



## wwPDB EM Validation Summary Report ⓘ

Feb 25, 2024 – 01:22 AM EST

PDB ID : 7LUP  
EMDB ID : EMD-23526  
Title : Human TRiC/CCT complex with reovirus outer capsid protein sigma-3  
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 : 6.20 Å(reported)

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We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev70  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

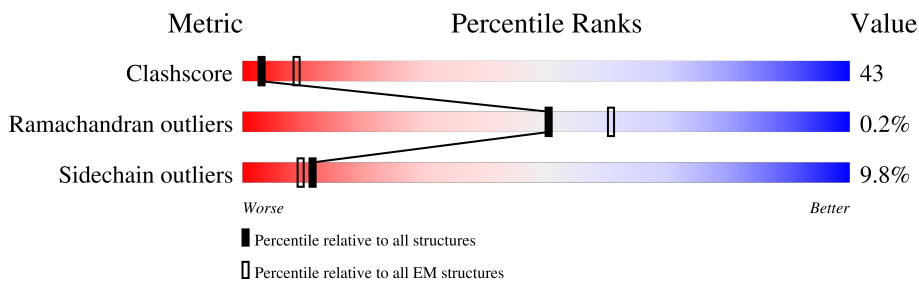
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	
1	L	541	
2	E	535	
2	M	535	
3	F	539	
3	N	539	
4	H	545	
4	P	545	

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Mol	Chain	Length	Quality of chain
5	C	543	
5	K	543	
6	B	548	
6	J	548	
7	A	531	
7	I	531	
8	G	556	
8	O	556	
9	Q	365	

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 67281 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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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
			Total	C	N	O	S		
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		

- Molecule 9 is a protein called Outer capsid protein sigma-3.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Q	365	Total	C	N	O	S	0	0
			2882	1821	507	527	27		

- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
10	Q	1	Total	Zn	0
			1	1	

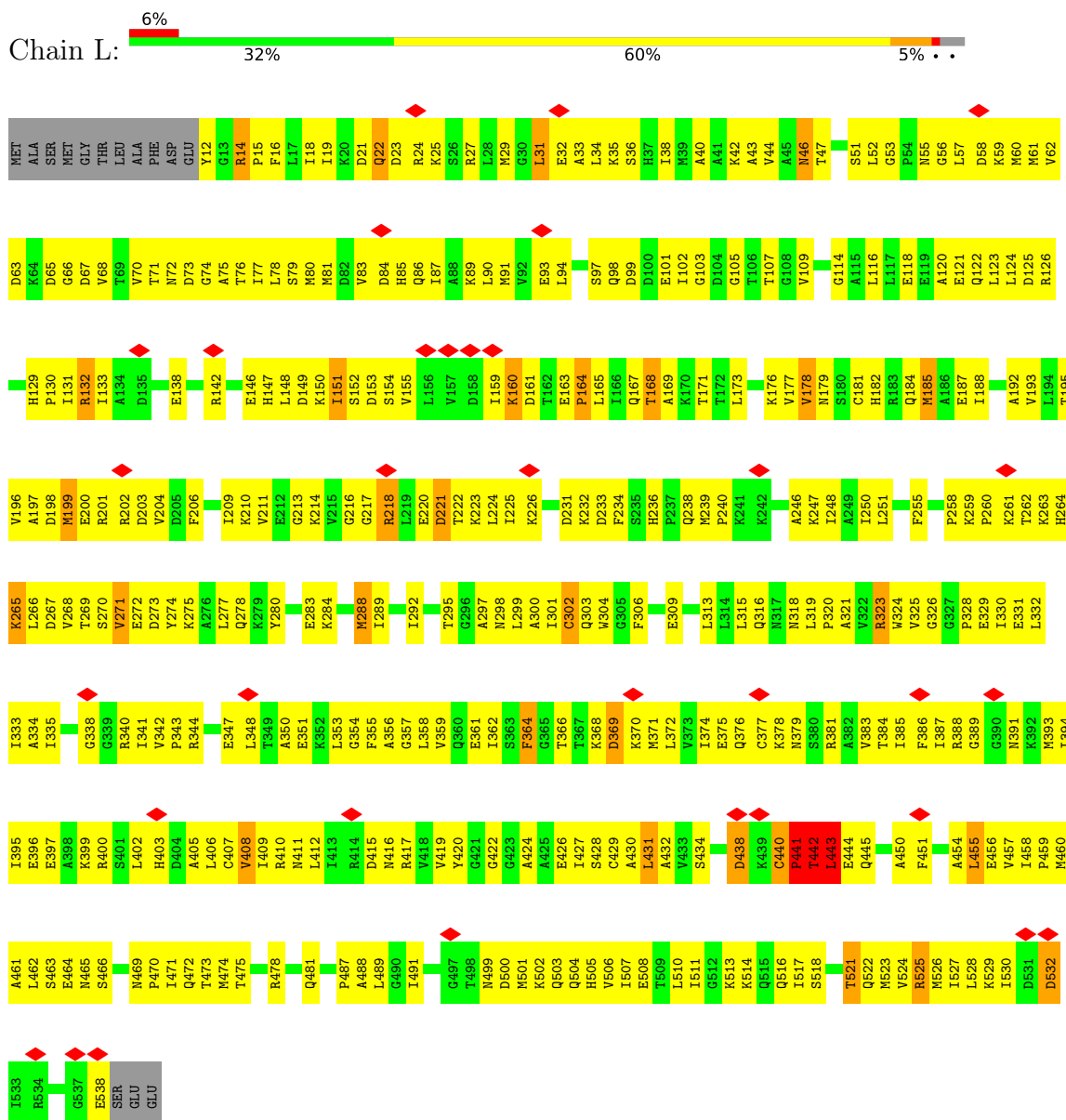
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	AltConf
11	D	1	Total O 1 1	0
11	H	1	Total O 1 1	0
11	C	4	Total O 4 4	0
11	A	3	Total O 3 3	0
11	G	10	Total O 10 10	0
11	Q	401	Total O 401 401	0

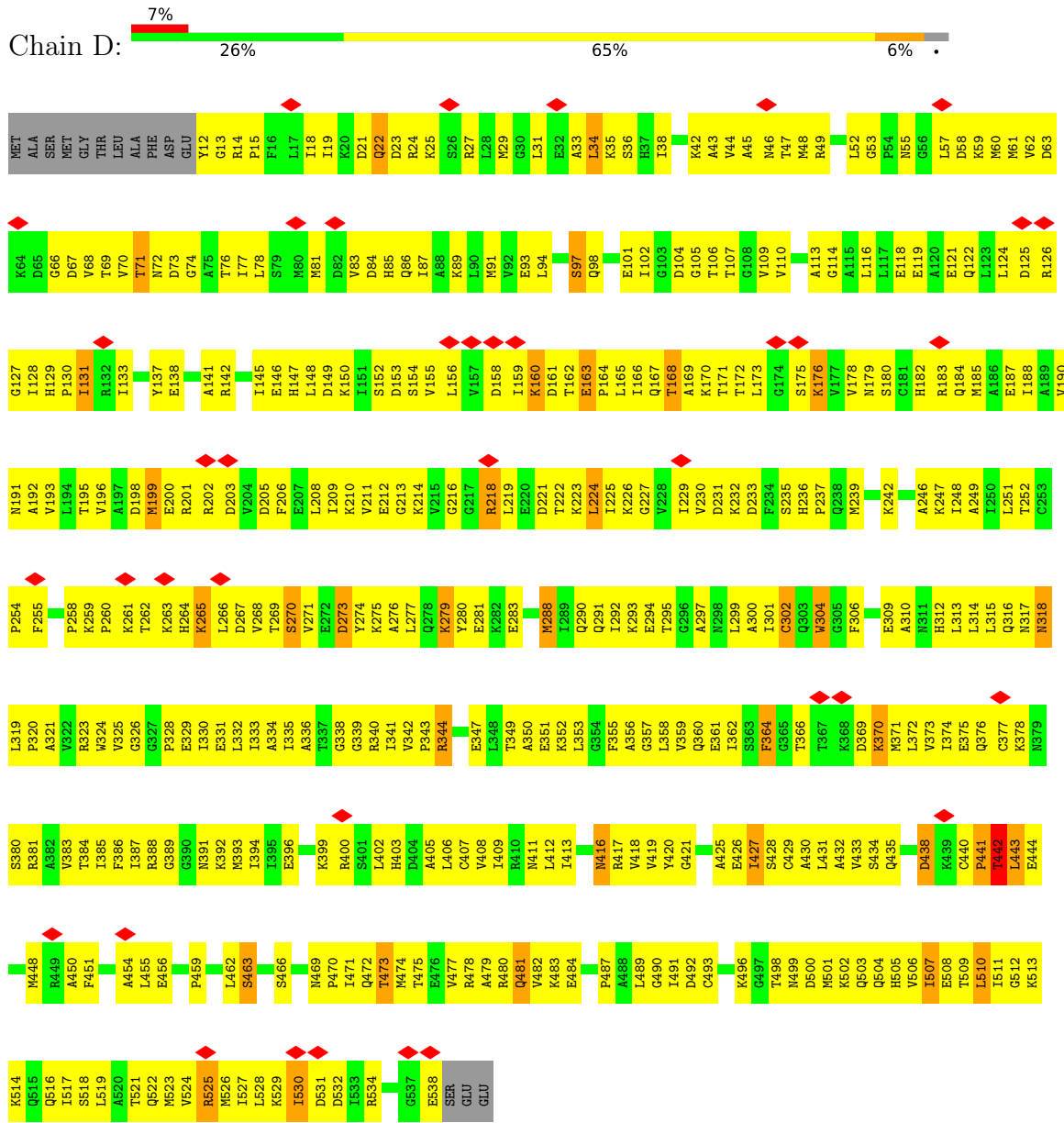
### 3 Residue-property plots

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.

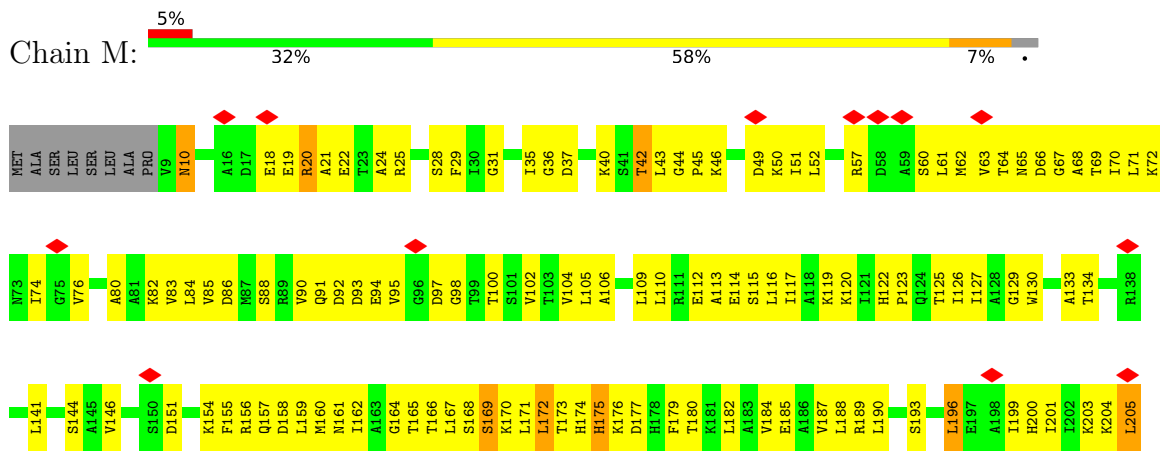
- Molecule 1: T-complex protein 1 subunit epsilon



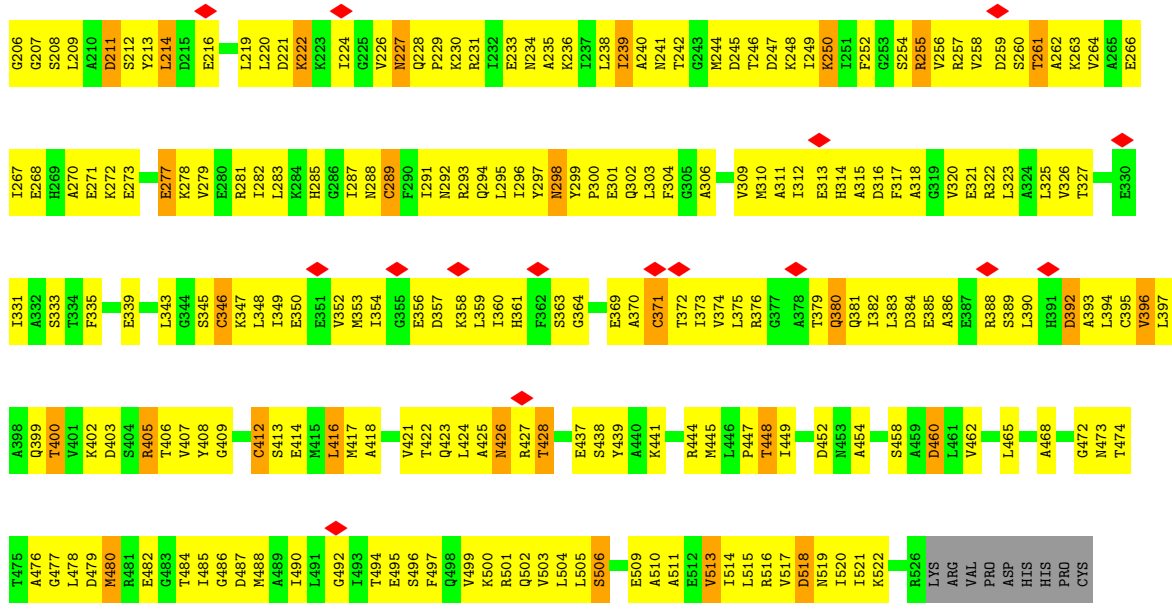
- Molecule 1: T-complex protein 1 subunit epsilon



