



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 06:12 AM UTC

PDB ID : 7WU7 / pdb_00007wu7
EMDB ID : EMD-32823
Title : Prefoldin-tubulin-TRiC complex
Authors : Gestaut, D.; Zhao, Y.; Park, J.; Ma, B.; Leitner, A.; Collier, M.; Pintilie, G.; Roh, S.-H.; Chiu, W.; Frydman, J.
Deposited on : 2022-02-07
Resolution : 3.85 Å(reported)
Based on initial model : 6NR8

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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

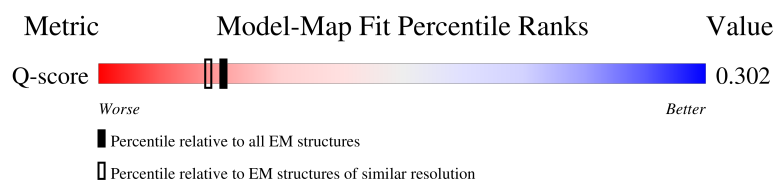
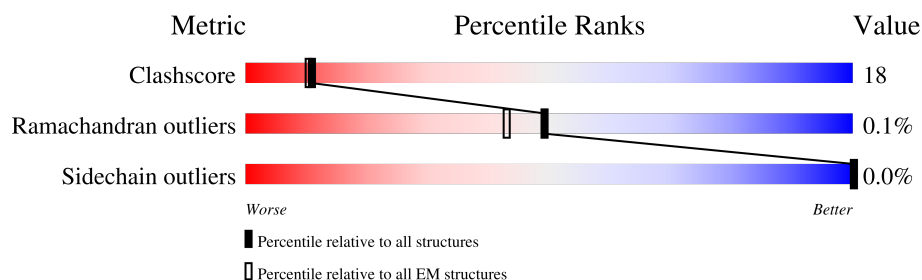
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.85 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	8989 (3.35 - 4.35)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	122	
2	2	154	
3	3	197	
4	4	140	

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Mol	Chain	Length	Quality of chain
5	5	140	
6	6	129	
7	A	556	
7	I	556	
8	B	535	
8	J	535	
9	C	545	
9	K	545	
10	D	539	
10	L	539	
11	E	541	
11	M	541	
12	F	531	
12	N	531	
13	G	543	
13	O	543	
14	H	547	
14	P	547	

2 Entry composition

There are 15 unique types of molecules in this entry. The entry contains 67031 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 Prefoldin subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	107	Total	C	N	O	S	0	0
			873	546	150	172	5		

- Molecule 2 is a protein called Prefoldin subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	83	Total	C	N	O	S	0	0
			667	413	121	130	3		

- Molecule 3 is a protein called Prefoldin subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	116	Total	C	N	O	S	0	0
			956	607	157	186	6		

- Molecule 4 is a protein called Prefoldin subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	88	Total	C	N	O	S	0	0
			711	437	118	151	5		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	135	HIS	-	expression tag	UNP Q9NQP4
4	136	HIS	-	expression tag	UNP Q9NQP4
4	137	HIS	-	expression tag	UNP Q9NQP4
4	138	HIS	-	expression tag	UNP Q9NQP4
4	139	HIS	-	expression tag	UNP Q9NQP4
4	140	HIS	-	expression tag	UNP Q9NQP4

- Molecule 5 is a protein called Prefoldin subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	127	Total	C	N	O	S	0	0
			1017	647	166	196	8		

- Molecule 6 is a protein called Prefoldin subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	102	Total	C	N	O	S	0	0
			825	511	148	165	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	516	Total	C	N	O	S	0	0
			3919	2456	685	755	23		
7	I	514	Total	C	N	O	S	0	0
			3903	2444	683	753	23		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	497	Total	C	N	O	S	0	0
			3736	2339	655	723	19		
8	J	497	Total	C	N	O	S	0	0
			3736	2339	655	723	19		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	505	Total	C	N	O	S	0	0
			3924	2448	690	756	30		
9	K	505	Total	C	N	O	S	0	0
			3924	2448	690	756	30		

- Molecule 10 is a protein called T-complex protein 1 subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	511	Total	C	N	O	S	0	0
			3847	2409	665	750	23		
10	L	511	Total	C	N	O	S	0	0
			3847	2407	666	751	23		

- Molecule 11 is a protein called T-complex protein 1 subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	506	Total	C	N	O	S	0	0
			3883	2431	673	749	30		
11	M	506	Total	C	N	O	S	0	0
			3883	2431	673	749	30		

- Molecule 12 is a protein called T-complex protein 1 subunit zeta.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	508	Total	C	N	O	S	0	0
			3903	2454	681	748	20		
12	N	508	Total	C	N	O	S	0	0
			3903	2454	681	748	20		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	528	PHE	SER	conflict	UNP P40227
N	528	PHE	SER	conflict	UNP P40227

- Molecule 13 is a protein called T-complex protein 1 subunit eta.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	509	Total	C	N	O	S	0	0
			3910	2471	676	740	23		
13	O	509	Total	C	N	O	S	0	0
			3910	2471	676	740	23		

- Molecule 14 is a protein called T-complex protein 1 subunit theta.

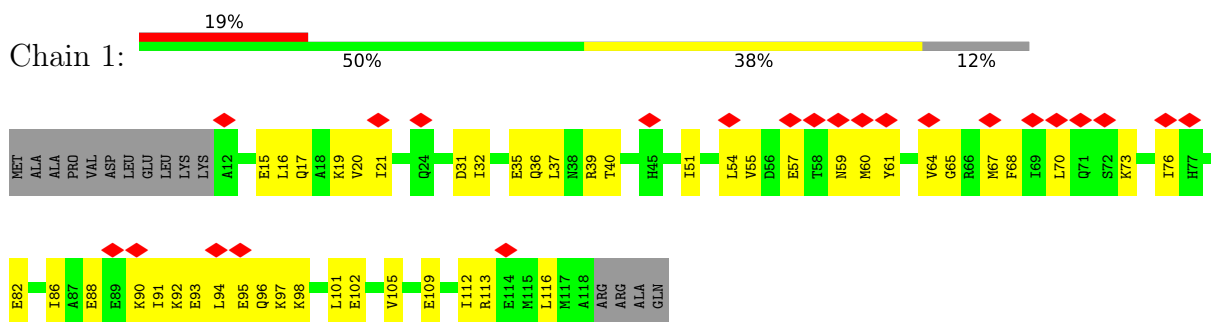
Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	500	Total	C	N	O	S	0	0
			3816	2404	647	739	26		
14	P	502	Total	C	N	O	S	0	0
			3830	2413	650	741	26		

- Molecule 15 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

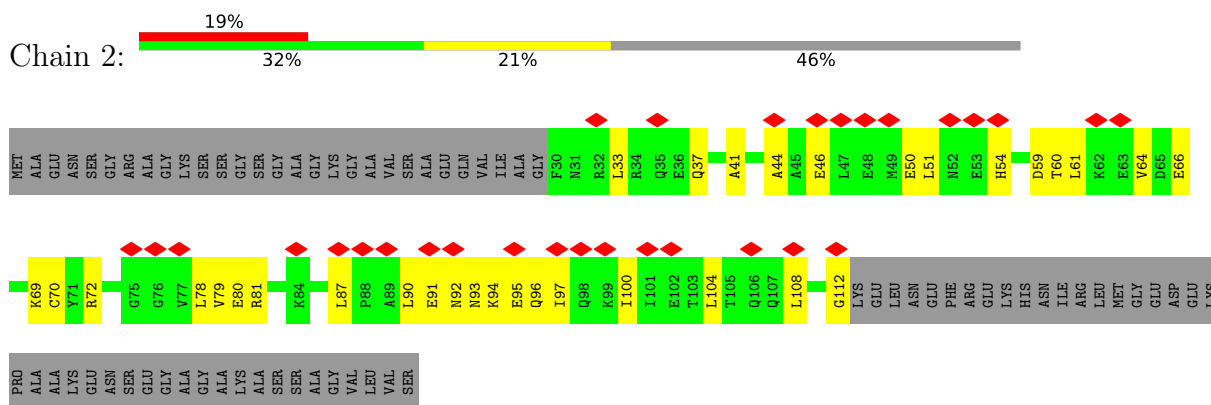
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

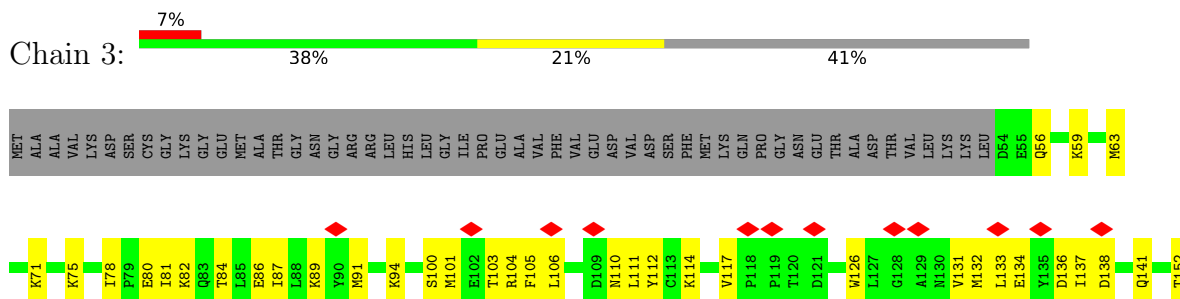
• Molecule 1: Prefoldin subunit 1

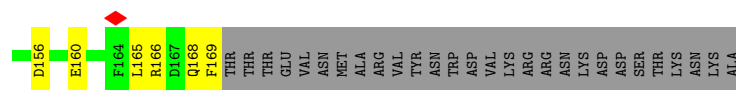


• Molecule 2: Prefoldin subunit 2

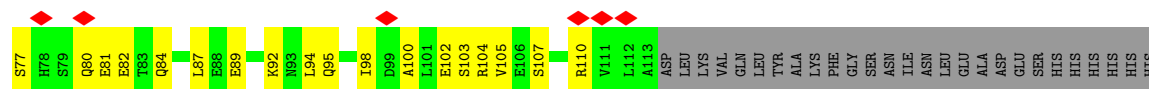
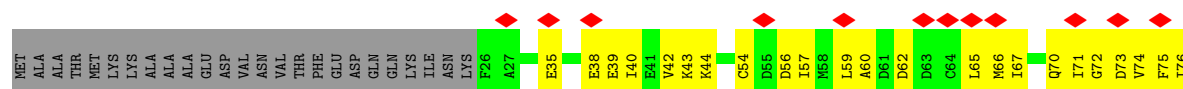


