



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:17 AM UTC

PDB ID : 6KS7 / pdb_00006ks7
EMDB ID : EMD-0759
Title : TRiC at 0.1 mM ADP-AlFx, Conformation 1, 0.1-C1
Authors : Jin, M.; Cong, Y.
Deposited on : 2019-08-23
Resolution : 4.62 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:

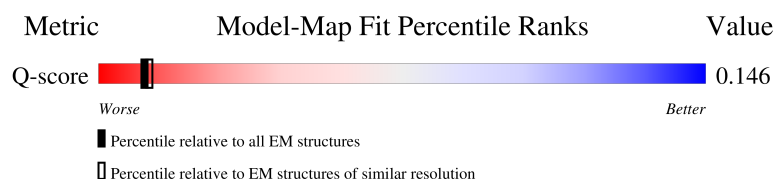
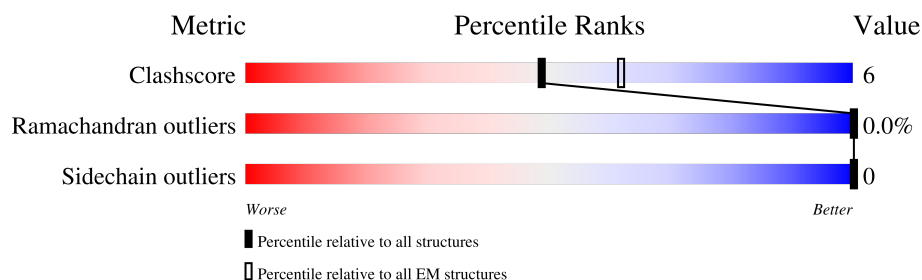
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.62 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	2088 (4.12 - 5.12)

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	H	550	58% 77% 15% 8%
1	h	550	56% 73% 15% 13%
2	A	559	53% 80% 13% 7%
2	a	559	56% 77% 15% 8%

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Mol	Chain	Length	Quality of chain
3	B	527	
3	b	527	
4	D	528	
4	d	528	
5	e	562	
6	E	518	
7	G	594	
7	g	594	
8	Q	568	
8	q	568	
9	Z	546	
9	z	546	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 62022 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 eta.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	506	Total	C	N	O	S	0	0
			3878	2445	663	751	19		
1	h	480	Total	C	N	O	S	0	0
			3658	2308	626	705	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	514	Total	C	N	O	S	0	0
			3879	2429	679	752	19		
2	A	521	Total	C	N	O	S	0	0
			3924	2457	687	760	20		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	505	Total	C	N	O	S	0	0
			3833	2397	662	760	14		
3	B	505	Total	C	N	O	S	0	0
			3833	2397	662	760	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	484	Total	C	N	O	S	0	0
			3687	2307	652	712	16		
4	D	492	Total	C	N	O	S	0	0
			3756	2348	667	724	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	e	501	Total	C	N	O	S	0	0
			3842	2411	656	754	21		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	518	Total	C	N	O	S	0	0
			3982	2500	678	783	21		

- Molecule 7 is a protein called fusion protein of T-complex protein 1 subunit gamma, rep-His-CBP and T-complex protein 1 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	g	487	Total	C	N	O	S	0	0
			3722	2339	650	708	25		
7	G	508	Total	C	N	O	S	0	0
			3905	2452	681	747	25		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
g	?	LEU	-	see sequence details	UNP P39077
g	?	GLU	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	TRP	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	PRO	-	see sequence details	UNP P39077
g	?	GLN	-	see sequence details	UNP P39077
g	?	PHE	-	see sequence details	UNP P39077
g	?	GLU	-	see sequence details	UNP P39077
g	?	LYS	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	LYS	-	see sequence details	UNP P39077
g	?	ARG	-	see sequence details	UNP P39077
g	?	ARG	-	see sequence details	UNP P39077
g	?	TRP	-	see sequence details	UNP P39077

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Chain	Residue	Modelled	Actual	Comment	Reference
g	?	LYS	-	see sequence details	UNP P39077
g	?	LYS	-	see sequence details	UNP P39077
g	?	ASN	-	see sequence details	UNP P39077
g	?	PHE	-	see sequence details	UNP P39077
g	?	ILE	-	see sequence details	UNP P39077
g	?	ALA	-	see sequence details	UNP P39077
g	?	VAL	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	ALA	-	see sequence details	UNP P39077
g	?	ALA	-	see sequence details	UNP P39077
g	?	ASN	-	see sequence details	UNP P39077
g	?	ARG	-	see sequence details	UNP P39077
g	?	PHE	-	see sequence details	UNP P39077
g	?	LYS	-	see sequence details	UNP P39077
g	?	LYS	-	see sequence details	UNP P39077
g	?	ILE	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	ALA	-	see sequence details	UNP P39077
g	?	LEU	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	HIS	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	SER	-	see sequence details	UNP P39077
g	?	GLY	-	see sequence details	UNP P39077
g	?	LEU	-	see sequence details	UNP P39077
g	?	GLN	-	see sequence details	UNP P39077
G	?	LEU	-	see sequence details	UNP P39077
G	?	GLU	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	GLY	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	TRP	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	PRO	-	see sequence details	UNP P39077
G	?	GLN	-	see sequence details	UNP P39077
G	?	PHE	-	see sequence details	UNP P39077
G	?	GLU	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	ARG	-	see sequence details	UNP P39077
G	?	ARG	-	see sequence details	UNP P39077
G	?	TRP	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	ASN	-	see sequence details	UNP P39077
G	?	PHE	-	see sequence details	UNP P39077
G	?	ILE	-	see sequence details	UNP P39077
G	?	ALA	-	see sequence details	UNP P39077
G	?	VAL	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	ALA	-	see sequence details	UNP P39077
G	?	ALA	-	see sequence details	UNP P39077
G	?	ASN	-	see sequence details	UNP P39077
G	?	ARG	-	see sequence details	UNP P39077
G	?	PHE	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	LYS	-	see sequence details	UNP P39077
G	?	ILE	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	ALA	-	see sequence details	UNP P39077
G	?	LEU	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077

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Chain	Residue	Modelled	Actual	Comment	Reference
G	?	GLY	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	HIS	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	SER	-	see sequence details	UNP P39077
G	?	GLY	-	see sequence details	UNP P39077
G	?	LEU	-	see sequence details	UNP P39077
G	?	GLN	-	see sequence details	UNP P39077

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	524	Total	C	N	O	S	0	0
			3978	2508	677	767	26		
8	Q	528	Total	C	N	O	S	0	0
			4005	2522	682	775	26		

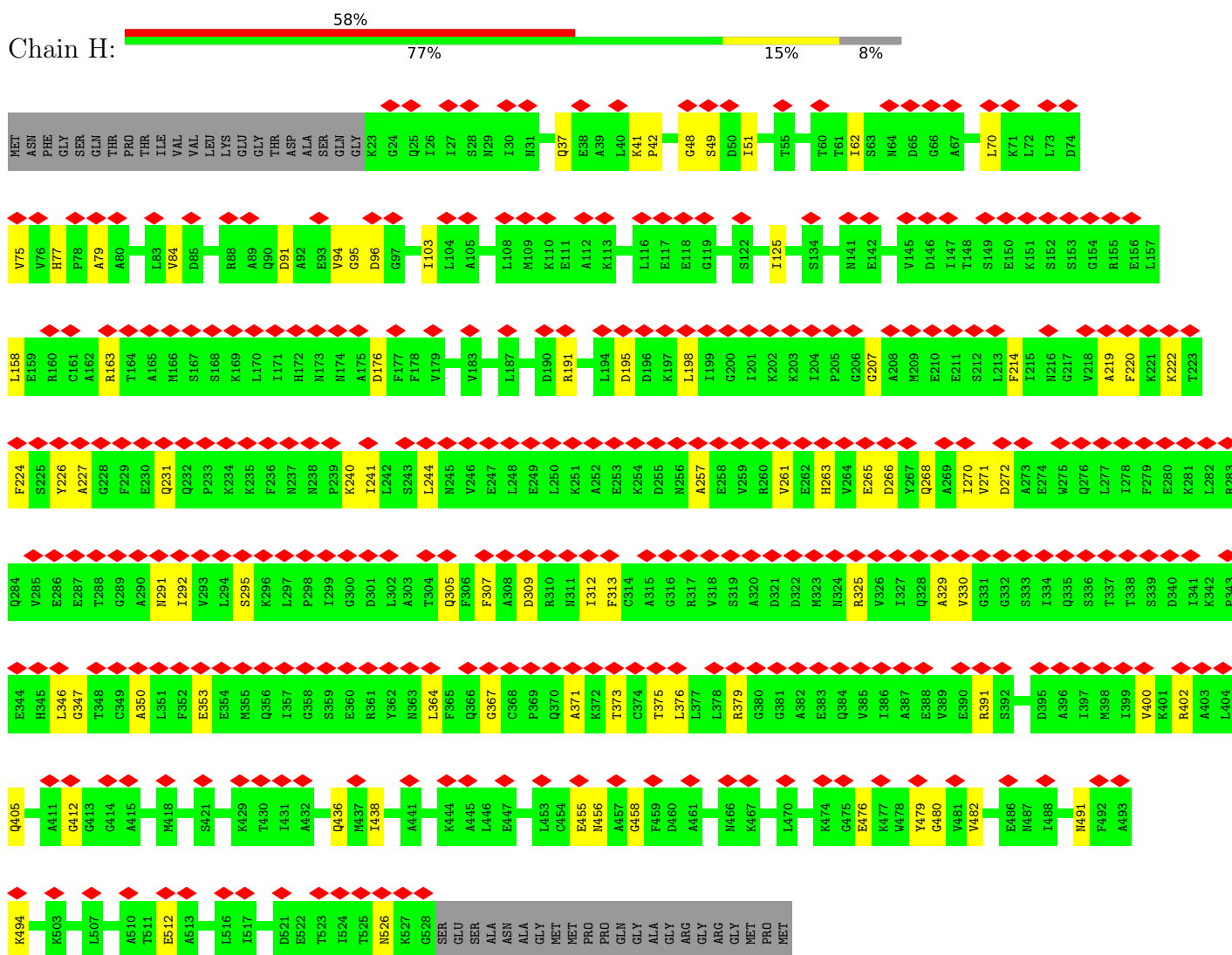
- Molecule 9 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	z	529	Total	C	N	O	S	0	0
			4070	2555	705	793	17		
9	Z	529	Total	C	N	O	S	0	0
			4070	2555	705	793	17		