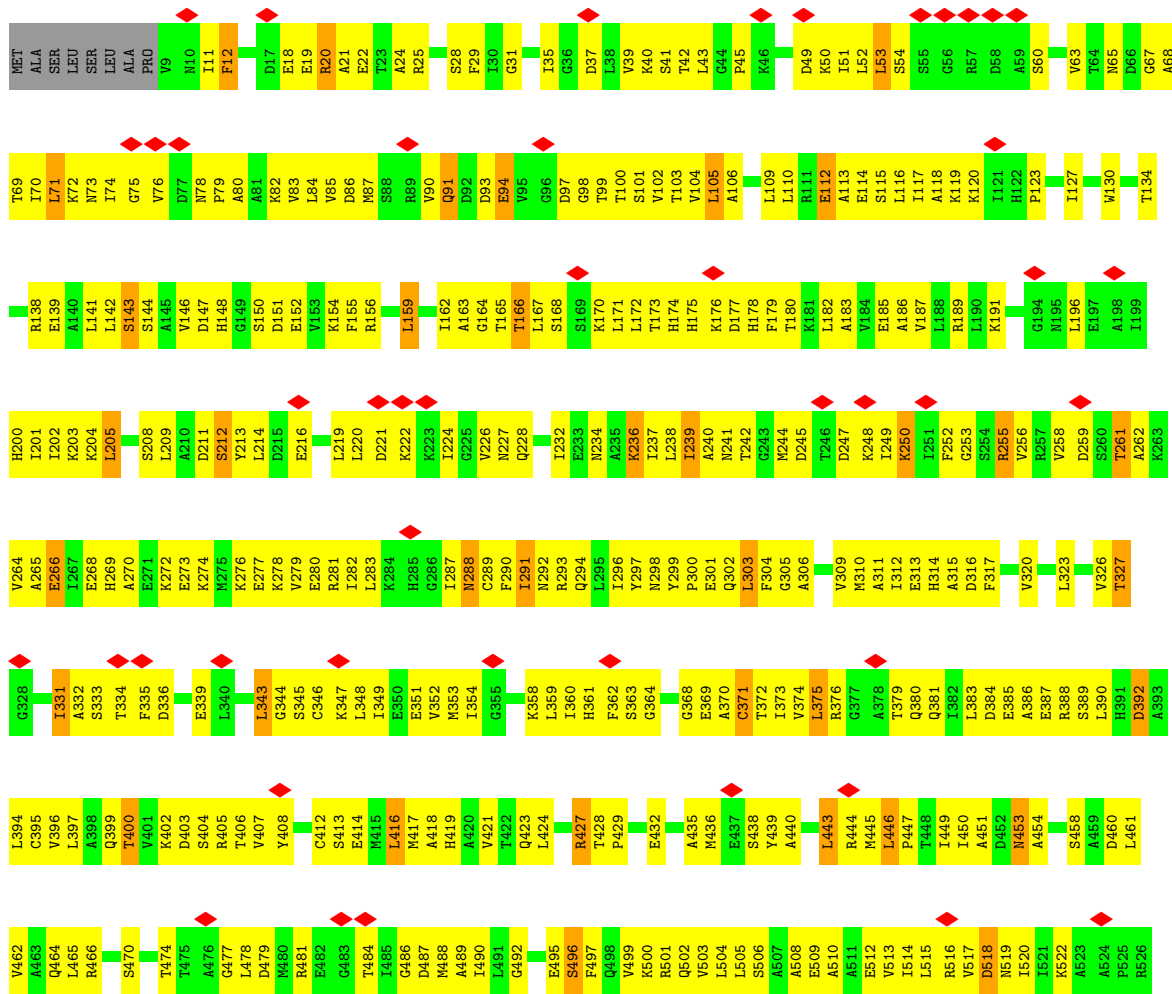
● Molecule 2: T-complex protein 1 subunit beta





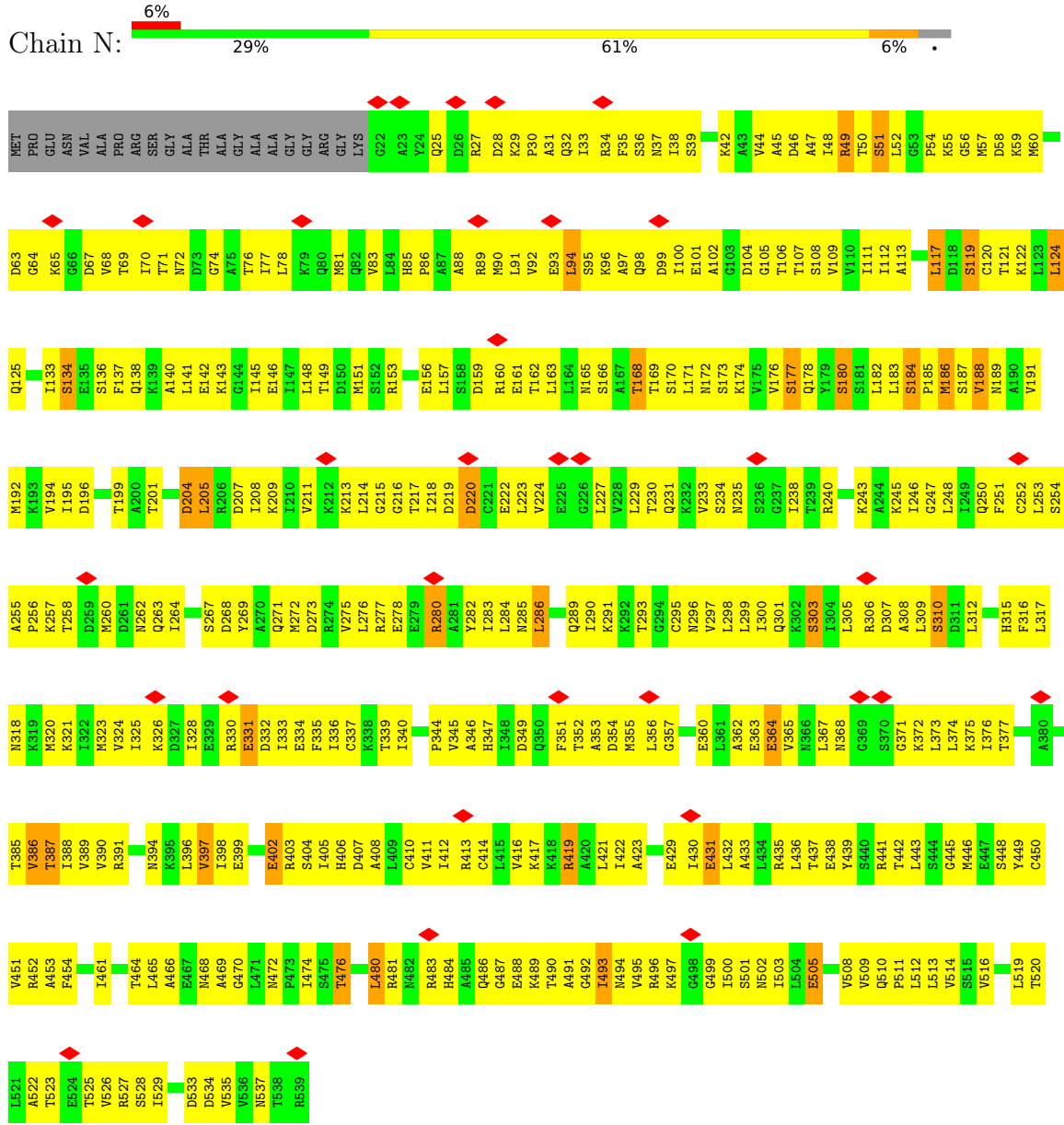


• Molecule 2: T-complex protein 1 subunit beta

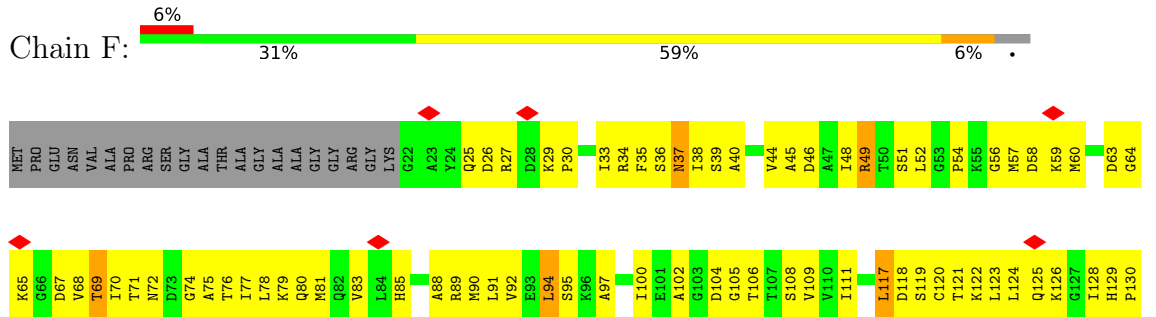


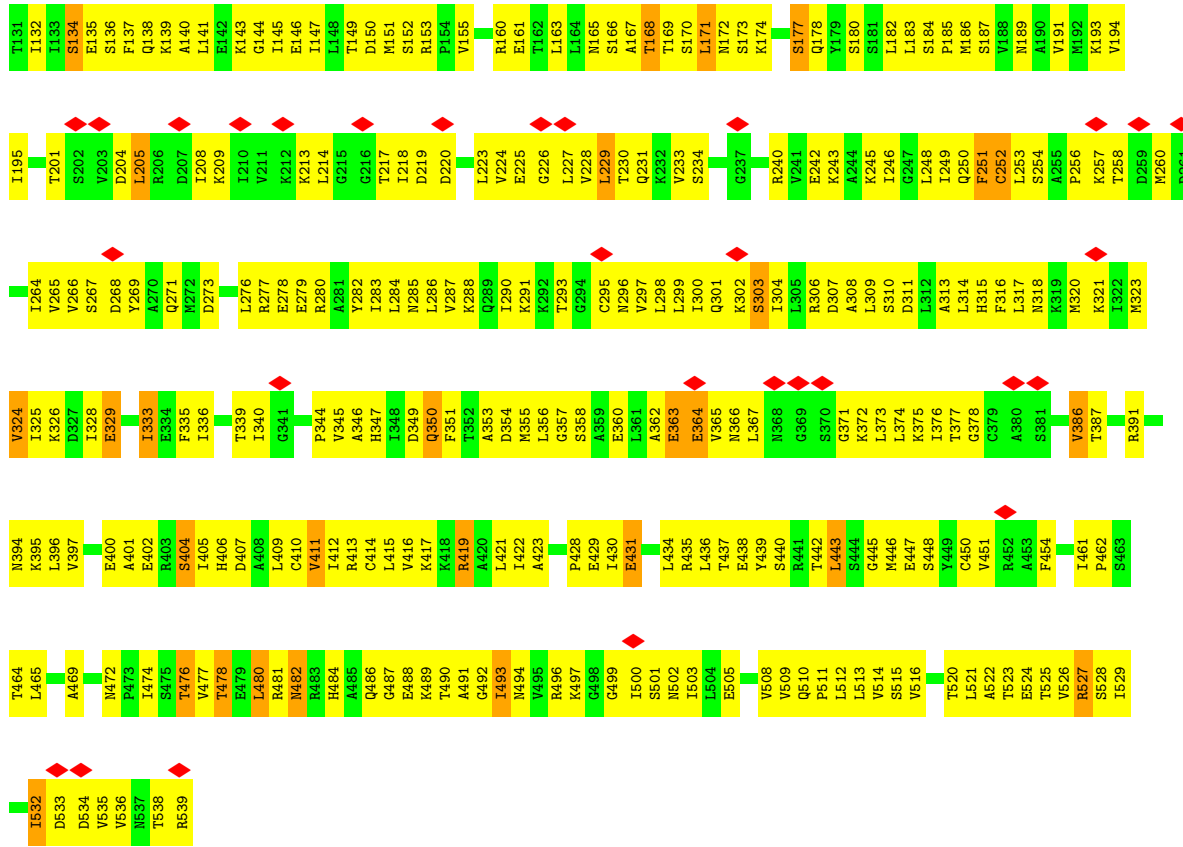
LYS  
ARG  
VAL  
PRO  
ASN  
ASP  
HIS  
HIS  
PRO  
CYS

