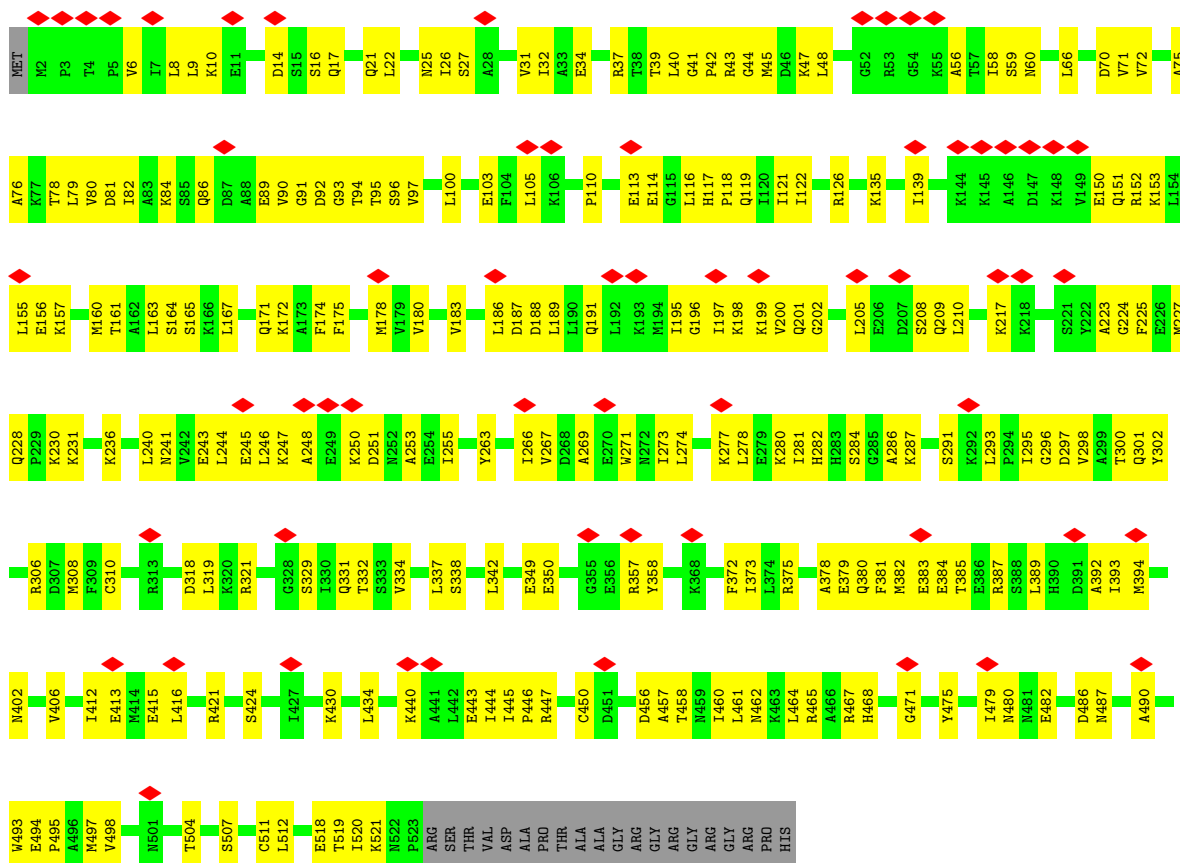


• Molecule 5: T-complex protein 1 subunit eta

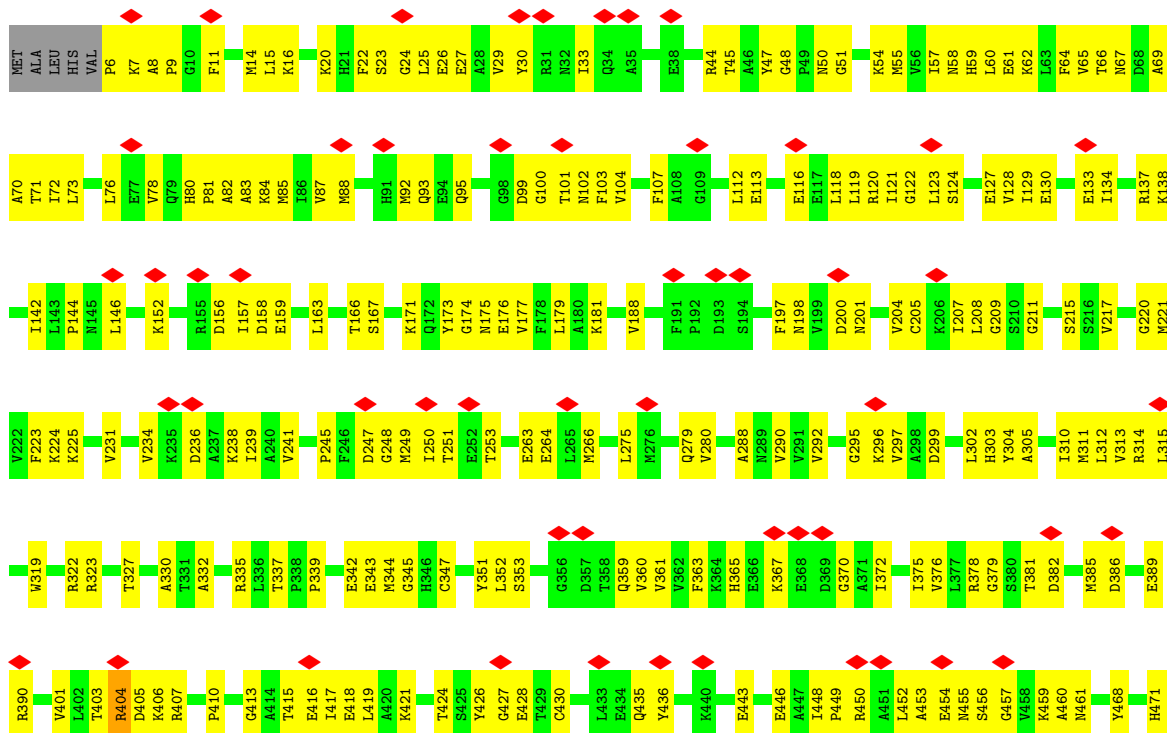


• Molecule 5: T-complex protein 1 subunit eta



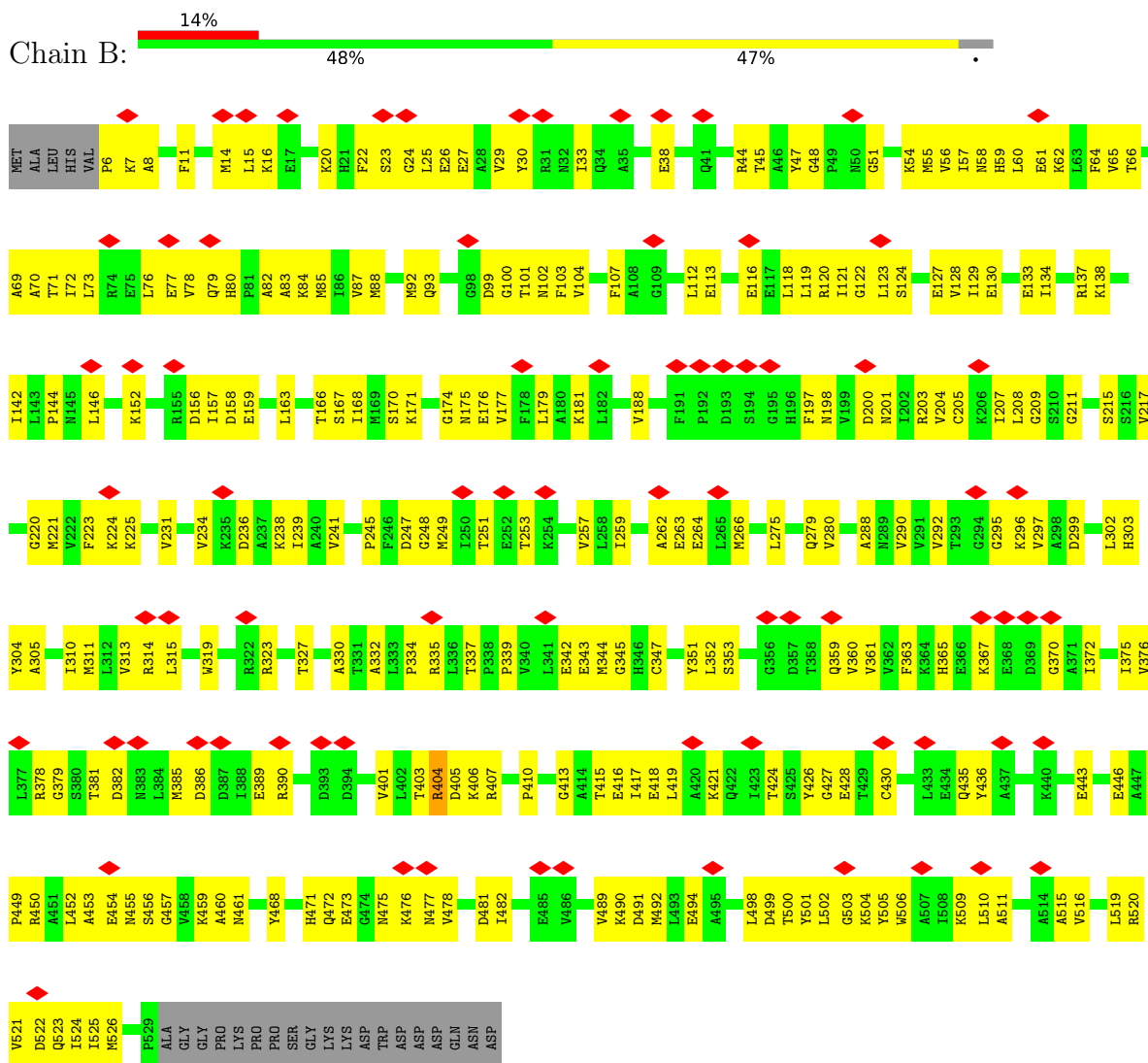


