



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:41 PM UTC

PDB ID : 4A0O / pdb_00004a0o
EMDB ID : EMD-1960
Title : Symmetry-free cryo-EM map of TRiC in the nucleotide-free (apo) state
Authors : Cong, Y.; Schroder, G.F.; Meyer, A.S.; Jakana, J.; Ma, B.; Dougherty, M.T.;
Schmid, M.F.; Reissmann, S.; Levitt, M.; Ludtke, S.L.; Frydman, J.; Chiu, W.
Deposited on : 2011-09-10
Resolution : 10.50 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

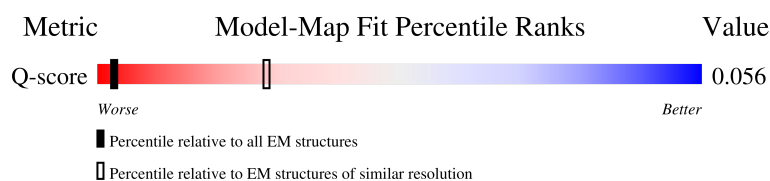
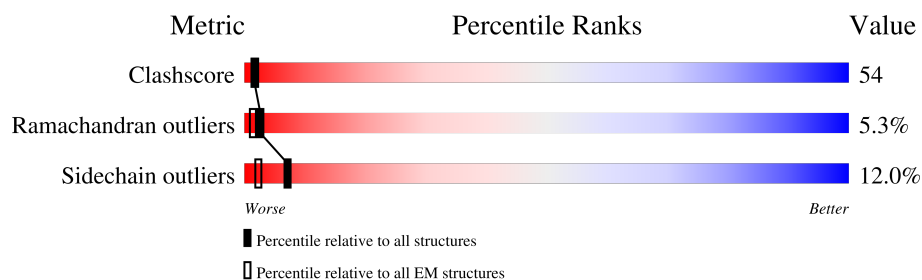
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.50 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	126 (10.00 - 11.00)

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	A	513	19% 25% 32% 7% • 34%
1	B	513	25% 35% 49% 9% • •
1	C	513	23% 34% 49% 10% • 6%
1	D	513	14% 33% 50% 10% • 5%

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Mol	Chain	Length	Quality of chain
1	E	513	
1	F	513	
1	G	513	
1	H	513	
1	I	513	
1	J	513	
1	K	513	
1	L	513	
1	M	513	
1	N	513	
1	O	513	
1	P	513	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 56830 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.

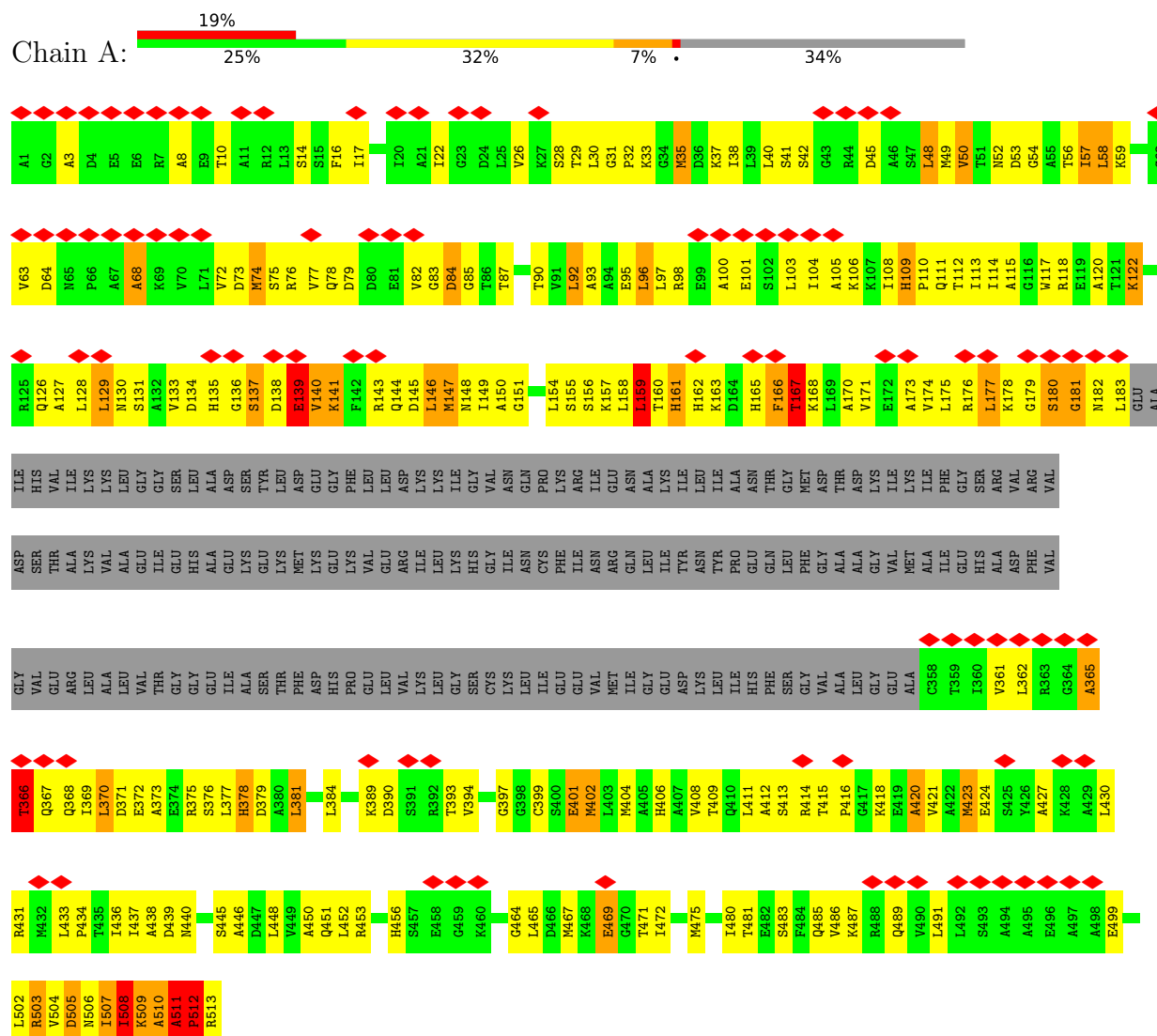
- Molecule 1 is a protein called T-COMPLEX PROTEIN 1 SUBUNIT BETA.

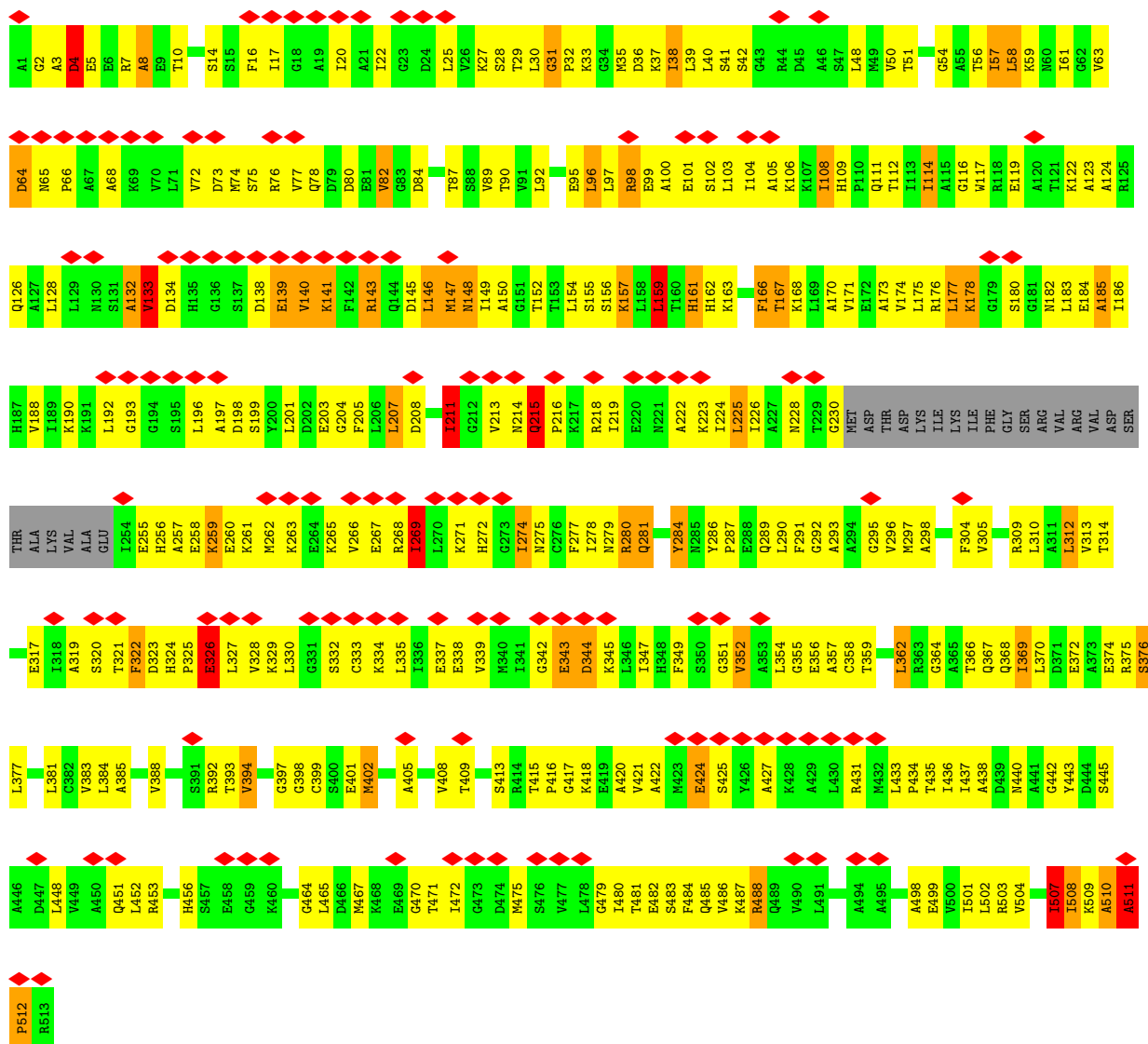
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	339	Total	C	N	O	S	0	0
			2510	1552	449	496	13		
1	B	490	Total	C	N	O	S	0	0
			3677	2299	647	713	18		
1	C	482	Total	C	N	O	S	0	0
			3608	2255	634	701	18		
1	D	489	Total	C	N	O	S	0	0
			3666	2291	644	712	19		
1	E	492	Total	C	N	O	S	0	0
			3693	2308	649	717	19		
1	F	488	Total	C	N	O	S	0	0
			3661	2288	643	711	19		
1	G	513	Total	C	N	O	S	0	0
			3855	2409	679	748	19		
1	H	493	Total	C	N	O	S	0	0
			3702	2313	650	720	19		
1	I	473	Total	C	N	O	S	0	0
			3530	2206	620	686	18		
1	J	490	Total	C	N	O	S	0	0
			3673	2295	645	714	19		
1	K	496	Total	C	N	O	S	0	0
			3723	2327	654	723	19		
1	L	491	Total	C	N	O	S	0	0
			3685	2304	648	714	19		
1	M	388	Total	C	N	O	S	0	0
			2881	1792	506	569	14		
1	N	486	Total	C	N	O	S	0	0
			3643	2277	640	707	19		
1	O	481	Total	C	N	O	S	0	0
			3600	2251	633	698	18		
1	P	496	Total	C	N	O	S	0	0
			3723	2327	654	723	19		