• Molecule 3: Prefoldin subunit 3

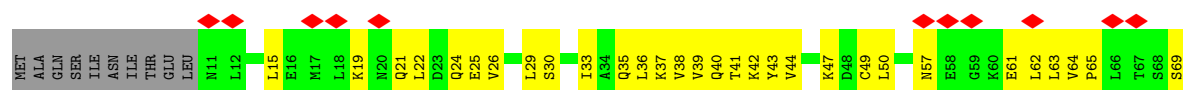




- Molecule 4: Prefoldin subunit 4



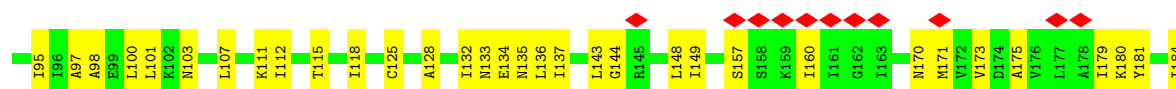
- Molecule 5: Prefoldin subunit 5

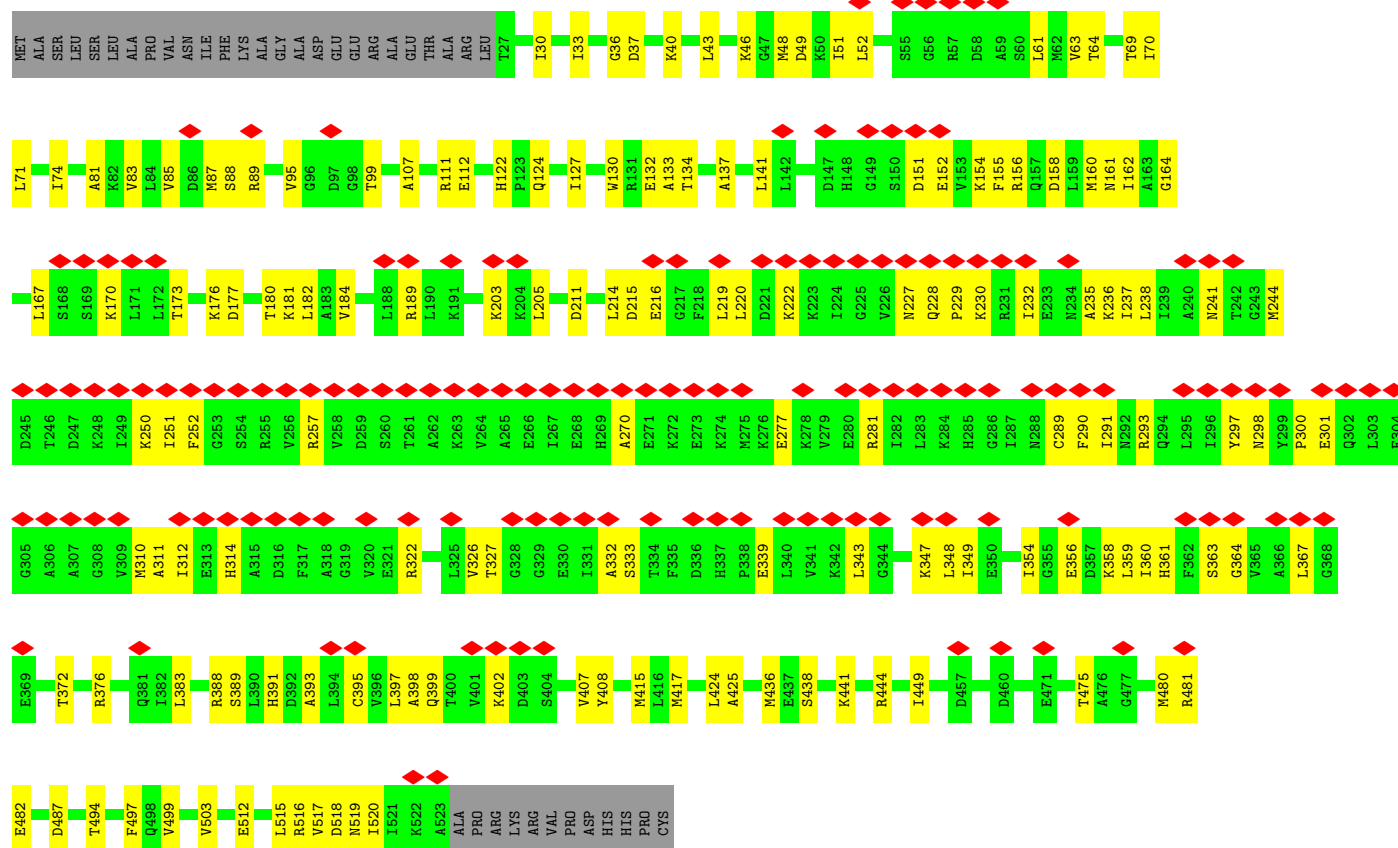


- Molecule 6: Prefoldin subunit 6

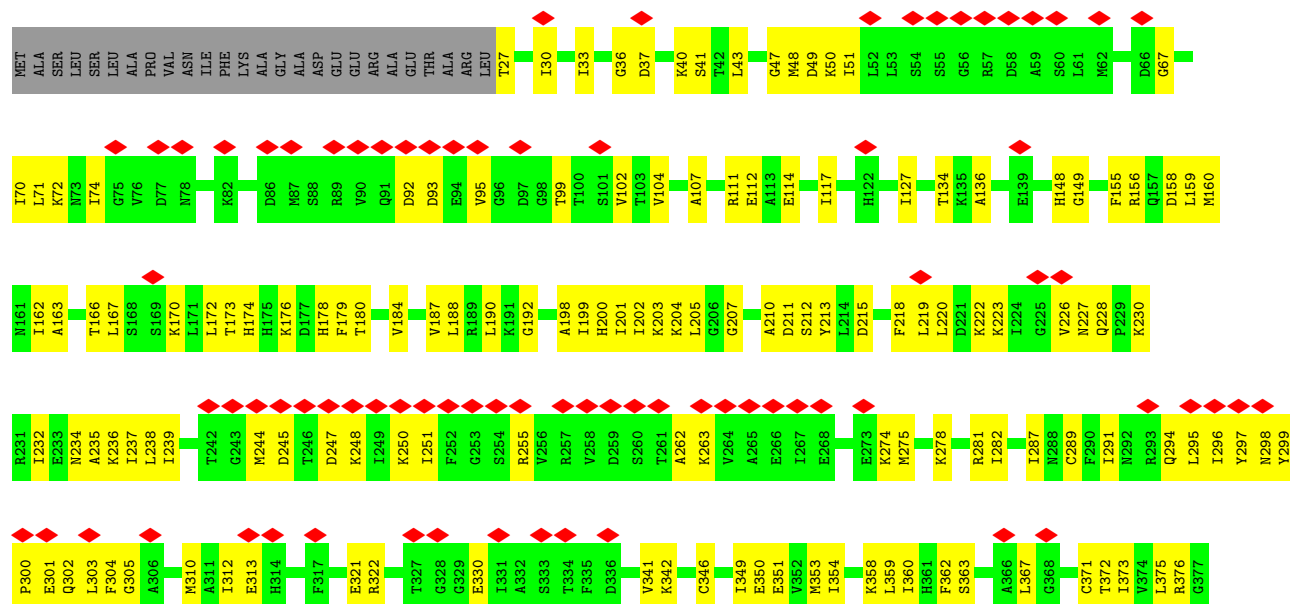


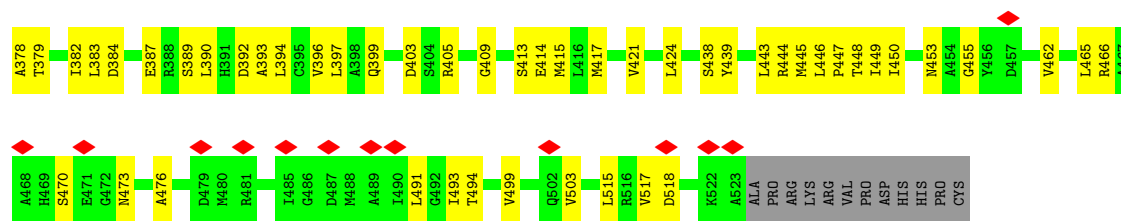
- Molecule 7: T-complex protein 1 subunit alpha



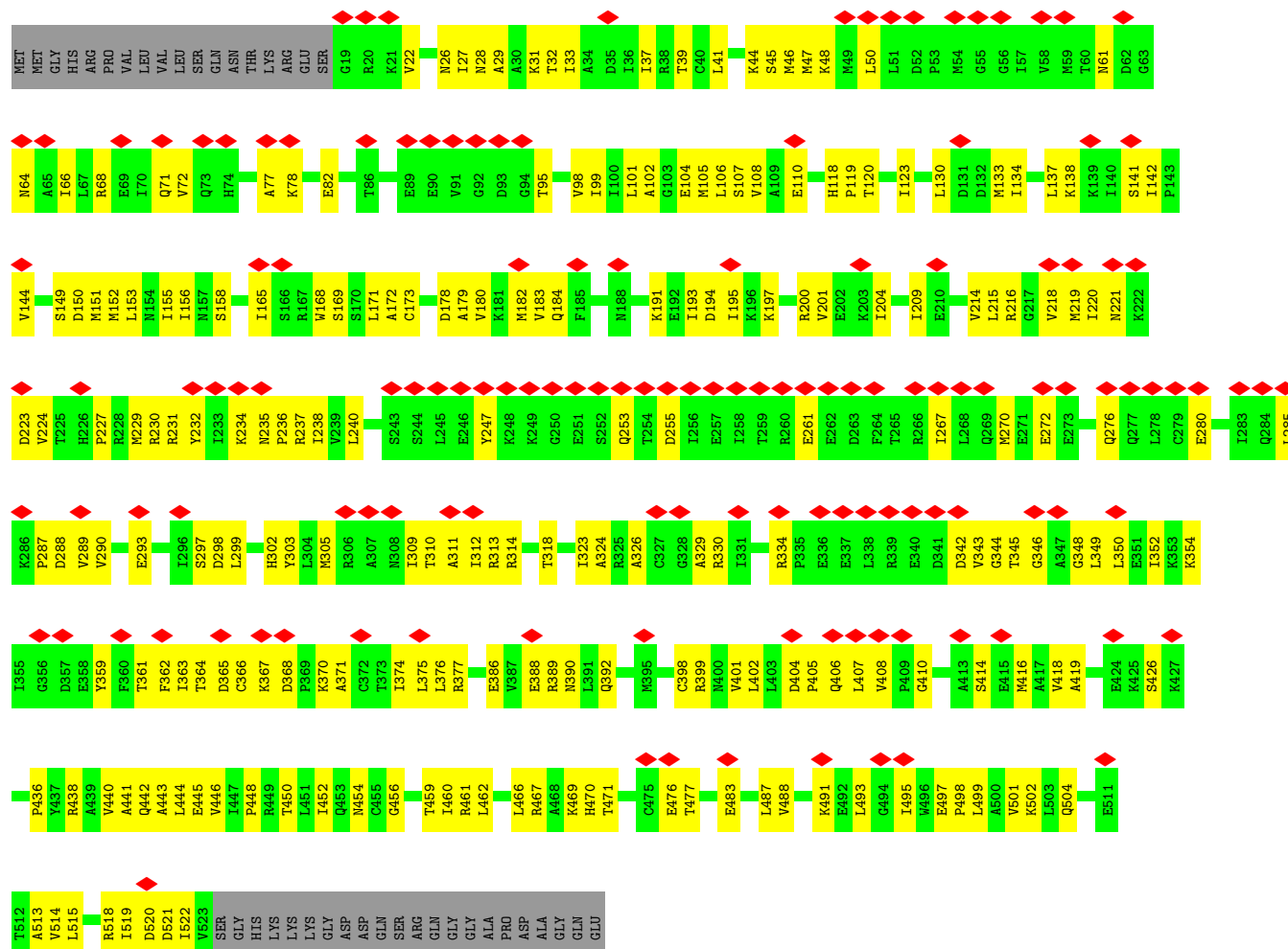


• Molecule 8: T-complex protein 1 subunit beta

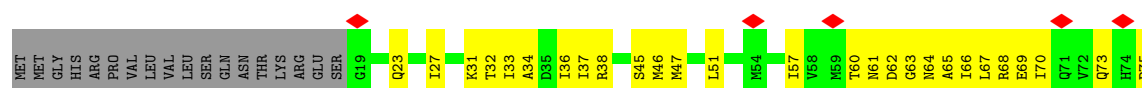


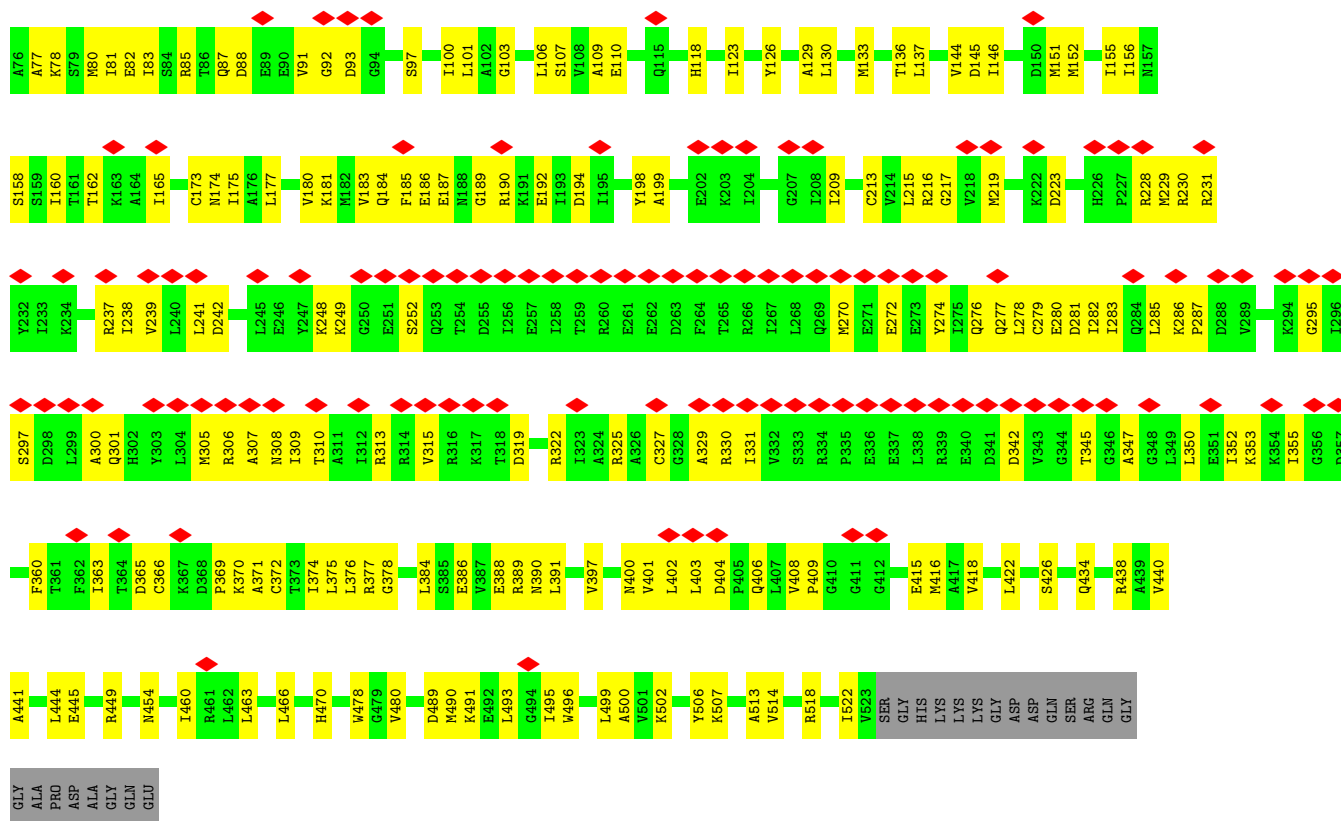


• Molecule 9: T-complex protein 1 subunit gamma

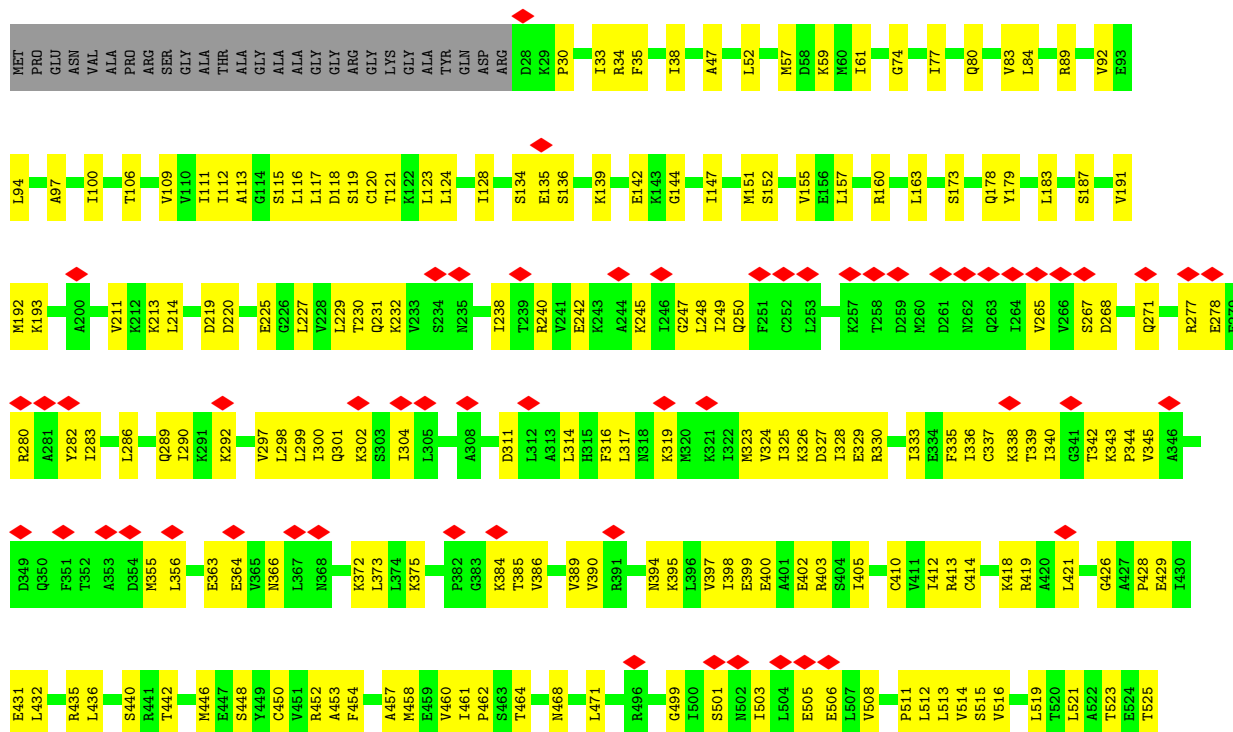


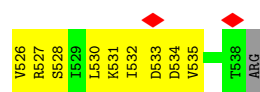
• Molecule 9: T-complex protein 1 subunit gamma