• Molecule 6: T-complex protein 1 subunit theta



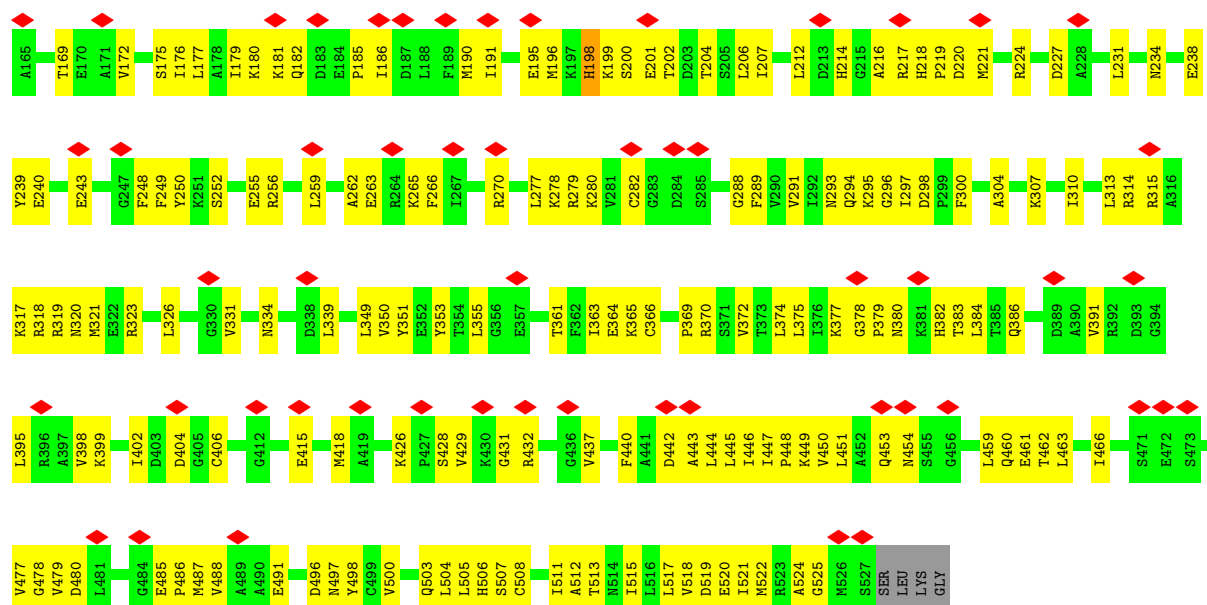


• Molecule 6: T-complex protein 1 subunit theta

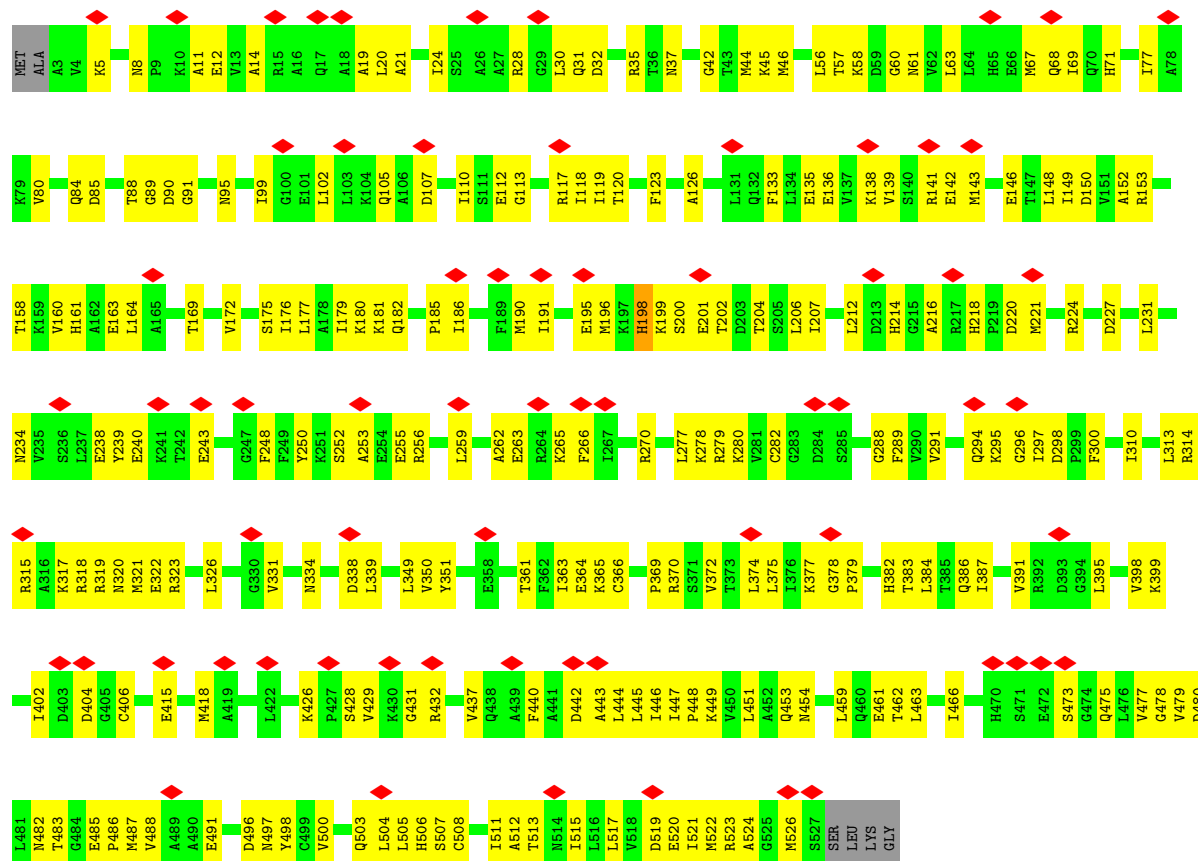