3 Residue-property plots

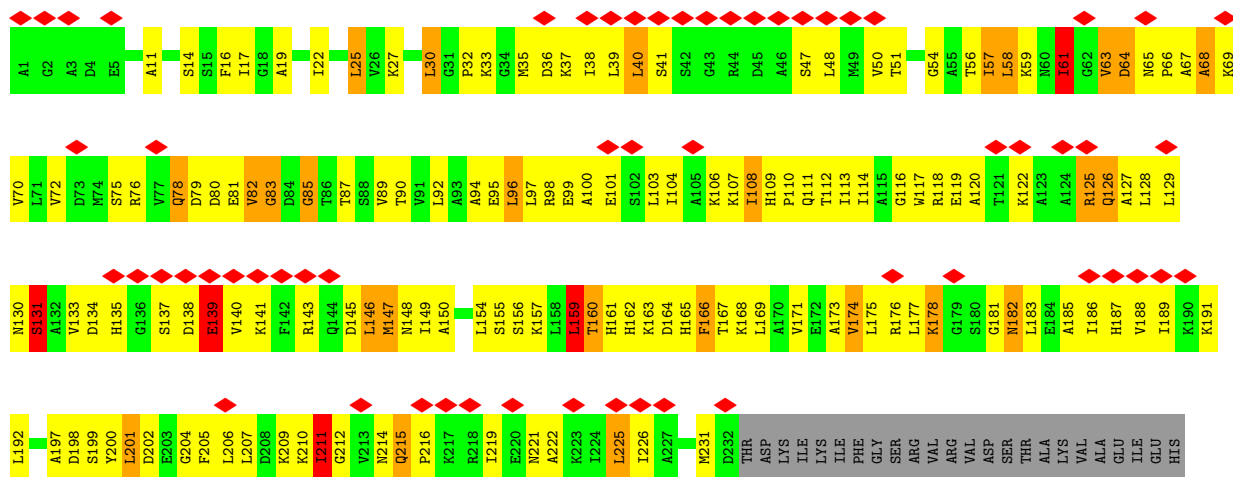
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

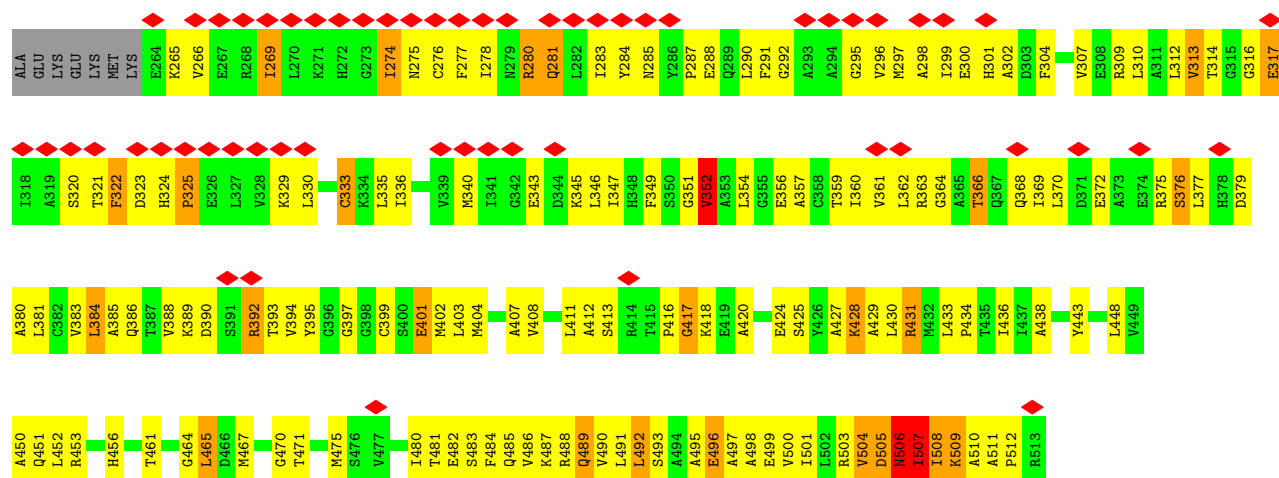
• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



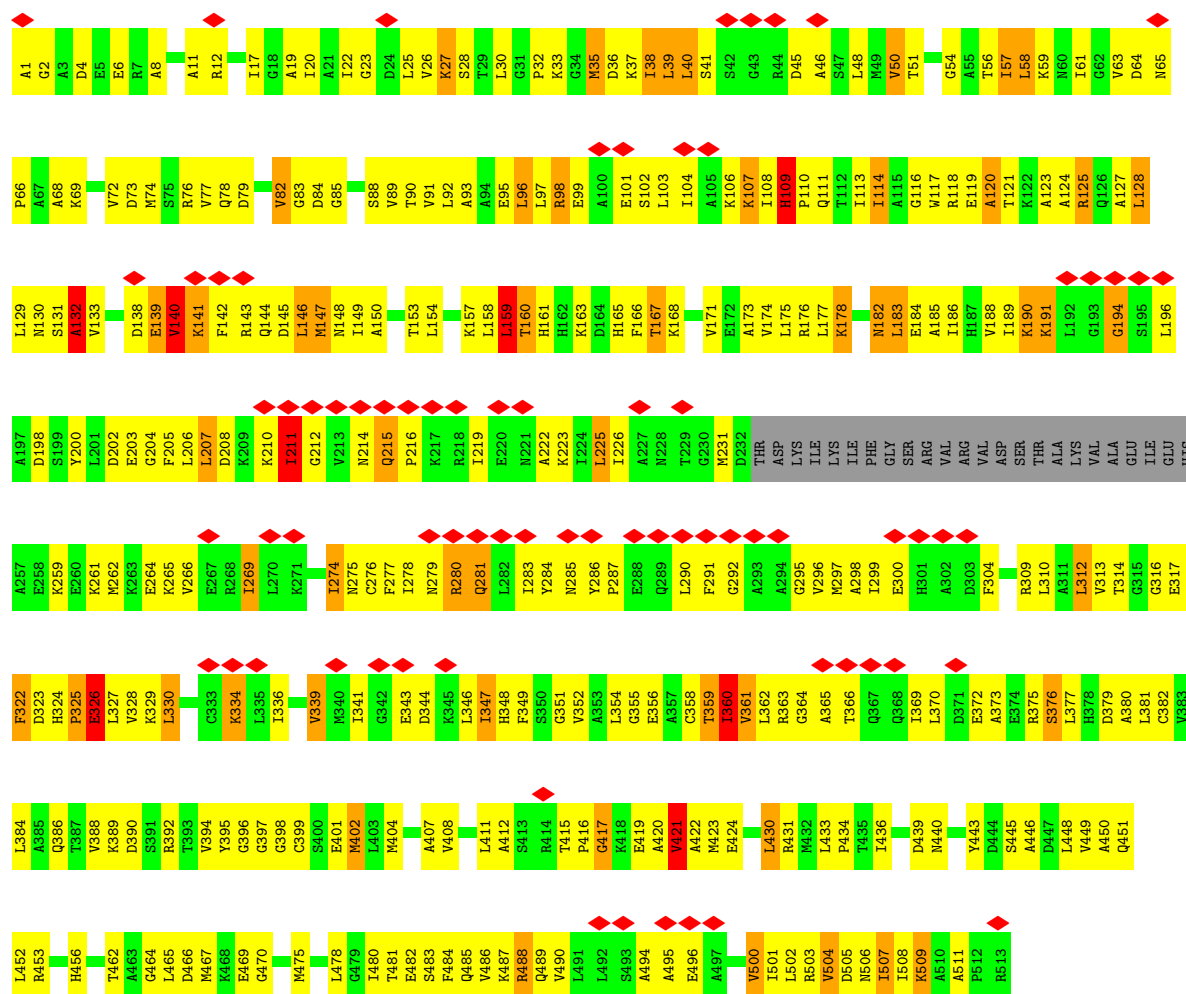


• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA





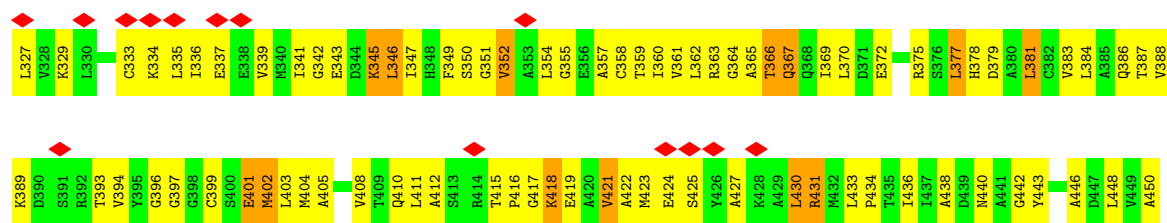
• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