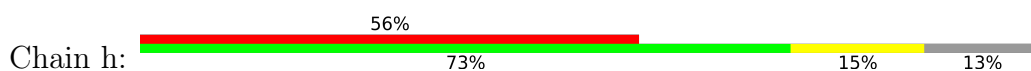
3 Residue-property plots

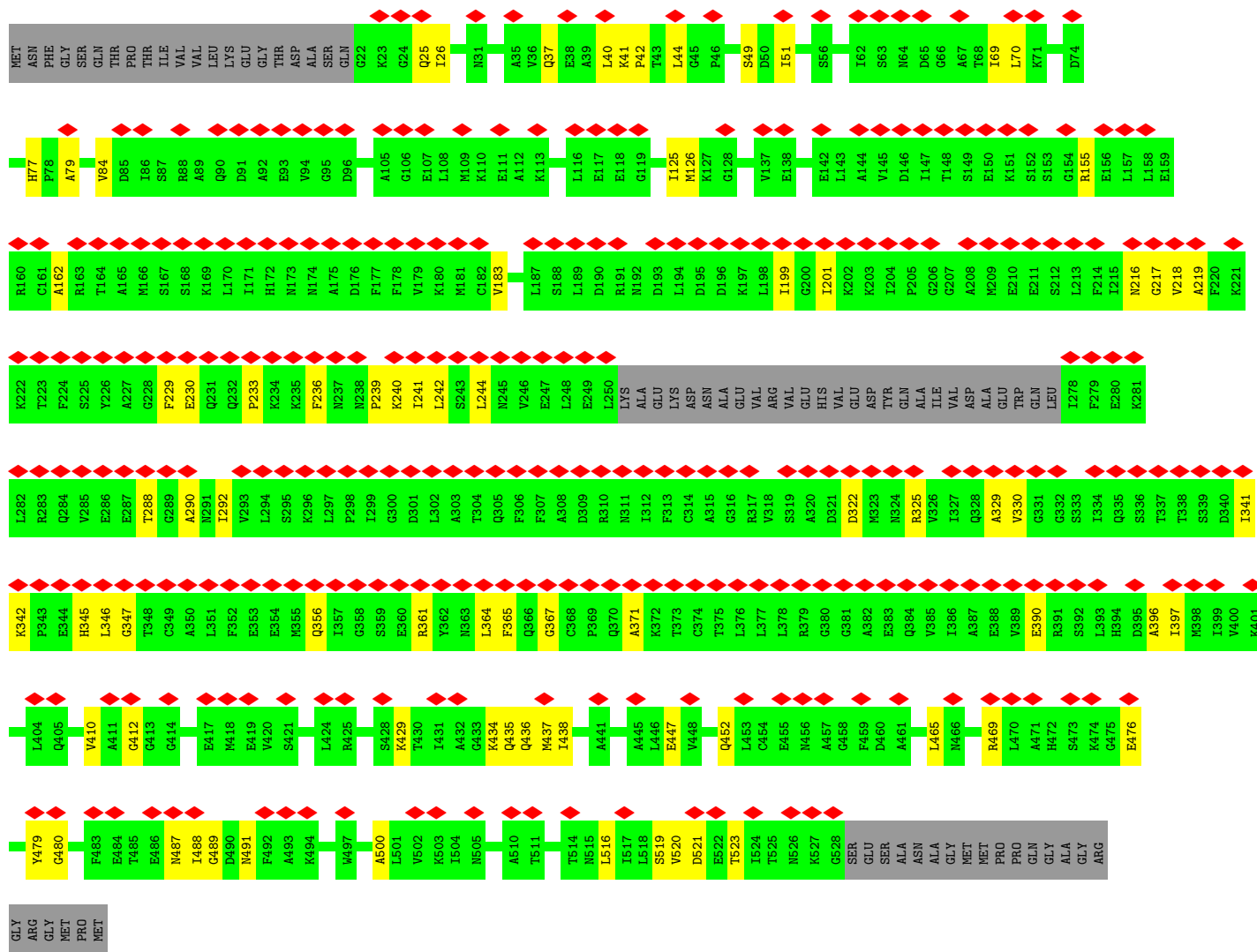
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

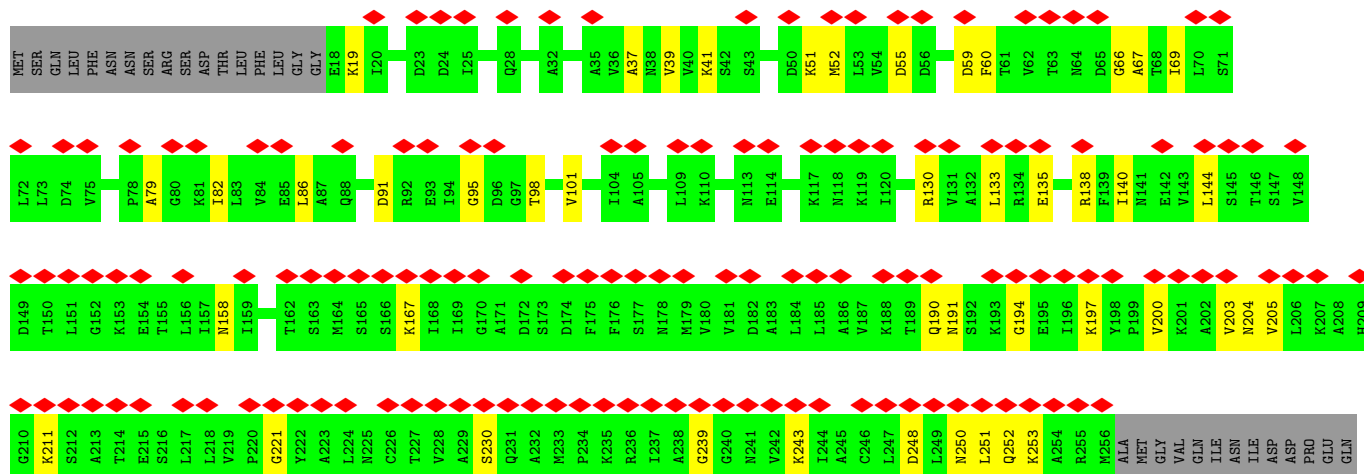
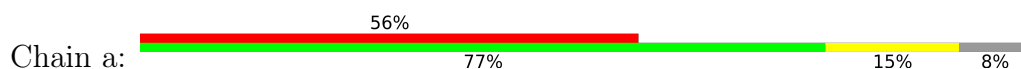


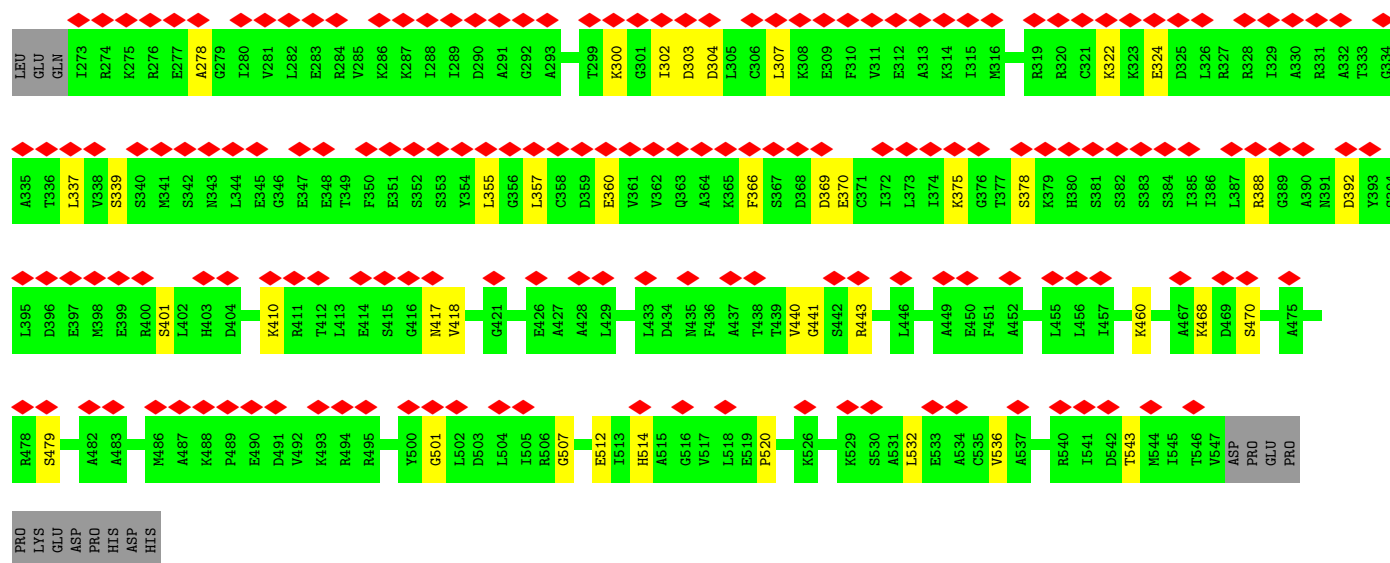
• Molecule 1: T-complex protein 1 subunit eta