• Molecule 3: T-complex protein 1 subunit delta

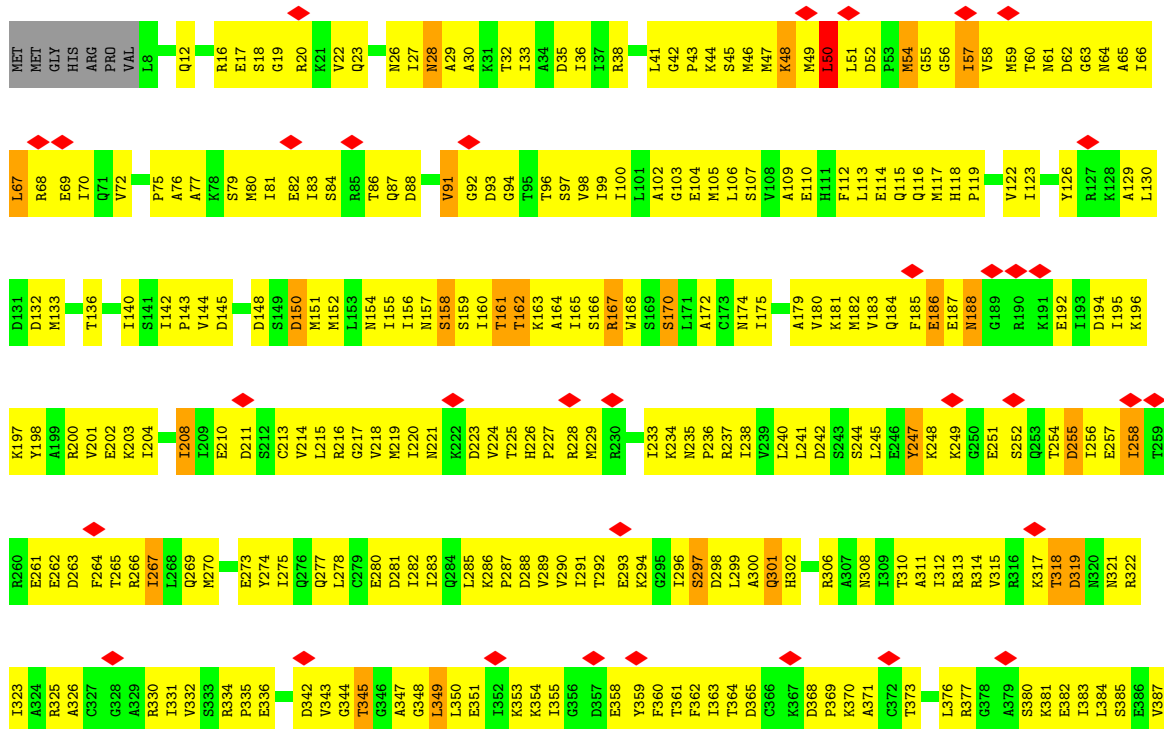


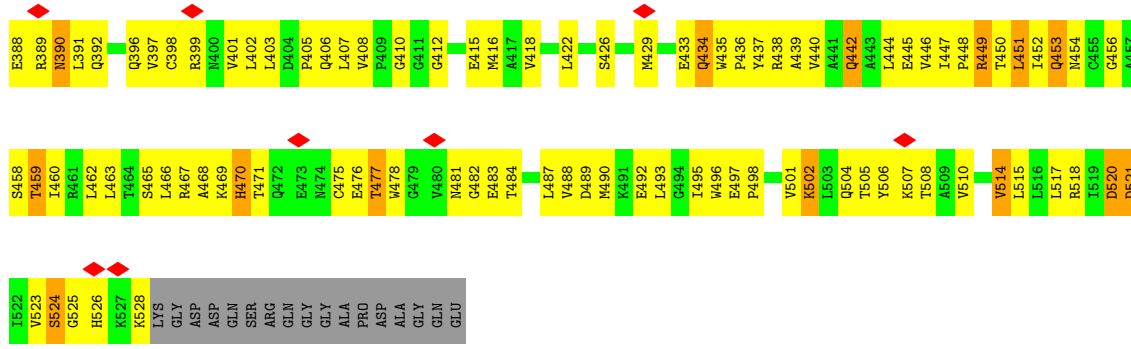
• Molecule 3: T-complex protein 1 subunit delta



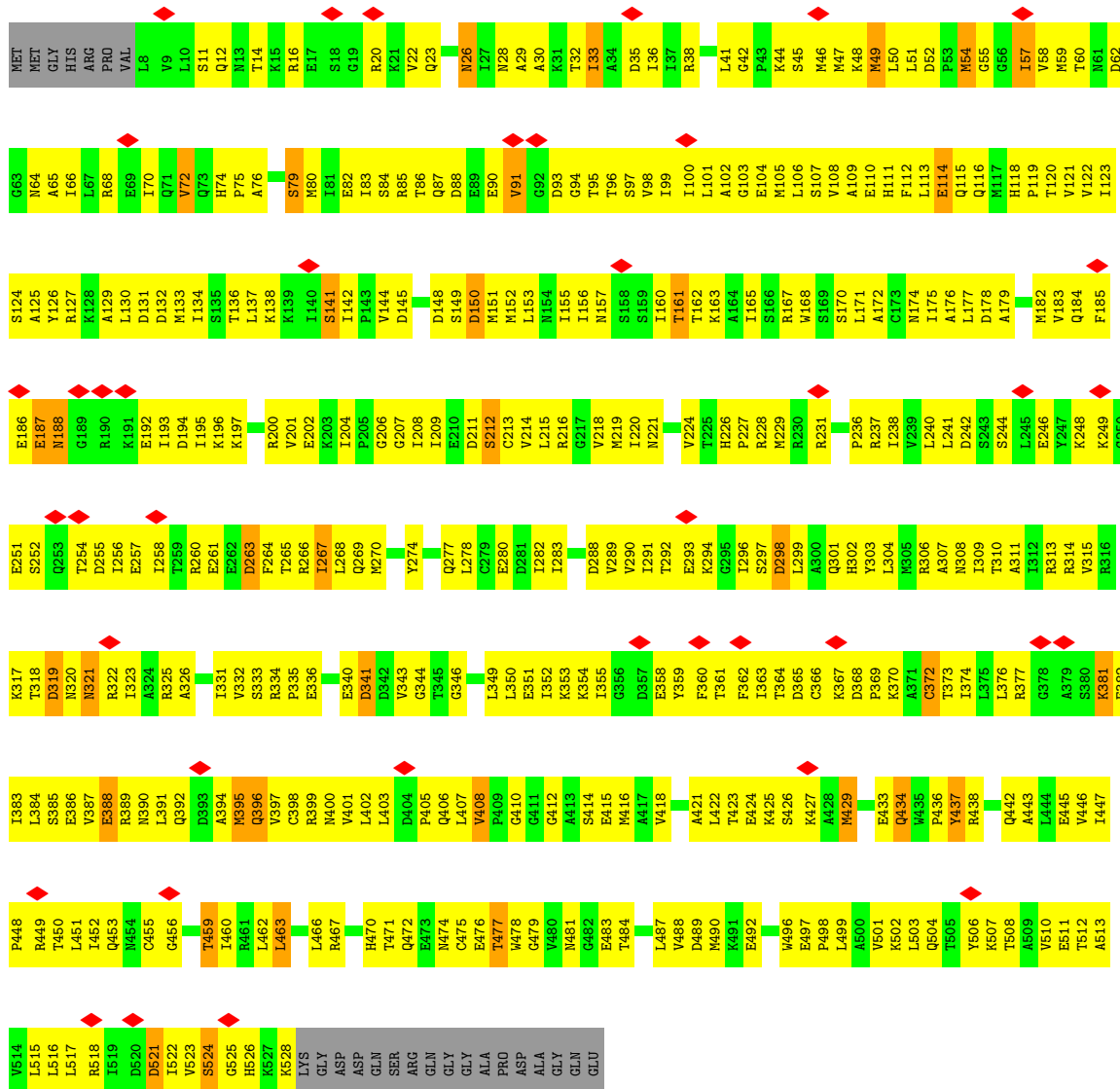


• Molecule 4: T-complex protein 1 subunit gamma

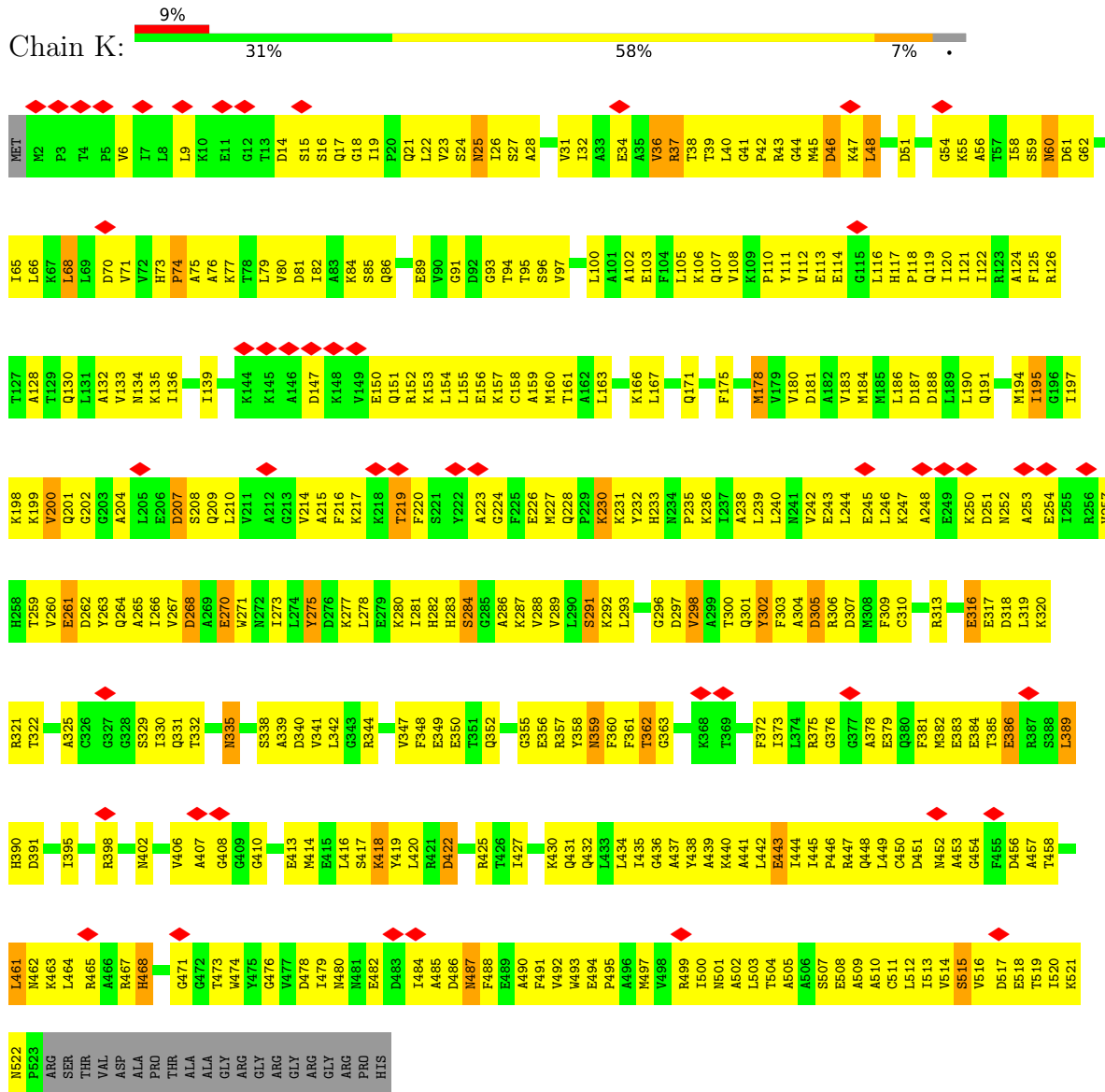




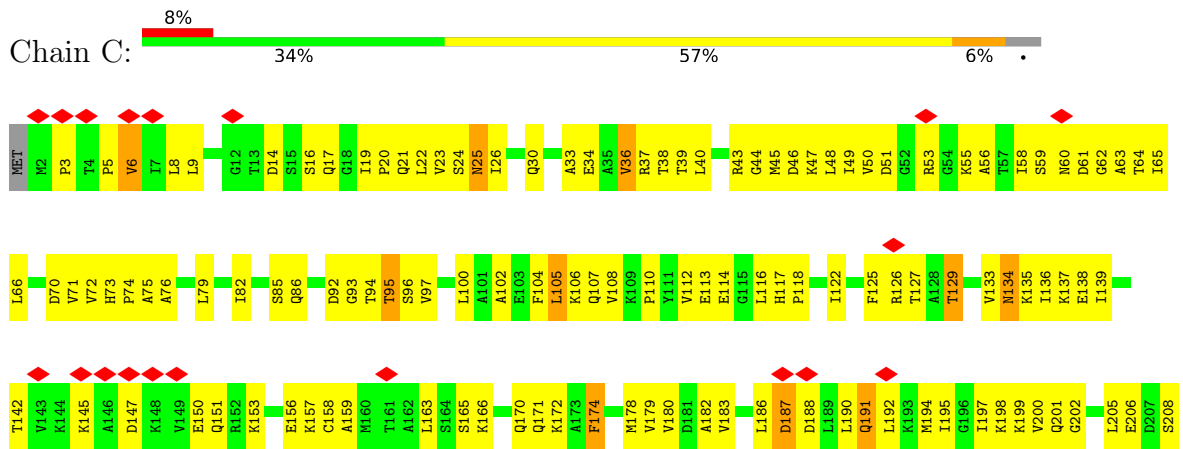
• Molecule 4: T-complex protein 1 subunit gamma