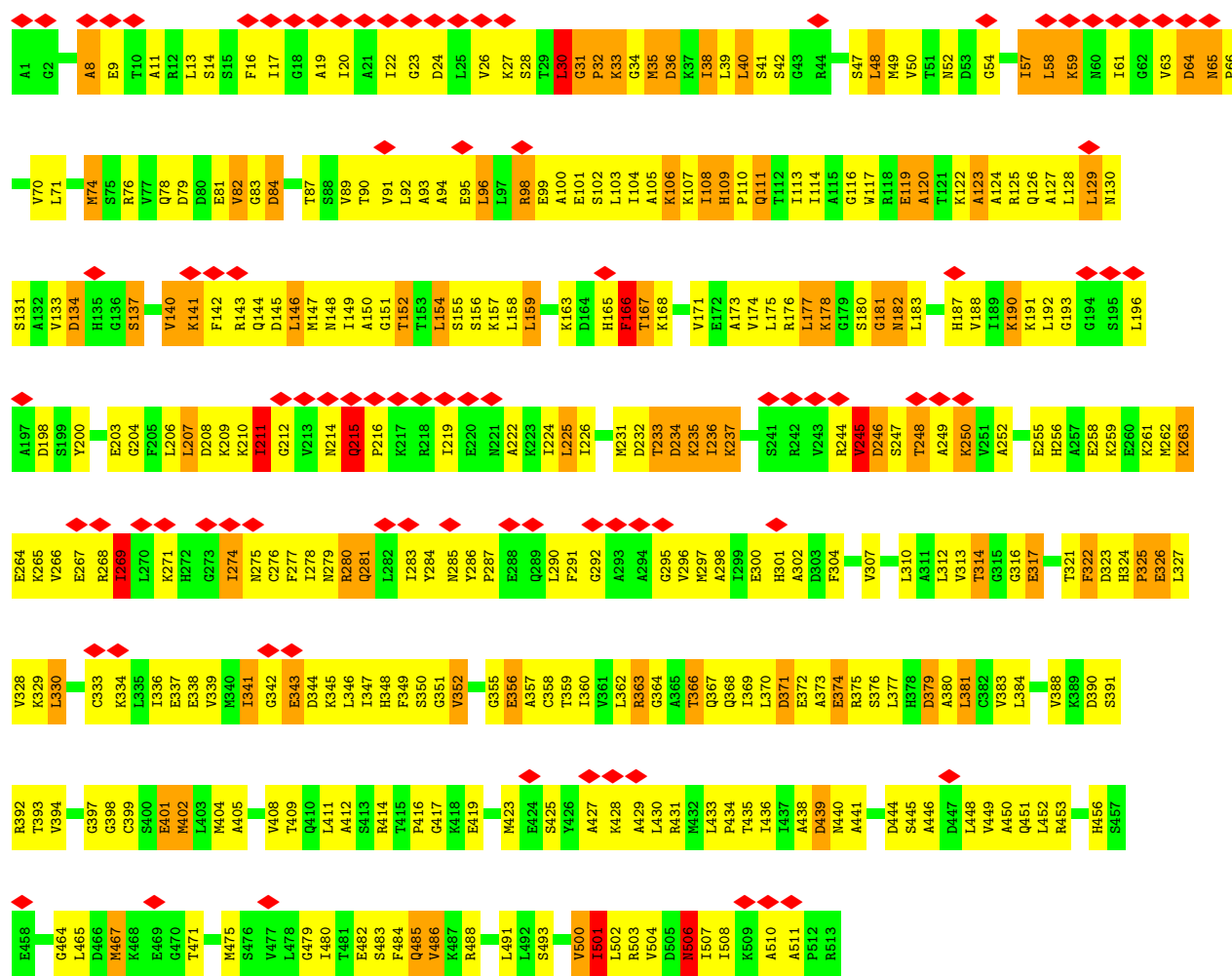
• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