• Molecule 7: T-complex protein 1 subunit zeta

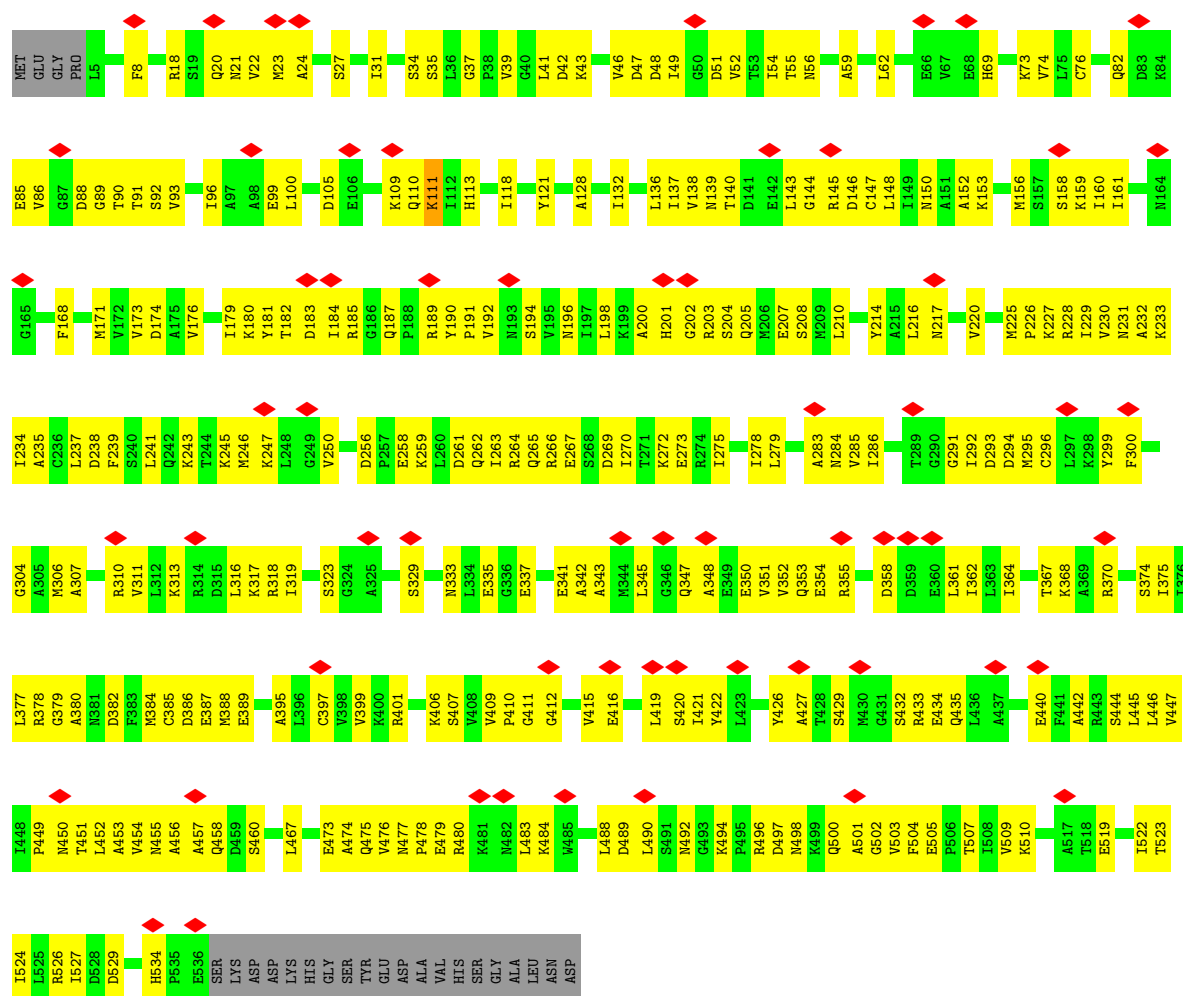




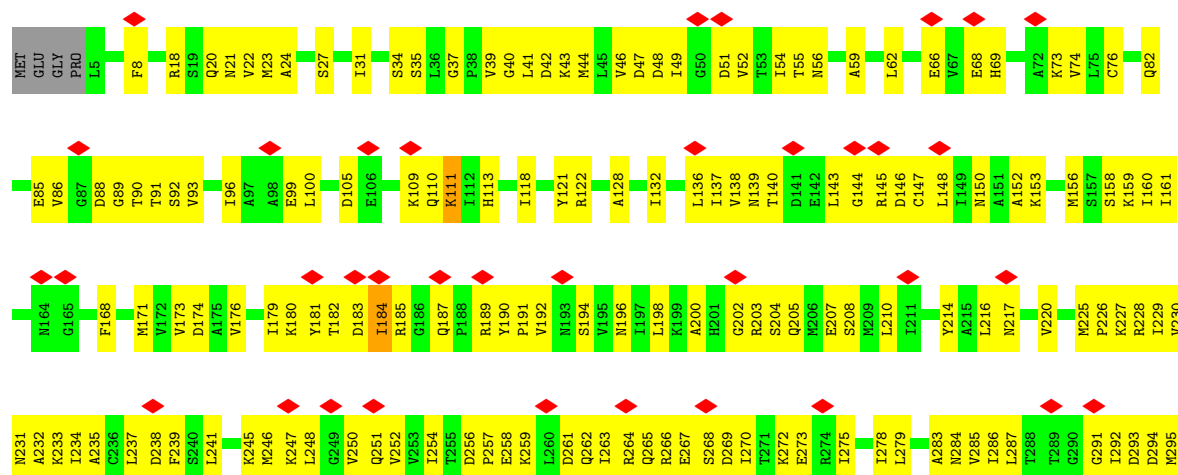
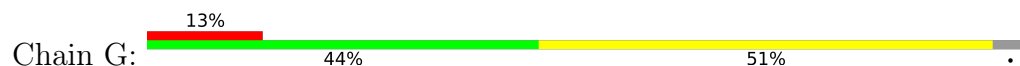
• Molecule 7: T-complex protein 1 subunit zeta