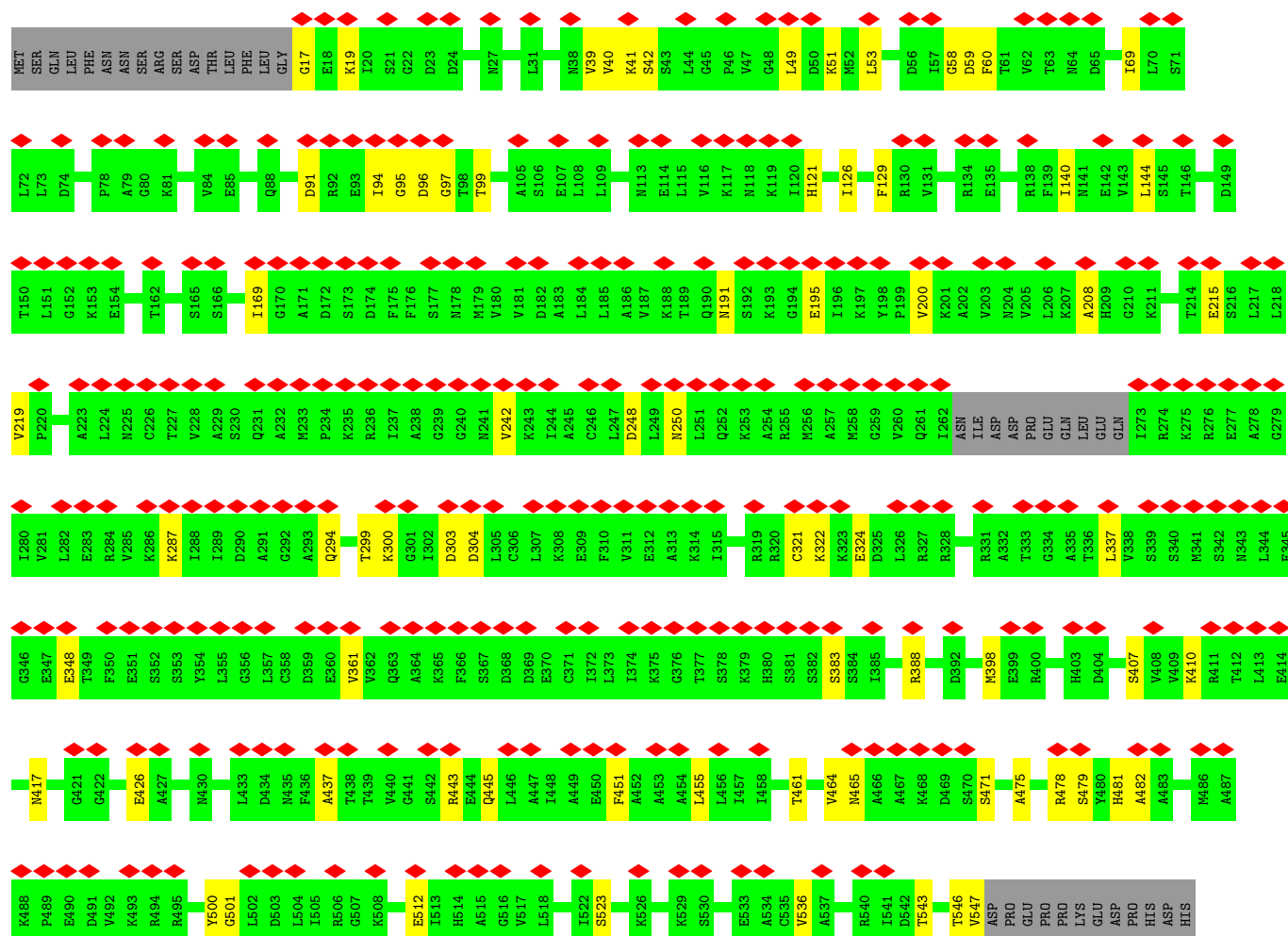


• Molecule 2: T-complex protein 1 subunit alpha



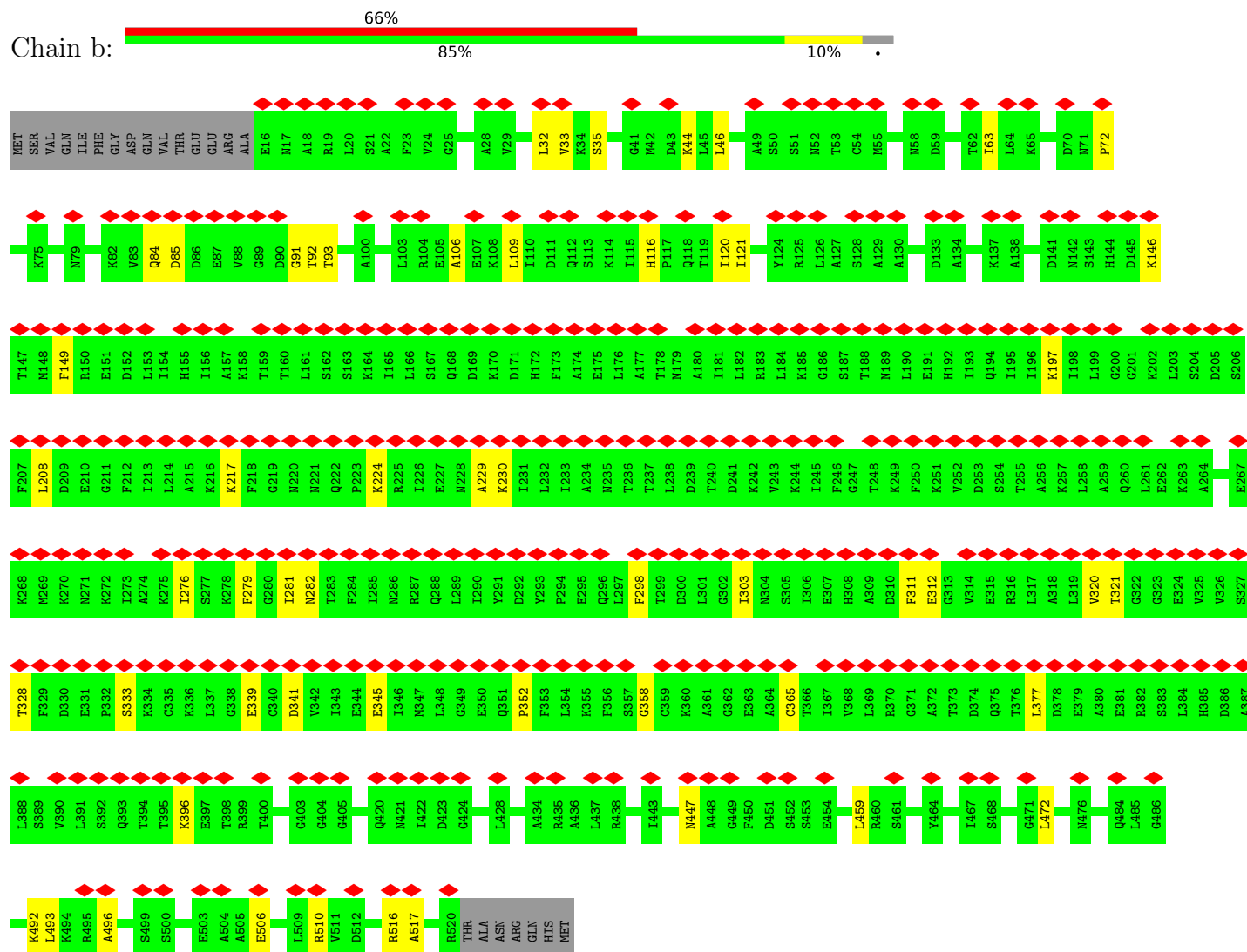


• Molecule 2: T-complex protein 1 subunit alpha



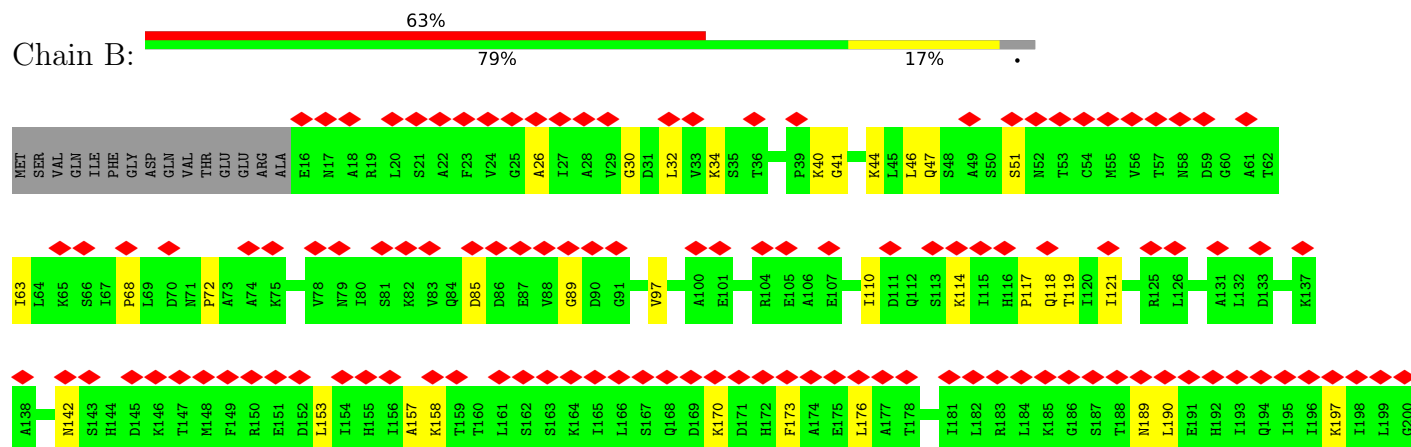
- Molecule 3: T-complex protein 1 subunit beta

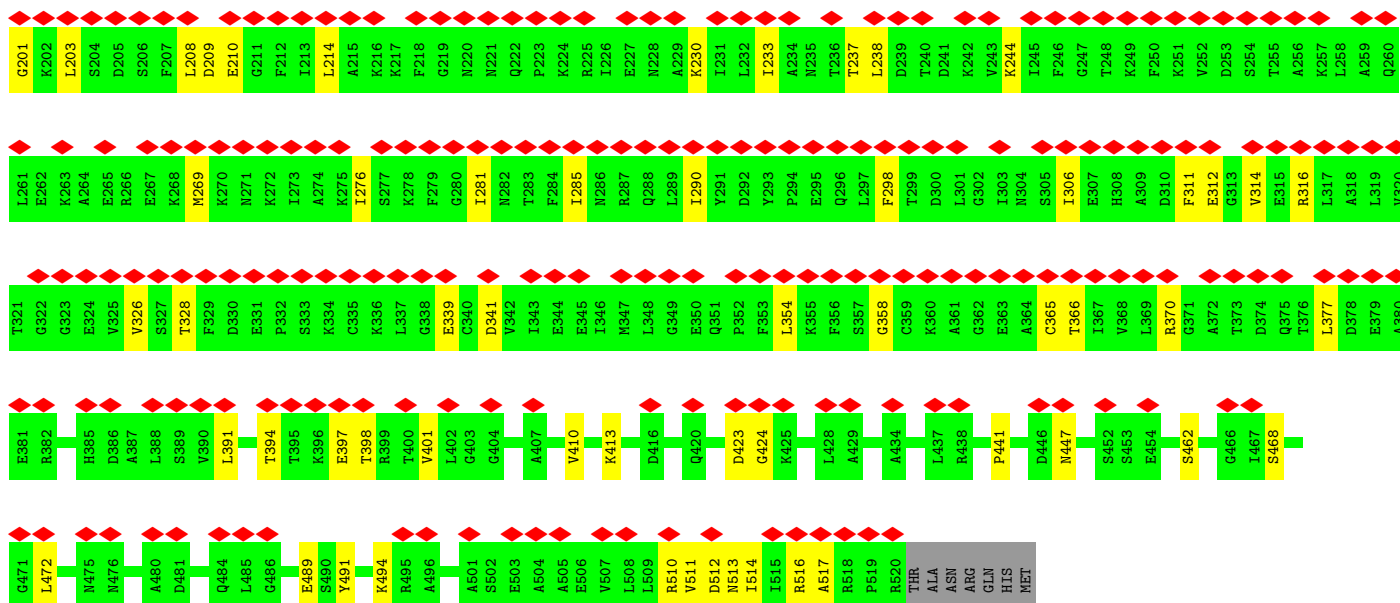
Chain b:



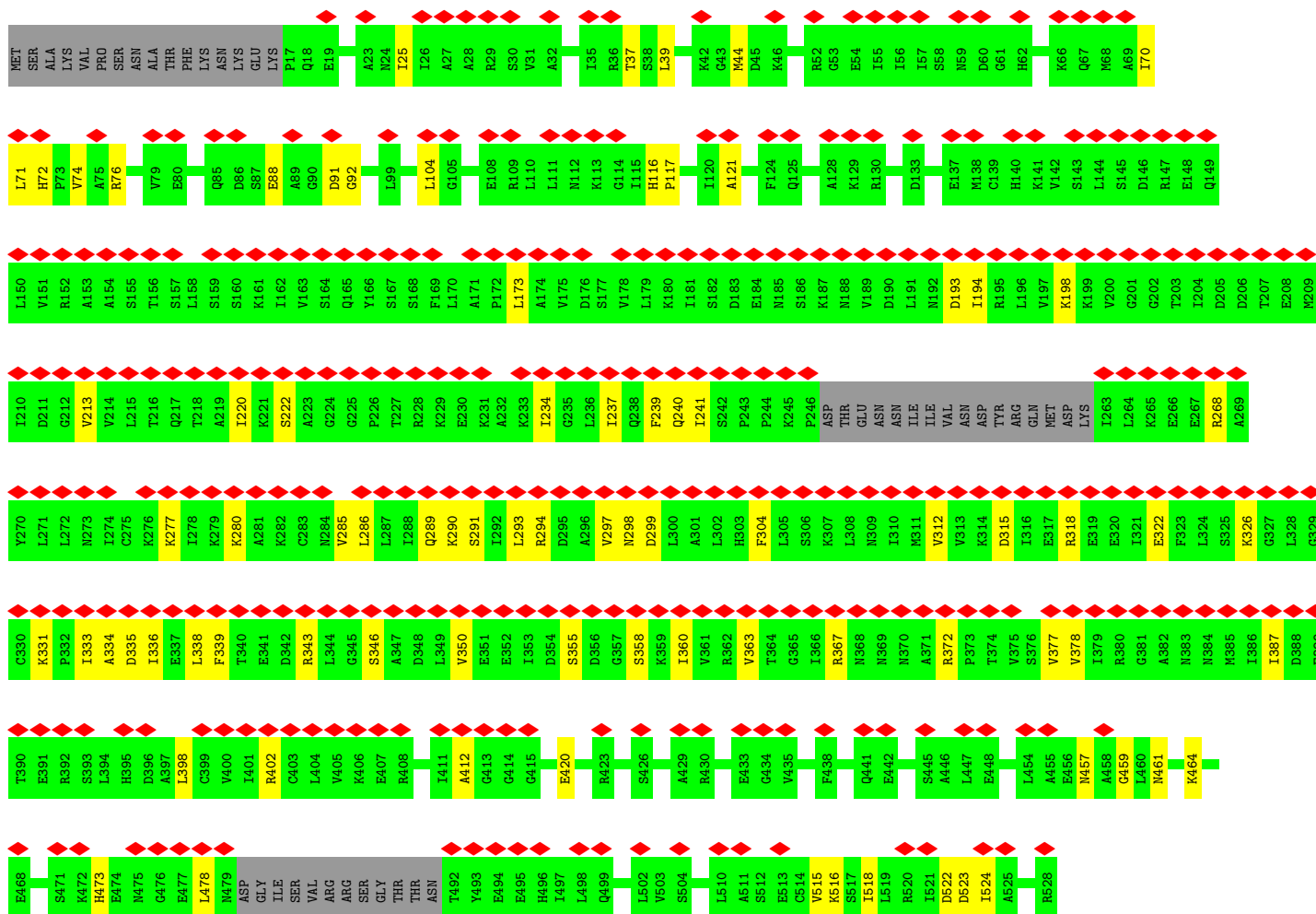
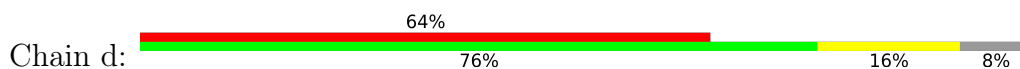
- Molecule 3: T-complex protein 1 subunit beta