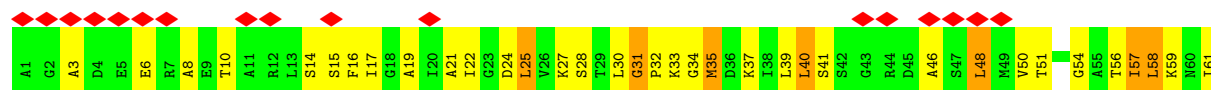


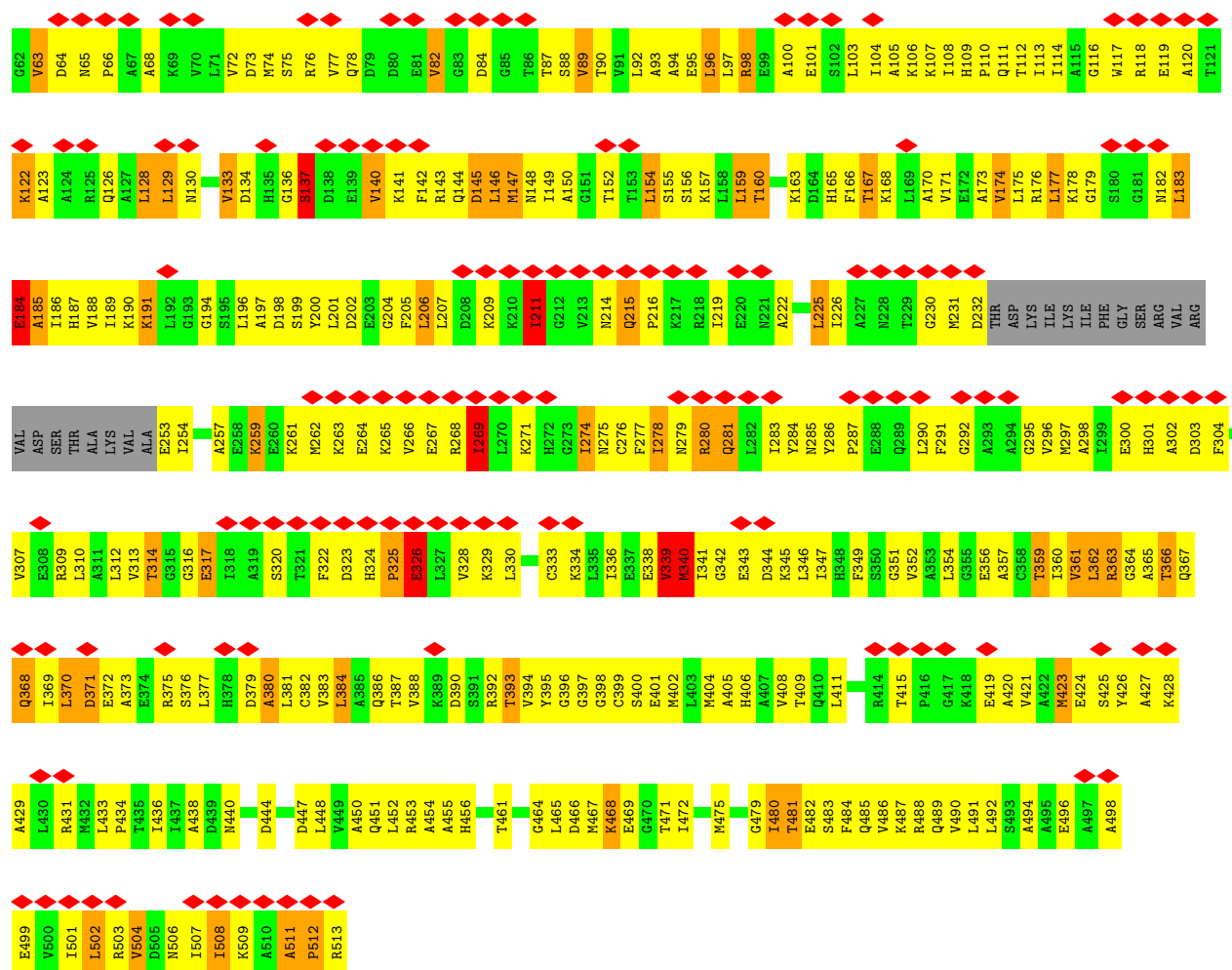


• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA

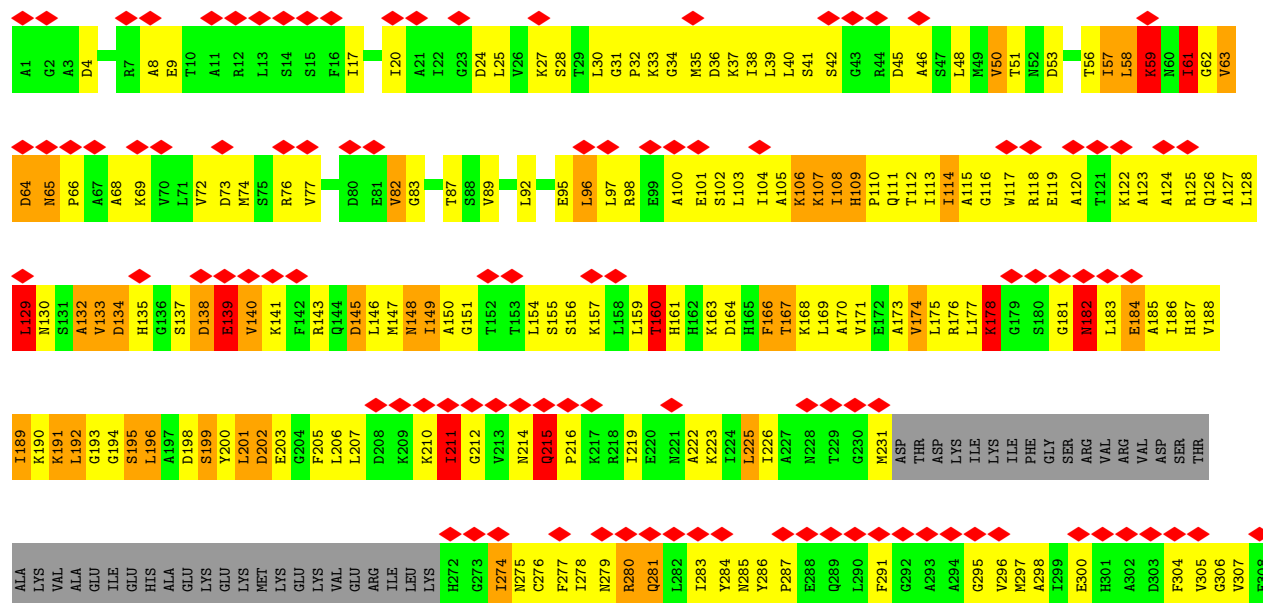


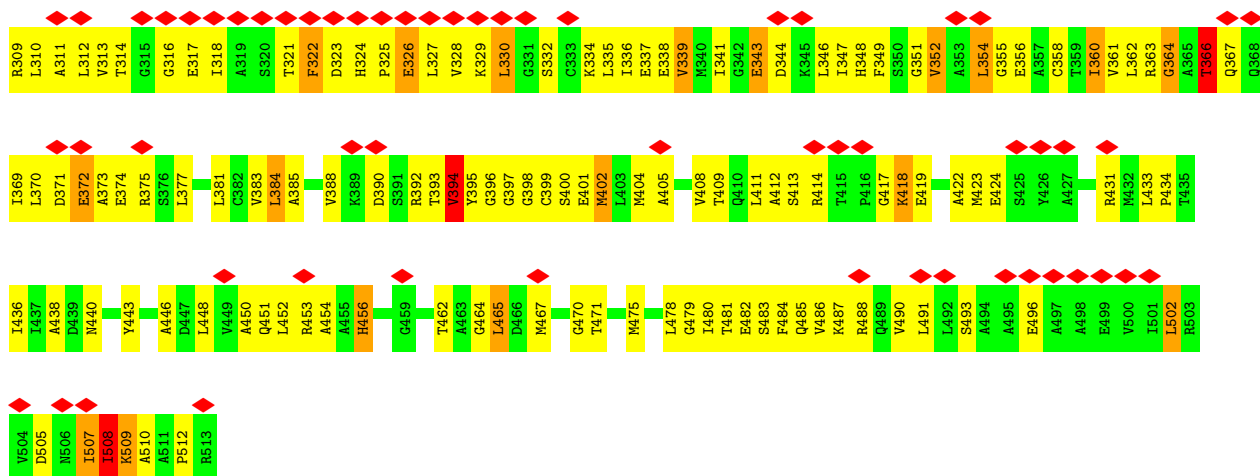
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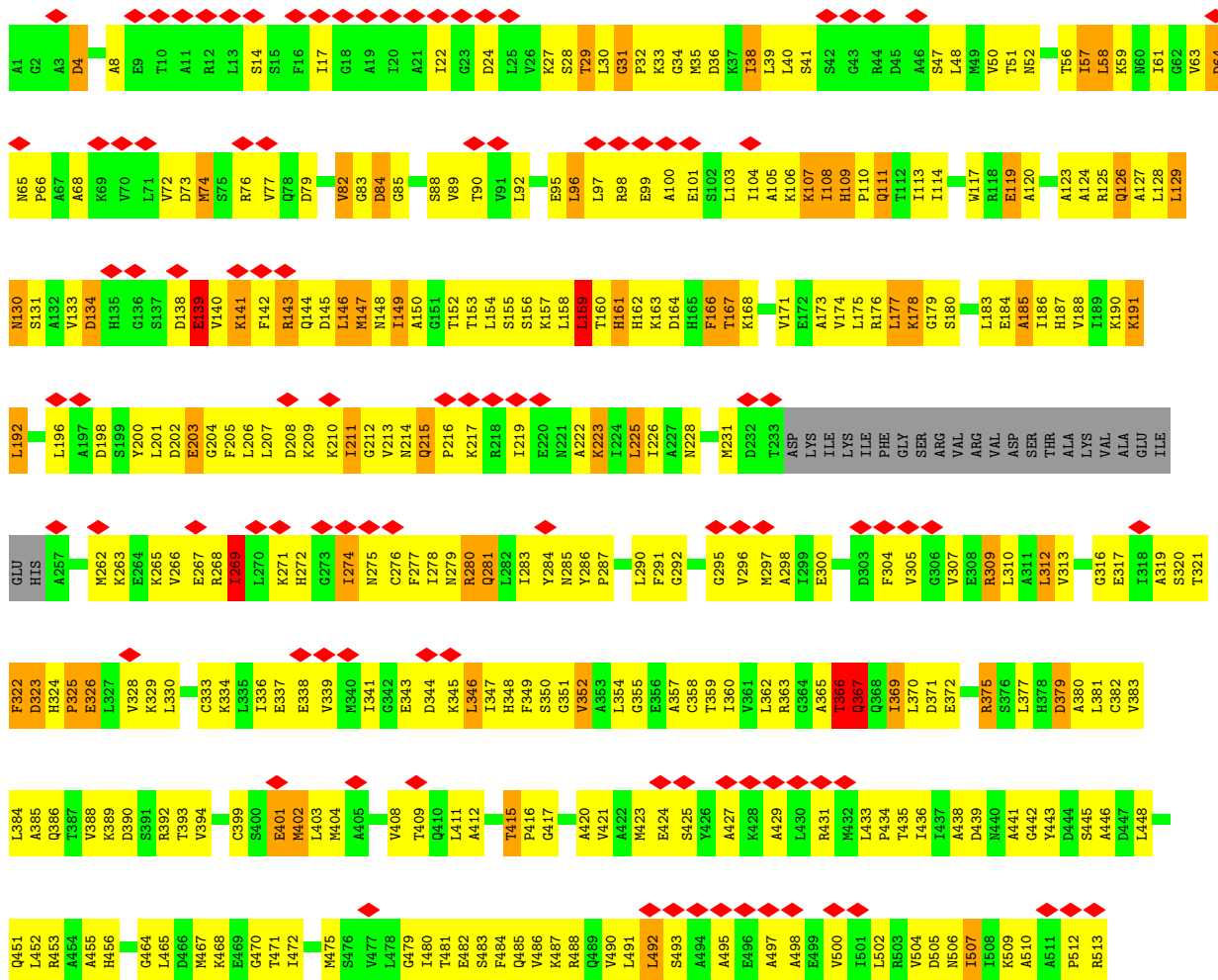


• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



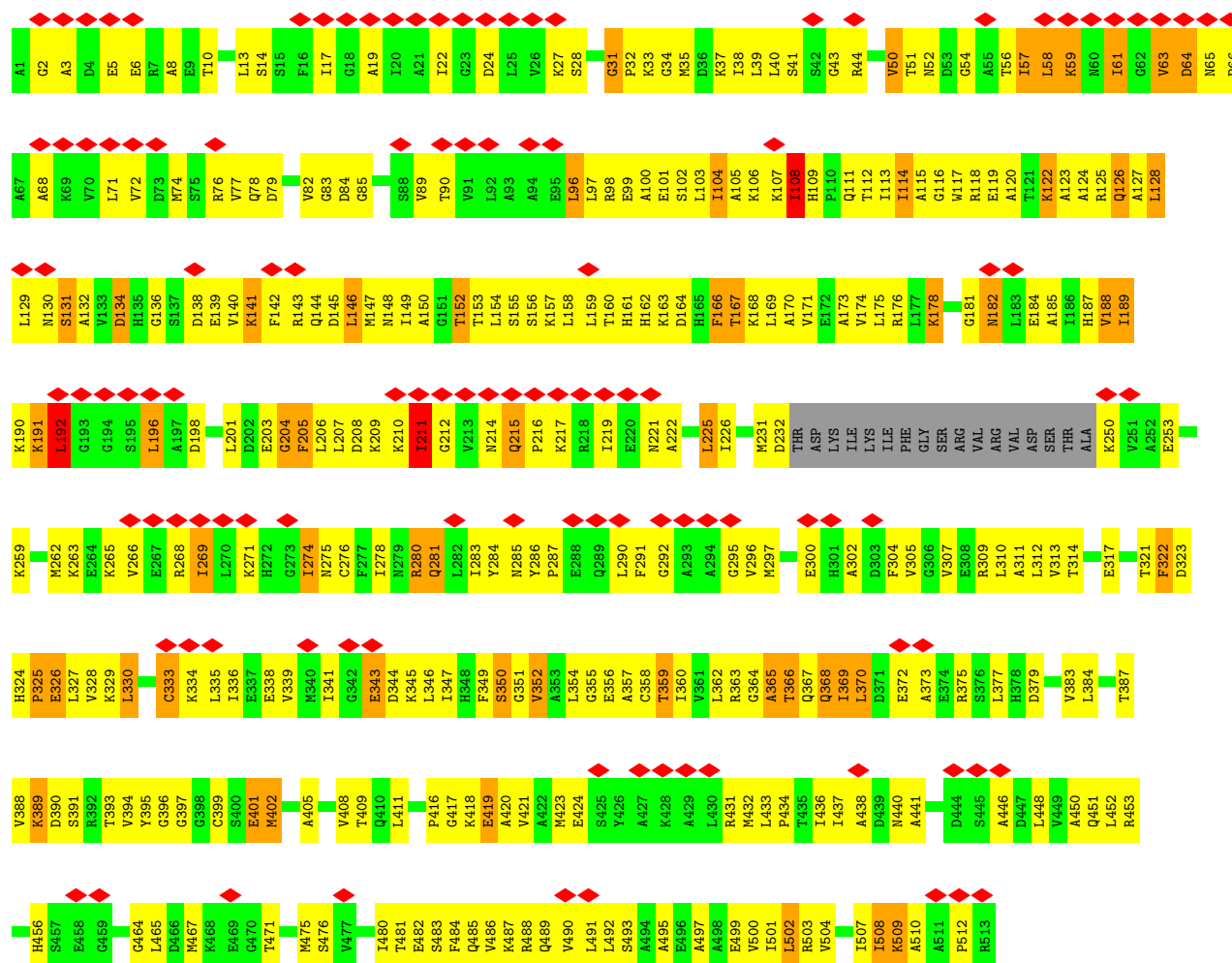


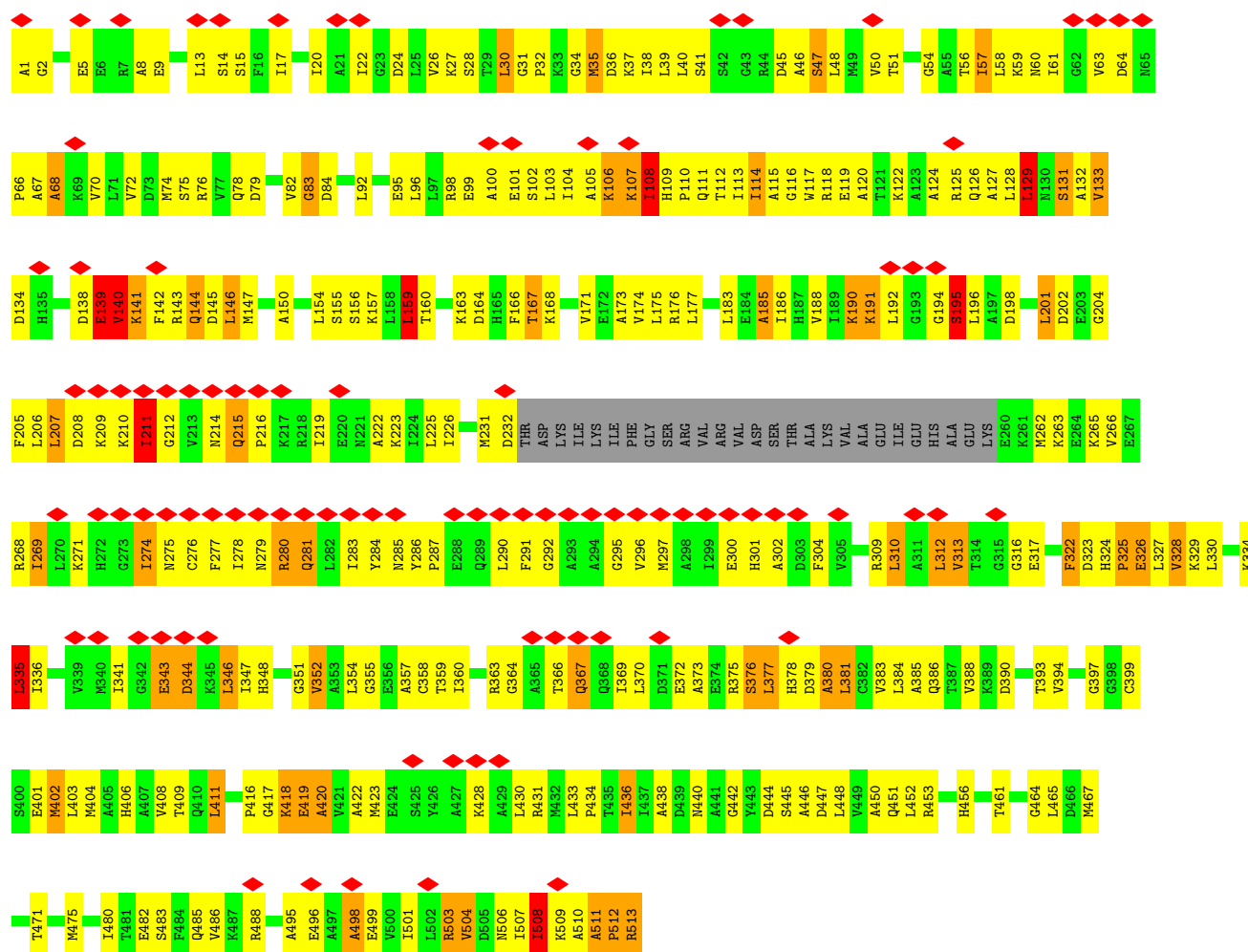
• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