• Molecule 8: T-complex protein 1 subunit alpha



• Molecule 8: T-complex protein 1 subunit alpha



I508	V509	K510	V511	K512	E519	A520	A521	I522	T523	I524	L525	R526	I527	D528	D529	H534	P535	F536	SER	LYS	ASP	ASP	LYS	HIS	GLY	SER	TYR	GLU	ASP	ALA	VAL	HIS	SER	GLY	ALA	LEU	ASN	ASP																	
L436	A437	E440	F441	A442	R443	S444	L445	L446	V447	I448	P449	N450	T451	L452	A453	V454	N455	A456	A457	Q458	D459	S460	L467	E473	A474	Q475	V476	N477	P478	E479	R480	K481	M482	L483	K484	L488	D489	L490	S491	N492	G493	K494	P495	R496	D497	N498	K499	Q500	A501	G502	V503	F504	E505	P506	T507
I364	T367	K368	A369	R370	I375	I376	L377	R378	G379	A380	N381	D382	F383	M384	C385	D386	E387	M388	E389	D394	A395	L396	C397	V398	V399	K400	R401	K406	S407	V408	V409	P410	G411	G412	G413	A414	V415	E416	L419	S420	I421	Y422	L423	Y426	A427	T428	S429	M430	G431	S432	R433	E434	Q435		
C296	L297	K298	Y299	F300	G304	A305	M306	A307	R310	V311	L312	K313	L316	K317	R318	I319	K321	A320	A322	S323	G324	A325	S329	T330	N333	L334	E335	G336	E337	F340	E341	A342	A343	P344	L345	Q346	Q347	A348	E349	E350	V351	V352	Q353	E354	R355	I356	C357	D358	D359	E360	L361	I362	L363		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	334000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.073	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	369.6, 369.6, 369.6	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	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	D	0.32	0/4112	0.52	2/5539 (0.0%)
1	L	0.32	0/4112	0.51	2/5539 (0.0%)
2	E	0.31	0/3940	0.46	0/5311
2	M	0.31	0/3940	0.46	0/5311
3	F	0.31	0/3943	0.50	0/5322
3	N	0.31	0/3943	0.50	0/5322
4	H	0.32	0/4095	0.52	1/5523 (0.0%)
4	P	0.33	0/4095	0.52	1/5523 (0.0%)
5	C	0.33	0/4064	0.50	0/5487
5	K	0.33	0/4064	0.50	0/5487
6	B	0.32	0/4051	0.51	2/5474 (0.0%)
6	J	0.31	0/4051	0.51	2/5474 (0.0%)
7	A	0.32	0/4070	0.47	0/5487
7	I	0.32	0/4070	0.47	0/5487
8	G	0.32	0/4082	0.49	0/5511
8	O	0.32	0/4082	0.49	0/5511
All	All	0.32	0/64714	0.50	10/87308 (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	D	0	5
1	L	0	5
2	E	0	3
2	M	0	3
6	B	0	1
6	J	0	1
7	A	0	1
7	I	0	1
8	G	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	O	0	1
All	All	0	22

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	J	404	ARG	CA-C-N	-5.37	115.14	121.90
6	J	404	ARG	C-N-CA	-5.37	115.14	121.90
6	B	404	ARG	CA-C-N	-5.36	115.15	121.90
6	B	404	ARG	C-N-CA	-5.36	115.15	121.90
4	H	46	MET	CB-CG-SD	-5.20	97.09	112.70

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	160	LYS	Peptide
1	L	163	GLU	Peptide
1	L	440	CYS	Peptide
1	L	441	PRO	Peptide
1	L	442	THR	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	D	4063	0	4183	270	0
1	L	4063	0	4183	257	0
2	E	3898	0	4008	198	0
2	M	3898	0	4008	216	0
3	F	3911	0	4115	238	0
3	N	3911	0	4115	232	0
4	H	4050	0	4185	247	0
4	P	4050	0	4185	254	0
5	C	4007	0	4110	235	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	K	4007	0	4110	211	0
6	B	3994	0	4063	245	0
6	J	3994	0	4063	251	0
7	A	4023	0	4161	217	0
7	I	4023	0	4161	230	0
8	G	4043	0	4203	267	0
8	O	4043	0	4203	255	0
All	All	63978	0	66056	3401	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 26.

The worst 5 of 3401 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)
3:F:269:TYR:HA	8:G:266:ARG:HH12	1.14	1.06
4:P:507:LYS:HE2	8:O:204:SER:HB3	1.44	0.98
6:J:522:ASP:OD1	7:I:45:LYS:NZ	1.97	0.97
4:H:507:LYS:HE2	8:G:204:SER:HB3	1.46	0.94
6:B:522:ASP:OD1	7:A:45:LYS:NZ	2.02	0.93

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	D	525/541 (97%)	484 (92%)	38 (7%)	3 (1%)	21 58
1	L	525/541 (97%)	484 (92%)	38 (7%)	3 (1%)	21 58
2	E	516/535 (96%)	477 (92%)	39 (8%)	0	100 100
2	M	516/535 (96%)	477 (92%)	39 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	516/539 (96%)	473 (92%)	42 (8%)	1 (0%)	43	77
3	N	516/539 (96%)	473 (92%)	42 (8%)	1 (0%)	43	77
4	H	519/545 (95%)	481 (93%)	37 (7%)	1 (0%)	43	77
4	P	519/545 (95%)	481 (93%)	37 (7%)	1 (0%)	43	77
5	C	520/543 (96%)	490 (94%)	30 (6%)	0	100	100
5	K	520/543 (96%)	490 (94%)	30 (6%)	0	100	100
6	B	522/548 (95%)	478 (92%)	44 (8%)	0	100	100
6	J	522/548 (95%)	478 (92%)	44 (8%)	0	100	100
7	A	523/531 (98%)	484 (92%)	39 (8%)	0	100	100
7	I	523/531 (98%)	484 (92%)	39 (8%)	0	100	100
8	G	530/556 (95%)	484 (91%)	44 (8%)	2 (0%)	30	67
8	O	530/556 (95%)	484 (91%)	44 (8%)	2 (0%)	30	67
All	All	8342/8676 (96%)	7702 (92%)	626 (8%)	14 (0%)	44	77

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	L	441	PRO
1	L	442	THR
1	L	443	LEU
1	D	441	PRO
1	D	442	THR

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	D	445/456 (98%)	445 (100%)	0	100	100
1	L	445/456 (98%)	445 (100%)	0	100	100
2	E	412/427 (96%)	412 (100%)	0	100	100
2	M	412/427 (96%)	412 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	441/452 (98%)	441 (100%)	0	100	100
3	N	441/452 (98%)	441 (100%)	0	100	100
4	H	452/469 (96%)	452 (100%)	0	100	100
4	P	452/469 (96%)	452 (100%)	0	100	100
5	C	429/443 (97%)	429 (100%)	0	100	100
5	K	429/443 (97%)	429 (100%)	0	100	100
6	B	433/452 (96%)	433 (100%)	0	100	100
6	J	433/452 (96%)	433 (100%)	0	100	100
7	A	438/442 (99%)	438 (100%)	0	100	100
7	I	438/442 (99%)	438 (100%)	0	100	100
8	G	444/463 (96%)	444 (100%)	0	100	100
8	O	444/463 (96%)	444 (100%)	0	100	100
All	All	6988/7208 (97%)	6988 (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 74 such sidechains are listed below:

Mol	Chain	Res	Type
8	O	20	GLN
8	G	425	ASN
8	O	113	HIS
8	G	20	GLN
4	P	116	GLN

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 [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.

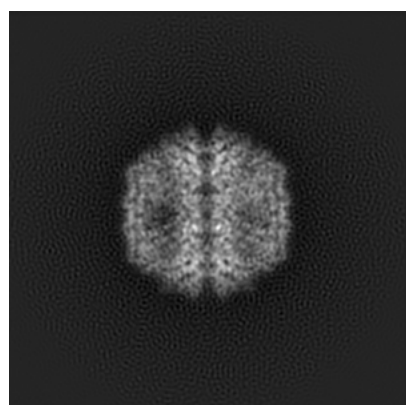
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23522. These allow visual inspection of the internal detail of the map and identification of artifacts.