Chain B:





• Molecule 4: T-complex protein 1 subunit delta



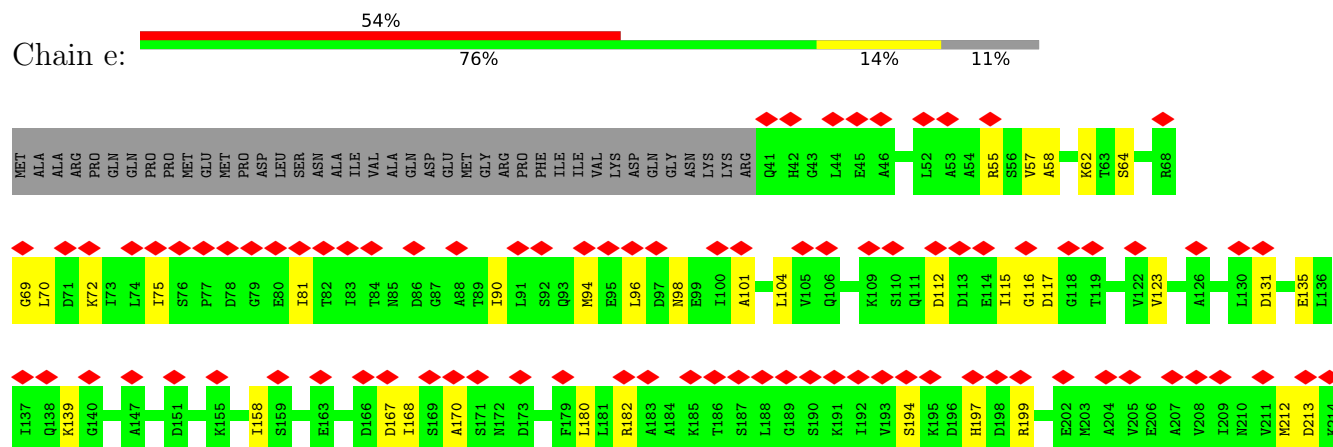
• Molecule 4: T-complex protein 1 subunit delta

Chain D:

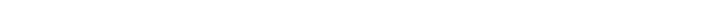


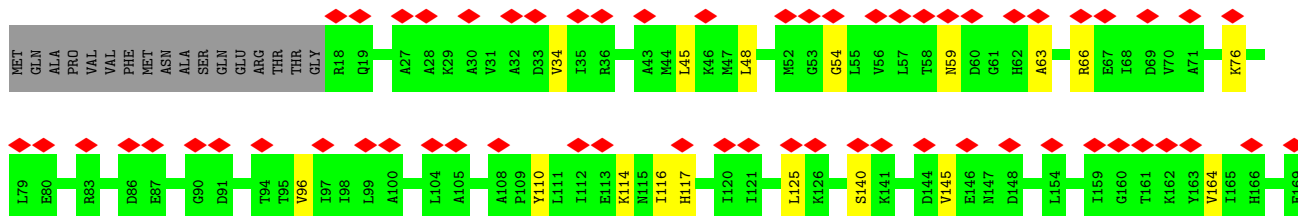
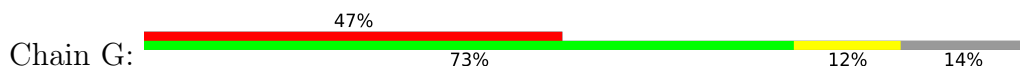
• Molecule 5: T-complex protein 1 subunit epsilon

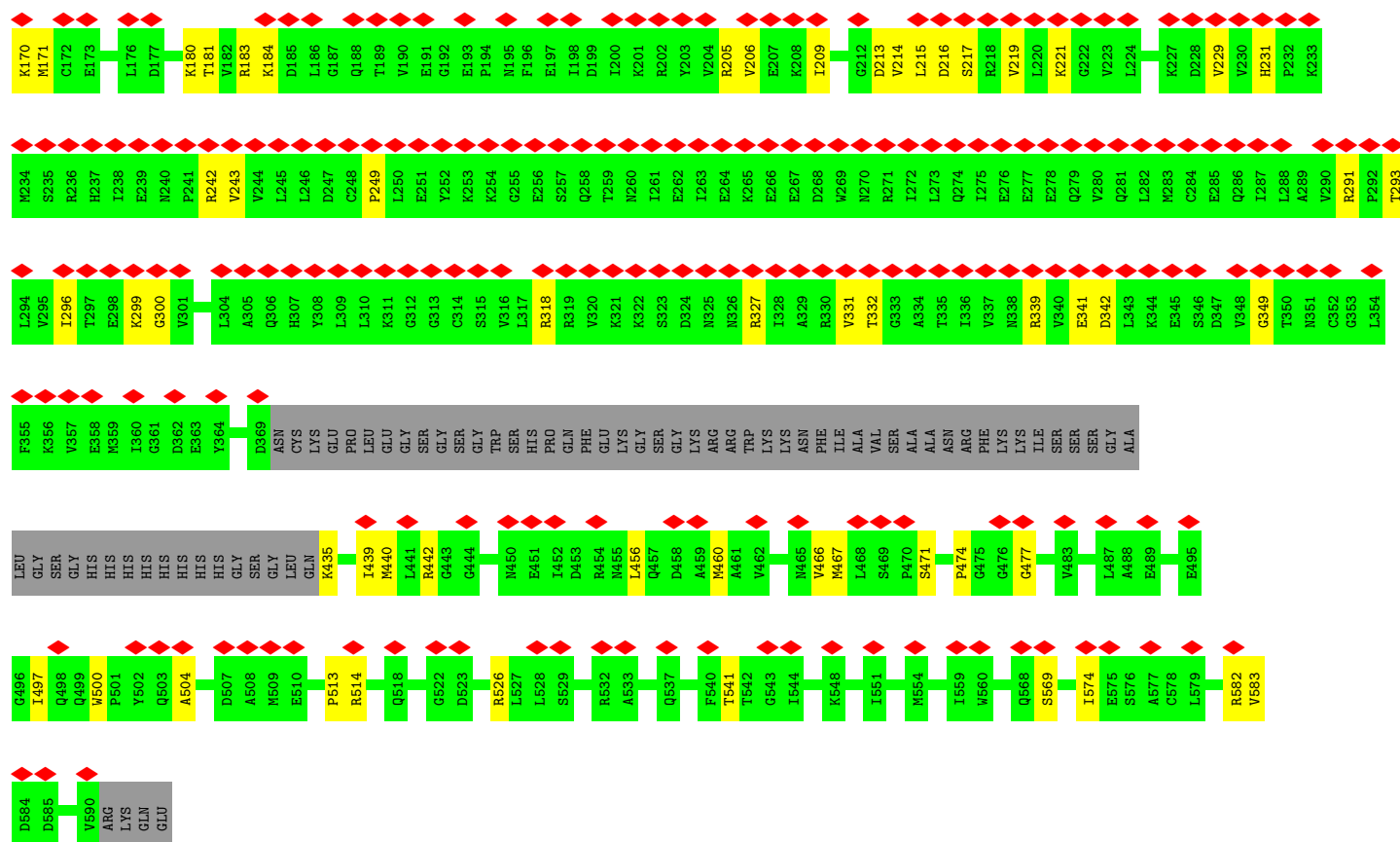
Chain e:



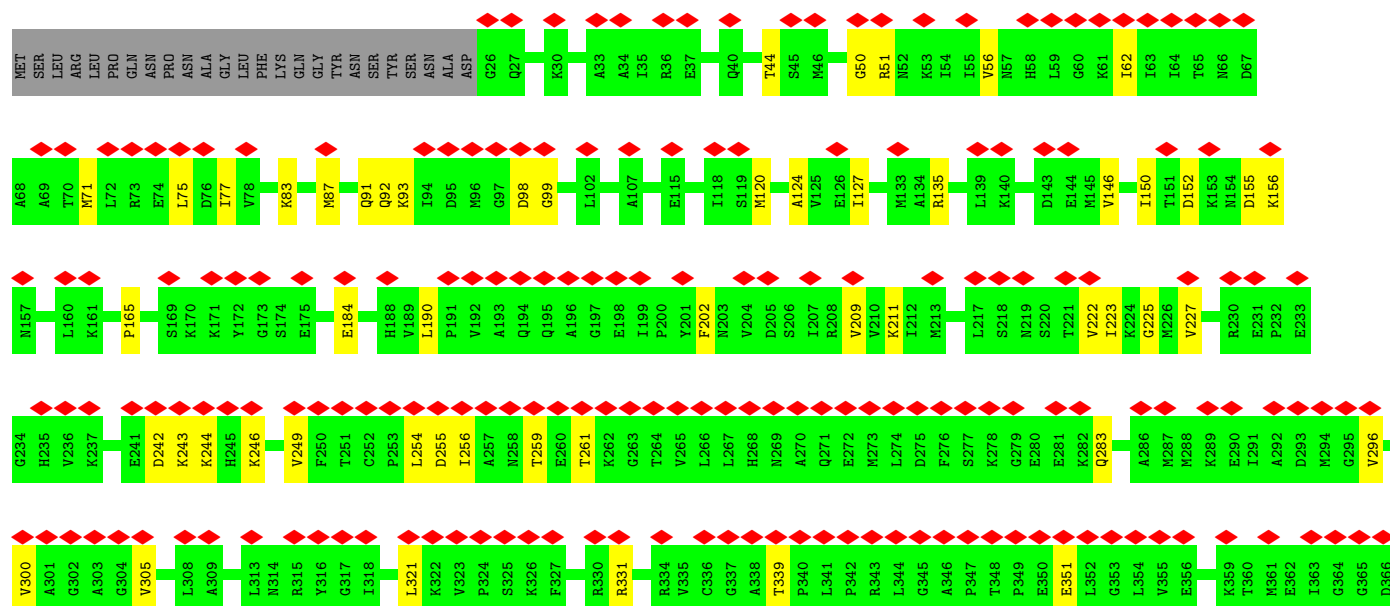
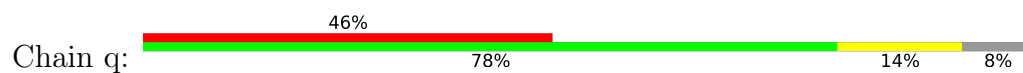


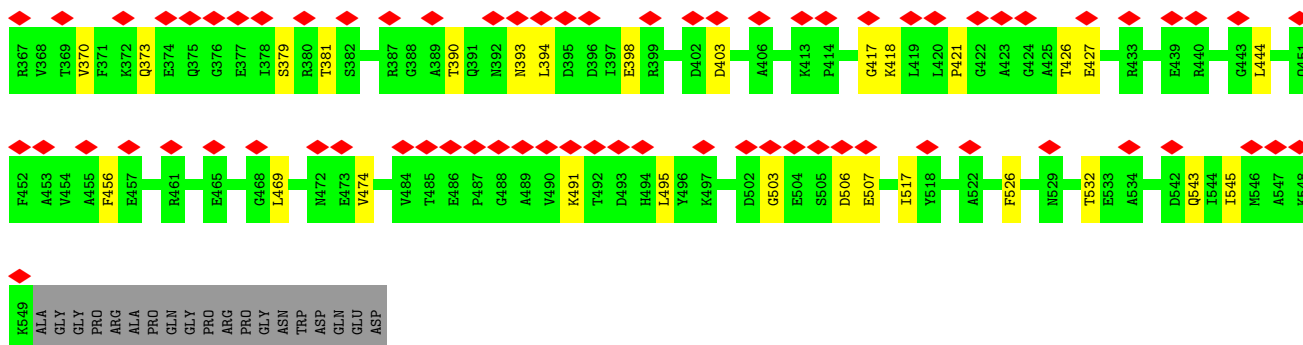
- Chain g: 