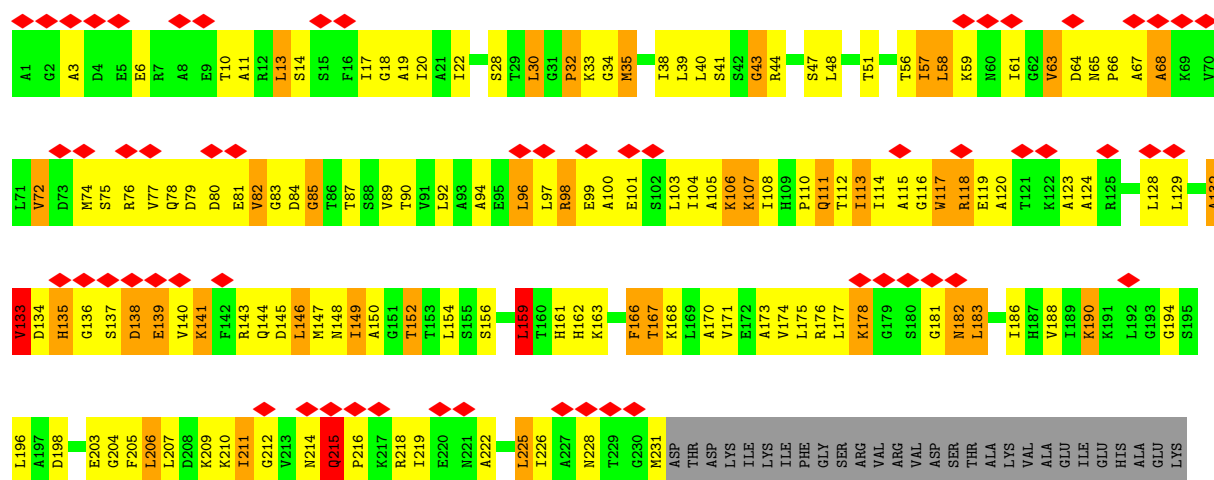
• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA

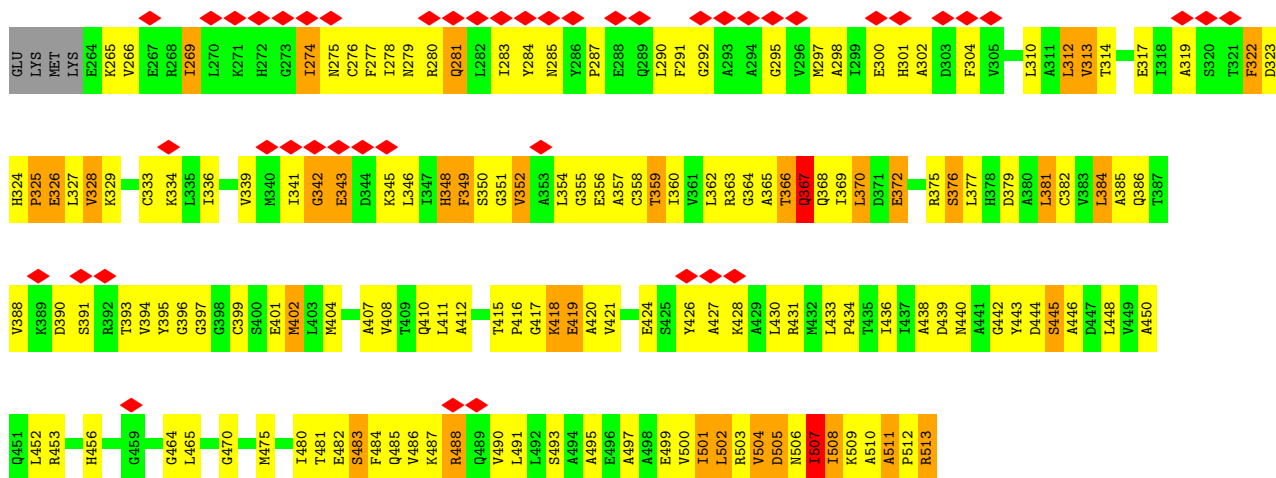




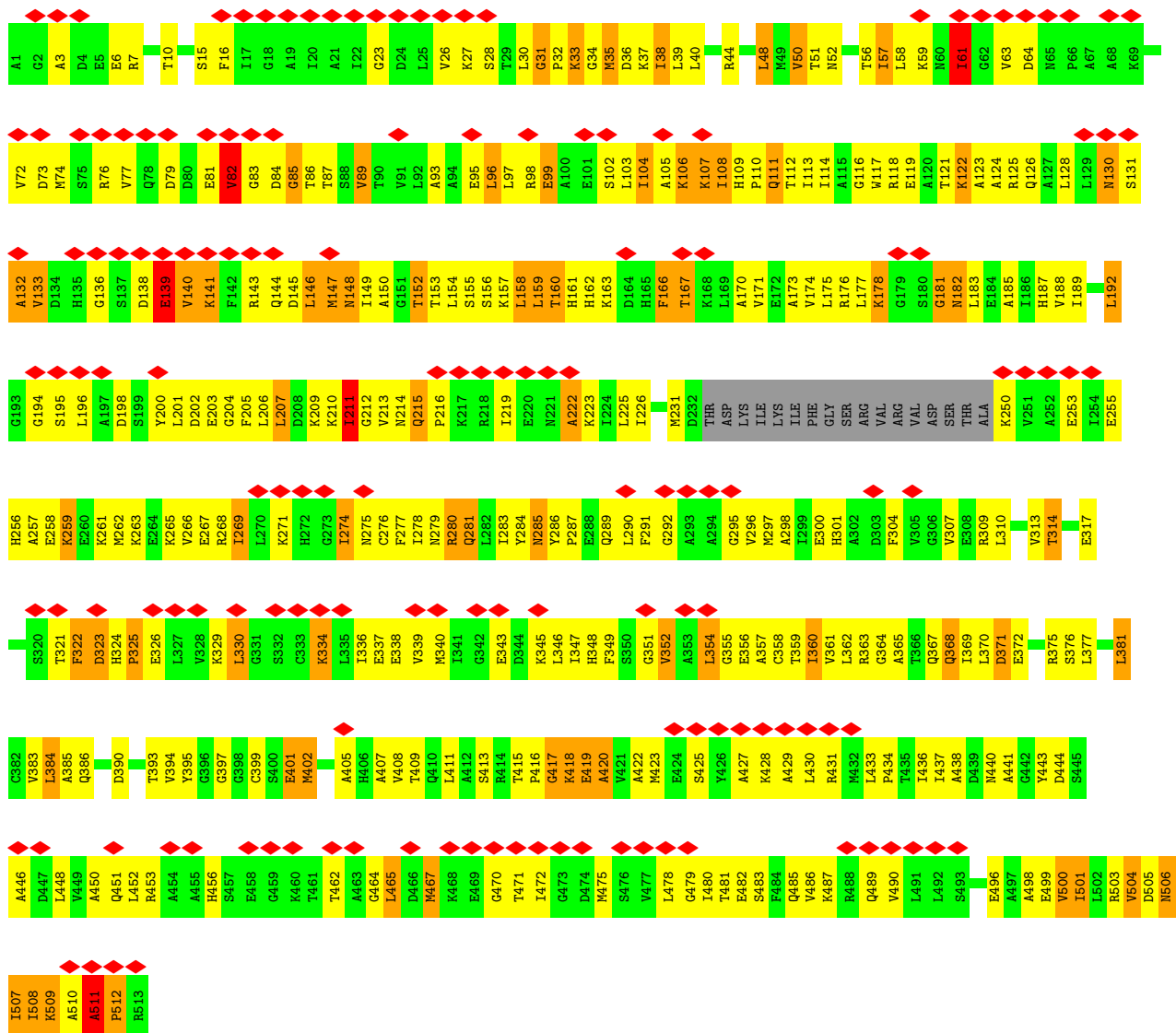


• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA





• Molecule 1: T-COMPLEX PROTEIN 1 SUBUNIT BETA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	47151	Depositor
Resolution determination method	Not provided	
CTF correction method	Not provided	
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	18	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	2.515	Depositor
Minimum map value	-0.425	Depositor
Average map value	0.075	Depositor
Map value standard deviation	0.283	Depositor
Recommended contour level	1.13	Depositor
Map size ($\text{\AA}$)	345.6, 345.6, 345.6	wwPDB
Map dimensions	144, 144, 144	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.4, 2.4, 2.4	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	0.86	1/2531 (0.0%)	1.32	18/3415 (0.5%)
1	B	0.76	0/3716	1.26	29/5007 (0.6%)
1	C	0.77	0/3646	1.27	20/4916 (0.4%)
1	D	0.79	1/3704 (0.0%)	1.29	25/4990 (0.5%)
1	E	0.72	0/3732	1.22	23/5028 (0.5%)
1	F	0.74	0/3699	1.25	20/4983 (0.4%)
1	G	0.79	0/3896	1.28	25/5249 (0.5%)
1	H	0.76	0/3741	1.33	35/5040 (0.7%)
1	I	0.78	0/3568	1.28	31/4813 (0.6%)
1	J	0.74	0/3711	1.23	21/5000 (0.4%)
1	K	0.77	0/3762	1.25	14/5068 (0.3%)
1	L	0.75	0/3724	1.27	24/5017 (0.5%)
1	M	0.79	0/2907	1.25	14/3920 (0.4%)
1	N	0.75	0/3681	1.24	23/4960 (0.5%)
1	O	0.79	0/3638	1.26	23/4905 (0.5%)
1	P	0.79	1/3762 (0.0%)	1.30	34/5068 (0.7%)
All	All	0.77	3/57418 (0.0%)	1.27	379/77379 (0.5%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	359	THR	CA-C	6.92	1.55	1.52
1	A	366	THR	N-CA	5.68	1.53	1.46
1	P	418	LYS	C-N	-5.28	1.27	1.33

The worst 5 of 379 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	183	LEU	N-CA-C	12.42	124.82	111.28
1	H	508	ILE	N-CA-C	11.48	124.24	108.17
1	L	344	ASP	N-CA-C	9.70	124.42	112.59
1	D	63	VAL	N-CA-C	9.42	120.23	110.62
1	J	63	VAL	N-CA-C	9.31	119.36	110.42

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	2510	0	2583	282	0
1	B	3677	0	3782	413	0
1	C	3608	0	3706	394	0
1	D	3666	0	3771	405	0
1	E	3693	0	3795	383	0
1	F	3661	0	3766	451	0
1	G	3855	0	3970	431	0
1	H	3702	0	3801	419	0
1	I	3530	0	3620	443	0
1	J	3673	0	3778	423	0
1	K	3723	0	3828	449	0
1	L	3685	0	3791	448	0
1	M	2881	0	2960	322	0
1	N	3643	0	3747	408	0
1	O	3600	0	3702	459	0
1	P	3723	0	3828	455	0
All	All	56830	0	58428	6177	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 54.