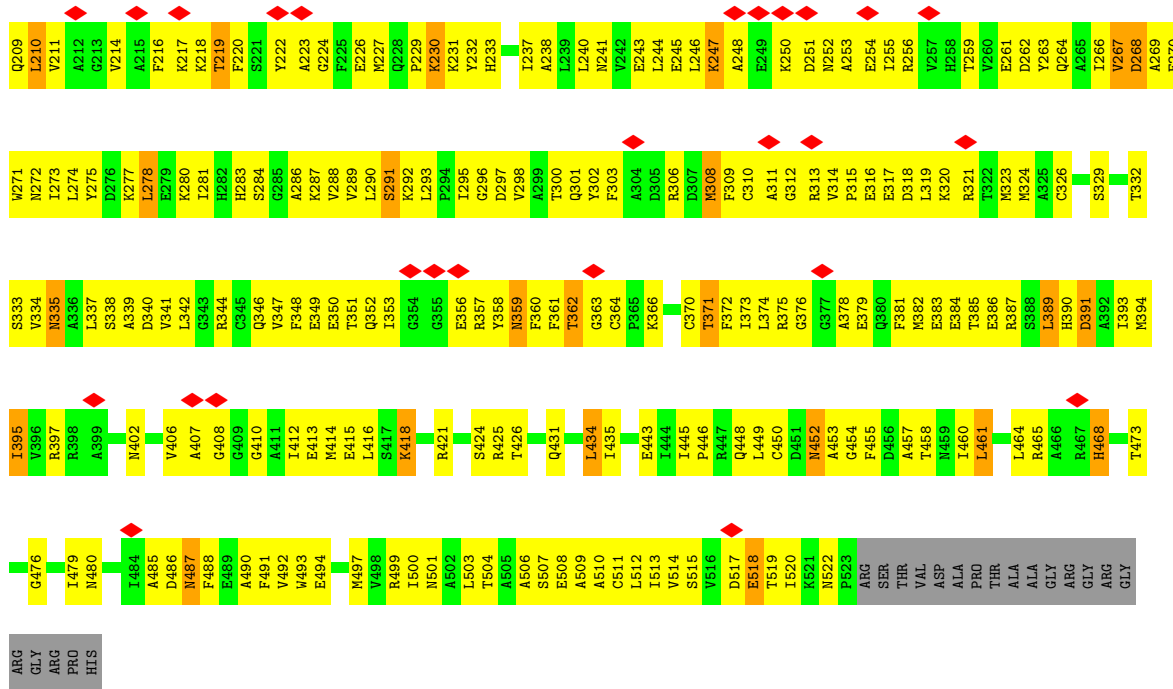


• Molecule 5: T-complex protein 1 subunit eta

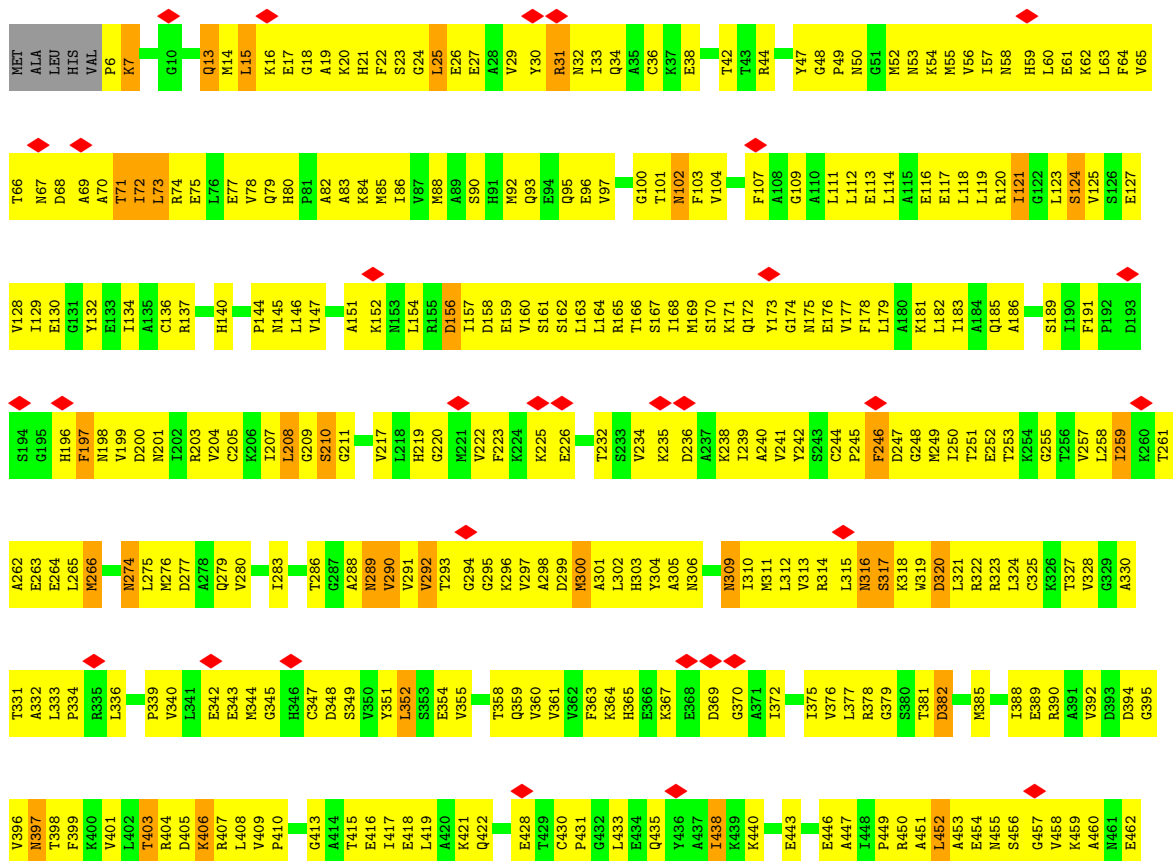


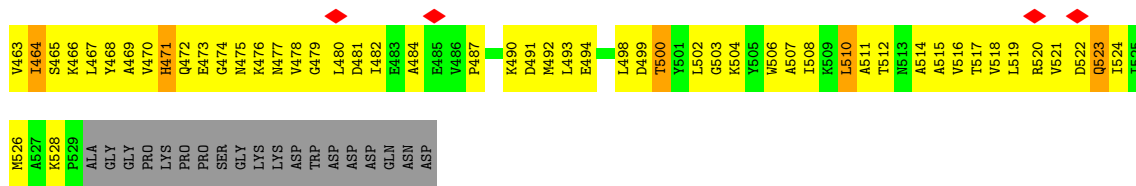
• Molecule 5: T-complex protein 1 subunit eta