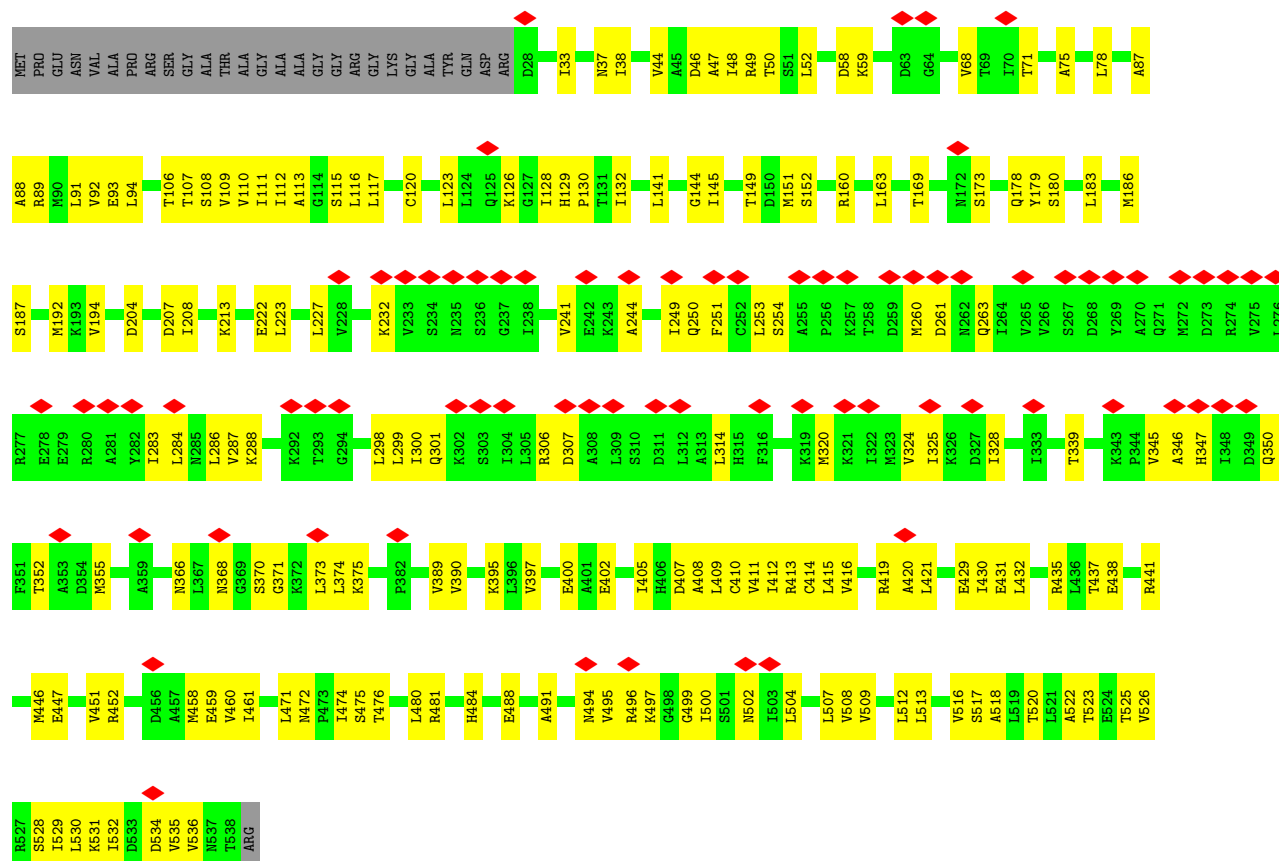


• Molecule 10: T-complex protein 1 subunit delta

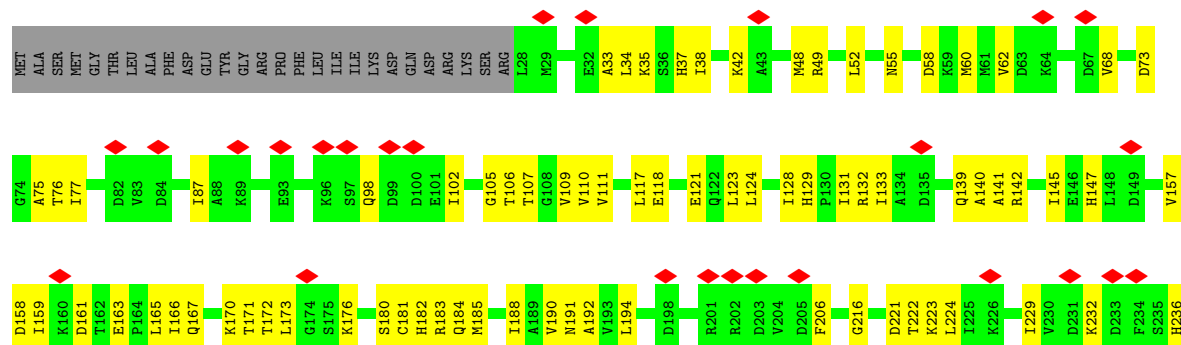


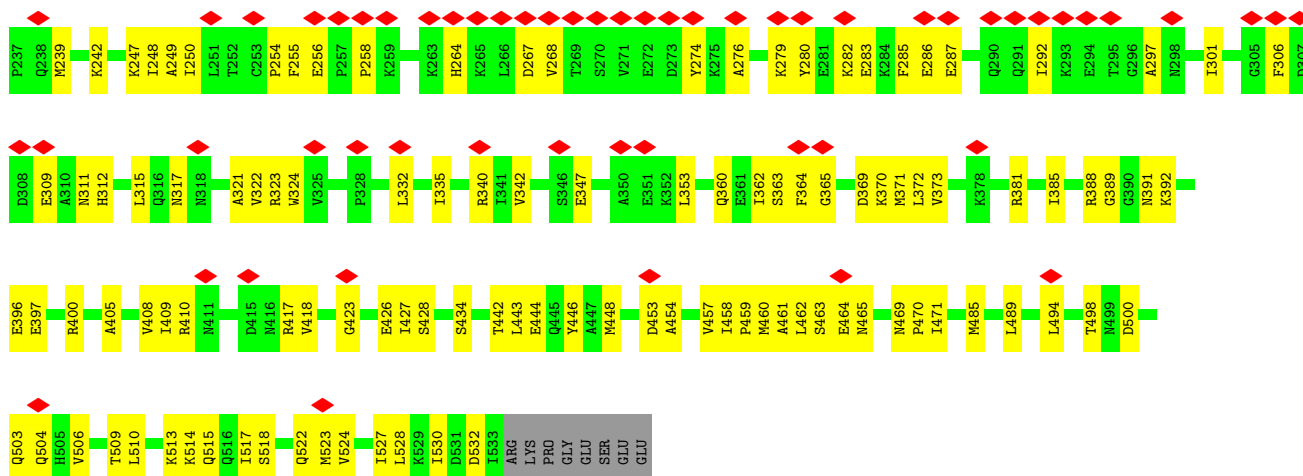


• Molecule 10: T-complex protein 1 subunit delta

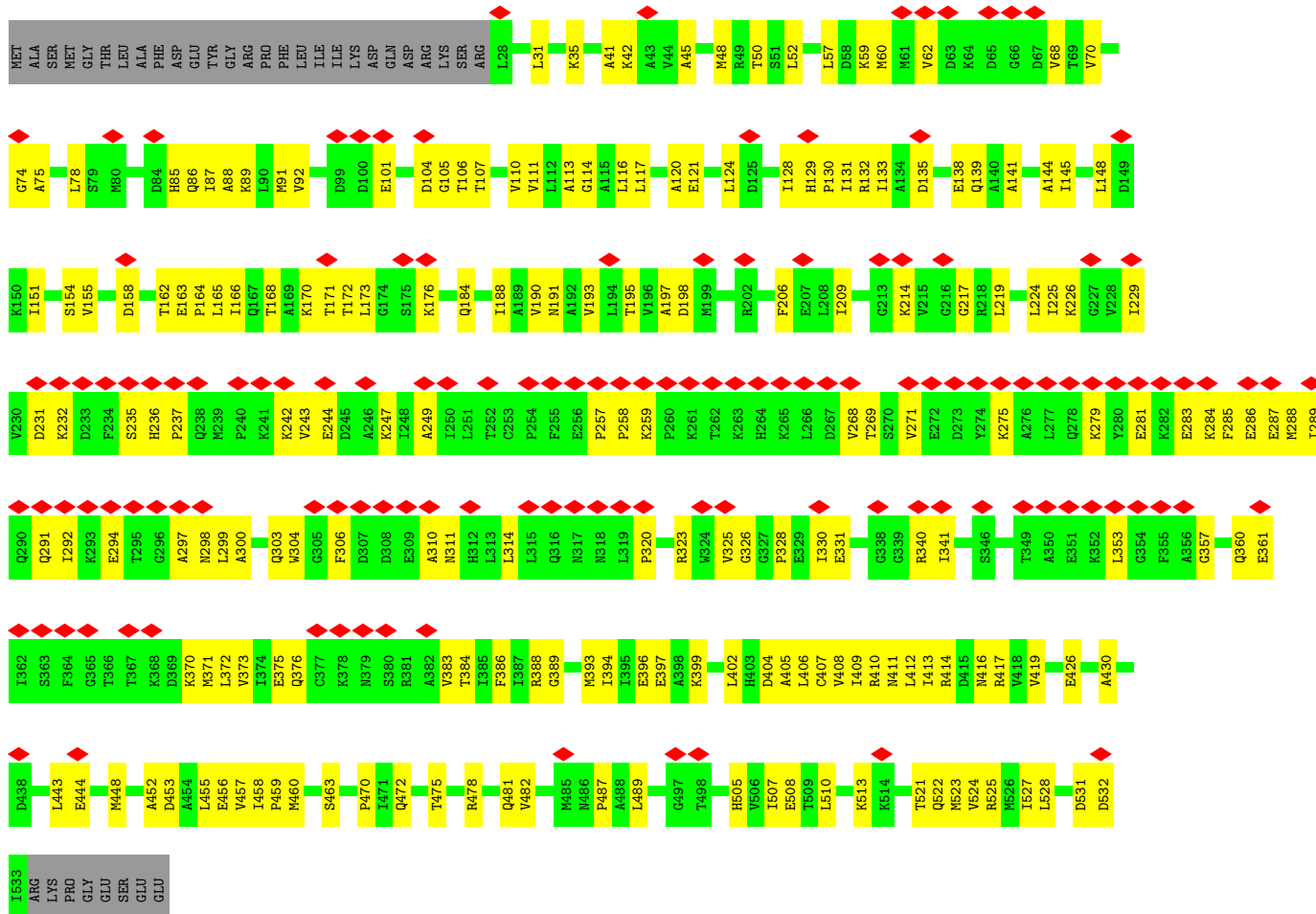


• Molecule 11: T-complex protein 1 subunit epsilon