The worst 5 of 6177 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:E:11:ALA:HB1	1:E:506:ASN:HB3	1.23	1.18
1:G:146:LEU:HD12	1:G:171:VAL:HG13	1.25	1.17
1:C:146:LEU:HD12	1:C:171:VAL:HG13	1.24	1.17
1:H:146:LEU:HD12	1:H:171:VAL:HG13	1.14	1.14
1:P:146:LEU:HD12	1:P:171:VAL:HG13	1.23	1.13

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	335/513 (65%)	299 (89%)	14 (4%)	22 (7%)	1	12
1	B	486/513 (95%)	441 (91%)	18 (4%)	27 (6%)	1	14
1	C	478/513 (93%)	425 (89%)	28 (6%)	25 (5%)	1	15
1	D	485/513 (94%)	439 (90%)	21 (4%)	25 (5%)	1	15
1	E	488/513 (95%)	443 (91%)	16 (3%)	29 (6%)	1	13
1	F	484/513 (94%)	439 (91%)	22 (4%)	23 (5%)	2	16
1	G	511/513 (100%)	450 (88%)	31 (6%)	30 (6%)	1	13
1	H	489/513 (95%)	434 (89%)	31 (6%)	24 (5%)	1	16
1	I	469/513 (91%)	421 (90%)	18 (4%)	30 (6%)	1	12
1	J	486/513 (95%)	438 (90%)	25 (5%)	23 (5%)	2	16
1	K	492/513 (96%)	438 (89%)	25 (5%)	29 (6%)	1	13
1	L	487/513 (95%)	450 (92%)	21 (4%)	16 (3%)	3	21
1	M	384/513 (75%)	347 (90%)	17 (4%)	20 (5%)	1	15
1	N	482/513 (94%)	429 (89%)	26 (5%)	27 (6%)	1	14
1	O	477/513 (93%)	422 (88%)	28 (6%)	27 (6%)	1	14
1	P	492/513 (96%)	449 (91%)	21 (4%)	22 (4%)	2	17
All	All	7525/8208 (92%)	6764 (90%)	362 (5%)	399 (5%)	2	15

5 of 399 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	ALA
1	A	37	LYS
1	A	68	ALA
1	A	139	GLU
1	A	180	SER

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	266/409 (65%)	238 (90%)	28 (10%)	6	21
1	B	389/409 (95%)	349 (90%)	40 (10%)	7	23
1	C	382/409 (93%)	336 (88%)	46 (12%)	5	17
1	D	388/409 (95%)	346 (89%)	42 (11%)	6	21
1	E	391/409 (96%)	343 (88%)	48 (12%)	4	17
1	F	388/409 (95%)	346 (89%)	42 (11%)	6	21
1	G	409/409 (100%)	343 (84%)	66 (16%)	2	11
1	H	392/409 (96%)	340 (87%)	52 (13%)	4	14
1	I	373/409 (91%)	320 (86%)	53 (14%)	3	13
1	J	389/409 (95%)	344 (88%)	45 (12%)	5	18
1	K	394/409 (96%)	351 (89%)	43 (11%)	6	21
1	L	390/409 (95%)	343 (88%)	47 (12%)	5	17
1	M	305/409 (75%)	276 (90%)	29 (10%)	8	25
1	N	386/409 (94%)	341 (88%)	45 (12%)	5	18
1	O	381/409 (93%)	337 (88%)	44 (12%)	5	18
1	P	394/409 (96%)	344 (87%)	50 (13%)	4	16
All	All	6017/6544 (92%)	5297 (88%)	720 (12%)	7	17

5 of 720 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	57	ILE
1	M	367	GLN
1	K	146	LEU
1	K	50	VAL
1	L	133	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
1	O	161	HIS
1	O	367	GLN
1	P	451	GLN
1	F	451	GLN
1	F	386	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.

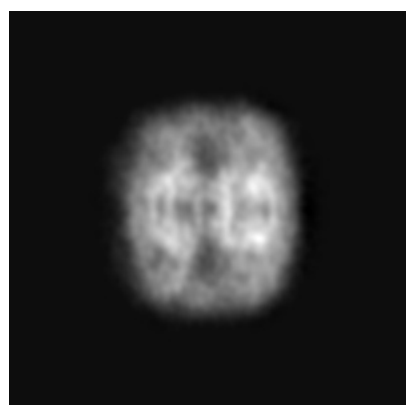
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1960. These allow visual inspection of the internal detail of the map and identification of artifacts.

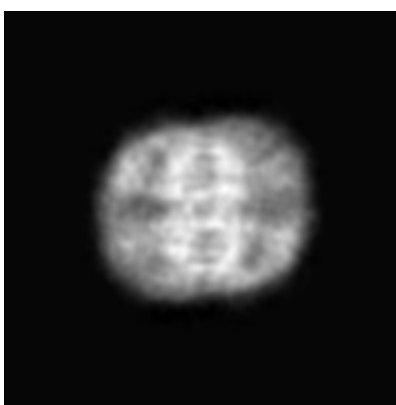
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

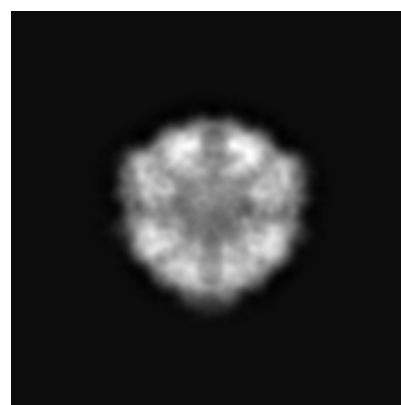
6.1.1 Primary map



X



Y

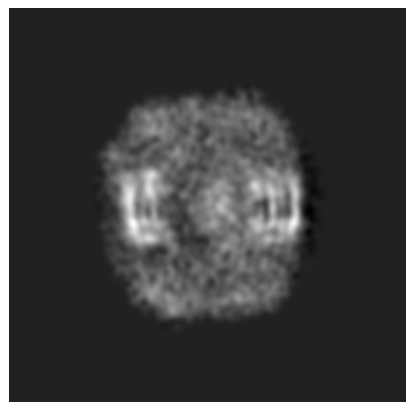


Z

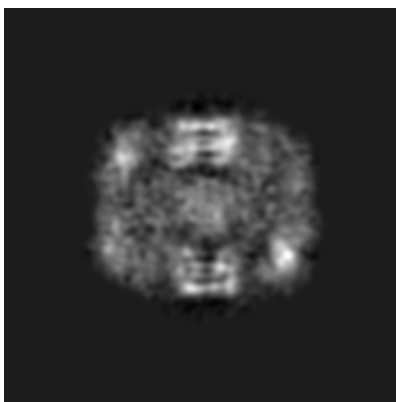
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

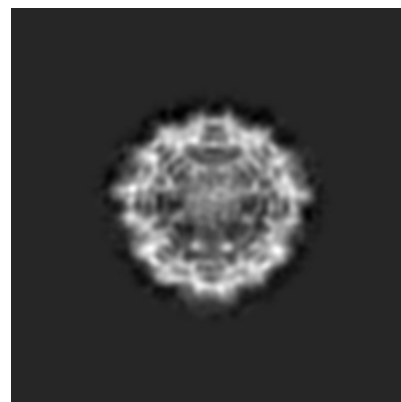
6.2.1 Primary map



X Index: 72



Y Index: 72

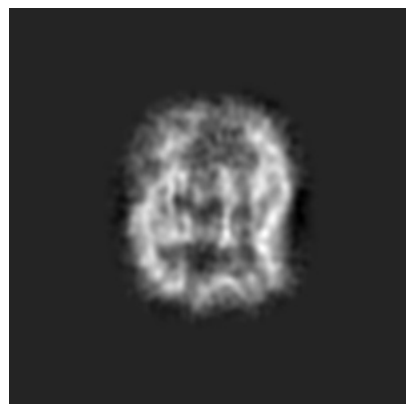


Z Index: 72

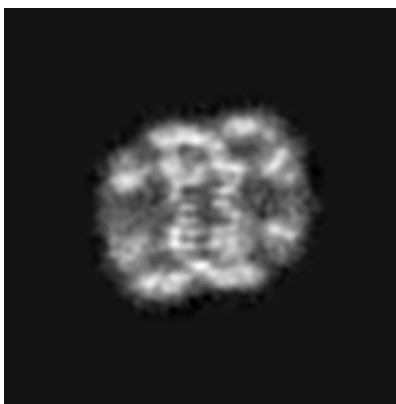
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

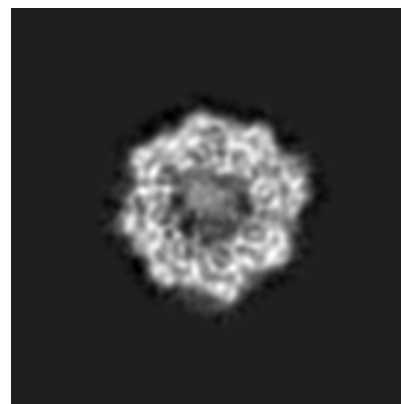
6.3.1 Primary map



X Index: 87



Y Index: 89

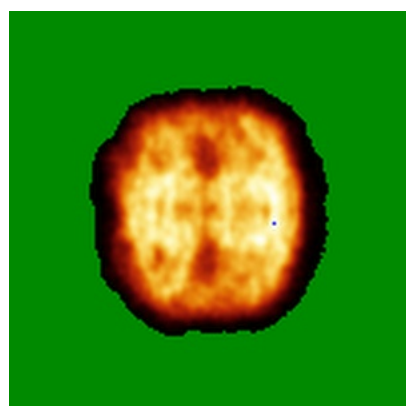


Z Index: 78

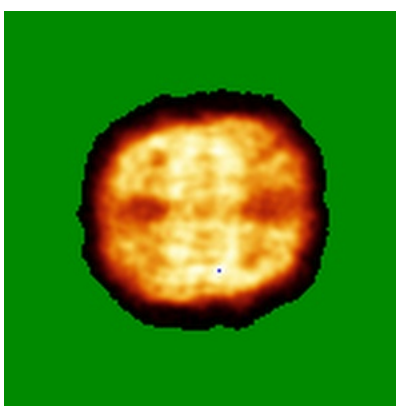
The images above show the largest variance slices of the map in three orthogonal directions.