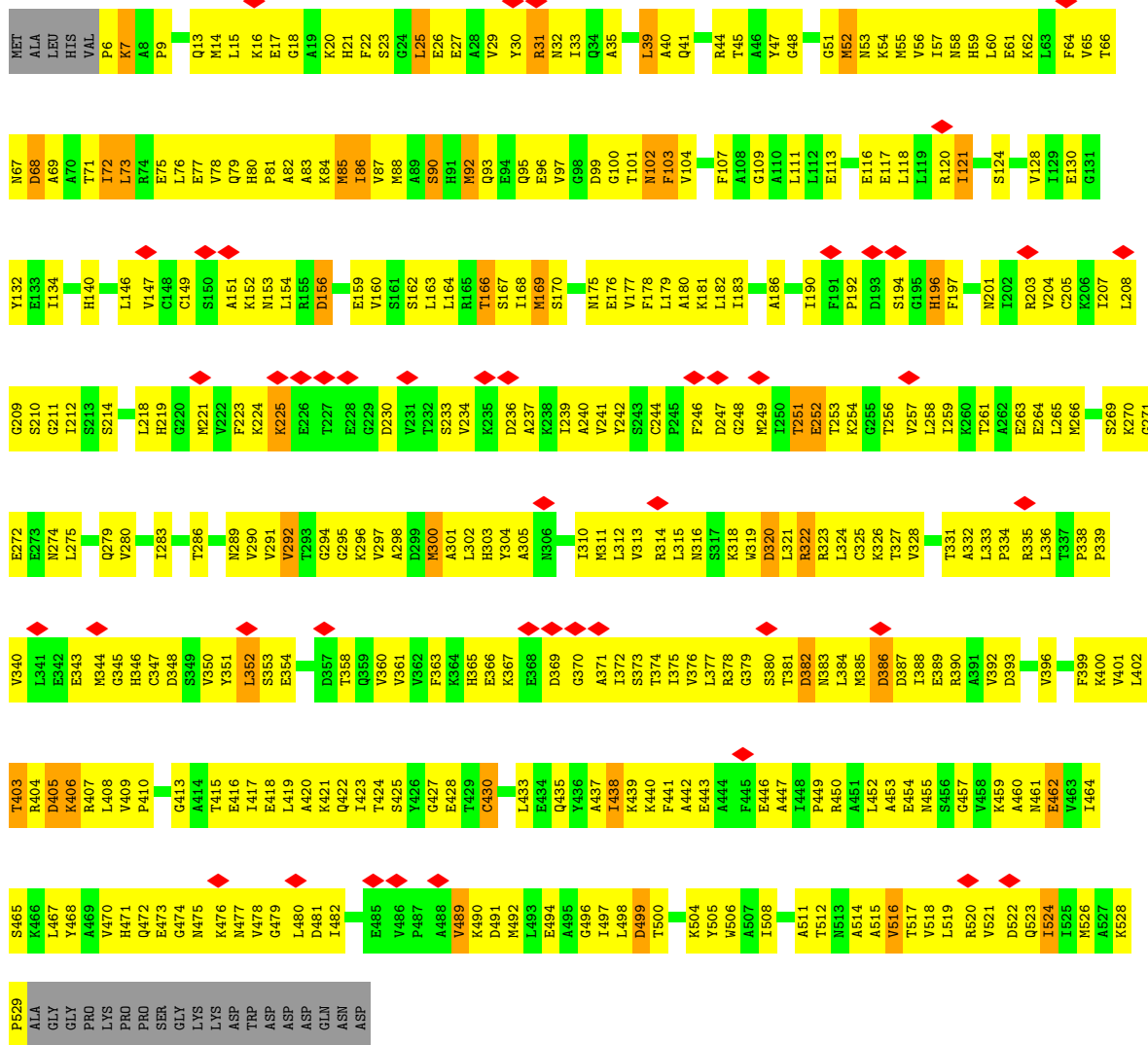


• Molecule 6: T-complex protein 1 subunit theta

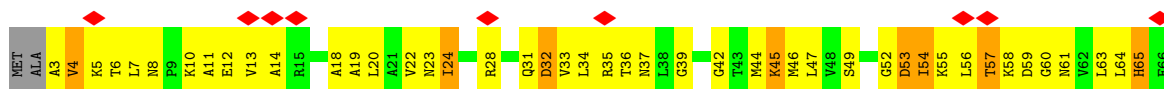


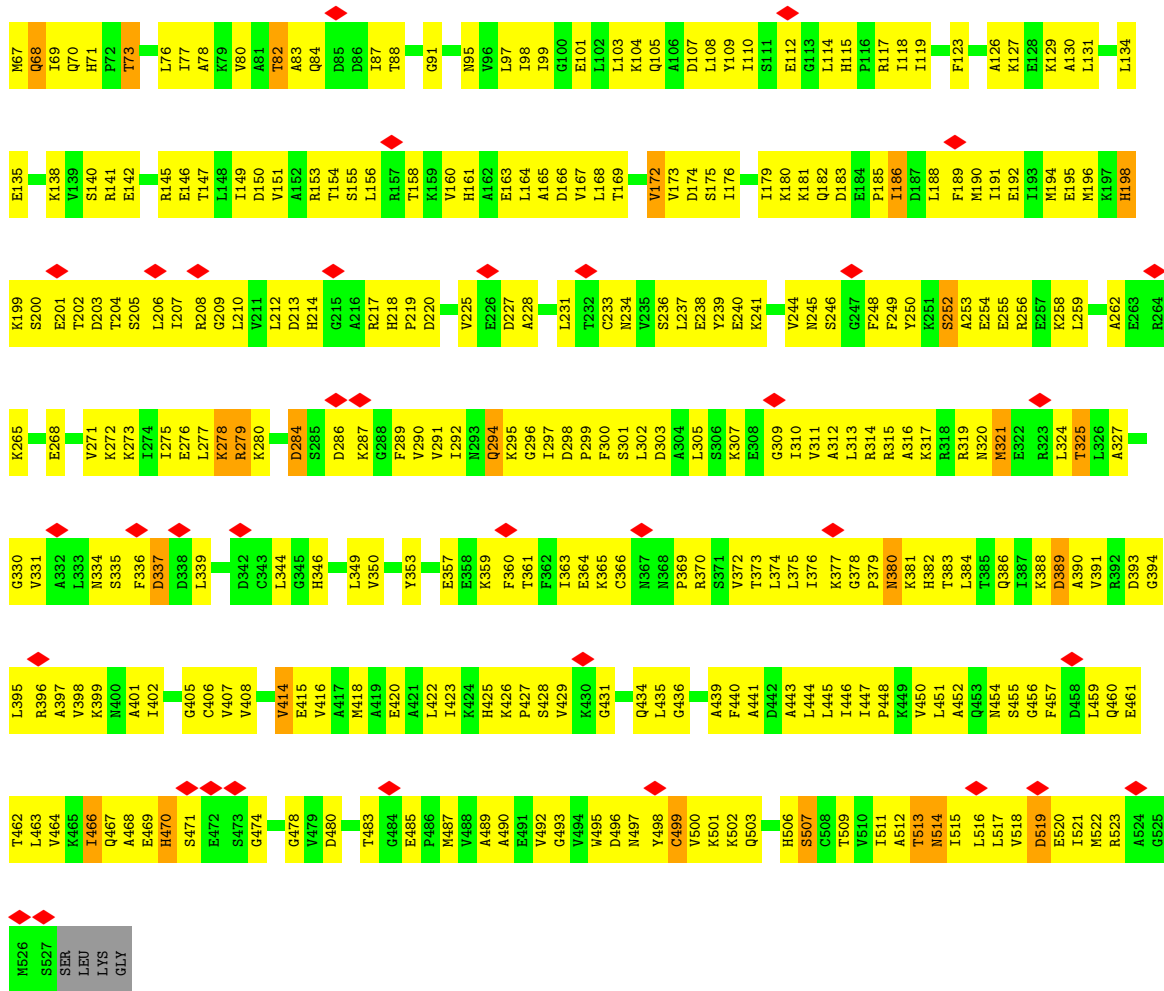


• Molecule 6: T-complex protein 1 subunit theta

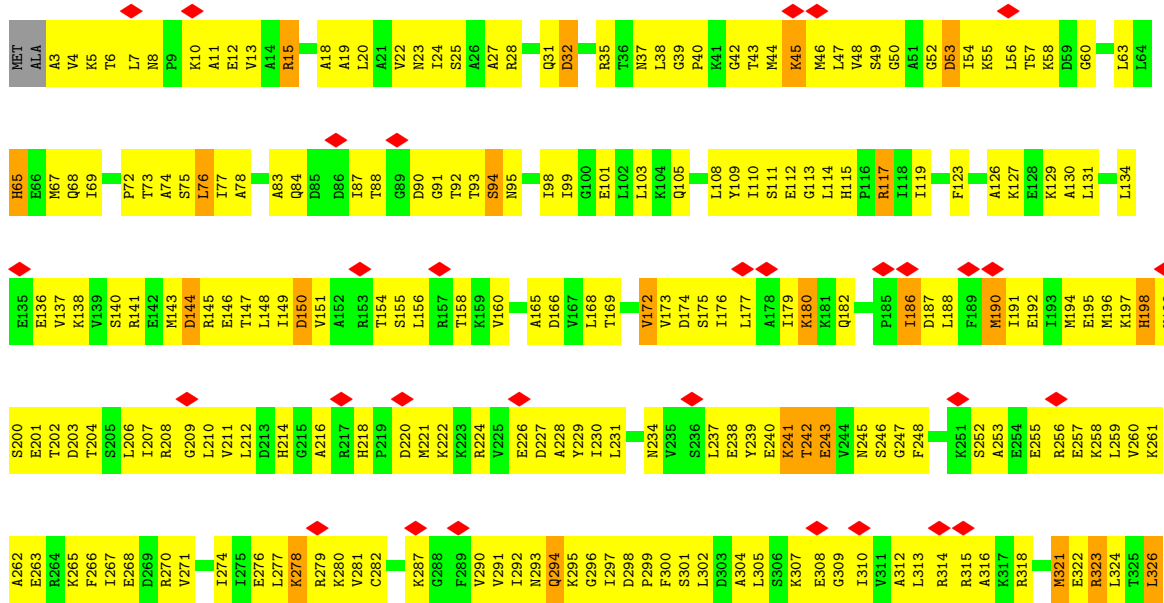


• Molecule 7: T-complex protein 1 subunit zeta

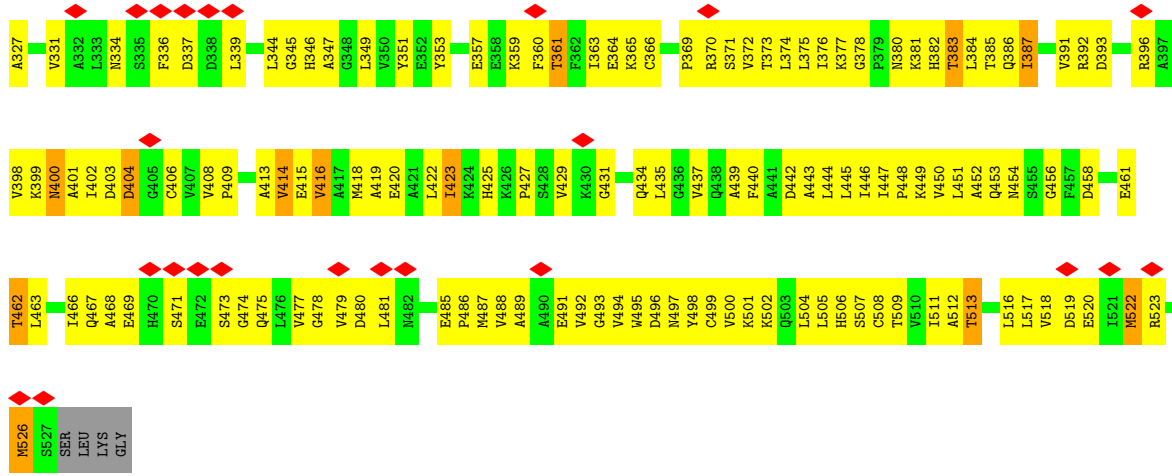




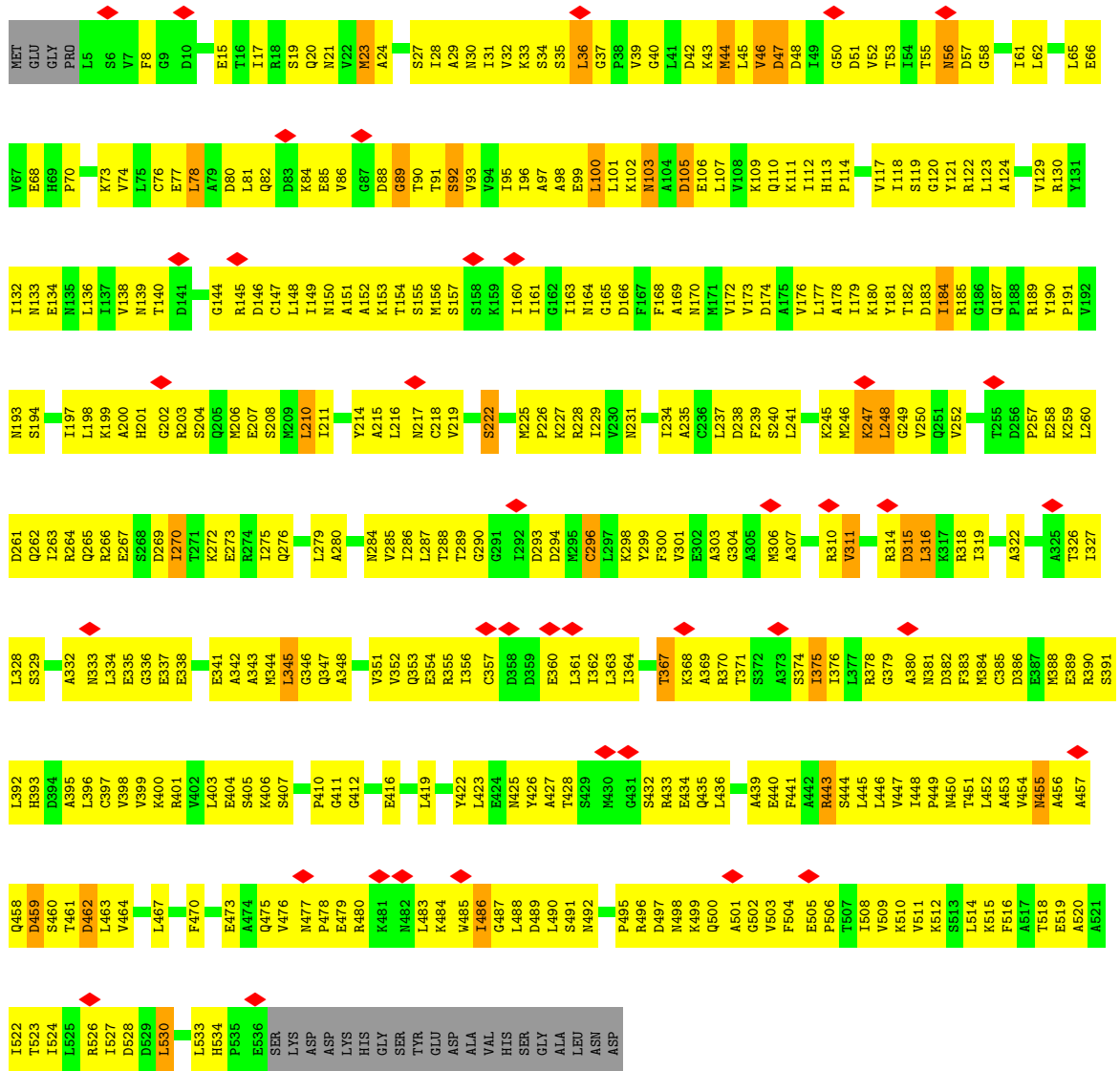
• Molecule 7: T-complex protein 1 subunit zeta



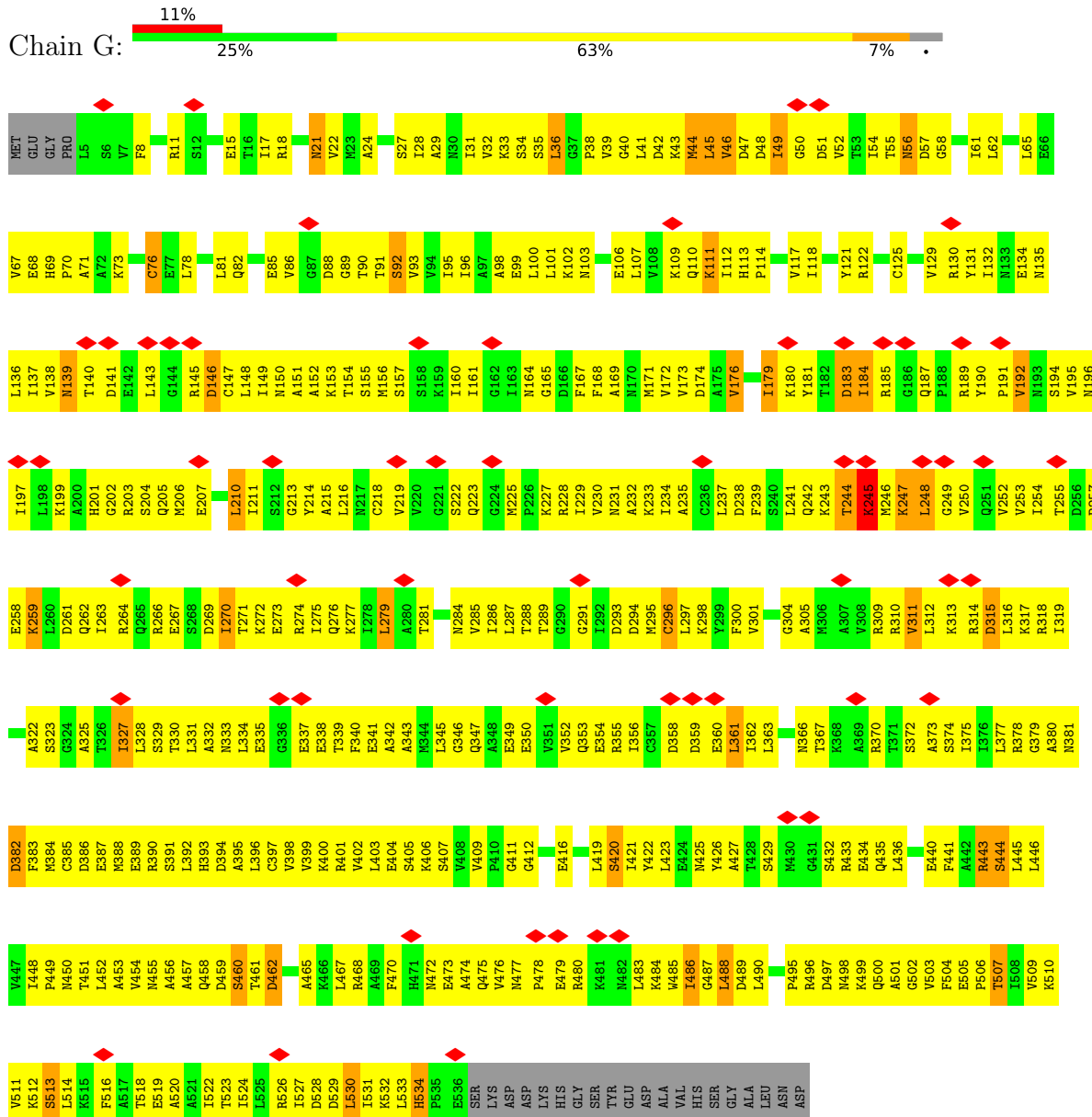




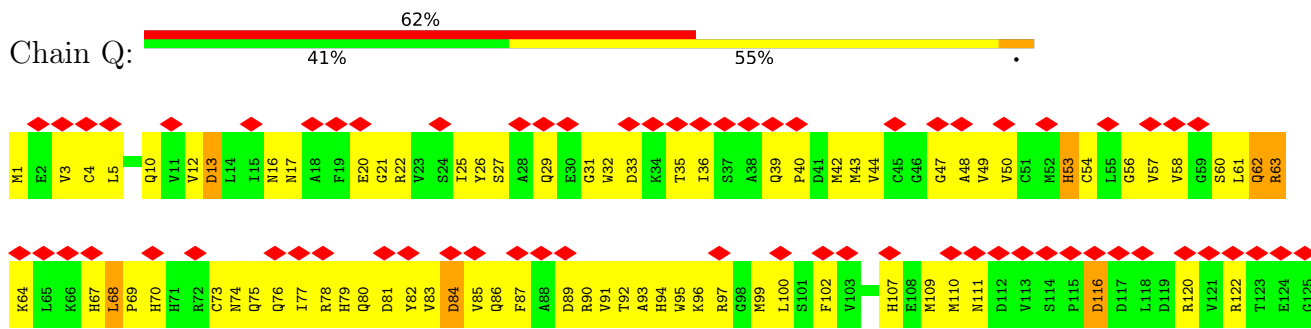
• Molecule 8: T-complex protein 1 subunit alpha