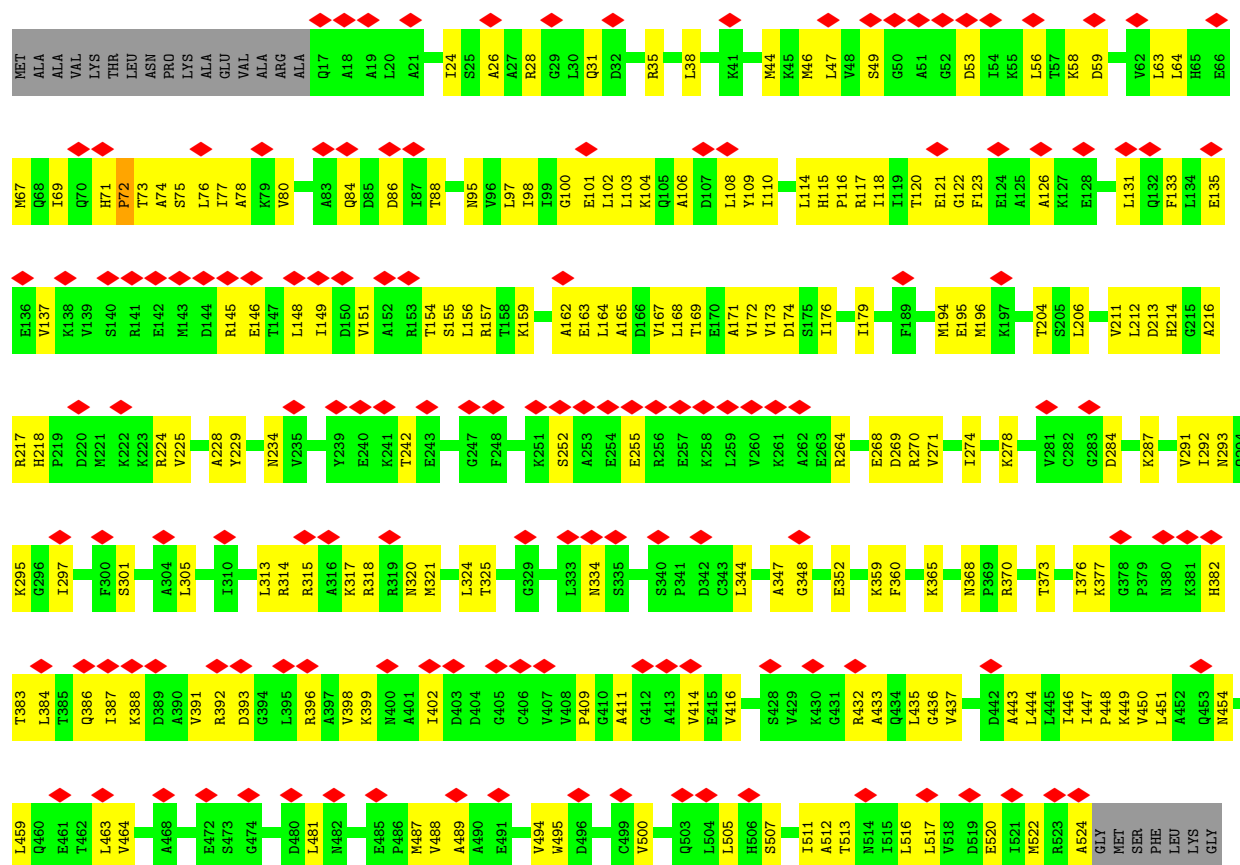


• Molecule 11: T-complex protein 1 subunit epsilon

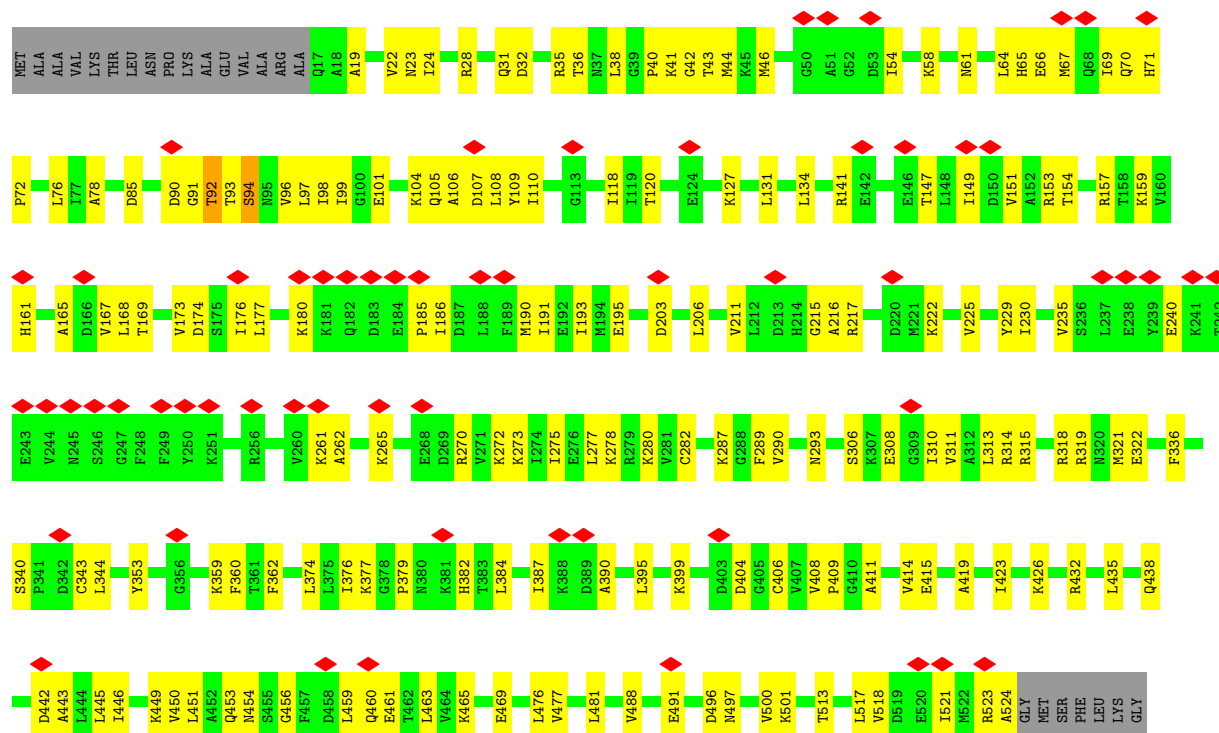


• Molecule 12: T-complex protein 1 subunit zeta

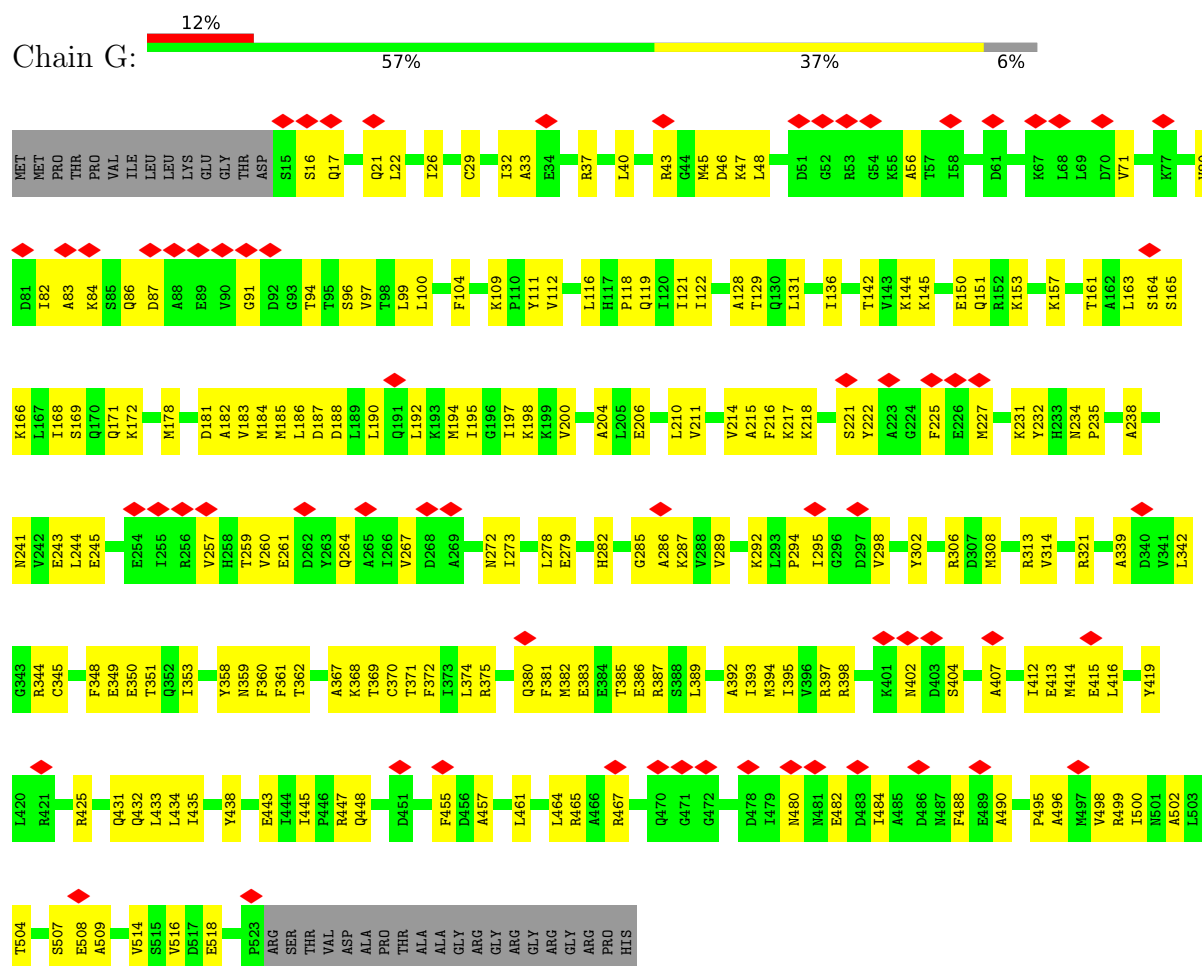




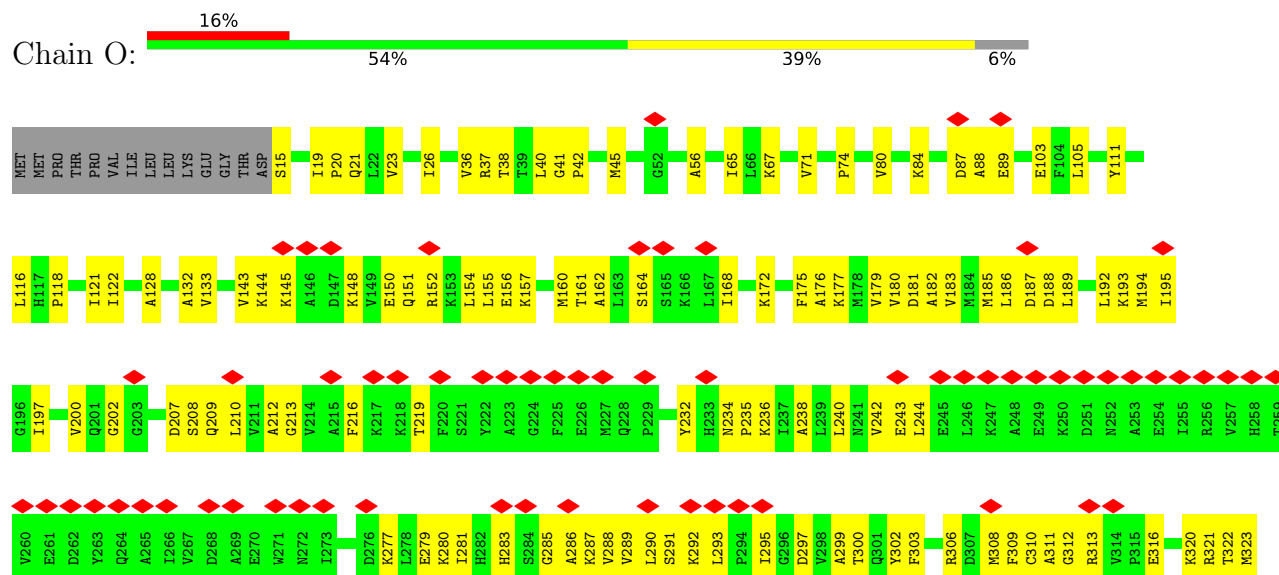
• Molecule 12: T-complex protein 1 subunit zeta