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

This section was not generated.

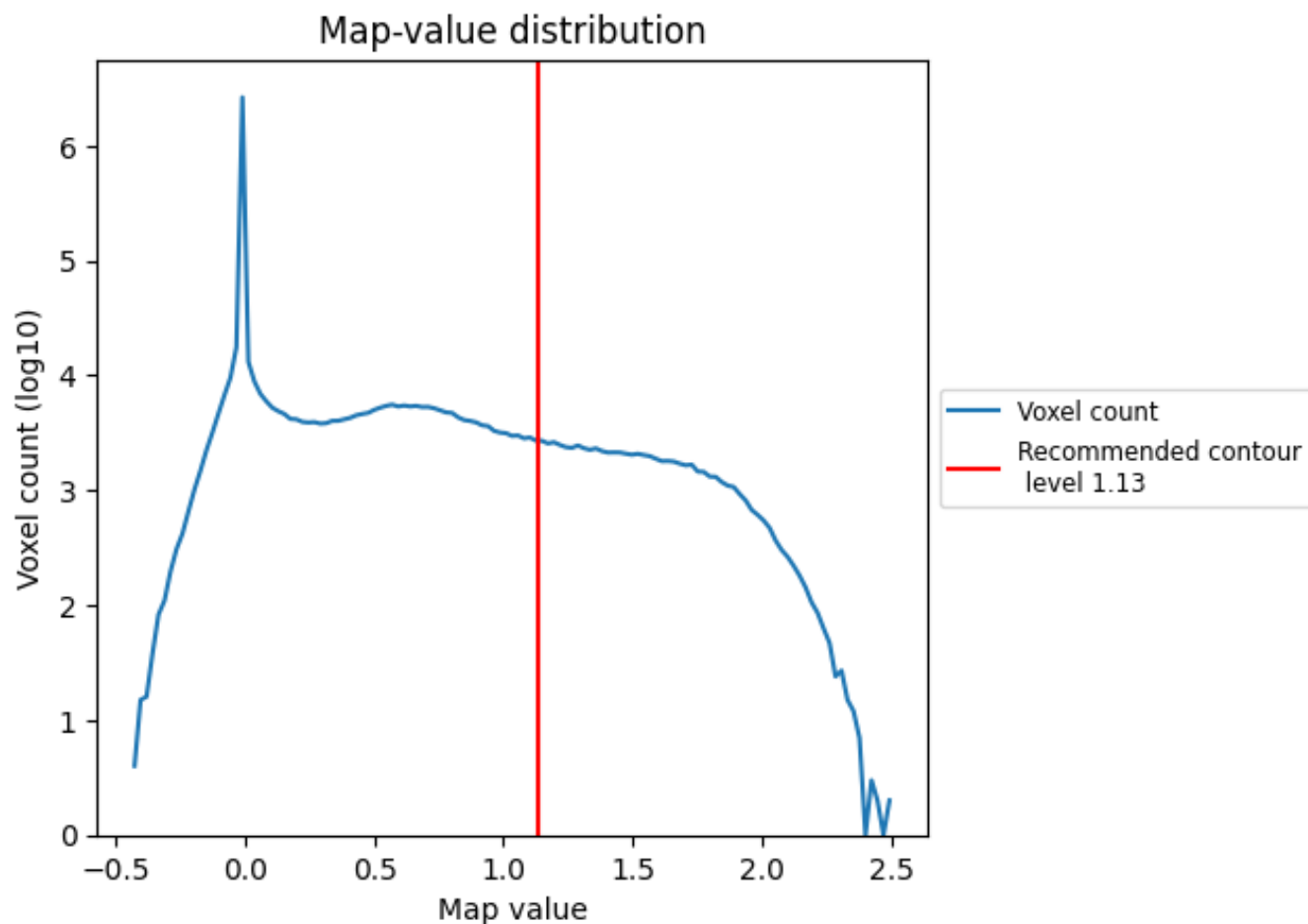
6.6 Mask visualisation

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

7 Map analysis [i](#)

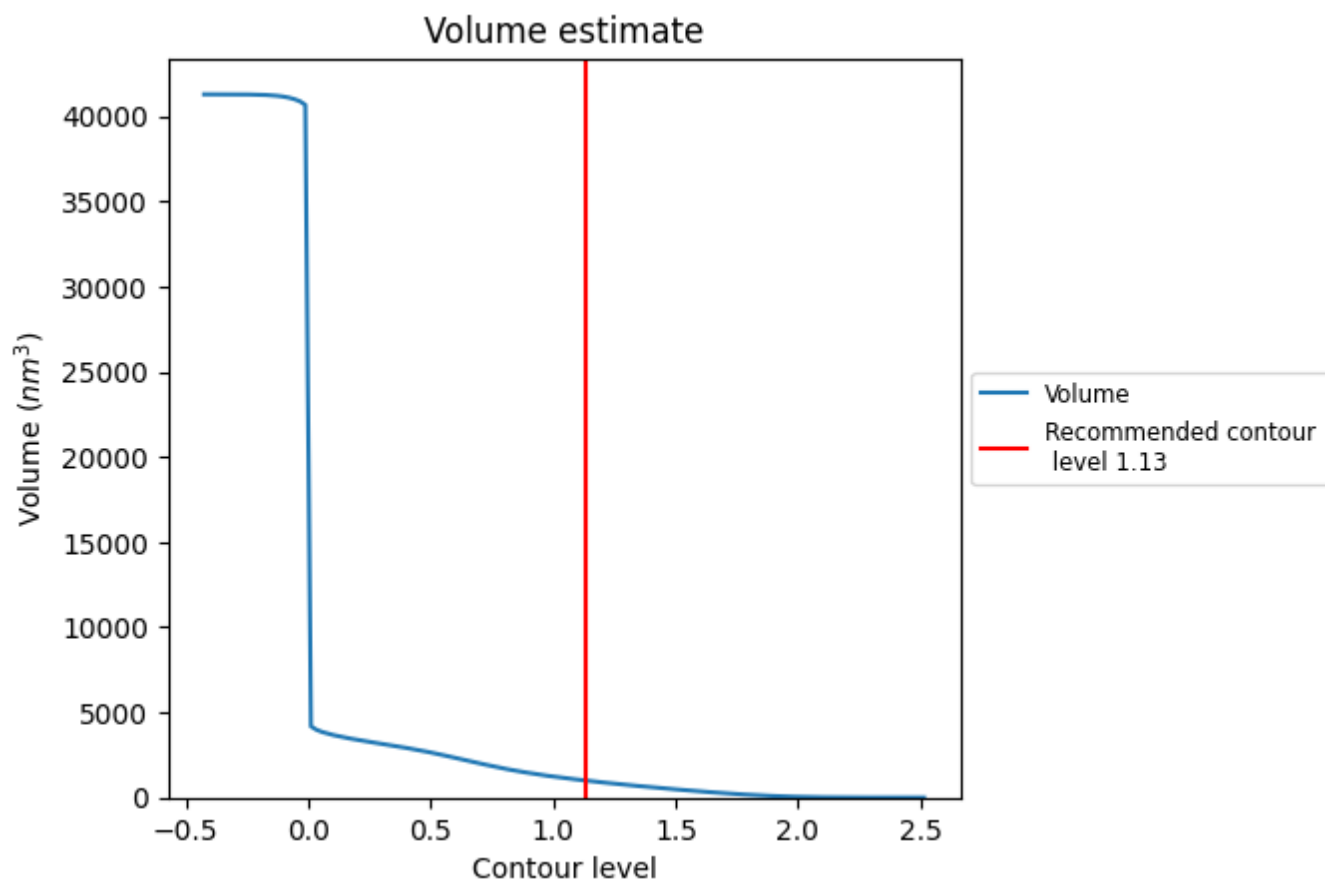
This section contains the results of statistical analysis of the map.

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.

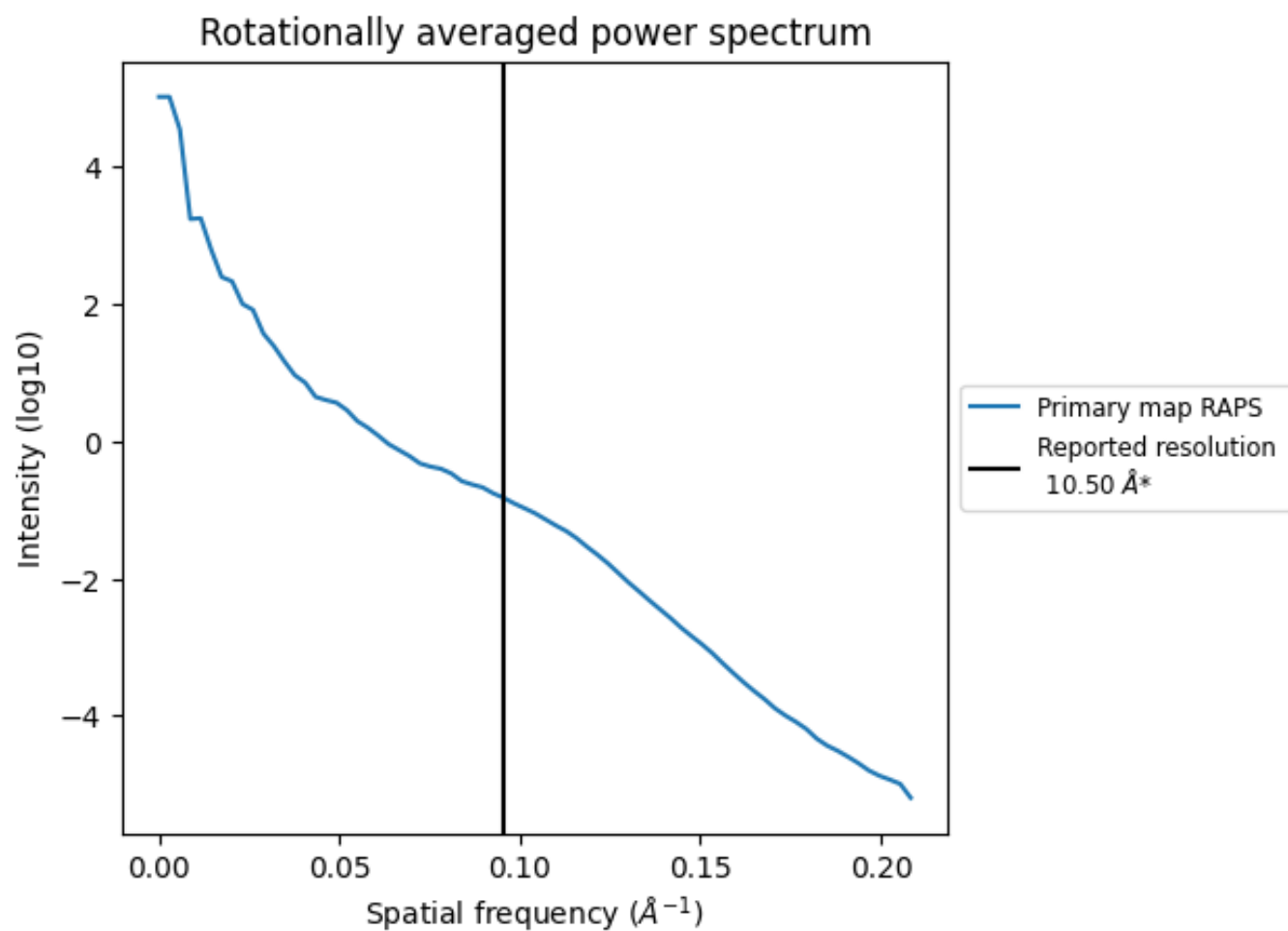
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1005 nm³; this corresponds to an approximate mass of 908 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 0.095 Å⁻¹