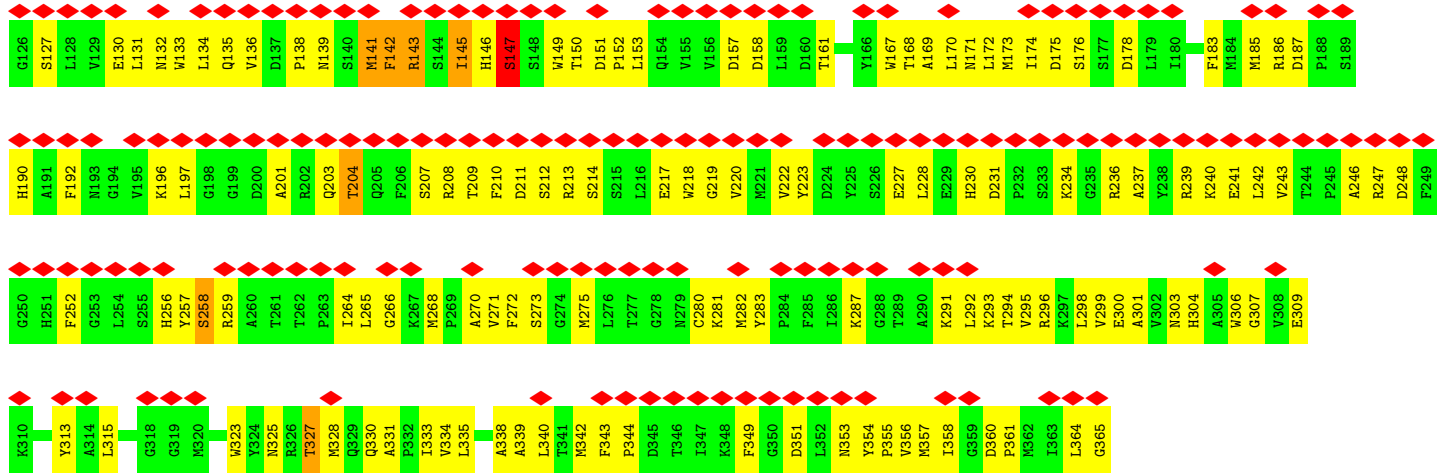


• Molecule 8: T-complex protein 1 subunit alpha



• Molecule 9: Outer capsid protein sigma-3





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26000	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	0.110	Depositor
Minimum map value	-0.048	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	364.0, 364.0, 364.0	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3, 1.3, 1.3	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section:  
ZN

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	0.37	0/4112	0.53	0/5539
1	L	0.35	0/4112	0.54	0/5539
2	E	0.36	0/3940	0.53	0/5311
2	M	0.36	0/3940	0.52	0/5311
3	F	0.34	0/3943	0.52	0/5322
3	N	0.35	0/3943	0.51	0/5322
4	H	0.37	0/4095	0.55	1/5523 (0.0%)
4	P	0.35	0/4095	0.51	0/5523
5	C	0.38	0/4064	0.53	0/5487
5	K	0.36	0/4064	0.51	0/5487
6	B	0.39	0/4051	0.55	0/5474
6	J	0.36	0/4051	0.53	0/5474
7	A	0.37	0/4070	0.55	0/5487
7	I	0.35	0/4070	0.52	0/5487
8	G	0.34	0/4082	0.55	1/5511 (0.0%)
8	O	0.34	0/4082	0.53	0/5511
9	Q	0.45	1/2955 (0.0%)	0.60	2/4003 (0.0%)
All	All	0.36	1/67669 (0.0%)	0.53	4/91311 (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	4
2	E	0	2
2	M	0	2
6	B	0	1
6	J	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	A	0	1
7	I	0	1
8	G	0	1
8	O	0	1
All	All	0	19

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	Q	147	SER	CB-OG	-5.75	1.34	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	G	245	LYS	CD-CE-NZ	-7.54	94.36	111.70
9	Q	145	ILE	CB-CA-C	-6.09	99.43	111.60
4	H	50	LEU	CA-CB-CG	5.87	128.79	115.30
9	Q	68	LEU	CB-CG-CD2	-5.20	102.15	111.00

There are no chirality outliers.

5 of 19 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	160	LYS	Peptide
1	L	160	LYS	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	420	0
1	L	4063	0	4183	364	0
2	E	3898	0	4008	347	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	M	3898	0	4008	335	0
3	F	3911	0	4115	343	0
3	N	3911	0	4115	364	0
4	H	4050	0	4185	406	0
4	P	4050	0	4185	403	0
5	C	4007	0	4110	360	0
5	K	4007	0	4110	349	0
6	B	3994	0	4063	391	0
6	J	3994	0	4063	385	0
7	A	4023	0	4161	363	0
7	I	4023	0	4161	369	0
8	G	4043	0	4203	414	0
8	O	4043	0	4203	379	0
9	Q	2882	0	2819	226	0
10	Q	1	0	0	0	0
11	A	3	0	0	0	0
11	C	4	0	0	0	0
11	D	1	0	0	1	0
11	G	10	0	0	1	0
11	H	1	0	0	0	0
11	Q	401	0	0	64	0
All	All	67281	0	68875	5796	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 43.

The worst 5 of 5796 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)
4:H:251:GLU:O	9:Q:203:GLN:NE2	1.93	1.01
9:Q:143:ARG:HH22	9:Q:219:GLY:HA2	1.22	1.00
7:A:257:GLU:OE1	7:A:261:LYS:NZ	1.96	0.98
8:G:99:GLU:OE2	8:G:103:ASN:ND2	1.98	0.96
8:O:238:ASP:HB3	8:O:329:SER:HA	1.49	0.95

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%)	481 (92%)	41 (8%)	3 (1%)	25	66
1	L	525/541 (97%)	481 (92%)	40 (8%)	4 (1%)	19	60
2	E	516/535 (96%)	477 (92%)	38 (7%)	1 (0%)	47	81
2	M	516/535 (96%)	477 (92%)	38 (7%)	1 (0%)	47	81
3	F	516/539 (96%)	480 (93%)	36 (7%)	0	100	100
3	N	516/539 (96%)	478 (93%)	38 (7%)	0	100	100
4	H	519/545 (95%)	484 (93%)	35 (7%)	0	100	100
4	P	519/545 (95%)	486 (94%)	33 (6%)	0	100	100
5	C	520/543 (96%)	477 (92%)	43 (8%)	0	100	100
5	K	520/543 (96%)	484 (93%)	35 (7%)	1 (0%)	47	81
6	B	522/548 (95%)	476 (91%)	46 (9%)	0	100	100
6	J	522/548 (95%)	474 (91%)	48 (9%)	0	100	100
7	A	523/531 (98%)	485 (93%)	38 (7%)	0	100	100
7	I	523/531 (98%)	477 (91%)	46 (9%)	0	100	100
8	G	530/556 (95%)	481 (91%)	48 (9%)	1 (0%)	47	81
8	O	530/556 (95%)	475 (90%)	52 (10%)	3 (1%)	25	66
9	Q	363/365 (100%)	354 (98%)	9 (2%)	0	100	100
All	All	8705/9041 (96%)	8027 (92%)	664 (8%)	14 (0%)	50	81

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 [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	D	445/456 (98%)	410 (92%)	35 (8%)	12	36
1	L	445/456 (98%)	408 (92%)	37 (8%)	11	34
2	E	412/427 (96%)	368 (89%)	44 (11%)	6	24
2	M	412/427 (96%)	373 (90%)	39 (10%)	8	28
3	F	441/452 (98%)	395 (90%)	46 (10%)	7	25
3	N	441/452 (98%)	394 (89%)	47 (11%)	6	24
4	H	452/469 (96%)	401 (89%)	51 (11%)	6	21
4	P	452/469 (96%)	404 (89%)	48 (11%)	6	24
5	C	429/443 (97%)	385 (90%)	44 (10%)	7	25
5	K	429/443 (97%)	387 (90%)	42 (10%)	8	27
6	B	433/452 (96%)	388 (90%)	45 (10%)	7	25
6	J	433/452 (96%)	381 (88%)	52 (12%)	5	20
7	A	438/442 (99%)	398 (91%)	40 (9%)	9	30
7	I	438/442 (99%)	400 (91%)	38 (9%)	10	31
8	G	444/463 (96%)	394 (89%)	50 (11%)	6	21
8	O	444/463 (96%)	406 (91%)	38 (9%)	10	32
9	Q	315/315 (100%)	296 (94%)	19 (6%)	19	44
All	All	7303/7523 (97%)	6588 (90%)	715 (10%)	11	27

5 of 715 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	J	290	VAL
7	A	54	ILE
6	J	403	THR
6	J	289	ASN
6	B	405	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 68

such sidechains are listed below:

Mol	Chain	Res	Type
8	O	21	ASN
8	O	133	ASN
9	Q	17	ASN
4	H	321	ASN
4	H	301	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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.

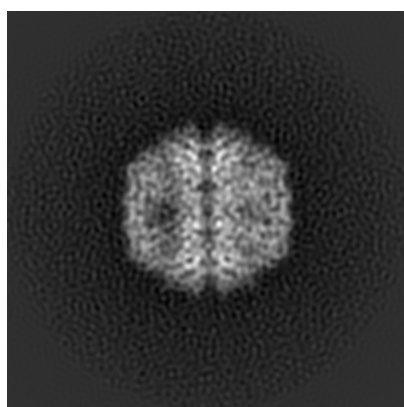
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23526. These allow visual inspection of the internal detail of the map and identification of artifacts.

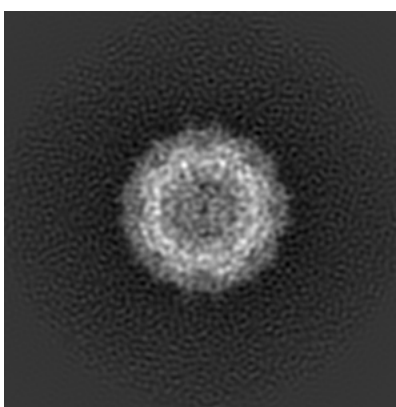
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

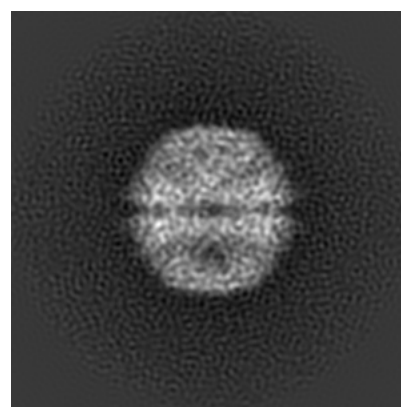
#### 6.1.1 Primary map



X



Y

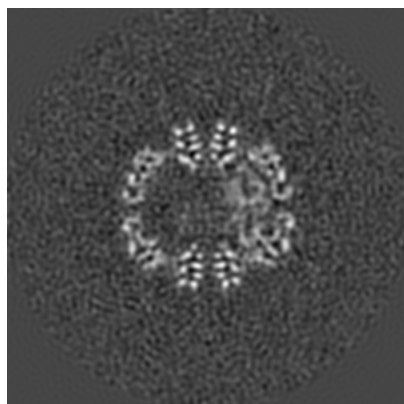


Z

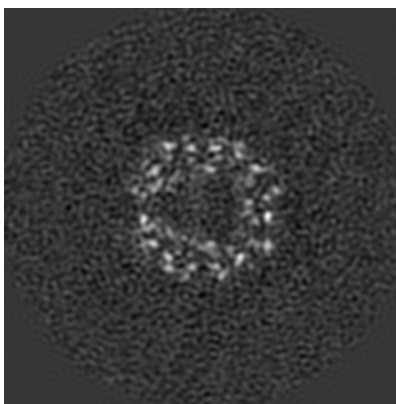
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