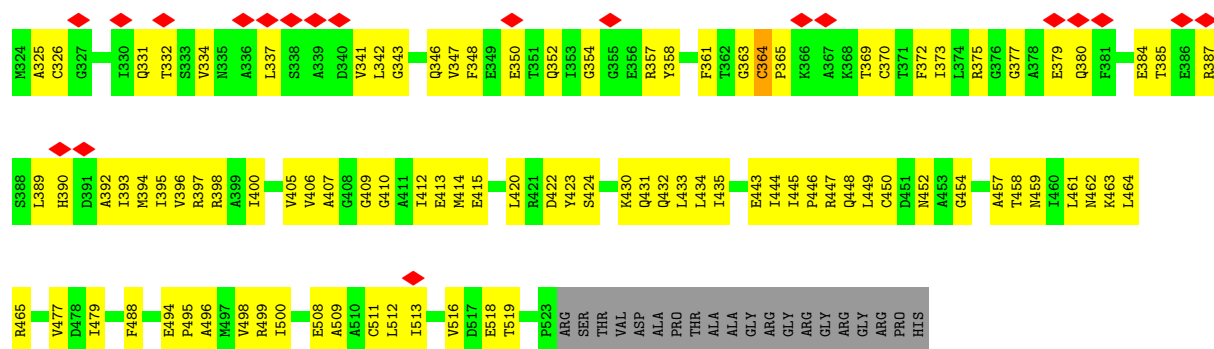


- Molecule 13: T-complex protein 1 subunit eta

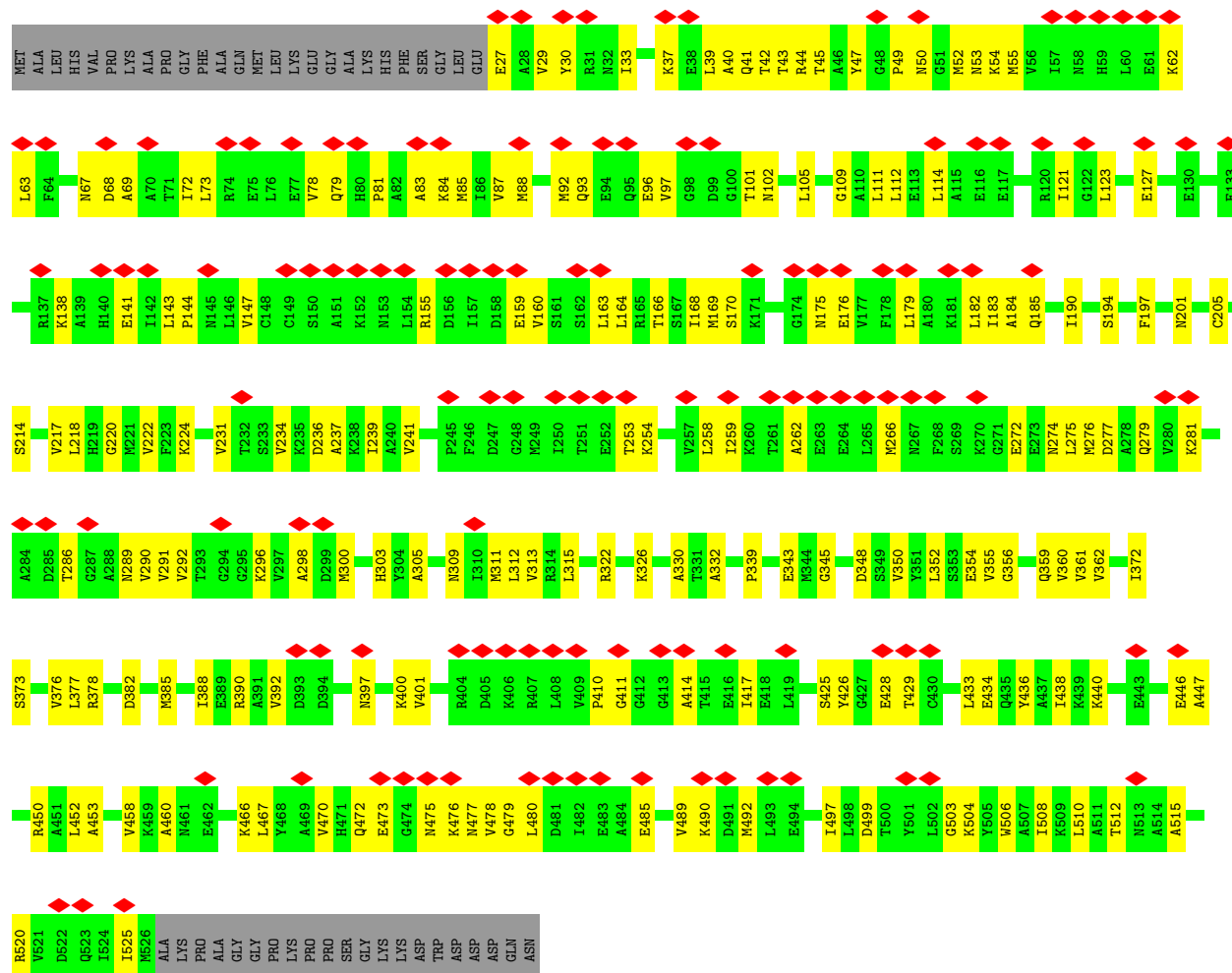


- Molecule 13: T-complex protein 1 subunit eta



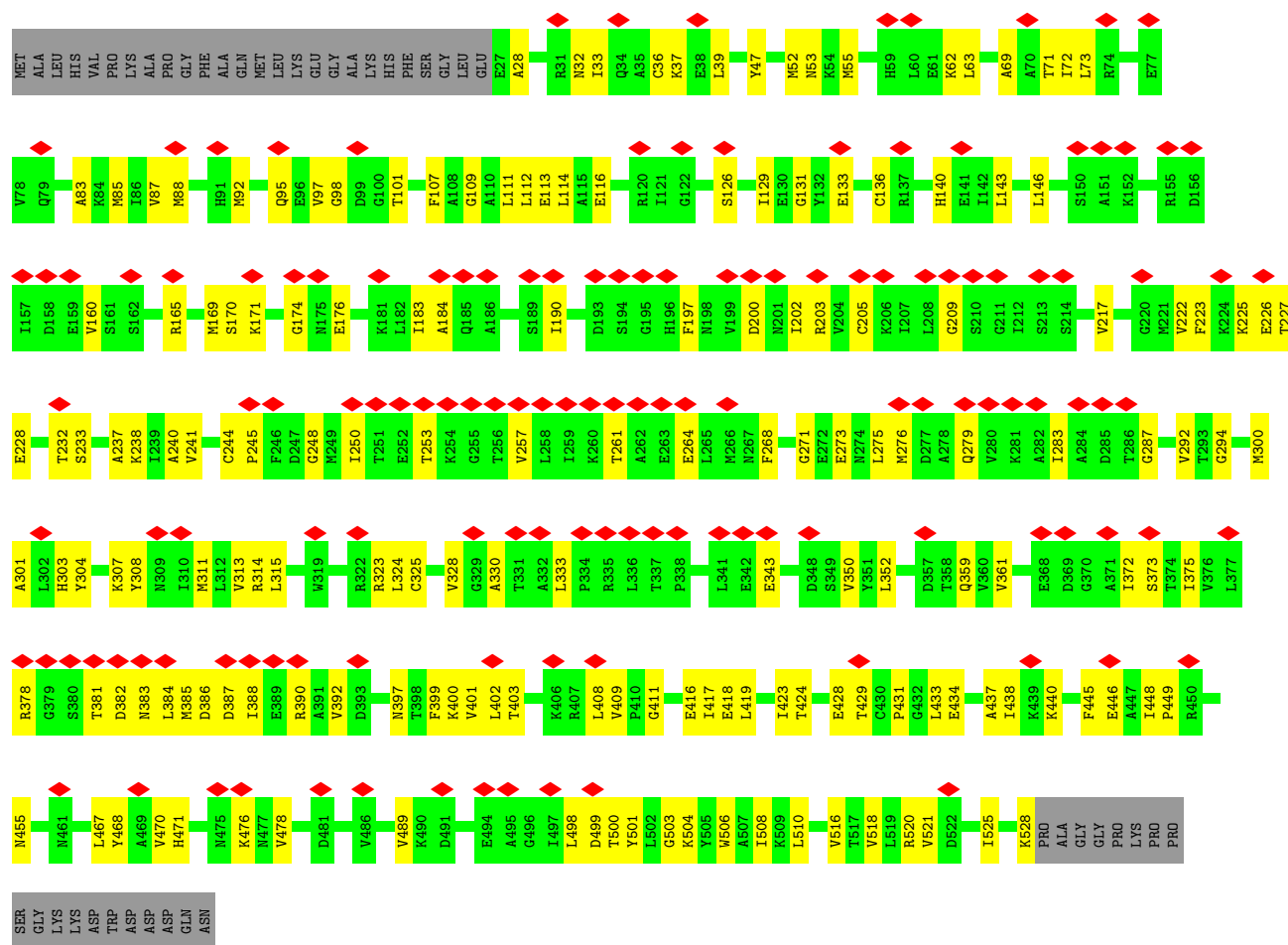


• Molecule 14: T-complex protein 1 subunit theta



• Molecule 14: T-complex protein 1 subunit theta





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	194013	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE; CTF correction was performed for every micrographs	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	11.117	Depositor
Minimum map value	-7.622	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.246	Depositor
Recommended contour level	0.943	Depositor
Map size (Å)	326.4, 326.4, 326.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.02, 1.02, 1.02	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.23	0/879	0.58	0/1173
2	2	0.15	0/670	0.41	0/897
3	3	0.18	0/969	0.53	0/1300
4	4	0.18	0/715	0.51	0/959
5	5	0.21	0/1031	0.59	0/1385
6	6	0.16	0/829	0.47	0/1109
7	A	0.15	0/3955	0.40	0/5340
7	I	0.15	0/3939	0.44	1/5318 (0.0%)
8	B	0.14	0/3776	0.39	0/5090
8	J	0.15	0/3776	0.40	0/5090
9	C	0.15	0/3968	0.42	0/5355
9	K	0.17	0/3968	0.46	0/5355
10	D	0.16	0/3878	0.41	0/5237
10	L	0.15	0/3878	0.40	0/5237
11	E	0.15	0/3928	0.40	0/5295
11	M	0.15	0/3928	0.44	0/5295
12	F	0.14	0/3949	0.40	0/5324
12	N	0.18	0/3949	0.46	1/5324 (0.0%)
13	G	0.15	0/3965	0.43	0/5351
13	O	0.17	0/3965	0.46	0/5351
14	H	0.14	0/3867	0.39	0/5229
14	P	0.14	0/3881	0.39	0/5247
All	All	0.16	0/67663	0.43	2/91261 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	N	92	THR	N-CA-C	10.94	123.21	111.28
7	I	39	VAL	N-CA-C	-5.08	107.51	112.29

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	1	873	0	902	47	0
2	2	667	0	693	27	0
3	3	956	0	970	39	0
4	4	711	0	699	36	0
5	5	1017	0	1042	76	0
6	6	825	0	850	50	0
7	A	3919	0	4084	134	0
7	I	3903	0	4062	129	0
8	B	3736	0	3846	123	0
8	J	3736	0	3846	139	0
9	C	3924	0	4050	188	0
9	K	3924	0	4050	169	0
10	D	3847	0	4056	150	0
10	L	3847	0	4051	139	0
11	E	3883	0	3994	158	0
11	M	3883	0	3994	153	0
12	F	3903	0	4030	169	0
12	N	3903	0	4030	142	0
13	G	3910	0	4005	160	0
13	O	3910	0	4005	179	0
14	H	3816	0	3879	142	0
14	P	3830	0	3897	125	0
15	F	27	0	11	1	0
15	H	27	0	11	4	0
15	N	27	0	11	1	0
15	P	27	0	11	2	0
All	All	67031	0	69079	2506	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 18.

The worst 5 of 2506 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)
12:F:71:HIS:ND1	12:F:72:PRO:HD2	1.39	1.31
9:K:152:MET:HE3	9:K:156:ILE:HD11	1.21	1.18
7:I:168:PHE:CZ	7:I:388:MET:HE1	1.80	1.15
13:O:186:LEU:HD12	13:O:186:LEU:O	1.42	1.15
7:I:168:PHE:HZ	7:I:388:MET:HE1	1.08	1.13

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	1	105/122 (86%)	103 (98%)	2 (2%)	0	100	100
2	2	81/154 (53%)	80 (99%)	1 (1%)	0	100	100
3	3	114/197 (58%)	108 (95%)	6 (5%)	0	100	100
4	4	86/140 (61%)	82 (95%)	4 (5%)	0	100	100
5	5	125/140 (89%)	118 (94%)	7 (6%)	0	100	100
6	6	100/129 (78%)	97 (97%)	3 (3%)	0	100	100
7	A	514/556 (92%)	495 (96%)	19 (4%)	0	100	100
7	I	512/556 (92%)	474 (93%)	38 (7%)	0	100	100
8	B	495/535 (92%)	472 (95%)	23 (5%)	0	100	100
8	J	495/535 (92%)	470 (95%)	25 (5%)	0	100	100
9	C	503/545 (92%)	477 (95%)	25 (5%)	1 (0%)	43	74
9	K	503/545 (92%)	466 (93%)	36 (7%)	1 (0%)	43	74
10	D	509/539 (94%)	486 (96%)	22 (4%)	1 (0%)	43	74
10	L	509/539 (94%)	479 (94%)	30 (6%)	0	100	100
11	E	504/541 (93%)	472 (94%)	32 (6%)	0	100	100
11	M	504/541 (93%)	478 (95%)	26 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	F	506/531 (95%)	484 (96%)	21 (4%)	1 (0%)	43	74
12	N	506/531 (95%)	471 (93%)	34 (7%)	1 (0%)	43	74
13	G	507/543 (93%)	477 (94%)	29 (6%)	1 (0%)	43	74
13	O	507/543 (93%)	472 (93%)	33 (6%)	2 (0%)	30	64
14	H	498/547 (91%)	482 (97%)	16 (3%)	0	100	100
14	P	500/547 (91%)	476 (95%)	24 (5%)	0	100	100
All	All	8683/9556 (91%)	8219 (95%)	456 (5%)	8 (0%)	49	80

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	365	ASP
12	F	72	PRO
12	N	94	SER
13	O	364	CYS
13	G	144	LYS

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	1	97/109 (89%)	97 (100%)	0	100	100
2	2	74/122 (61%)	74 (100%)	0	100	100
3	3	107/175 (61%)	107 (100%)	0	100	100
4	4	81/125 (65%)	81 (100%)	0	100	100
5	5	116/128 (91%)	116 (100%)	0	100	100
6	6	91/108 (84%)	91 (100%)	0	100	100
7	A	430/463 (93%)	430 (100%)	0	100	100
7	I	428/463 (92%)	427 (100%)	1 (0%)	87	87
8	B	397/427 (93%)	397 (100%)	0	100	100
8	J	397/427 (93%)	397 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	C	437/469 (93%)	437 (100%)	0	100	100
9	K	437/469 (93%)	437 (100%)	0	100	100
10	D	435/452 (96%)	435 (100%)	0	100	100
10	L	435/452 (96%)	435 (100%)	0	100	100
11	E	426/456 (93%)	426 (100%)	0	100	100
11	M	426/456 (93%)	426 (100%)	0	100	100
12	F	426/442 (96%)	426 (100%)	0	100	100
12	N	426/442 (96%)	426 (100%)	0	100	100
13	G	417/443 (94%)	417 (100%)	0	100	100
13	O	417/443 (94%)	417 (100%)	0	100	100
14	H	416/451 (92%)	416 (100%)	0	100	100
14	P	417/451 (92%)	417 (100%)	0	100	100
All	All	7333/7973 (92%)	7332 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	I	389	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
9	K	434	GLN
10	L	482	ASN
13	O	487	ASN
9	K	454	ASN
10	L	350	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
15	ADP	P	601	-	28,29,29	3.05	11 (39%)	43,45,45	1.81	8 (18%)
15	ADP	N	601	-	28,29,29	3.09	12 (42%)	43,45,45	1.82	8 (18%)
15	ADP	F	601	-	28,29,29	3.05	11 (39%)	43,45,45	1.88	9 (20%)
15	ADP	H	5000	-	28,29,29	3.06	11 (39%)	43,45,45	1.85	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
15	ADP	P	601	-	-	6/16/32/32	0/3/3/3
15	ADP	N	601	-	-	1/16/32/32	0/3/3/3
15	ADP	F	601	-	-	5/16/32/32	0/3/3/3
15	ADP	H	5000	-	-	6/16/32/32	0/3/3/3

The worst 5 of 45 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	N	601	ADP	O4'-C4'	7.79	1.62	1.45
15	P	601	ADP	O4'-C4'	7.61	1.61	1.45
15	F	601	ADP	O4'-C4'	7.57	1.61	1.45
15	H	5000	ADP	O4'-C4'	7.45	1.61	1.45
15	P	601	ADP	C3'-C4'	-7.37	1.34	1.53

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	601	ADP	C5-C4-N3	-5.53	119.10	126.72
15	P	601	ADP	C5-C4-N3	-5.46	119.20	126.72
15	F	601	ADP	C5-C4-N3	-5.41	119.27	126.72
15	H	5000	ADP	C5-C4-N3	-5.37	119.32	126.72
15	N	601	ADP	N3-C2-N1	-4.60	121.62	128.58