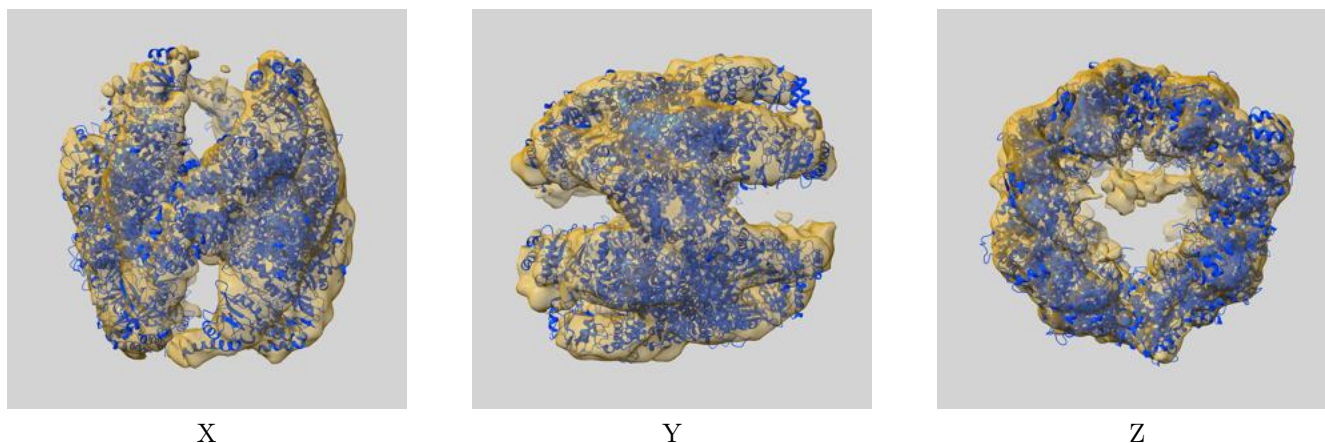
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

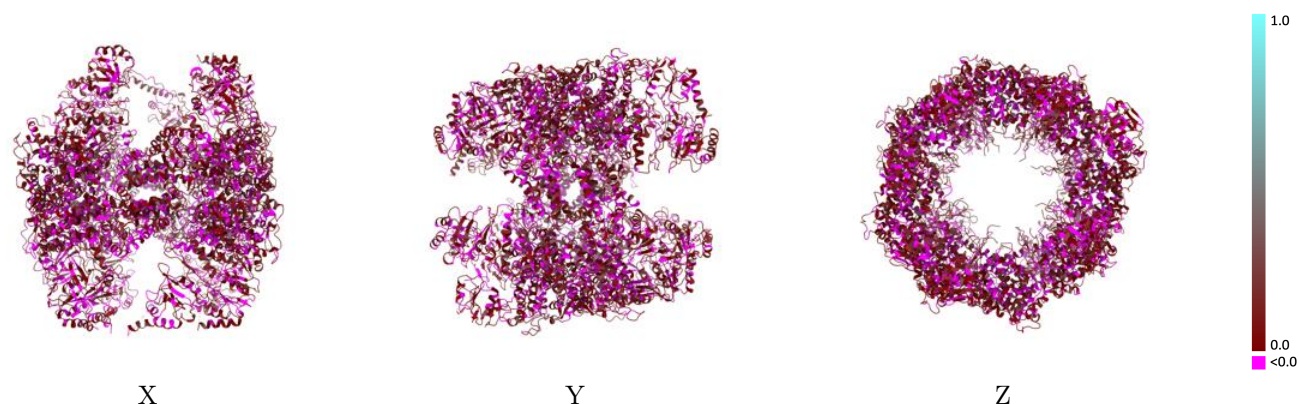
This section contains information regarding the fit between EMDB map EMD-1960 and PDB model 4A0O. Per-residue inclusion information can be found in section [3](#) on page [5](#).

9.1 Map-model overlay [i](#)



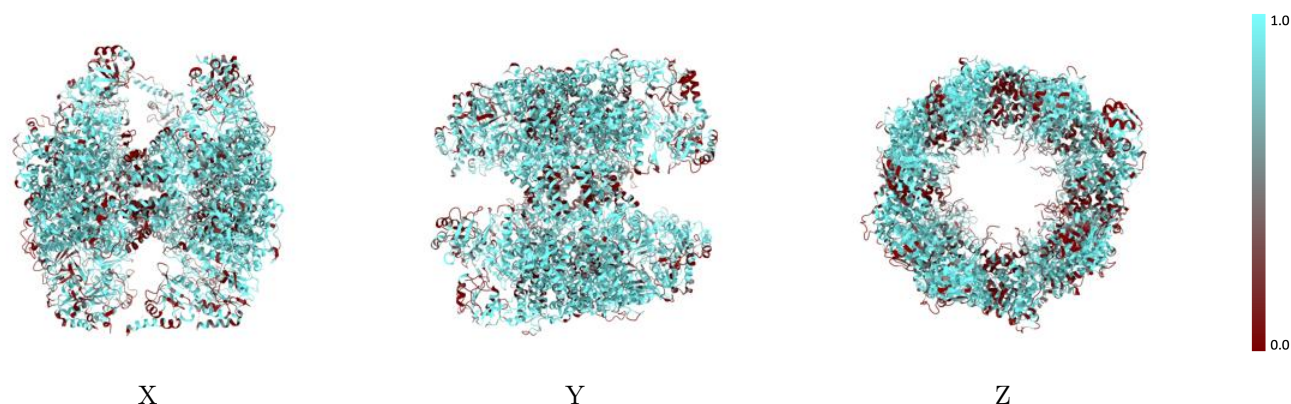
The images above show the 3D surface view of the map at the recommended contour level 1.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



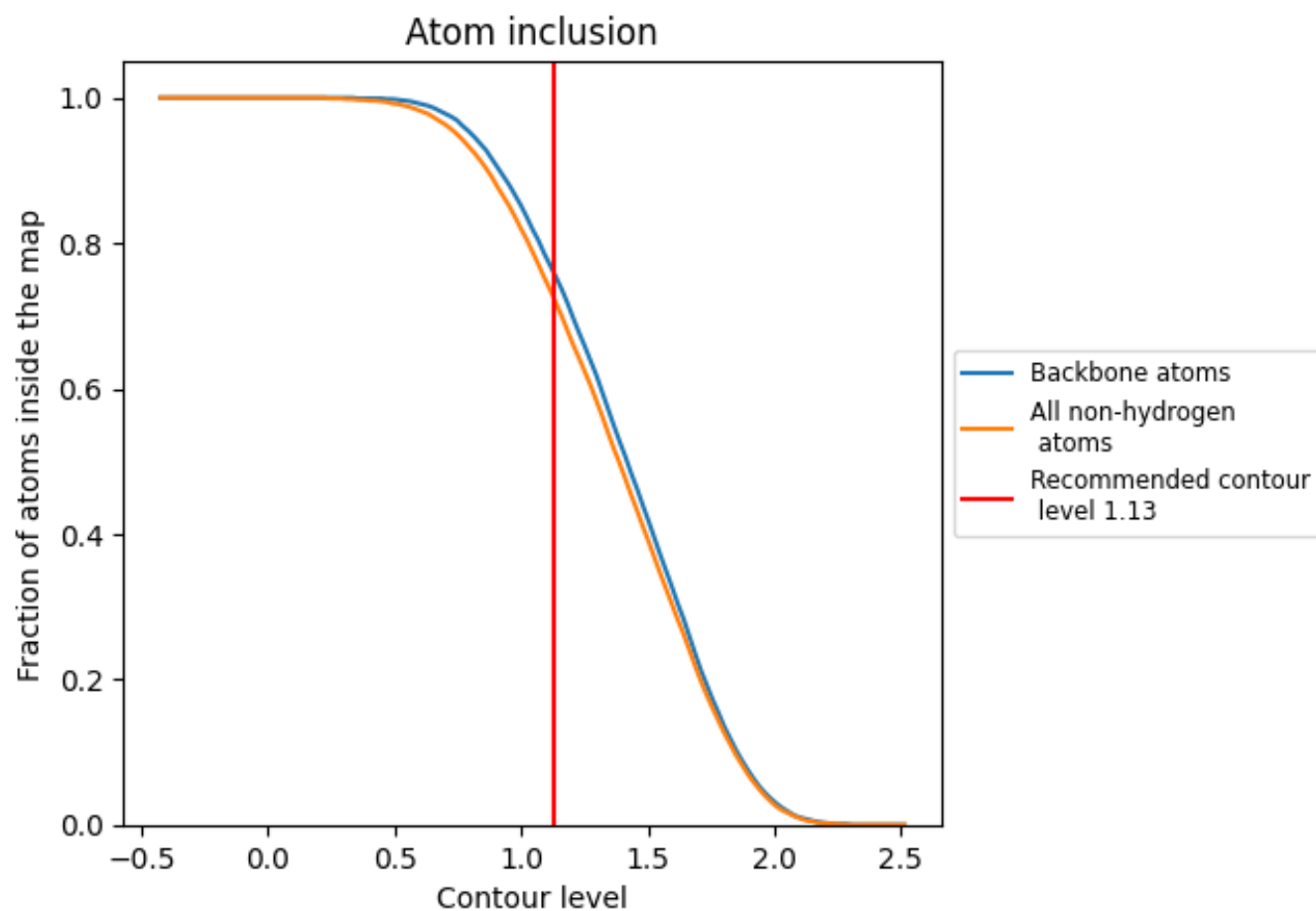
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (1.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7240	 0.0560
A	 0.6770	 0.0560
B	 0.6950	 0.0490
C	 0.7050	 0.0600
D	 0.7980	 0.0710
E	 0.7440	 0.0660
F	 0.7960	 0.0660
G	 0.7870	 0.0570
H	 0.6380	 0.0520
I	 0.6290	 0.0510
J	 0.7690	 0.0610
K	 0.7310	 0.0460
L	 0.7690	 0.0570
M	 0.6310	 0.0400
N	 0.7690	 0.0610
O	 0.7320	 0.0520
P	 0.6690	 0.0410