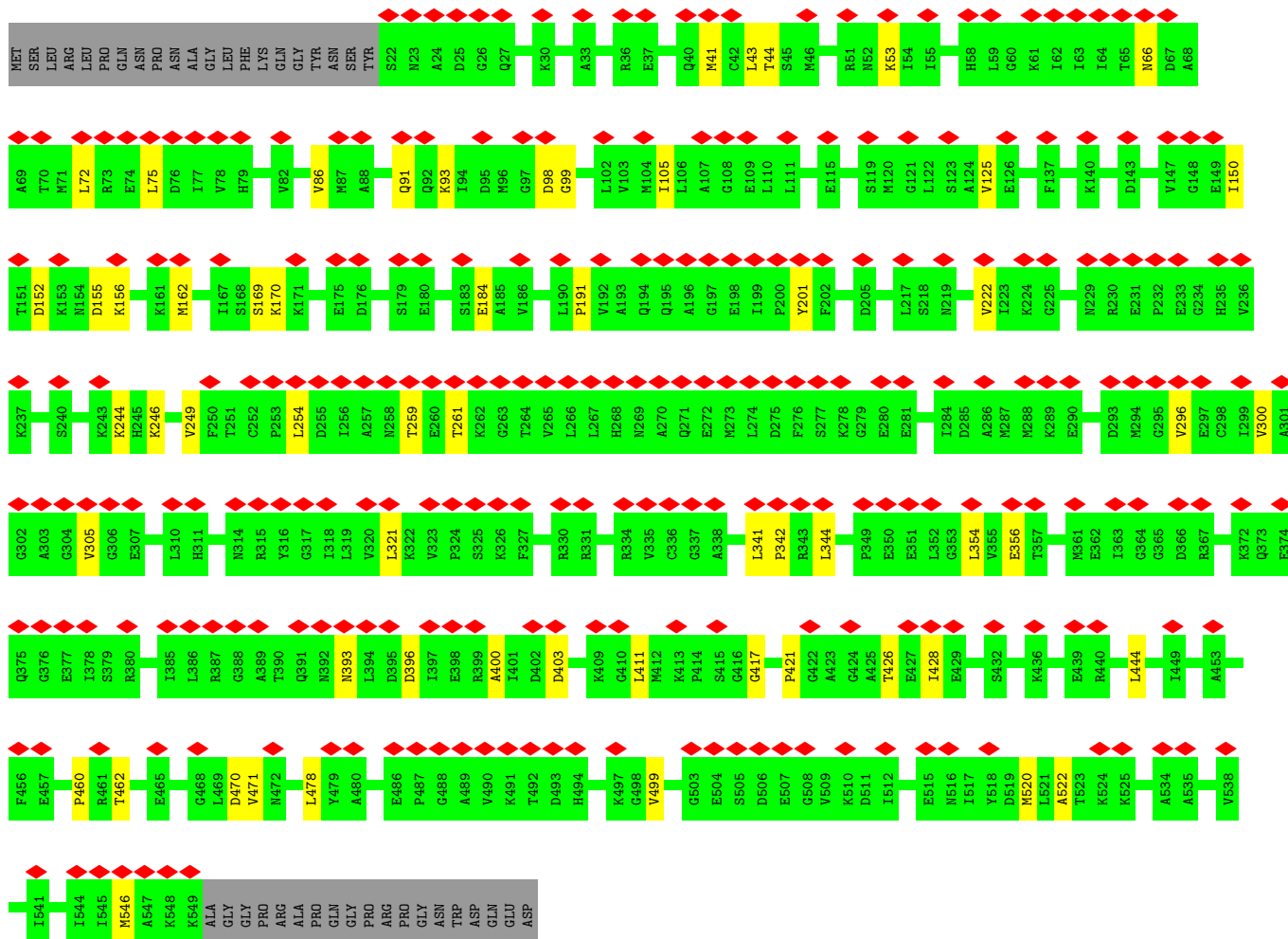
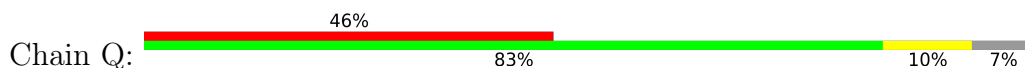


• Molecule 8: T-complex protein 1 subunit theta

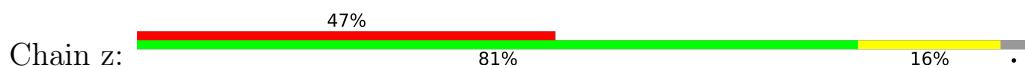


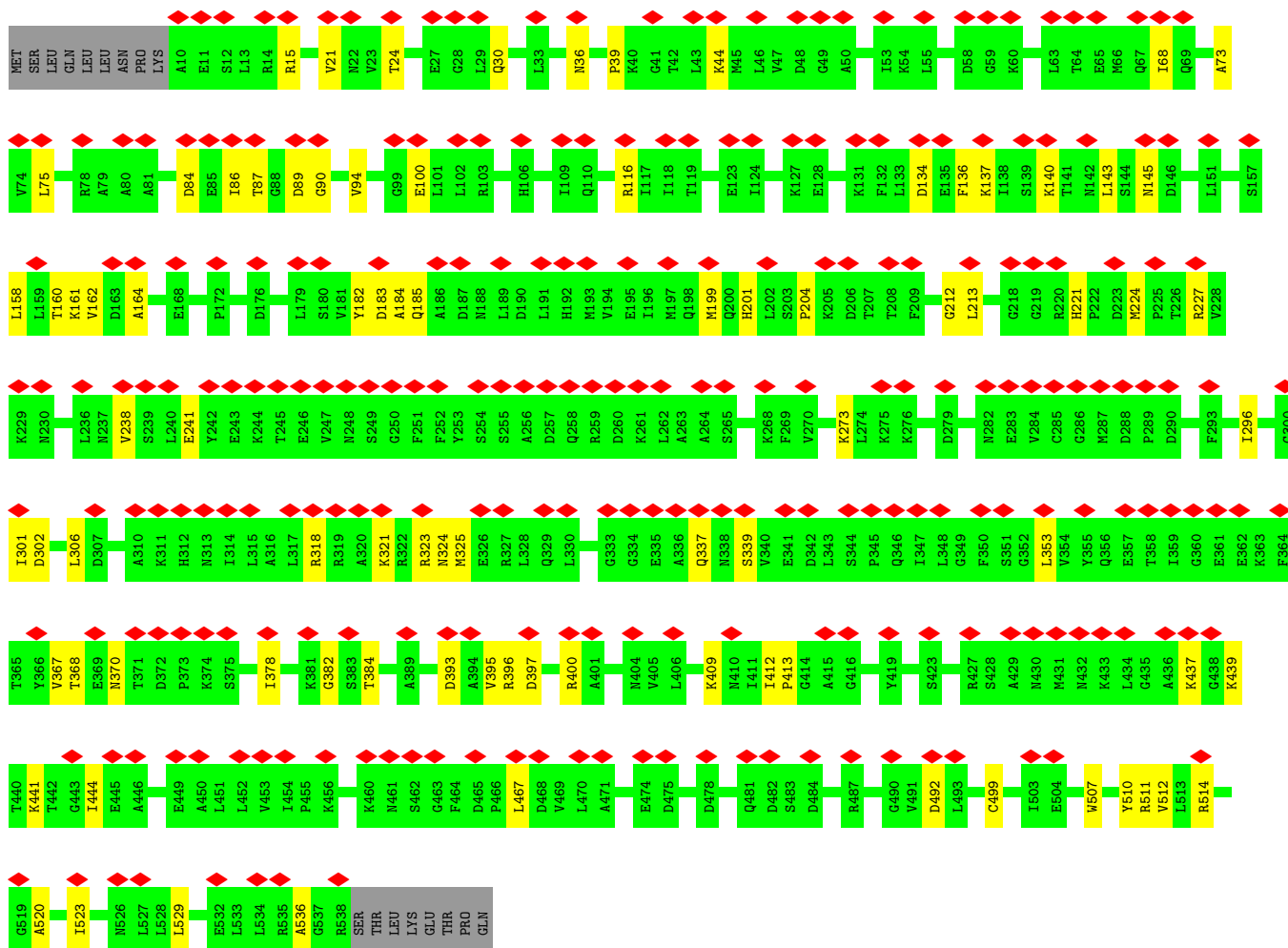


• Molecule 8: T-complex protein 1 subunit theta

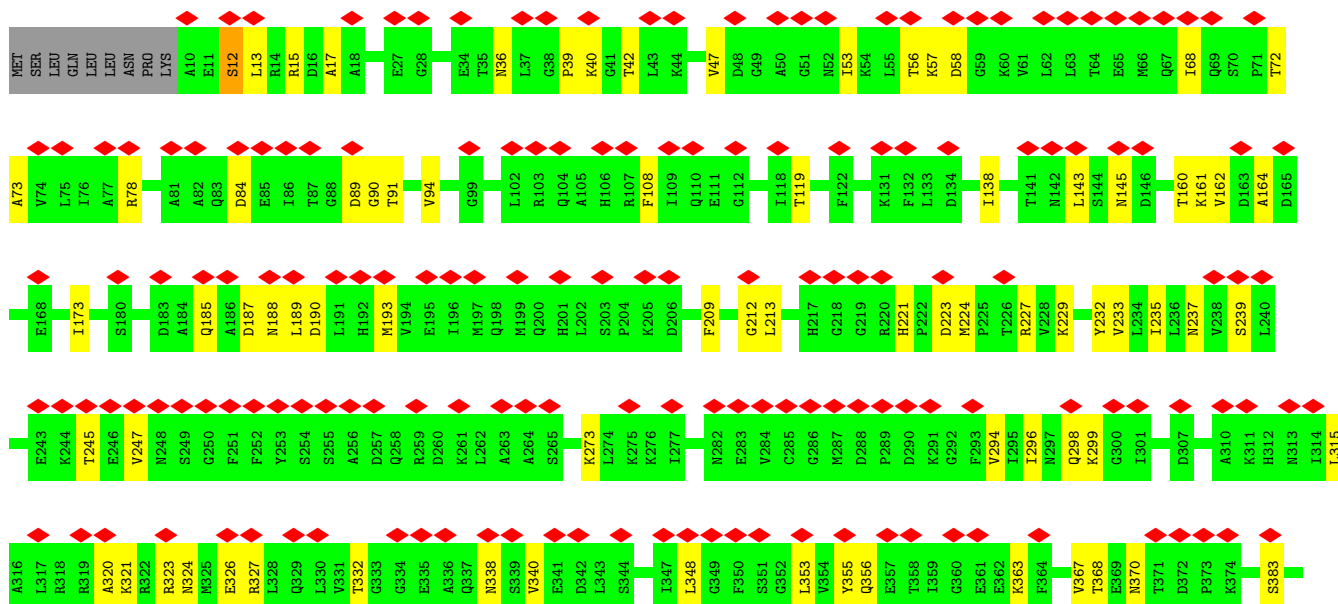
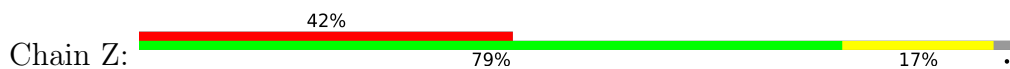