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

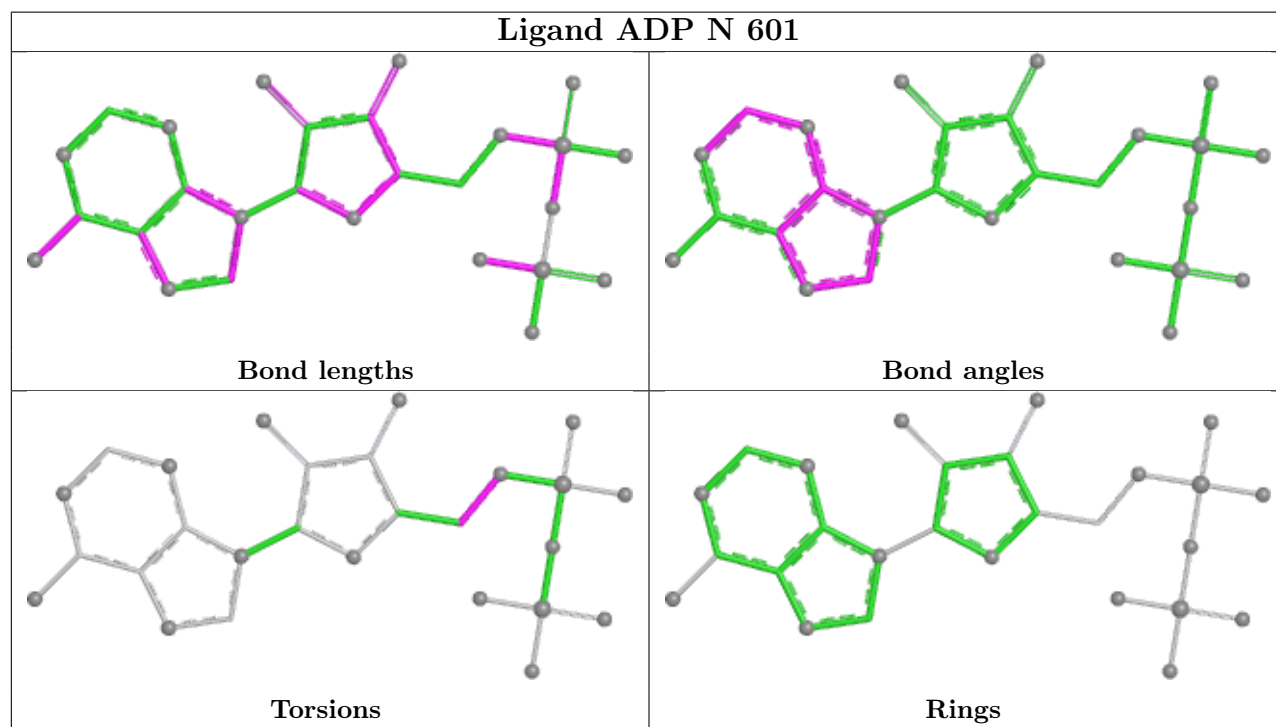
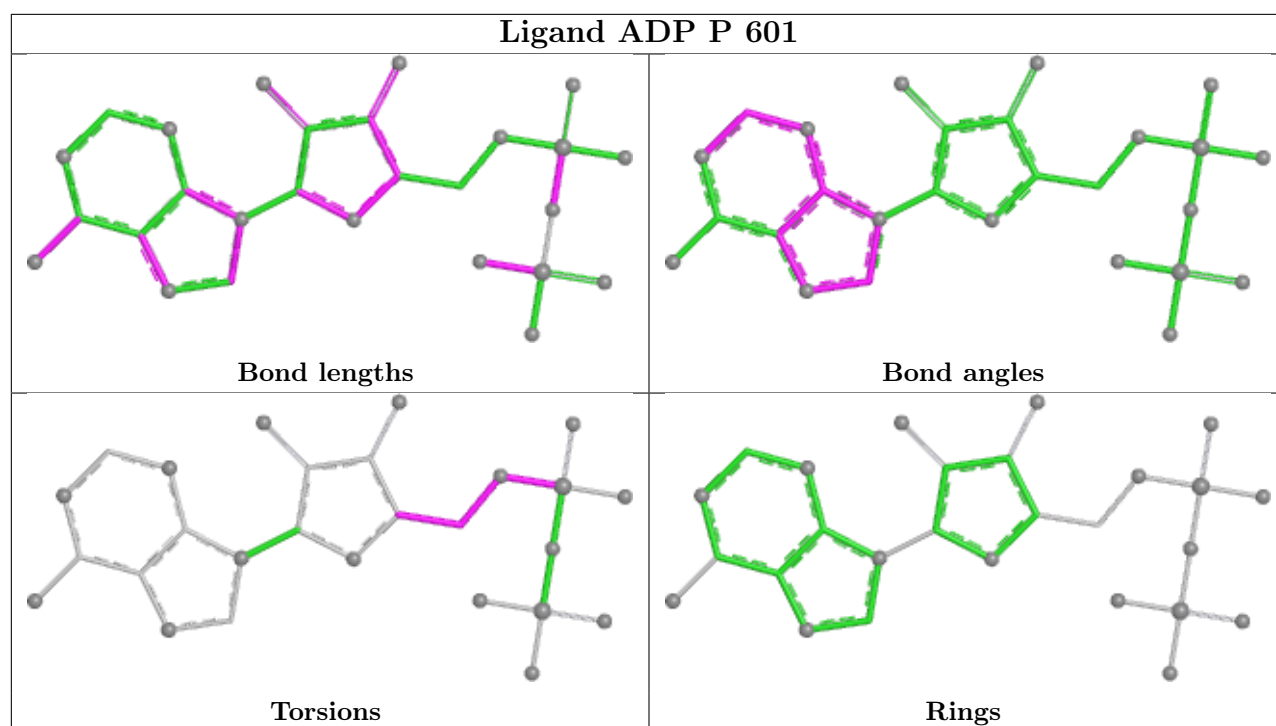
Mol	Chain	Res	Type	Atoms
15	F	601	ADP	C5'-O5'-PA-O1A
15	F	601	ADP	C5'-O5'-PA-O2A
15	F	601	ADP	C5'-O5'-PA-O3A
15	F	601	ADP	O4'-C4'-C5'-O5'
15	H	5000	ADP	PA-O3A-PB-O2B

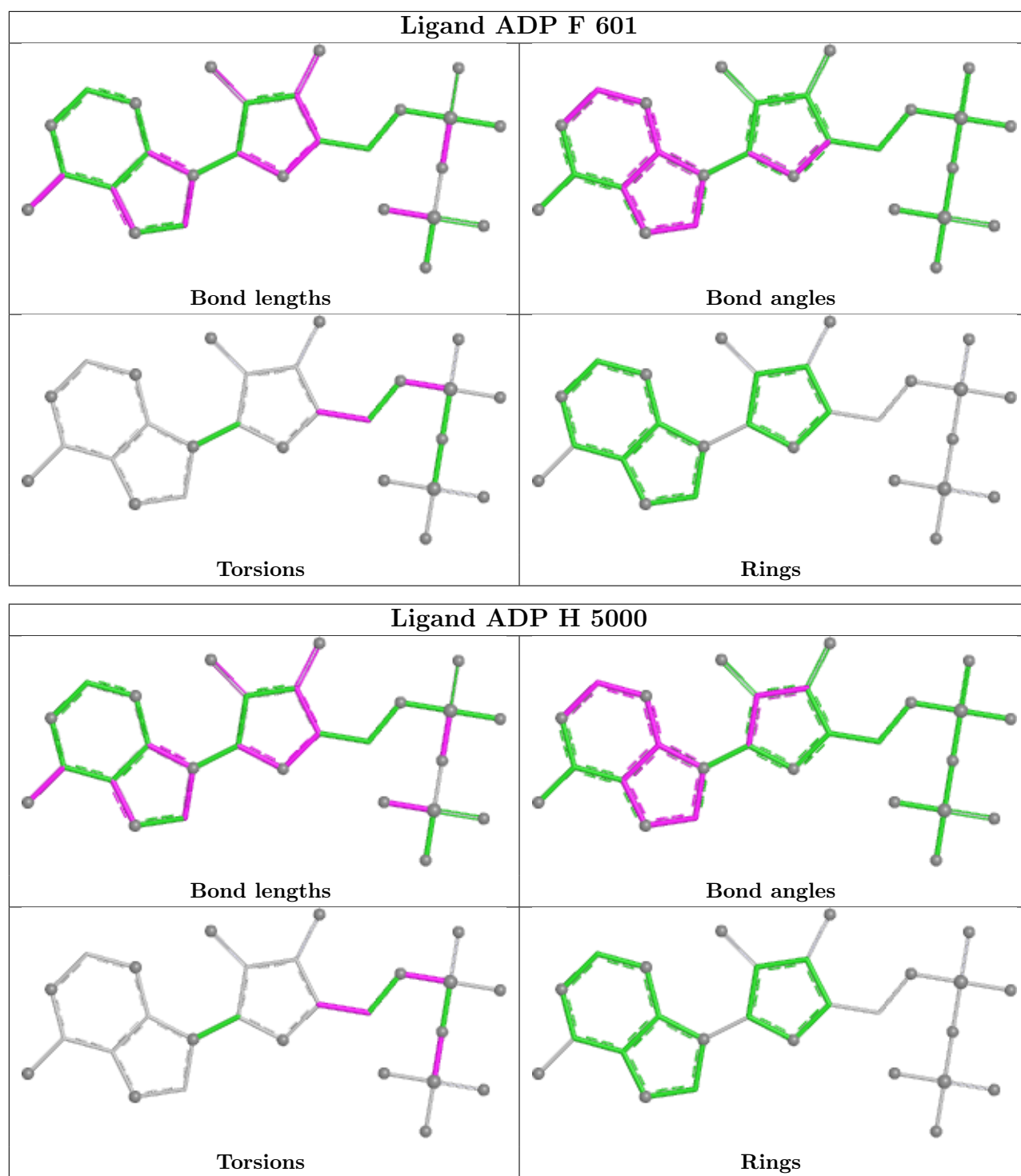
There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
15	P	601	ADP	2	0
15	N	601	ADP	1	0
15	F	601	ADP	1	0
15	H	5000	ADP	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

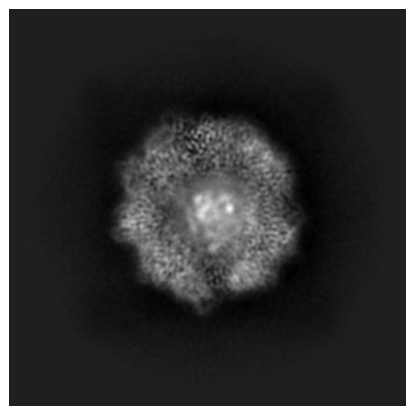
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32823. These allow visual inspection of the internal detail of the map and identification of artifacts.

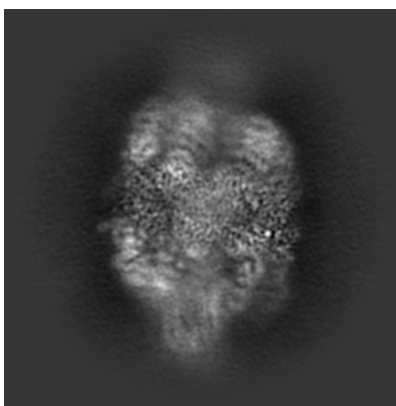
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

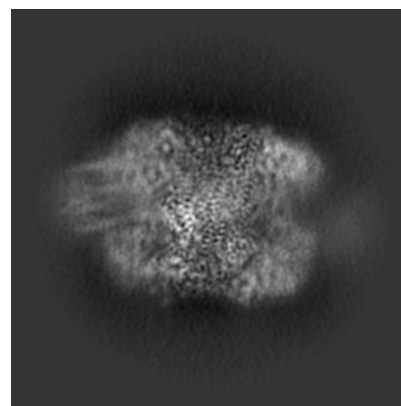
6.1.1 Primary map



X

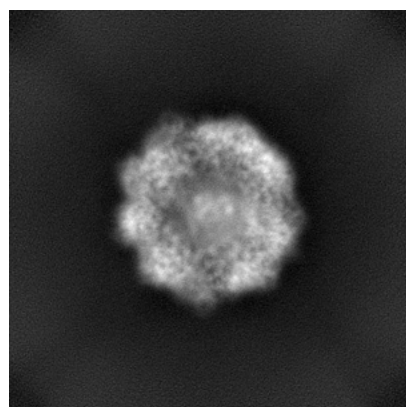


Y

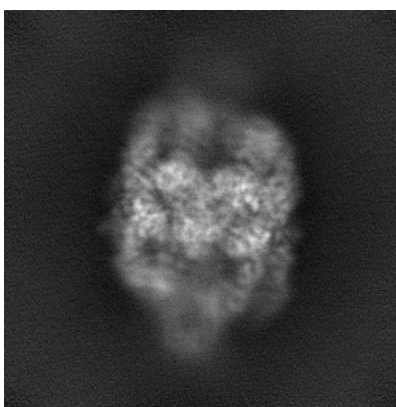


Z

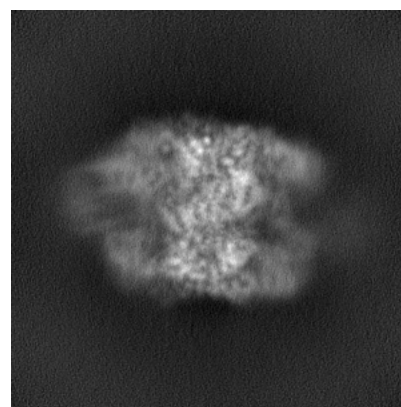
6.1.2 Raw map



X



Y

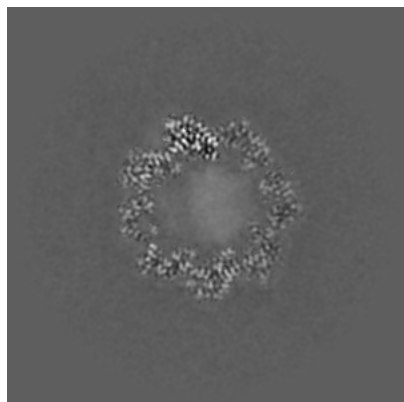


Z

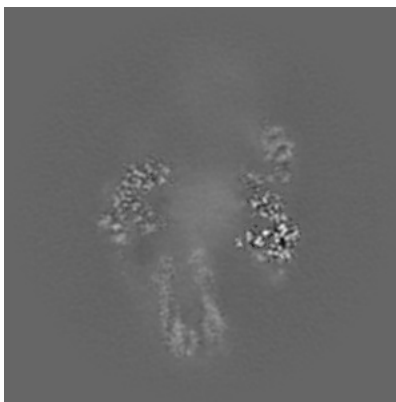
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