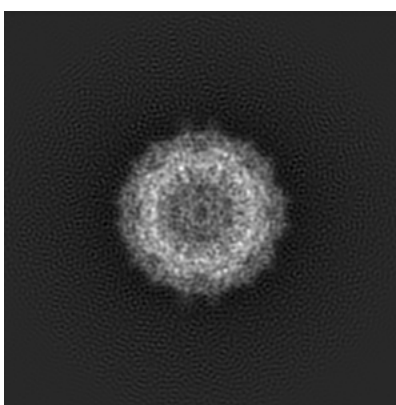
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

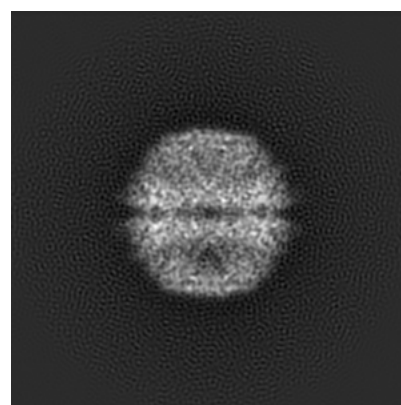
6.1.1 Primary map



X



Y

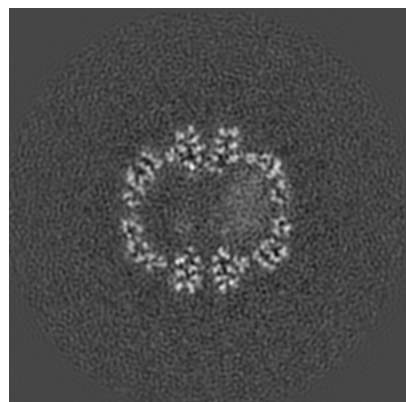


Z

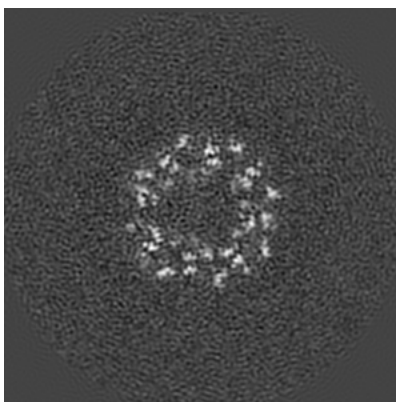
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

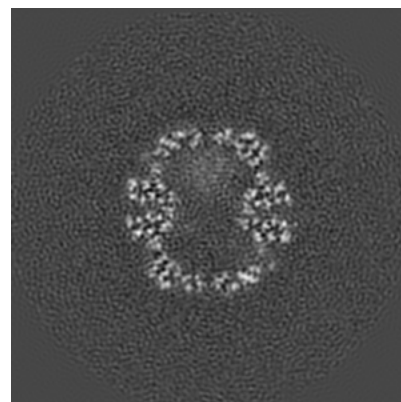
6.2.1 Primary map



X Index: 140



Y Index: 140

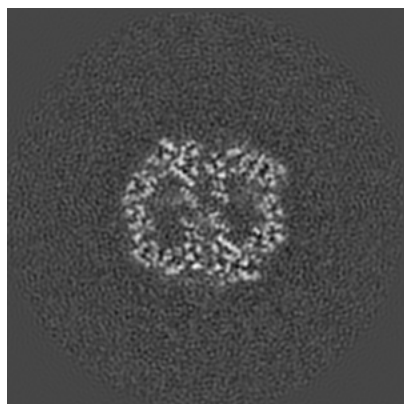


Z Index: 140

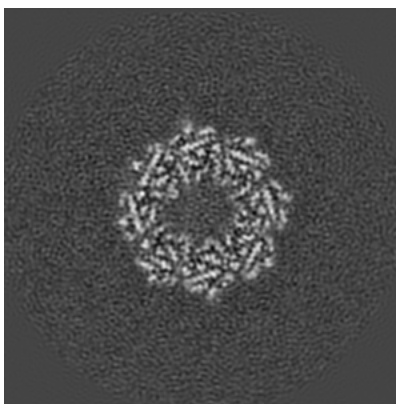
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

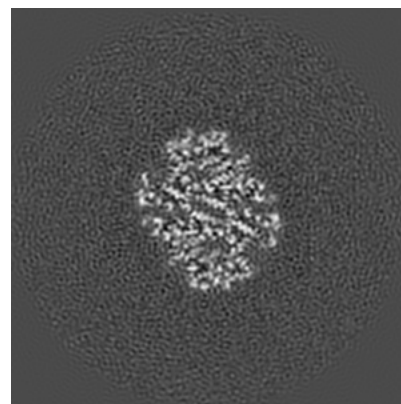
6.3.1 Primary map



X Index: 160



Y Index: 146

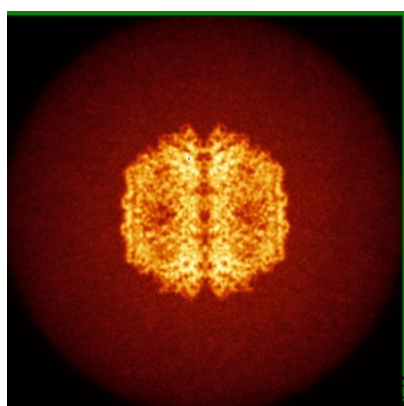


Z Index: 105

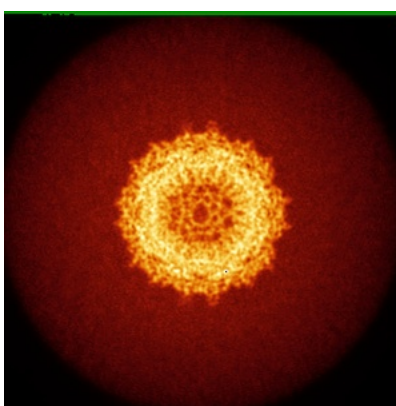
The images above show the largest variance slices of the map in three orthogonal directions.

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

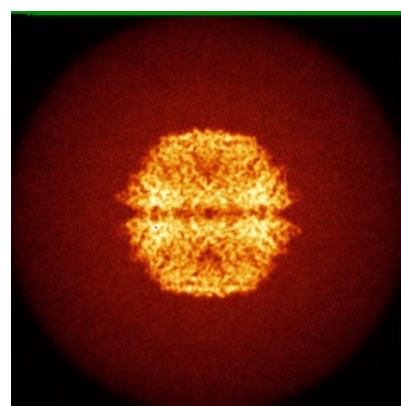
6.4.1 Primary map



X



Y

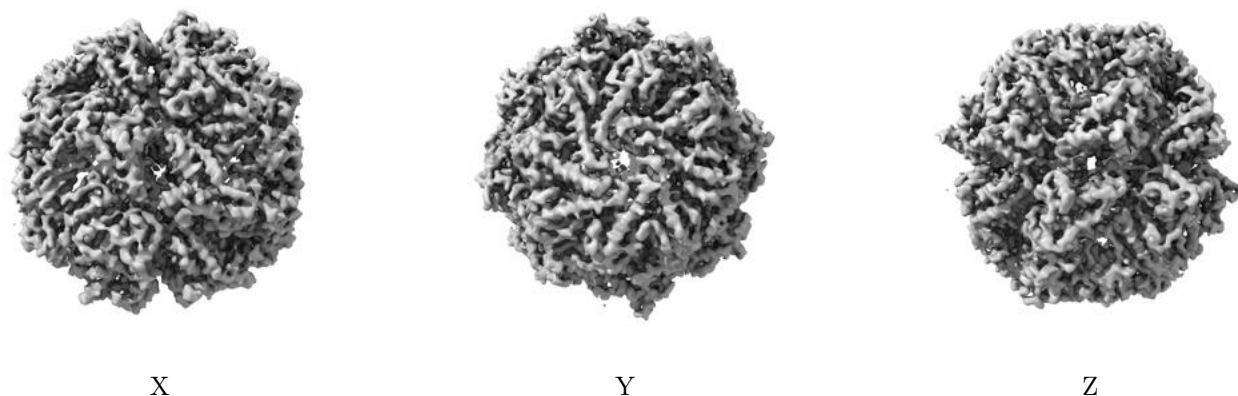


Z

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 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