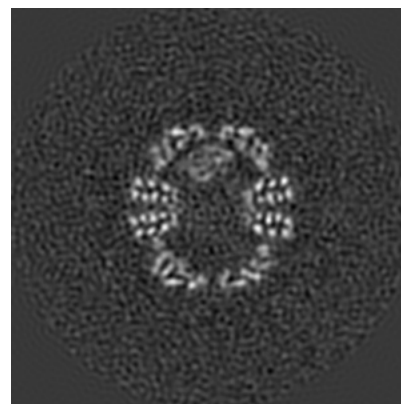
#### 6.2.1 Primary map



X Index: 140



Y Index: 140

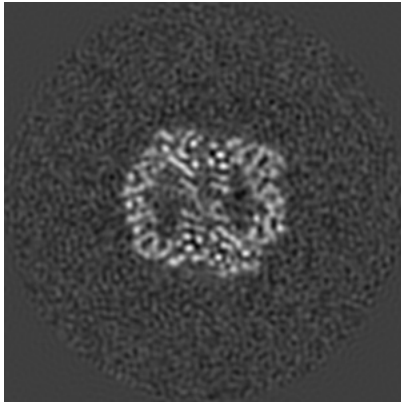


Z Index: 140

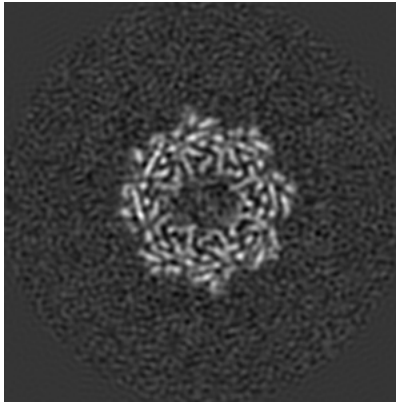
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [\(i\)](#)

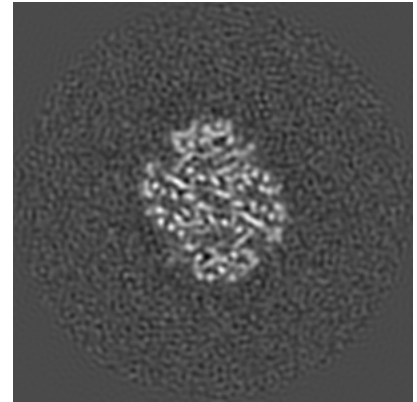
### 6.3.1 Primary map



X Index: 163



Y Index: 149

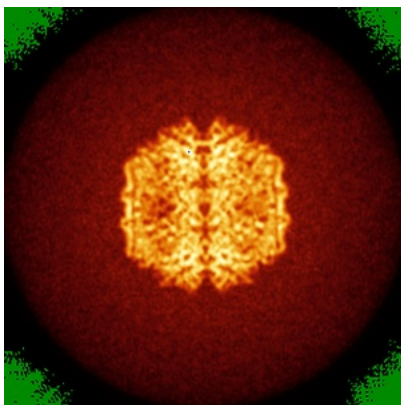


Z Index: 108

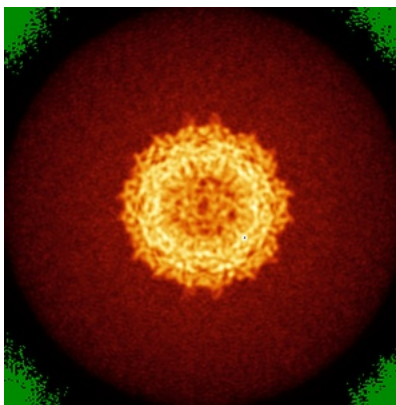
The images above show the largest variance slices of the map in three orthogonal directions.

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

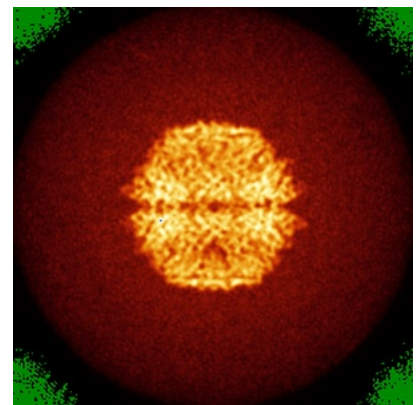
### 6.4.1 Primary map



X



Y

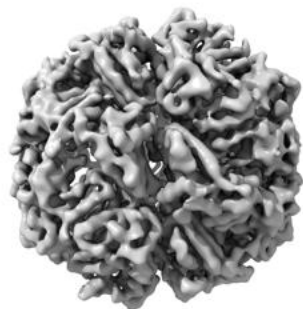


Z

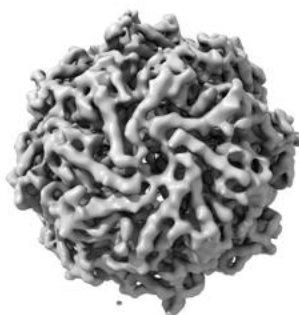
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

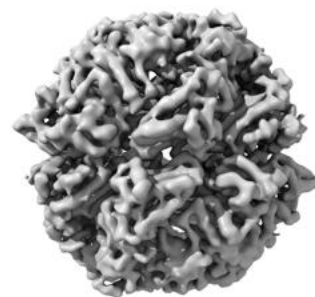
### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

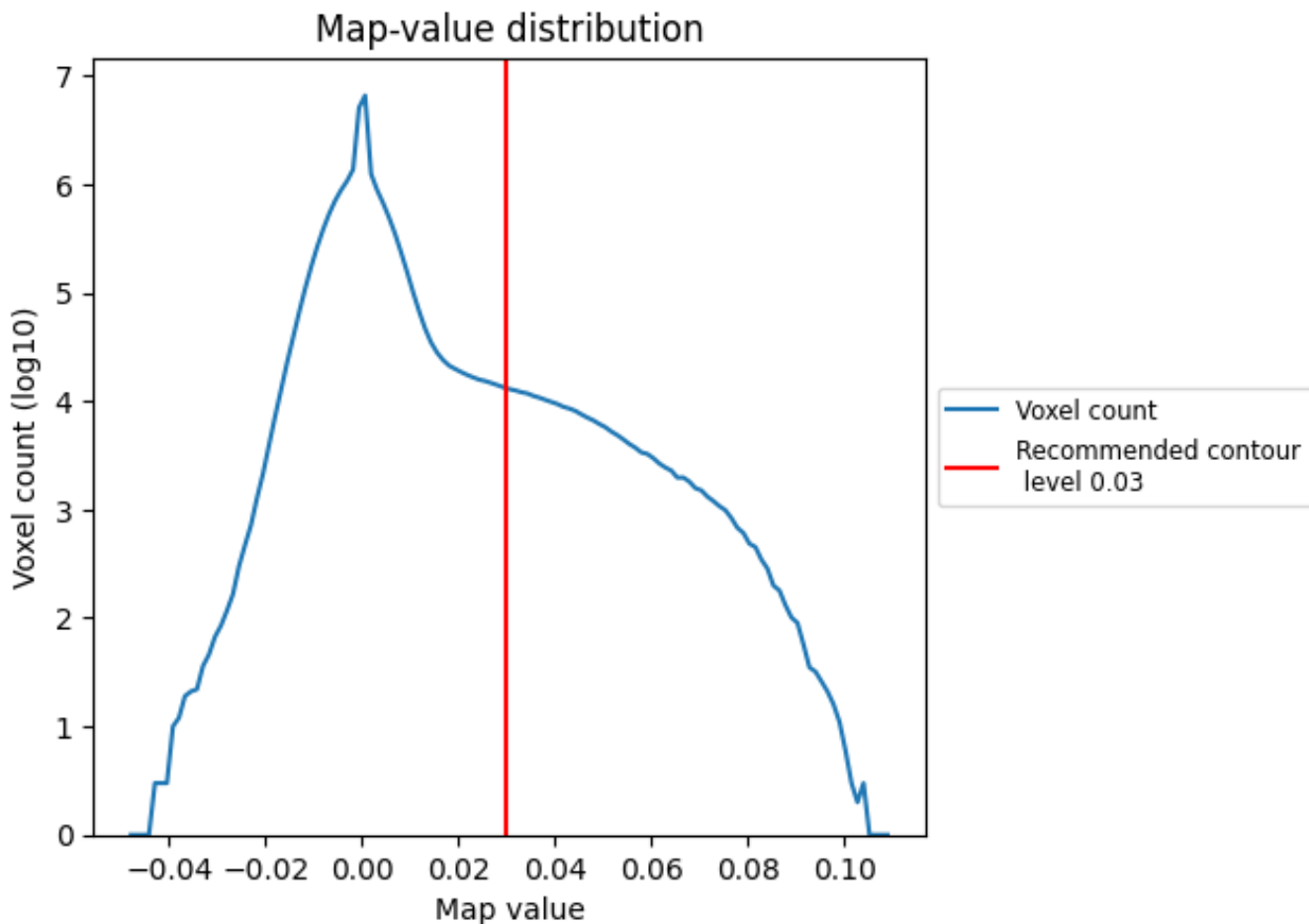
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

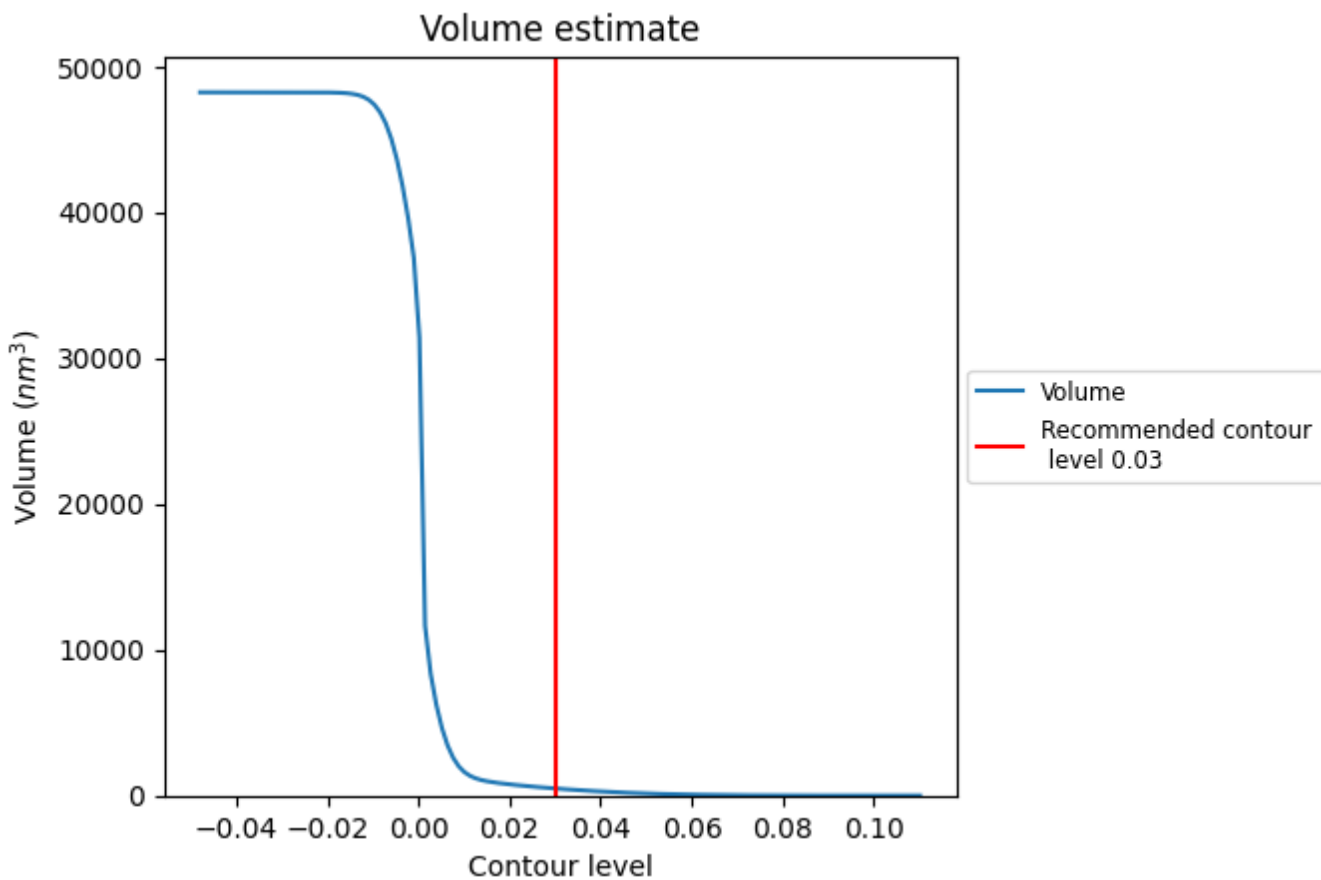
This section contains the results of statistical analysis of the map.