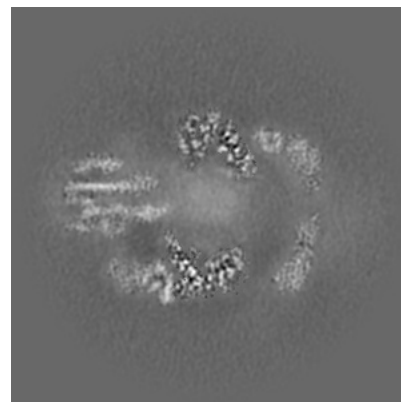
6.2.1 Primary map



X Index: 160

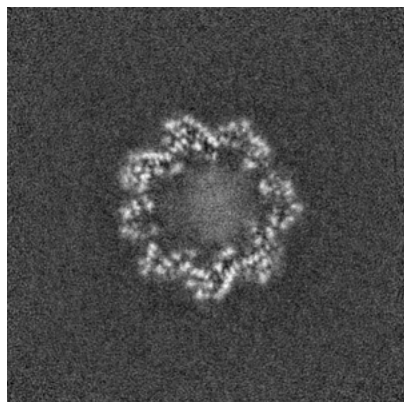


Y Index: 160

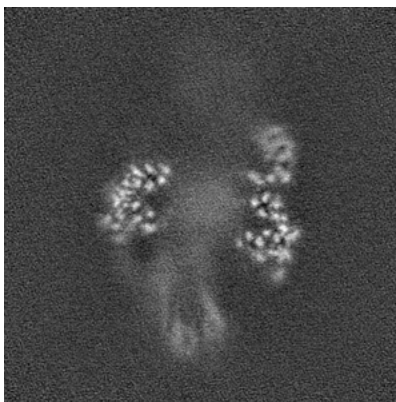


Z Index: 160

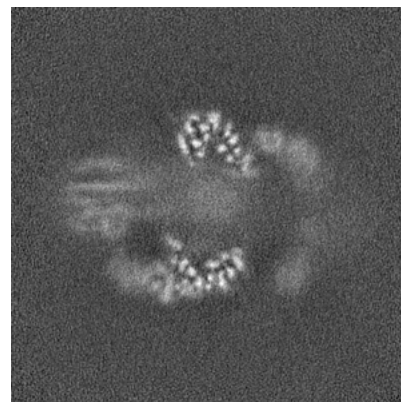
6.2.2 Raw map



X Index: 160



Y Index: 160

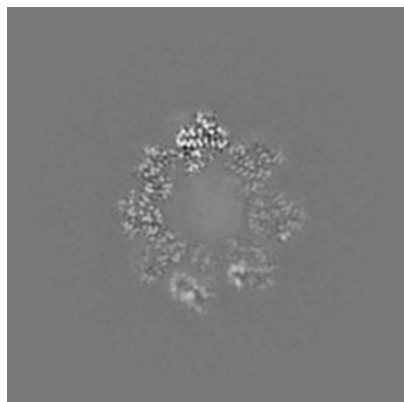


Z Index: 160

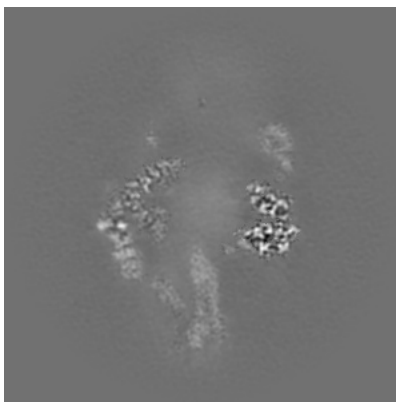
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

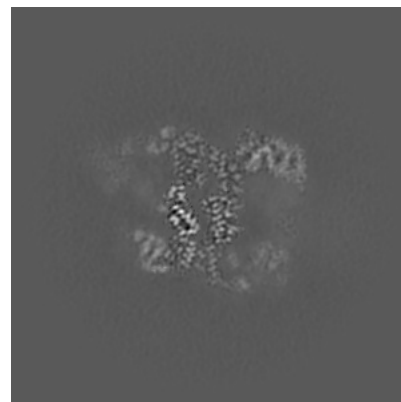
6.3.1 Primary map



X Index: 141

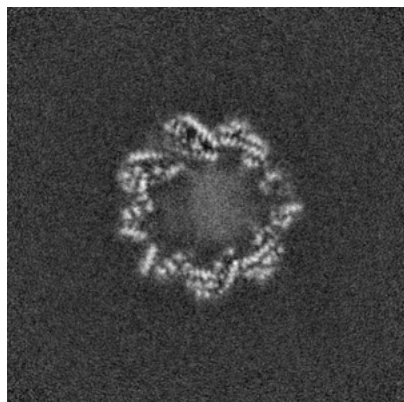


Y Index: 153

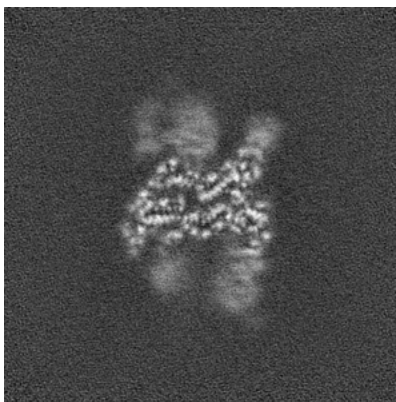


Z Index: 202

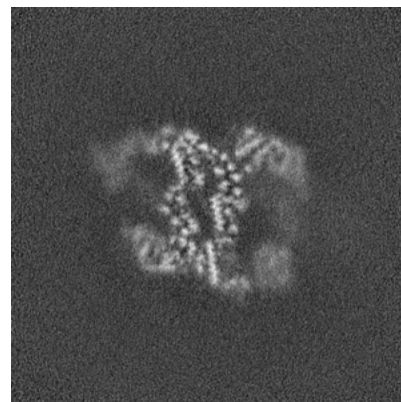
6.3.2 Raw map



X Index: 162



Y Index: 207

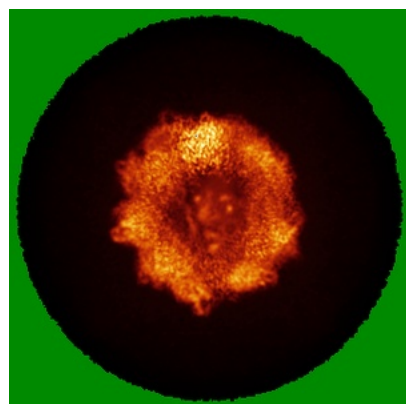


Z Index: 200

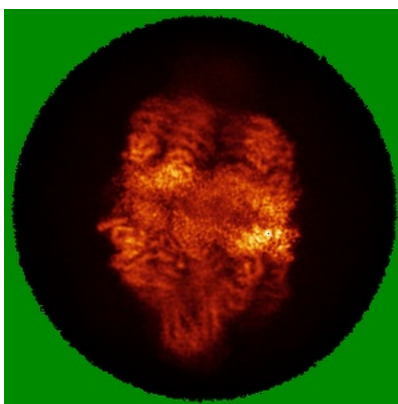
The images above show the largest variance slices of the map in three orthogonal directions.

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

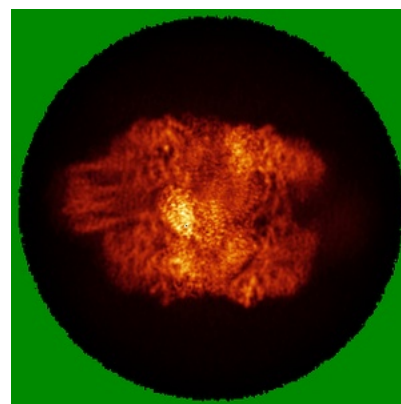
6.4.1 Primary map



X

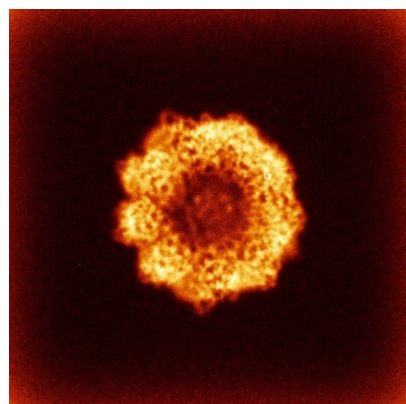


Y

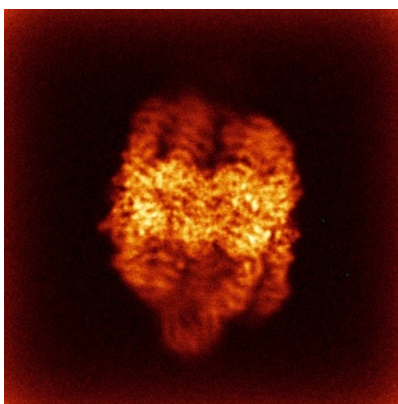


Z

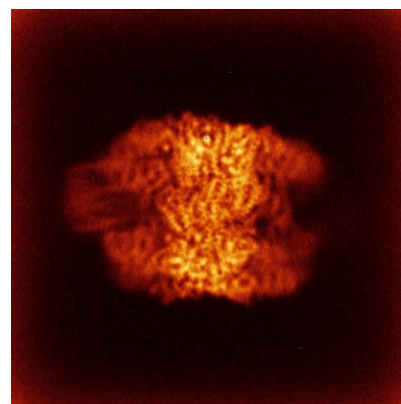
6.4.2 Raw map



X



Y

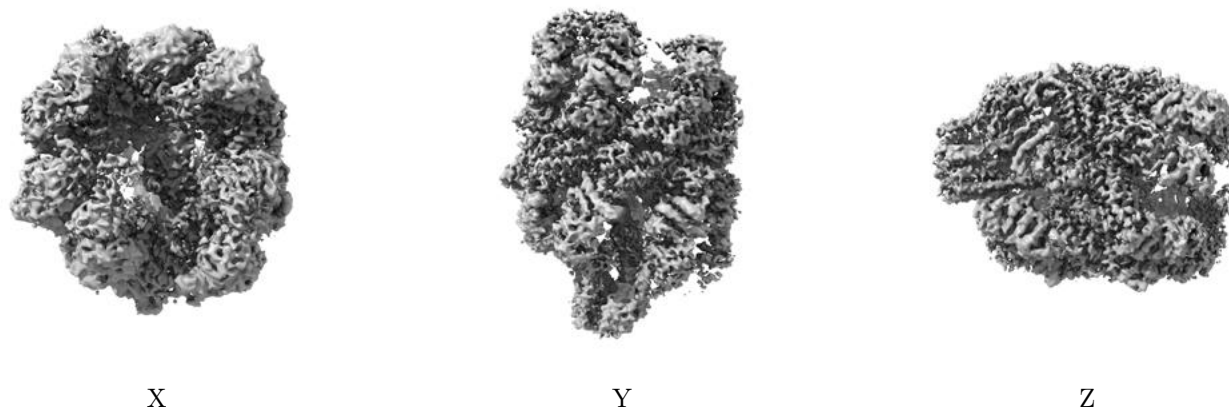


Z

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.

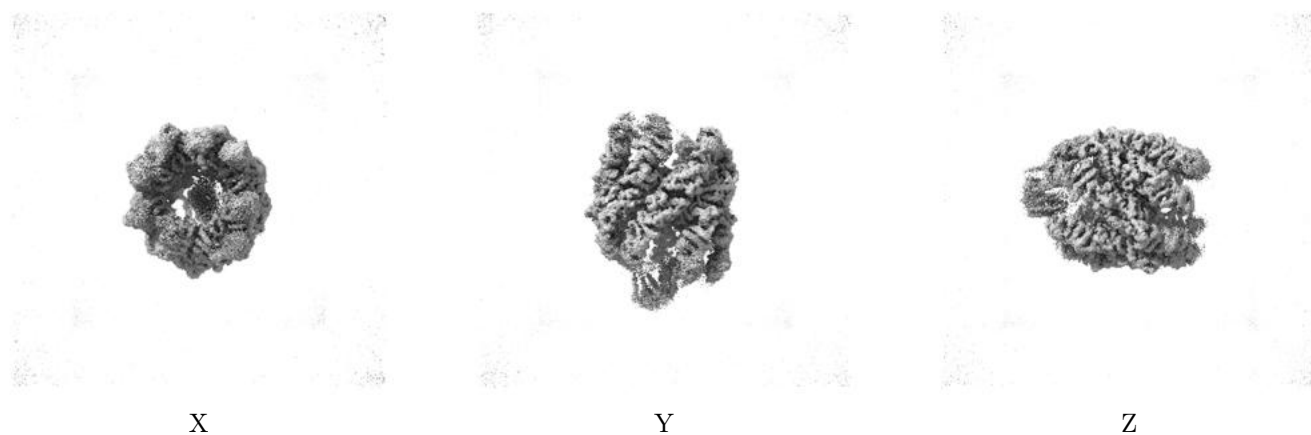
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.943. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

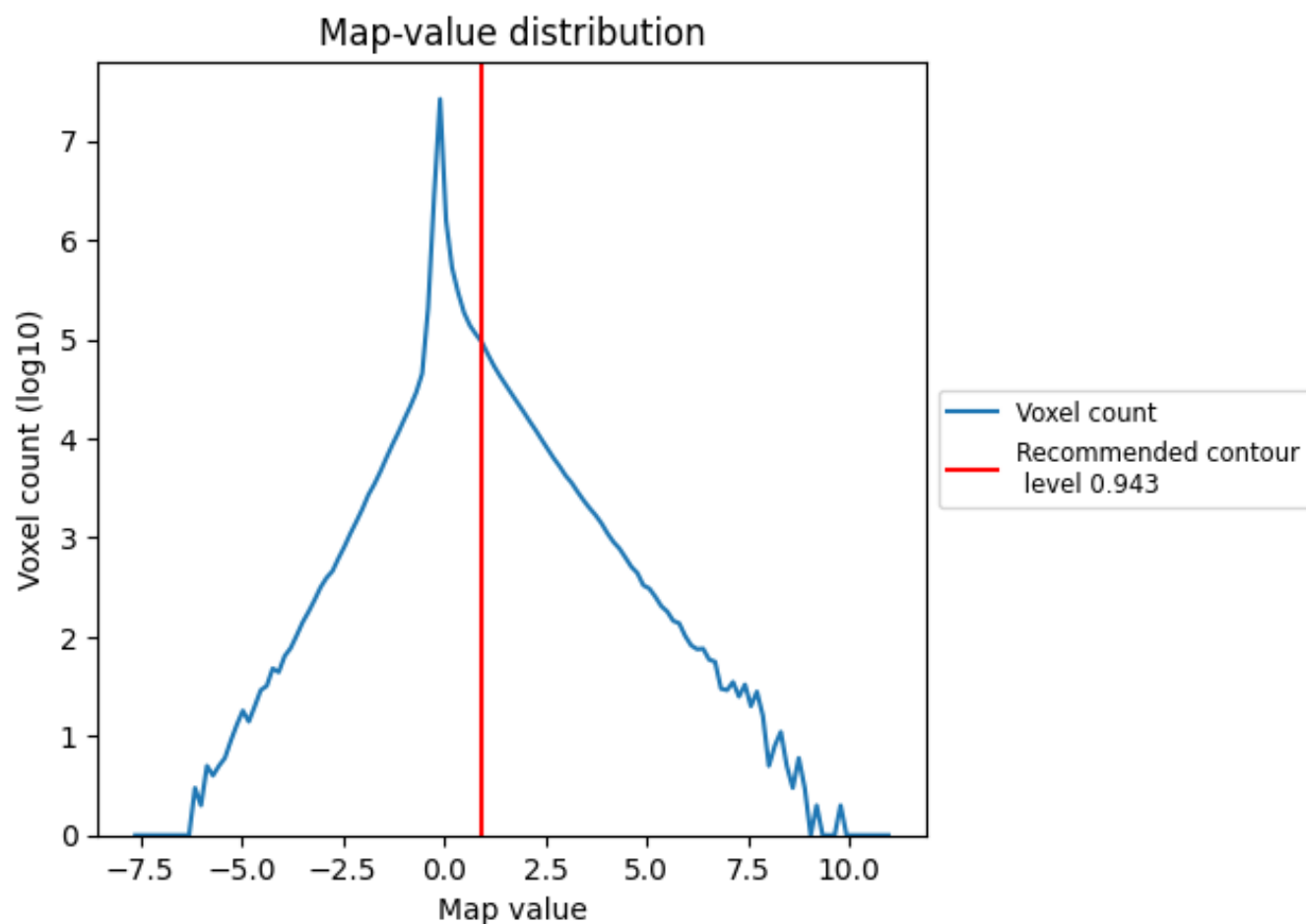
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