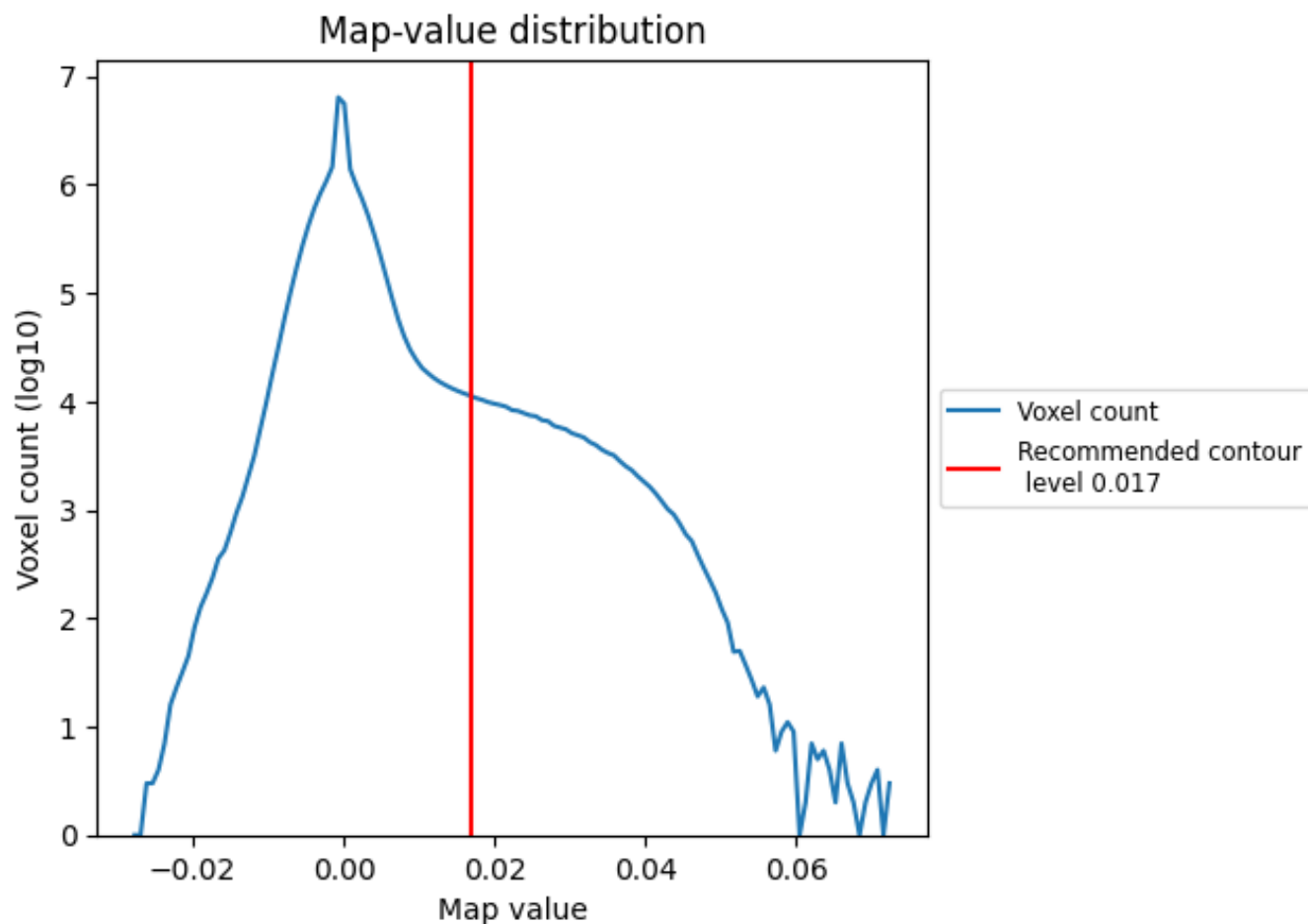
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

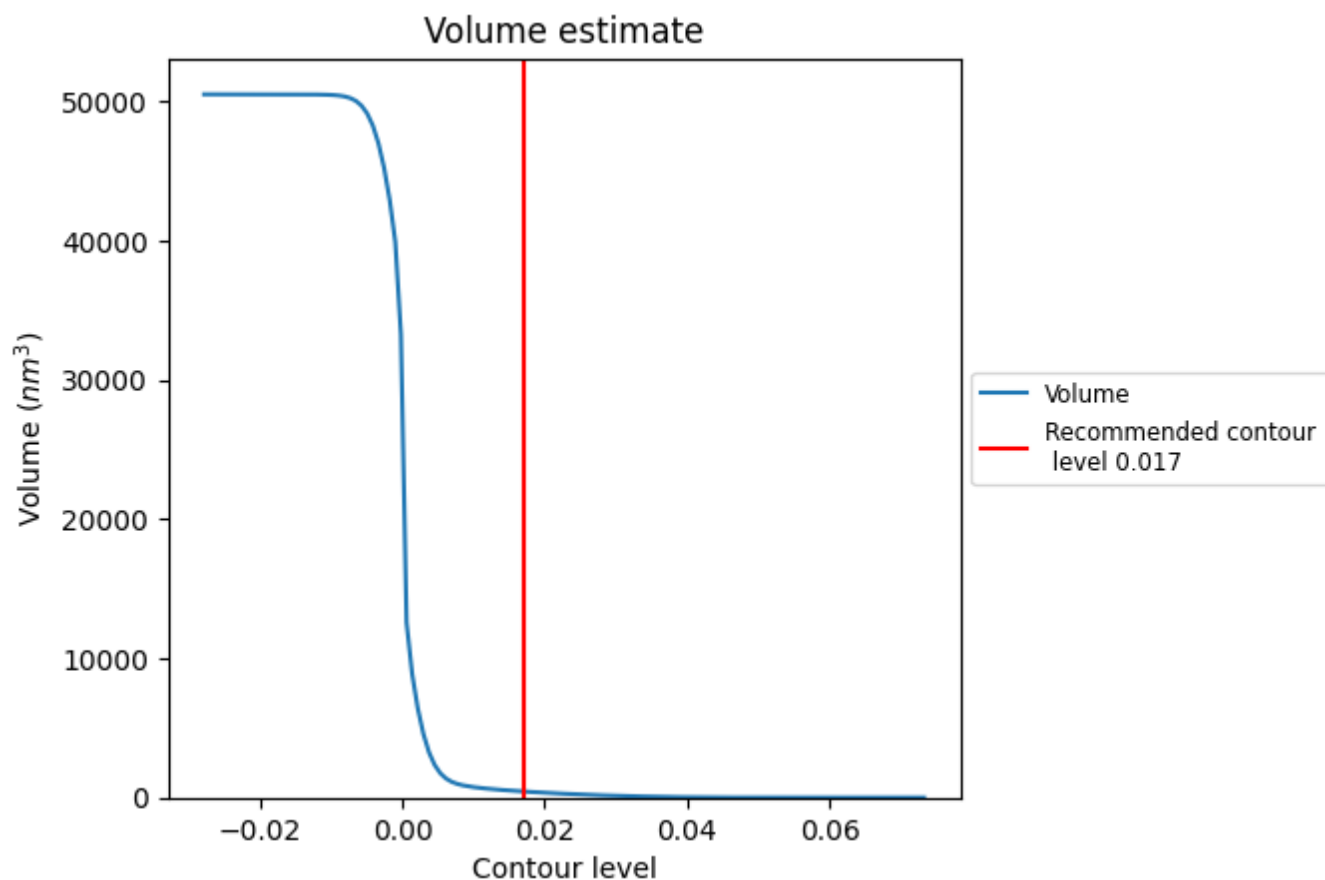
This section contains the results of statistical analysis of the map.