### 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.

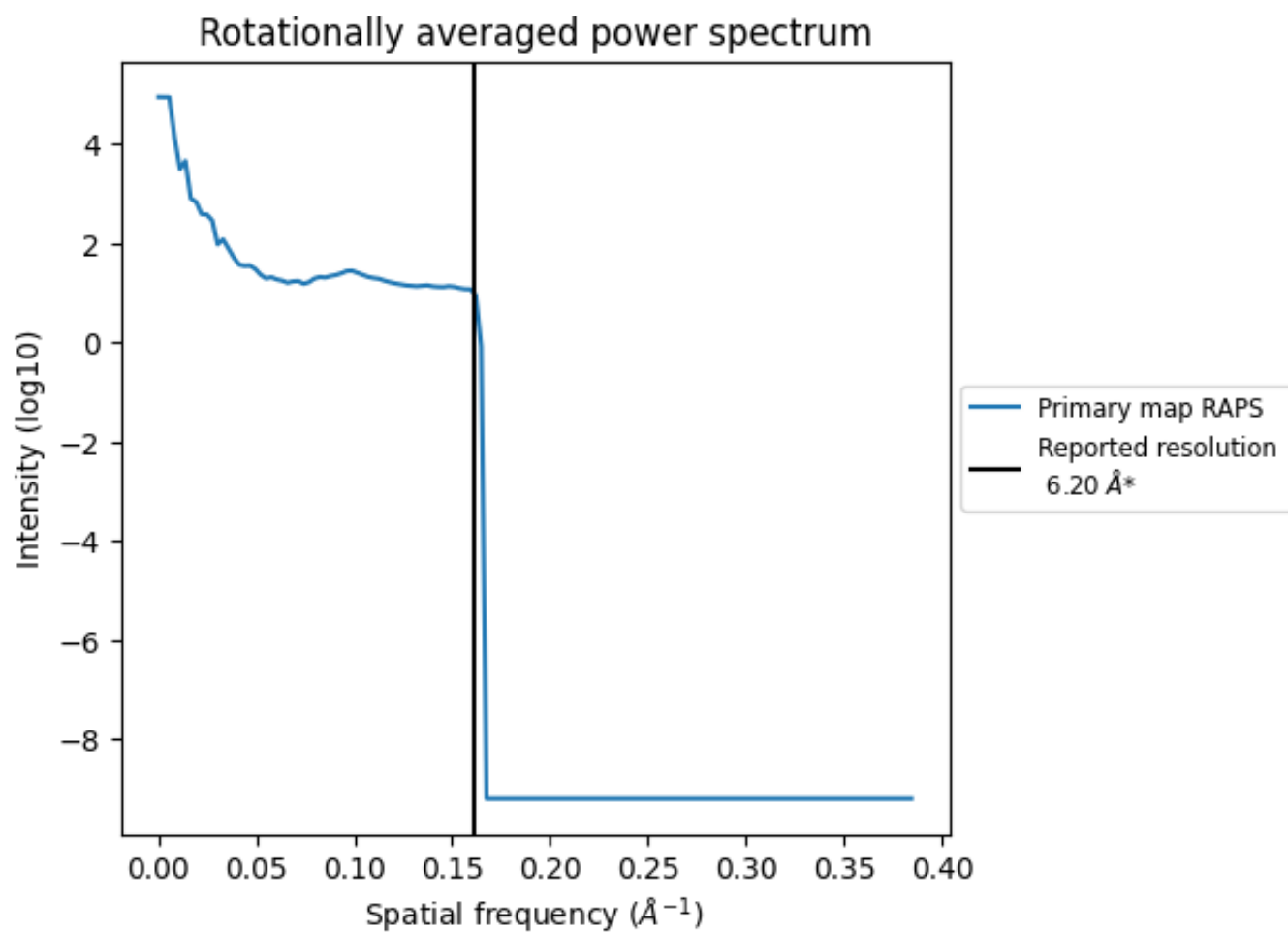
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 487 nm<sup>3</sup>; this corresponds to an approximate mass of 440 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 [i](#)



\*Reported resolution corresponds to spatial frequency of 0.161 Å<sup>-1</sup>



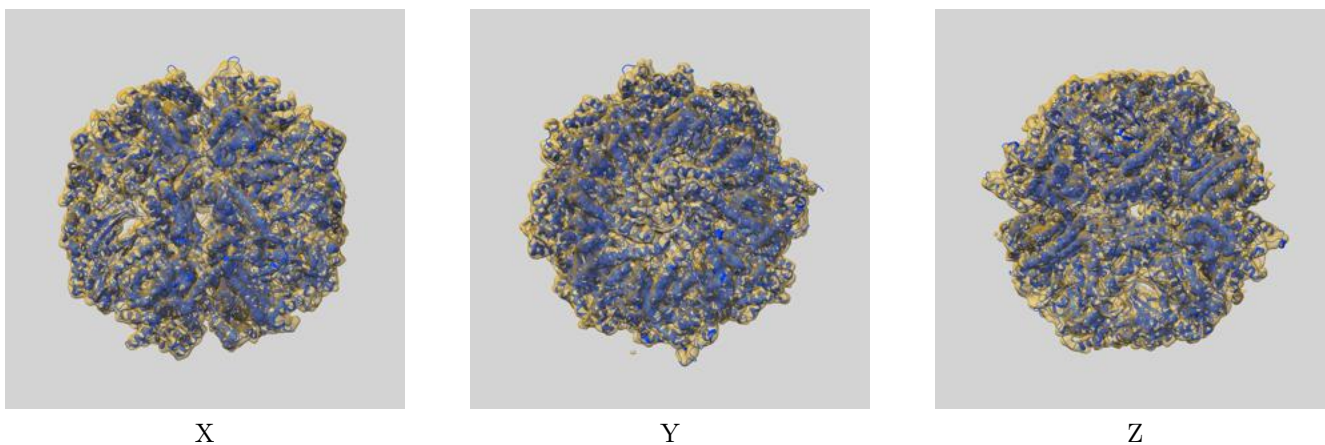
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

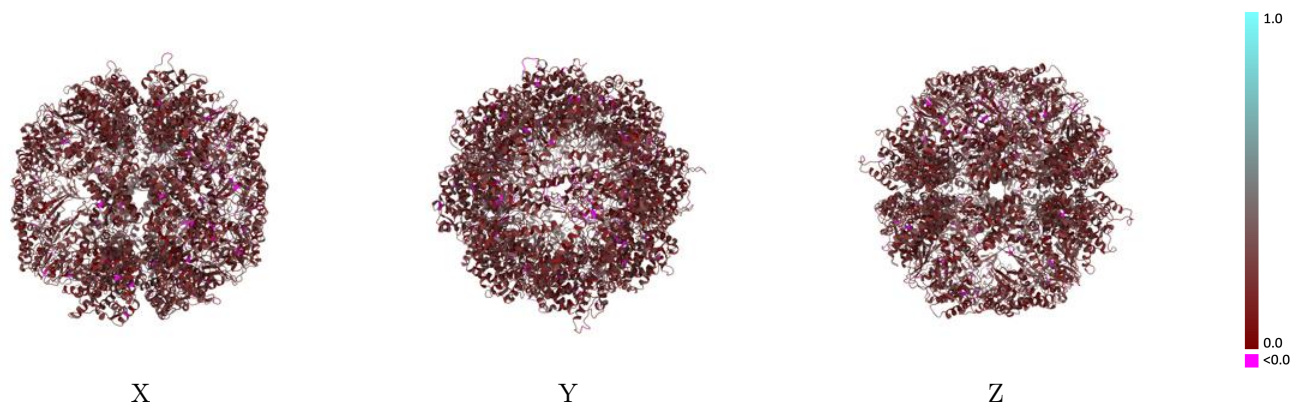
This section contains information regarding the fit between EMDB map EMD-23526 and PDB model 7LUP. Per-residue inclusion information can be found in section 3 on page 7.

### 9.1 Map-model overlay [i](#)



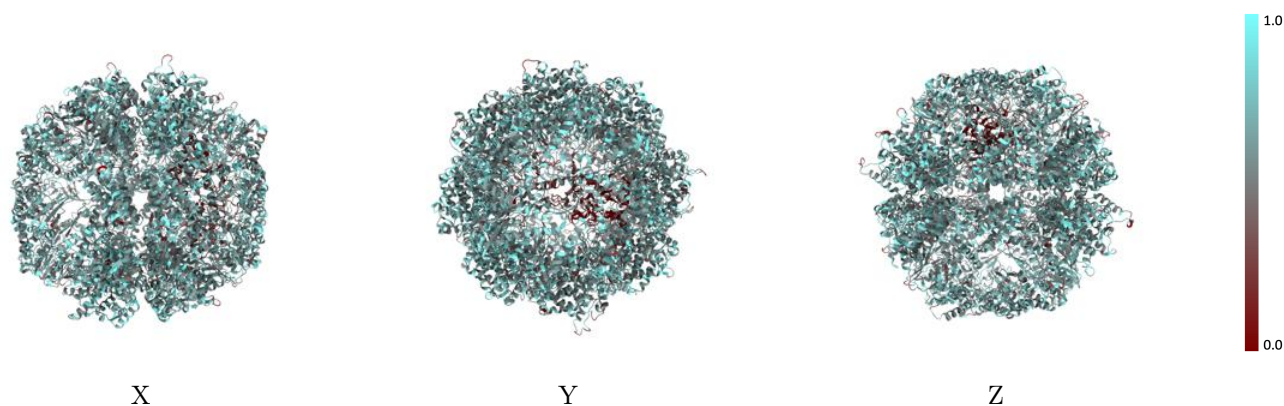
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



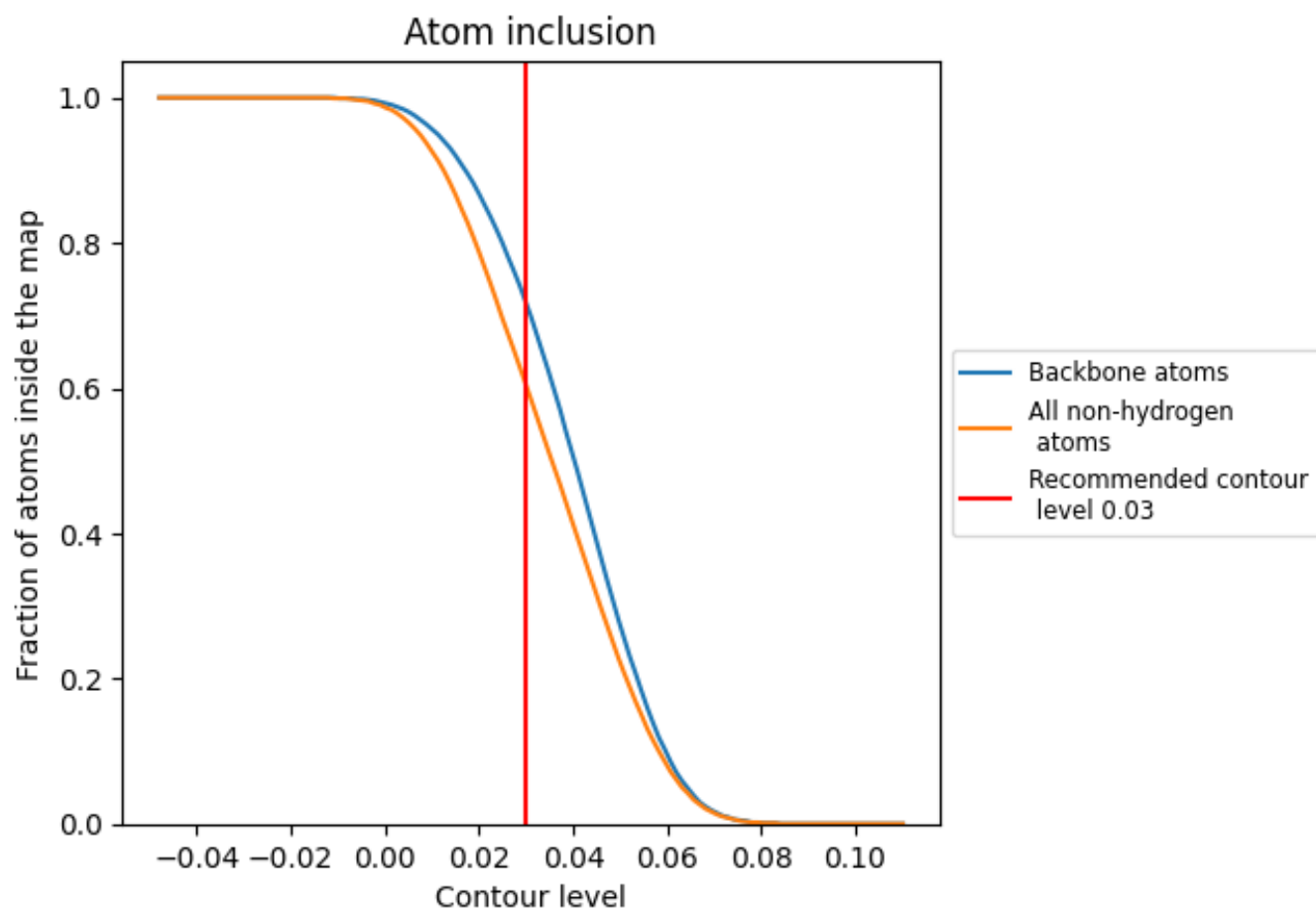
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).





































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6050	 0.2170
A	 0.6130	 0.2170
B	 0.6450	 0.2240
C	 0.6140	 0.2130
D	 0.6160	 0.2170
E	 0.6310	 0.2270
F	 0.6300	 0.2250
G	 0.6150	 0.2150
H	 0.6350	 0.2190
I	 0.6160	 0.2170
J	 0.6380	 0.2260
K	 0.6110	 0.2140
L	 0.6310	 0.2210
M	 0.6420	 0.2250
N	 0.6260	 0.2250
O	 0.6250	 0.2210
P	 0.6240	 0.2180
Q	 0.3150	 0.1500