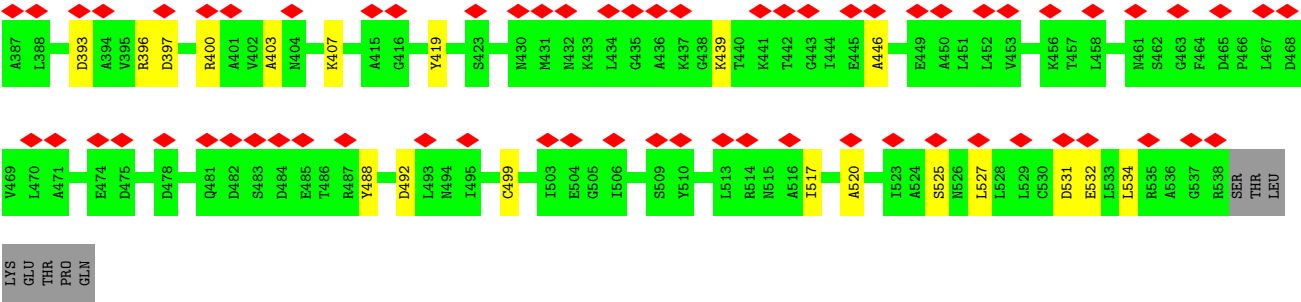
• Molecule 9: T-complex protein 1 subunit zeta





• Molecule 9: T-complex protein 1 subunit zeta





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	61702	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	38	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	3.670	Depositor
Minimum map value	-2.012	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.164	Depositor
Recommended contour level	1.05	Depositor
Map size ($\text{\AA}$)	337.408, 337.408, 337.408	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.318, 1.318, 1.318	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	H	0.07	0/3927	0.22	0/5299
1	h	0.07	0/3702	0.21	0/4991
2	A	0.07	0/3957	0.23	0/5335
2	a	0.09	0/3912	0.24	0/5275
3	B	0.07	0/3871	0.23	0/5216
3	b	0.07	0/3871	0.22	0/5216
4	D	0.07	0/3788	0.23	0/5100
4	d	0.07	0/3720	0.23	0/5012
5	e	0.07	0/3888	0.22	0/5235
6	E	0.08	0/4030	0.22	0/5426
7	G	0.08	0/3950	0.24	0/5334
7	g	0.08	0/3764	0.23	0/5082
8	Q	0.06	0/4051	0.21	0/5468
8	q	0.09	0/4024	0.20	0/5431
9	Z	0.08	0/4121	0.28	1/5568 (0.0%)
9	z	0.07	0/4121	0.26	0/5568
All	All	0.07	0/62697	0.23	1/84556 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	Z	12	SER	CB-CA-C	-5.05	109.77	115.79

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	H	3878	0	3961	58	0
1	h	3658	0	3756	52	0
2	A	3924	0	4108	48	0
2	a	3879	0	4060	47	0
3	B	3833	0	3945	58	0
3	b	3833	0	3945	33	0
4	D	3756	0	3939	49	0
4	d	3687	0	3866	45	0
5	e	3842	0	3923	46	0
6	E	3982	0	4075	72	0
7	G	3905	0	4049	47	0
7	g	3722	0	3870	51	0
8	Q	4005	0	4152	37	0
8	q	3978	0	4132	48	0
9	Z	4070	0	4156	62	0
9	z	4070	0	4156	51	0
All	All	62022	0	64093	729	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 6.

The worst 5 of 729 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)
9:z:212:GLY:H	9:z:368:THR:HG22	1.42	0.84
9:Z:212:GLY:H	9:Z:368:THR:HG22	1.41	0.84
6:E:247:LYS:HG3	6:E:249:PHE:H	1.52	0.74
4:d:121:ALA:HB1	4:d:516:LYS:HG3	1.71	0.71
1:h:25:GLN:HG2	1:h:523:THR:H	1.55	0.71

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	H	504/550 (92%)	482 (96%)	22 (4%)	0	100	100
1	h	476/550 (86%)	462 (97%)	14 (3%)	0	100	100
2	A	517/559 (92%)	488 (94%)	29 (6%)	0	100	100
2	a	510/559 (91%)	485 (95%)	24 (5%)	1 (0%)	43	77
3	B	503/527 (95%)	481 (96%)	22 (4%)	0	100	100
3	b	503/527 (95%)	479 (95%)	24 (5%)	0	100	100
4	D	485/528 (92%)	466 (96%)	18 (4%)	1 (0%)	43	77
4	d	478/528 (90%)	456 (95%)	21 (4%)	1 (0%)	43	77
5	e	497/562 (88%)	480 (97%)	17 (3%)	0	100	100
6	E	516/518 (100%)	487 (94%)	29 (6%)	0	100	100
7	G	504/594 (85%)	484 (96%)	20 (4%)	0	100	100
7	g	481/594 (81%)	461 (96%)	19 (4%)	1 (0%)	43	77
8	Q	526/568 (93%)	505 (96%)	21 (4%)	0	100	100
8	q	522/568 (92%)	499 (96%)	23 (4%)	0	100	100
9	Z	527/546 (96%)	507 (96%)	20 (4%)	0	100	100
9	z	527/546 (96%)	506 (96%)	21 (4%)	0	100	100
All	All	8076/8824 (92%)	7728 (96%)	344 (4%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	g	195	ASN
4	d	213	VAL
2	a	203	VAL
4	D	213	VAL

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	H	422/454 (93%)	422 (100%)	0	100	100
1	h	399/454 (88%)	399 (100%)	0	100	100
2	A	434/471 (92%)	434 (100%)	0	100	100
2	a	430/471 (91%)	430 (100%)	0	100	100
3	B	422/441 (96%)	422 (100%)	0	100	100
3	b	422/441 (96%)	422 (100%)	0	100	100
4	D	421/453 (93%)	421 (100%)	0	100	100
4	d	413/453 (91%)	413 (100%)	0	100	100
5	e	428/483 (89%)	428 (100%)	0	100	100
6	E	445/445 (100%)	445 (100%)	0	100	100
7	G	432/501 (86%)	432 (100%)	0	100	100
7	g	411/501 (82%)	411 (100%)	0	100	100
8	Q	442/473 (93%)	442 (100%)	0	100	100
8	q	439/473 (93%)	439 (100%)	0	100	100
9	Z	446/463 (96%)	446 (100%)	0	100	100
9	z	446/463 (96%)	446 (100%)	0	100	100
All	All	6852/7440 (92%)	6852 (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 65 such sidechains are listed below:

Mol	Chain	Res	Type
9	z	36	ASN
9	z	313	ASN
4	D	289	GLN
4	D	284	ASN
9	z	385	HIS

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 [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.

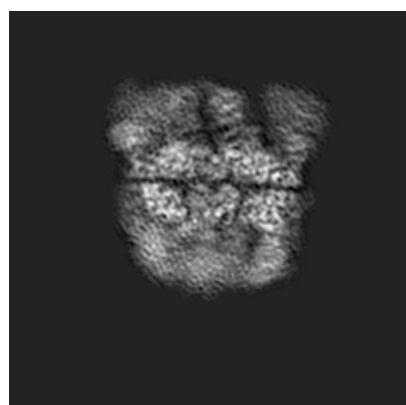
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0759. These allow visual inspection of the internal detail of the map and identification of artifacts.

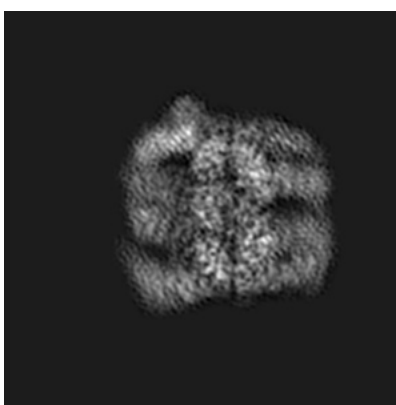
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

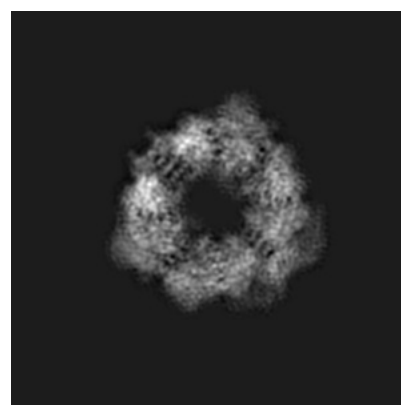
6.1.1 Primary map



X



Y



Z

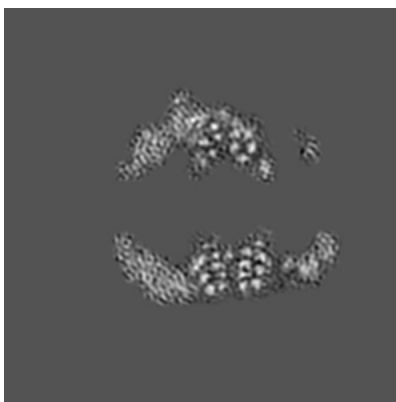
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

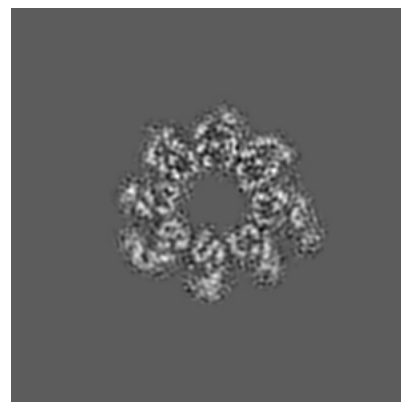
6.2.1 Primary map



X Index: 128



Y Index: 128

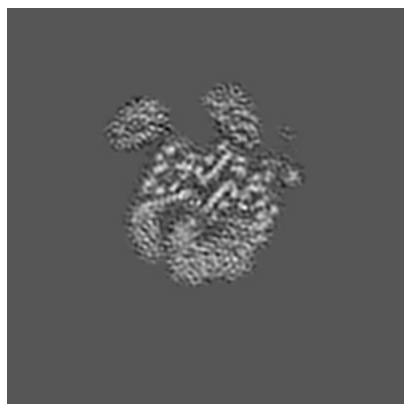


Z Index: 128

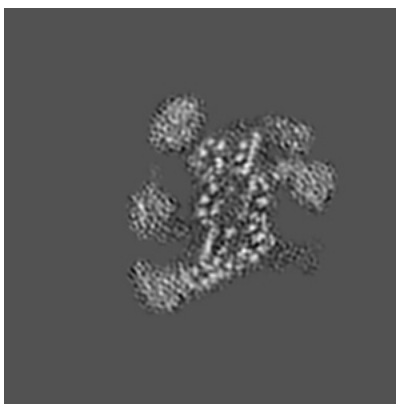
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

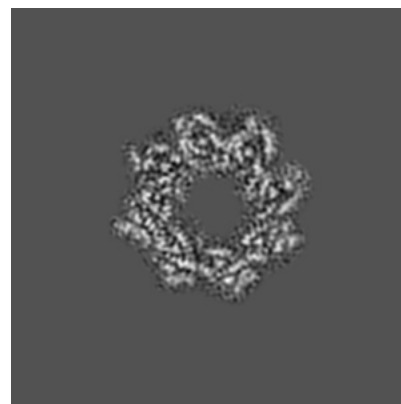
6.3.1 Primary map



X Index: 168



Y Index: 97

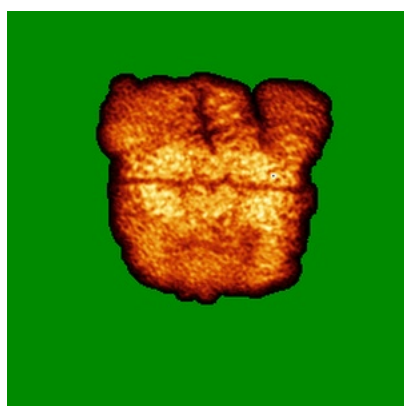


Z Index: 156

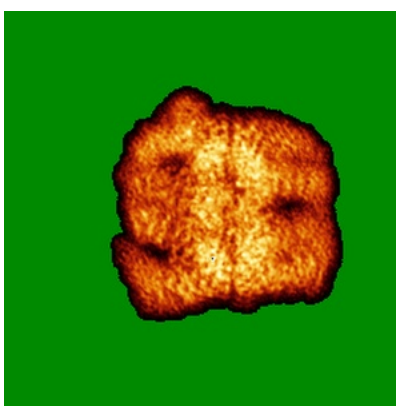
The images above show the largest variance slices of the map in three orthogonal directions.