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.

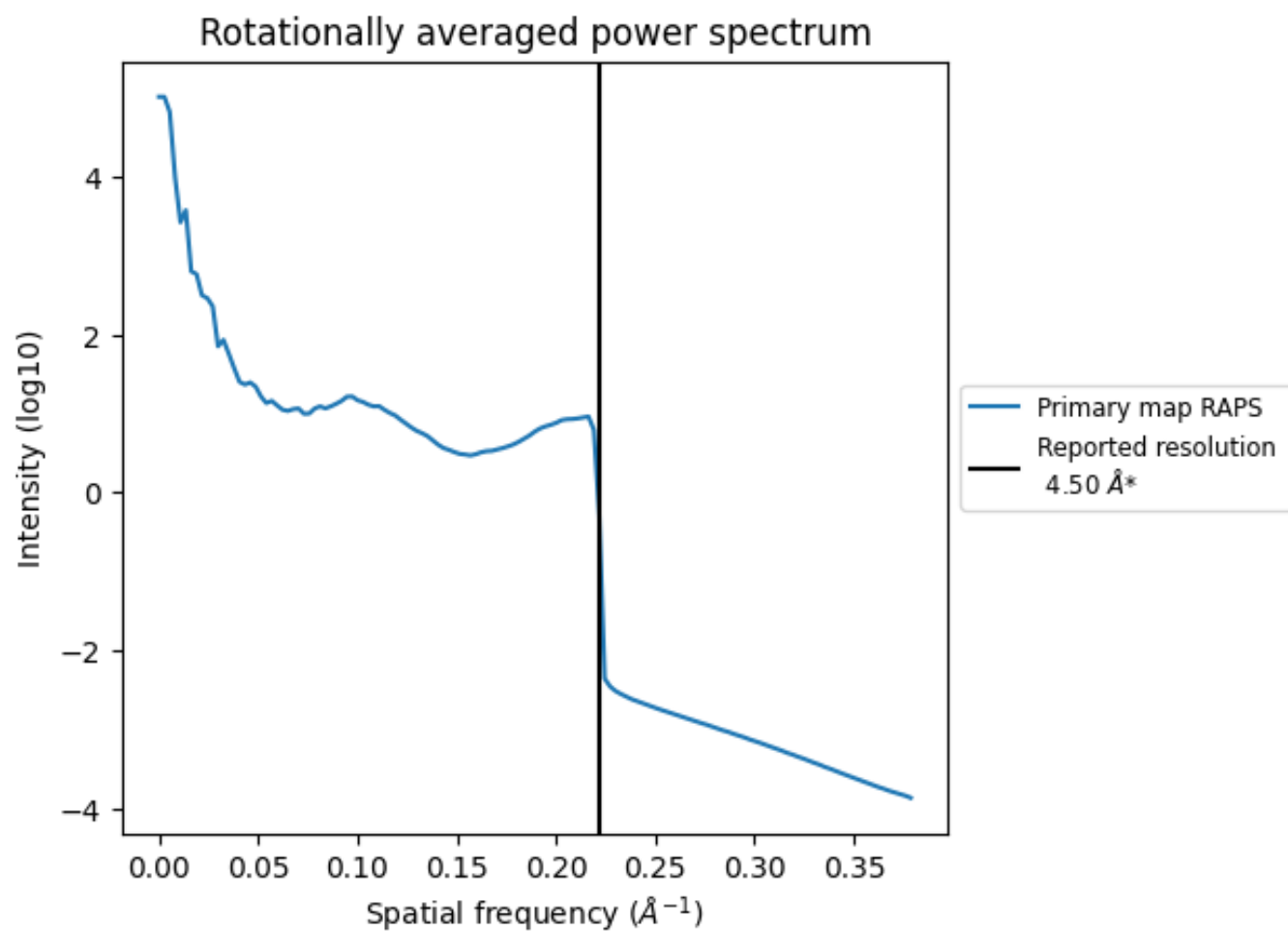
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 438 nm³; this corresponds to an approximate mass of 396 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 0.222 Å⁻¹

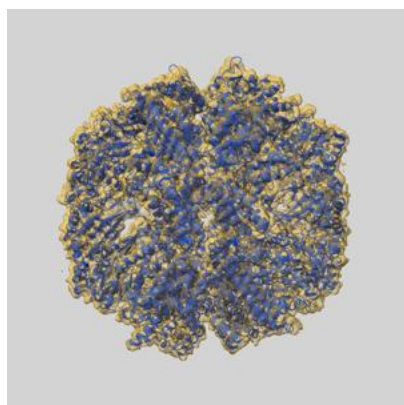
8 Fourier-Shell correlation ⓘ

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

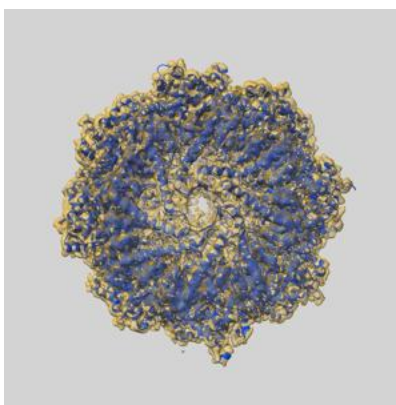
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-23522 and PDB model 7LUM. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

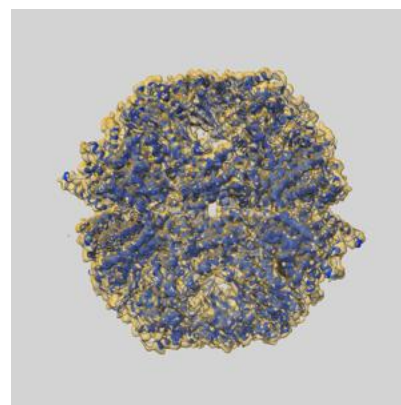
9.1 Map-model overlay [i](#)



X



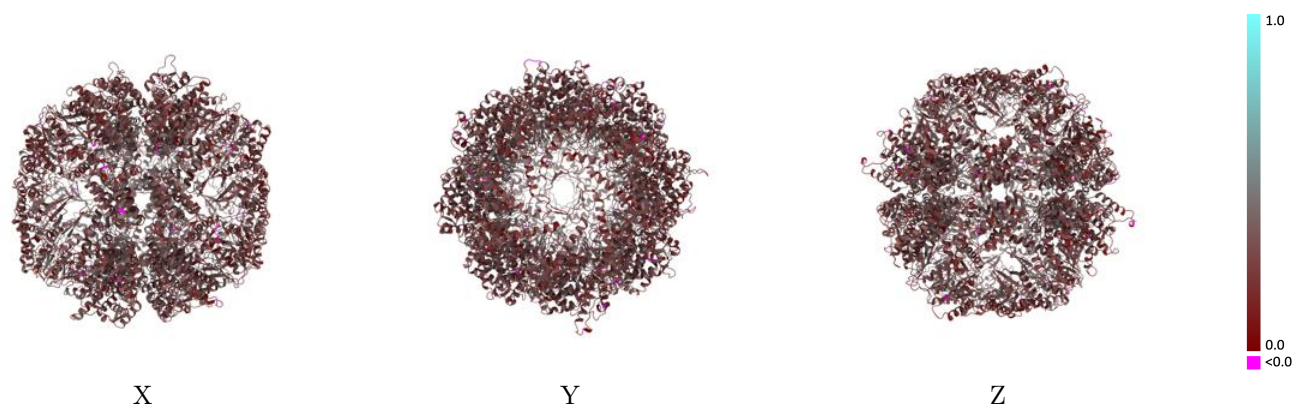
Y



Z

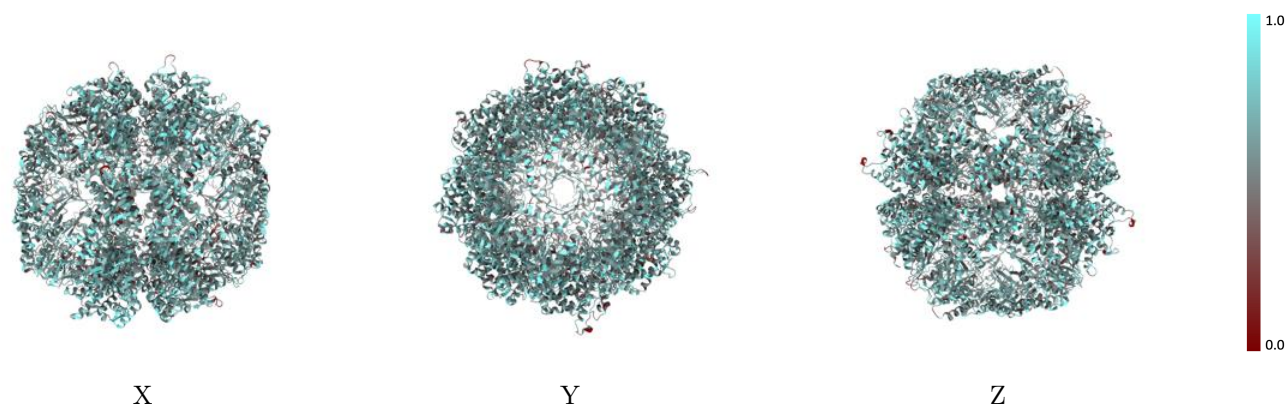
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



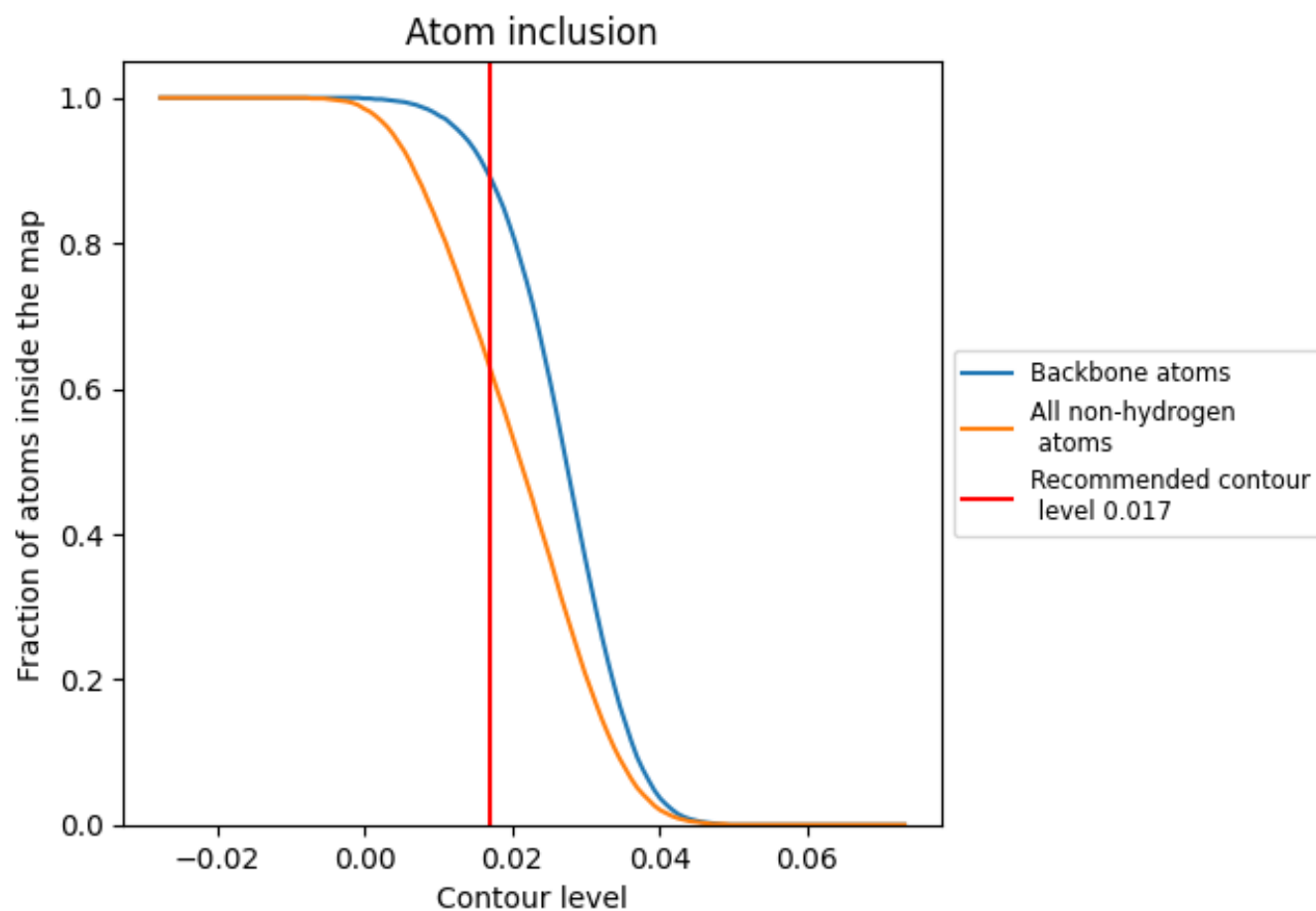
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 63% 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 (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6270	 0.2910
A	 0.6130	 0.2740
B	 0.6180	 0.2730
C	 0.6180	 0.2920
D	 0.6270	 0.3010
E	 0.6370	 0.2910
F	 0.6290	 0.2950
G	 0.6240	 0.2920
H	 0.6270	 0.2910
I	 0.6170	 0.2860
J	 0.6420	 0.3020
K	 0.6280	 0.2940
L	 0.6260	 0.2880
M	 0.6480	 0.3130
N	 0.6330	 0.2990
O	 0.6160	 0.2830
P	 0.6260	 0.2870