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

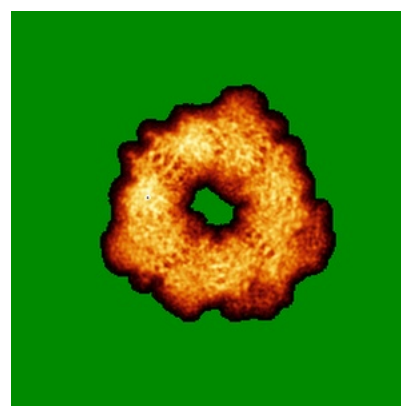
6.4.1 Primary map



X



Y

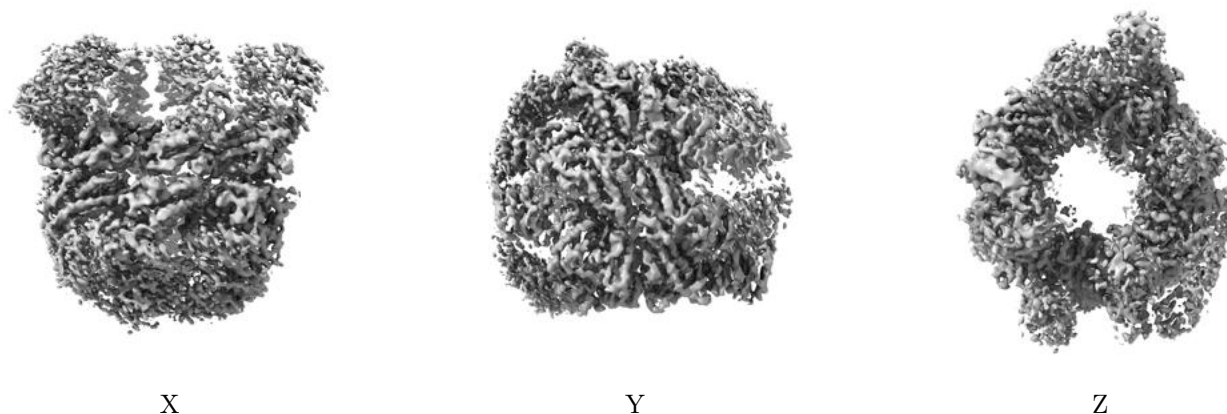


Z

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

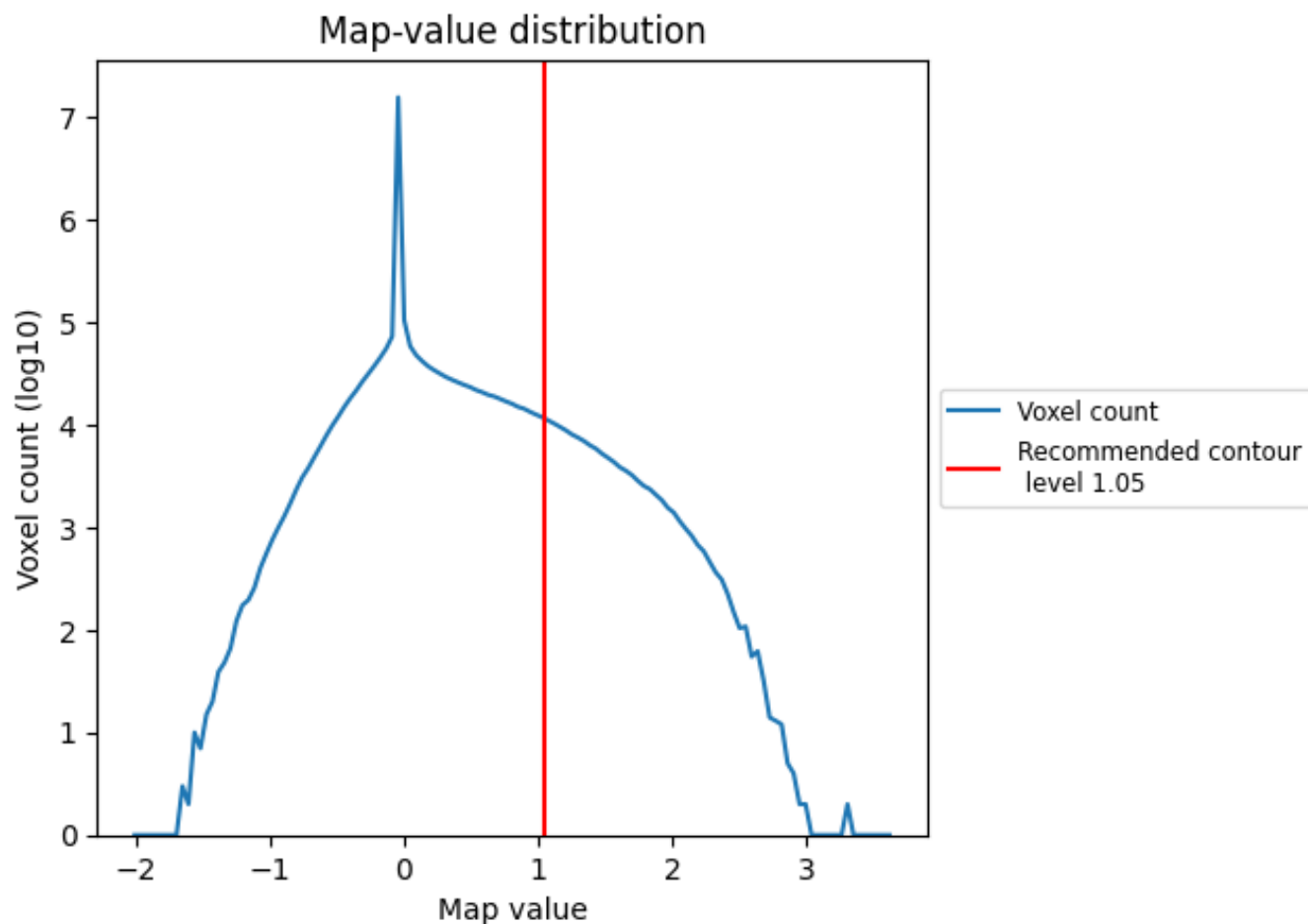
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

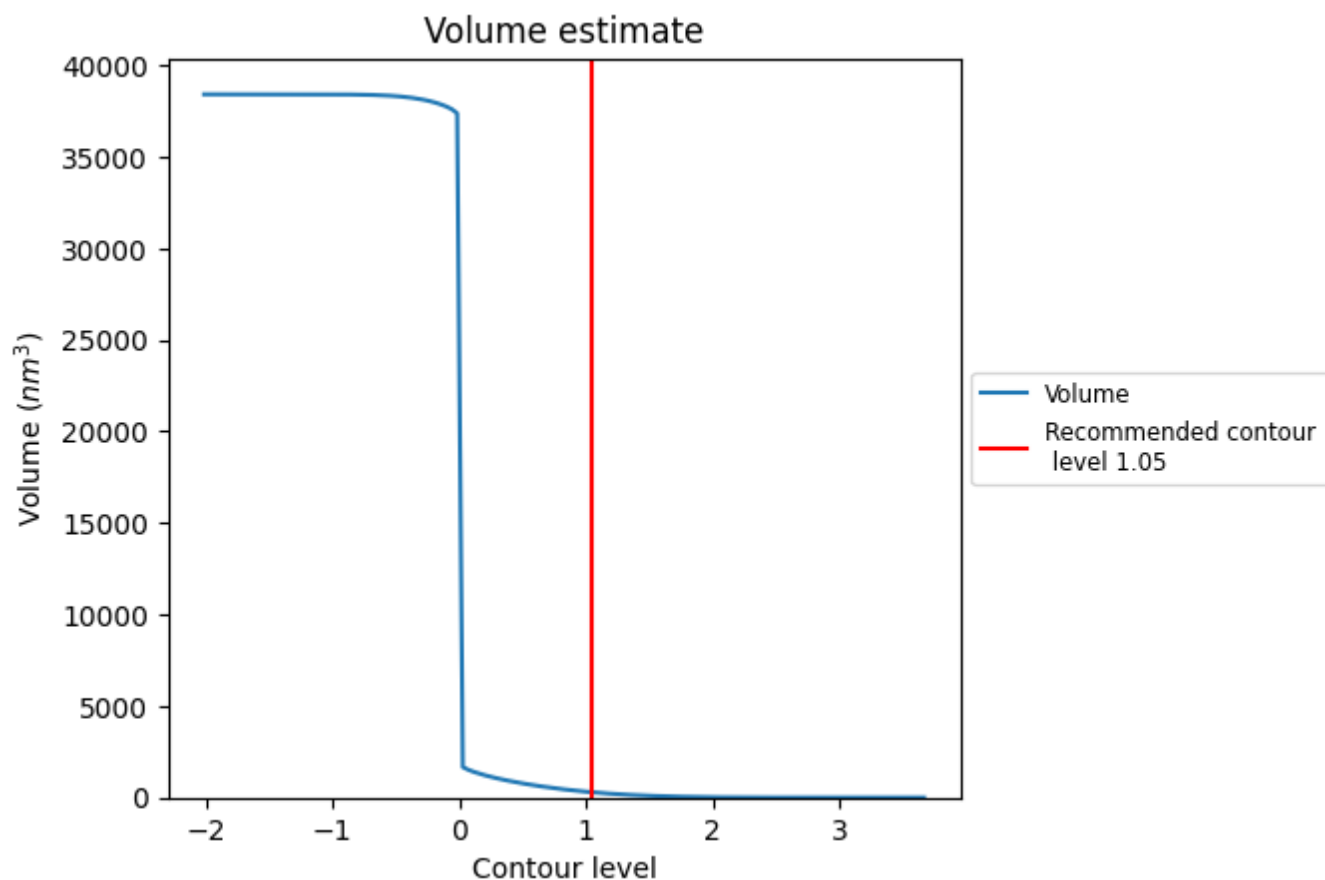
This section contains the results of statistical analysis of the map.

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.

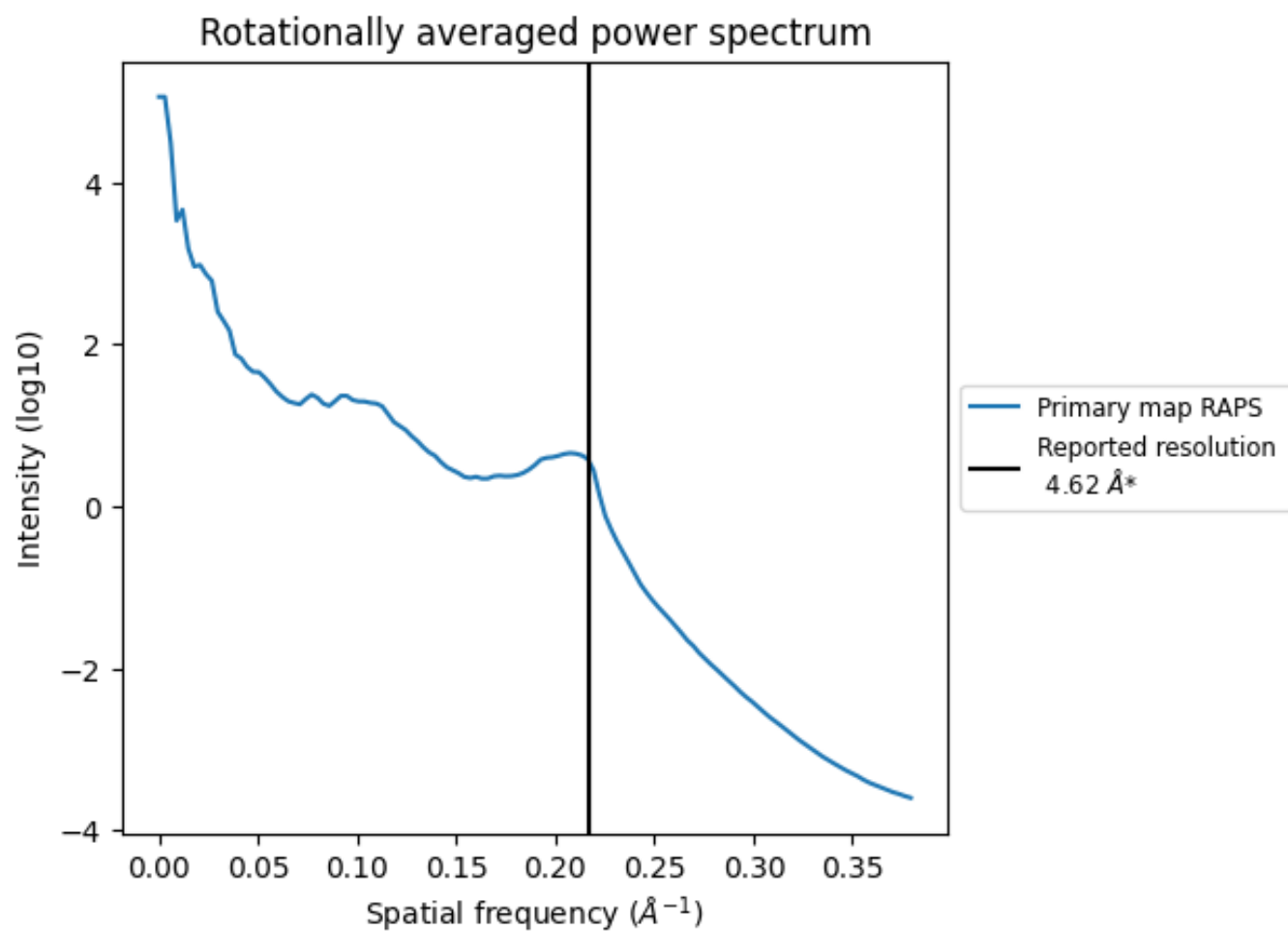
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 290 nm³; this corresponds to an approximate mass of 262 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 0.216 $\text{\AA}^{-1}$

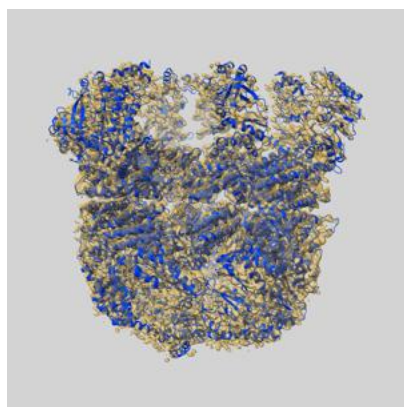
8 Fourier-Shell correlation ⓘ

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

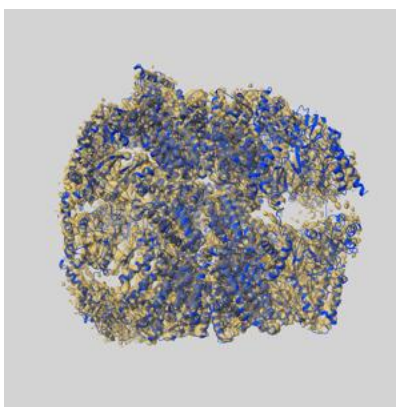
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0759 and PDB model 6KS7. Per-residue inclusion information can be found in section [3](#) on page [9](#).

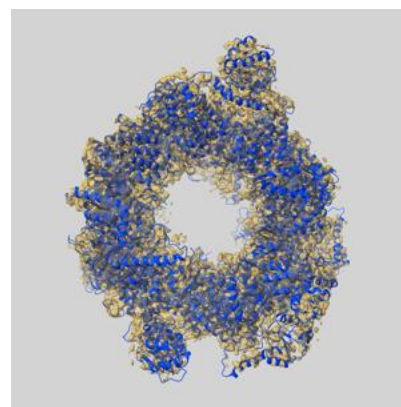
9.1 Map-model overlay [i](#)



X



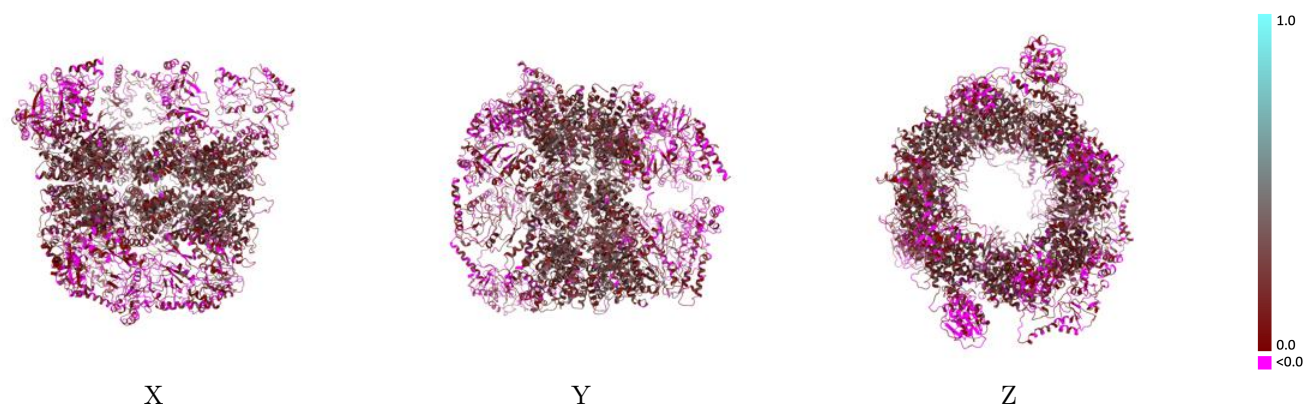
Y



Z

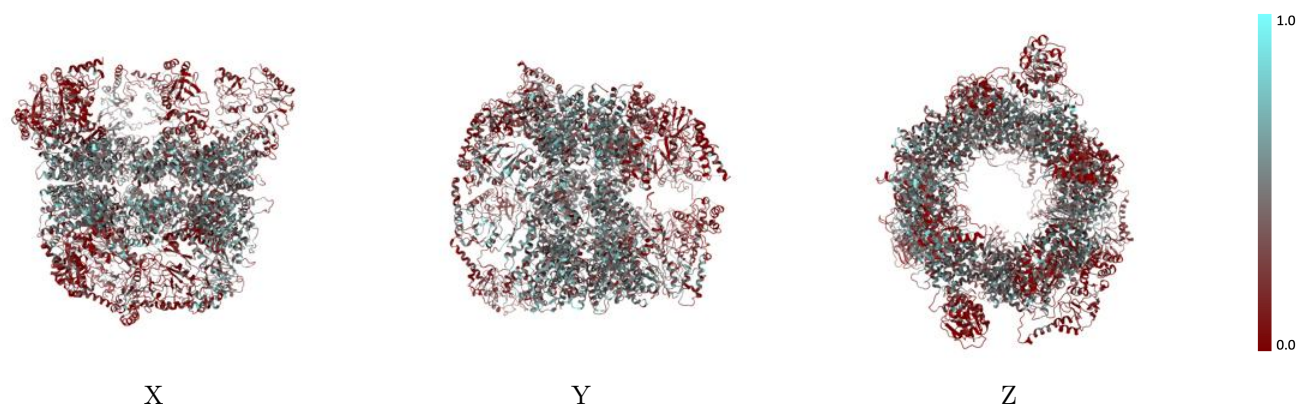
The images above show the 3D surface view of the map at the recommended contour level 1.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



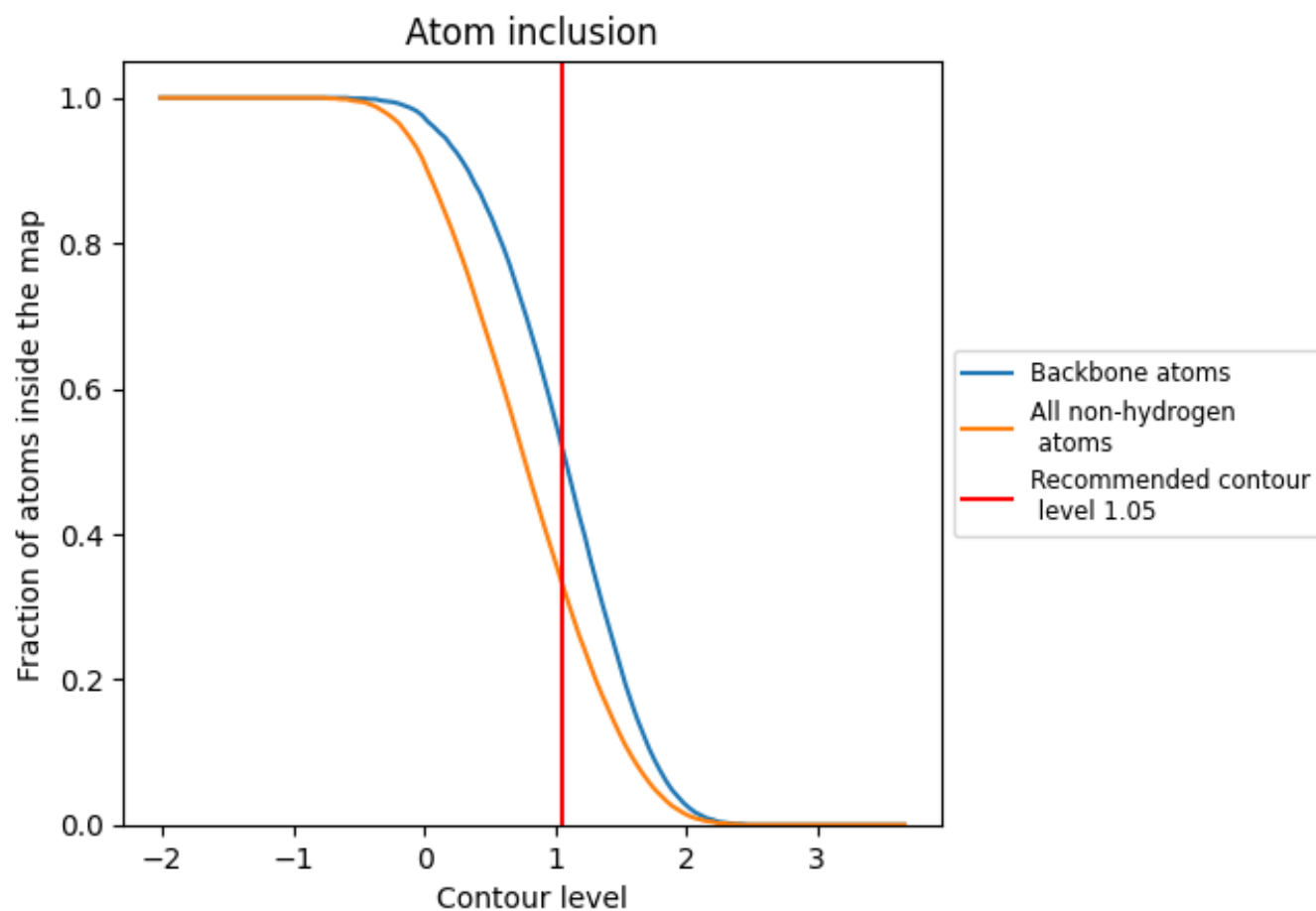
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 33% 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 (1.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3340	 0.1460
A	 0.3540	 0.1500
B	 0.2920	 0.1120
D	 0.3160	 0.1430
E	 0.3380	 0.1280
G	 0.3470	 0.1420
H	 0.3120	 0.1410
Q	 0.3920	 0.1660
Z	 0.4320	 0.2000
a	 0.3200	 0.1470
b	 0.2580	 0.1200
d	 0.2600	 0.1220
e	 0.3150	 0.1310
g	 0.3280	 0.1450
h	 0.2830	 0.1120
q	 0.3690	 0.1700
z	 0.4150	 0.1990