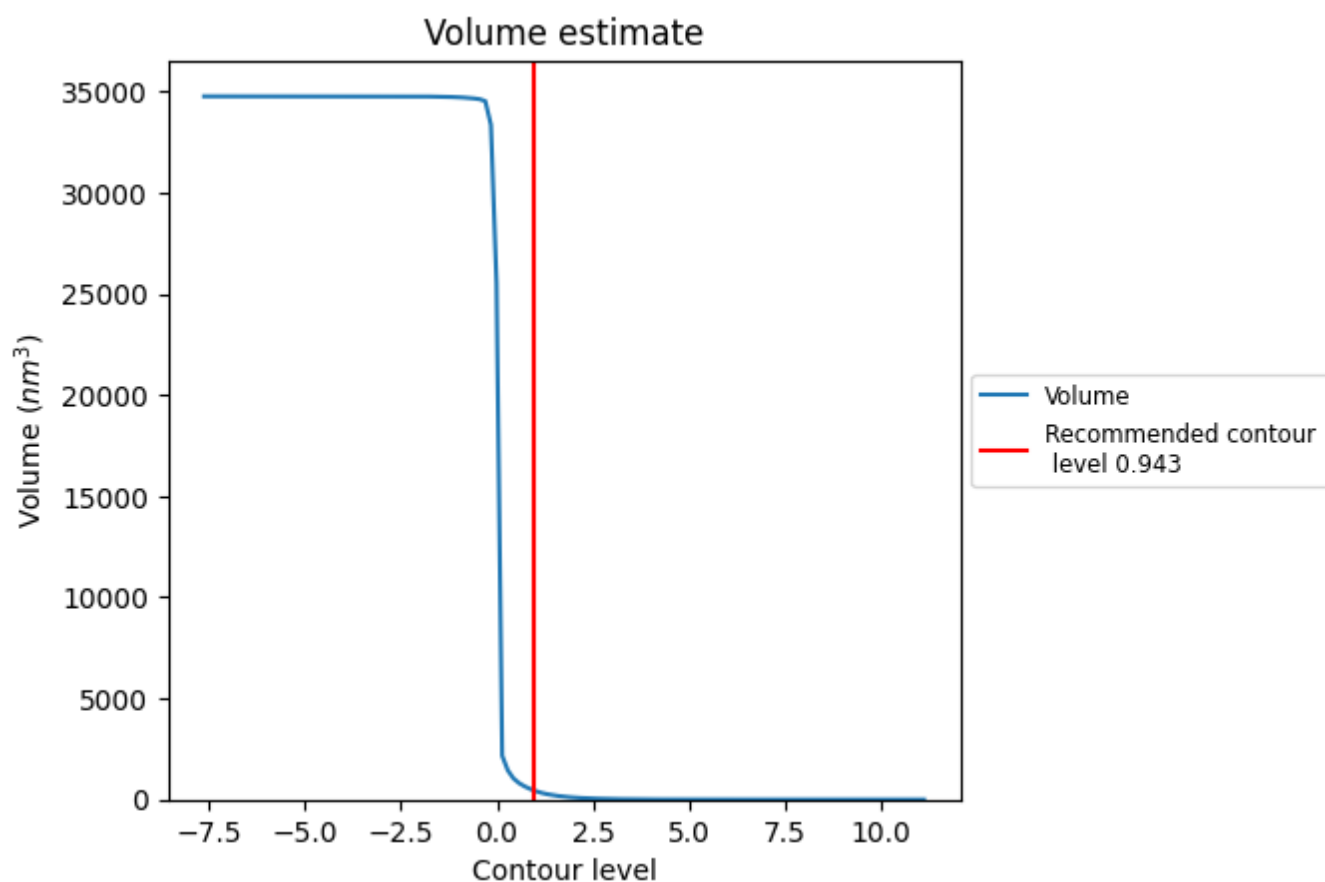
This section contains the results of statistical analysis of the map.

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.

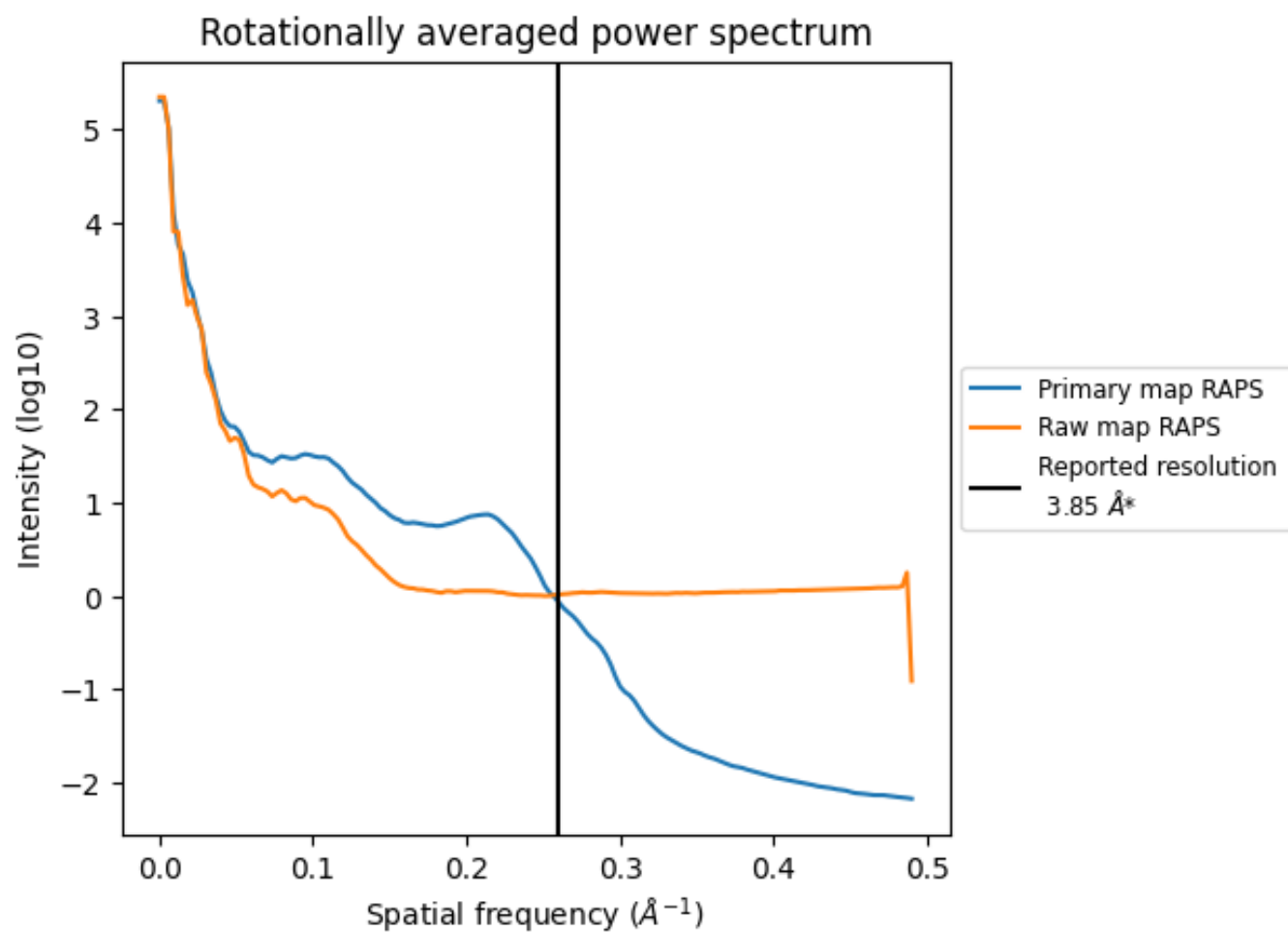
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 469 nm³; this corresponds to an approximate mass of 423 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 ⓘ

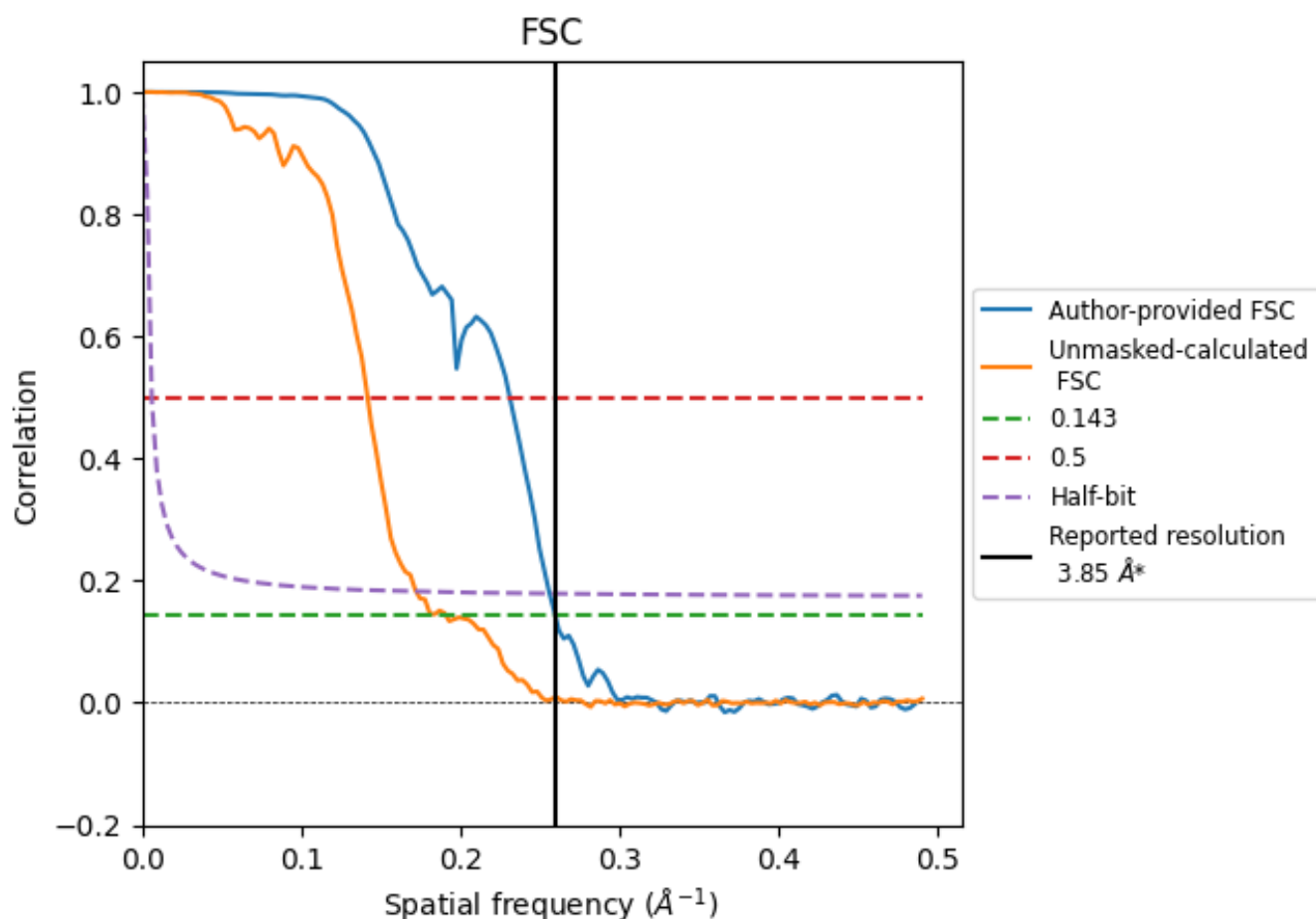


*Reported resolution corresponds to spatial frequency of $0.260 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.260 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

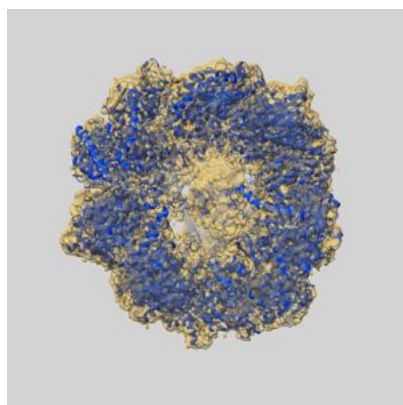
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.85	-	-
Author-provided FSC curve	3.85	4.33	3.90
Unmasked-calculated*	5.24	7.06	5.81

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.24 differs from the reported value 3.85 by more than 10 %

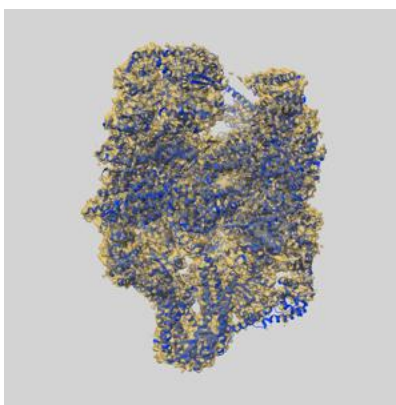
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32823 and PDB model 7WU7. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

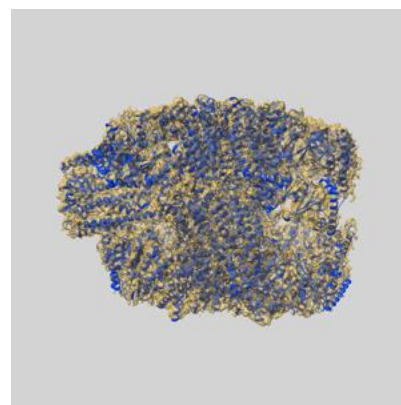
9.1 Map-model overlay [i](#)



X



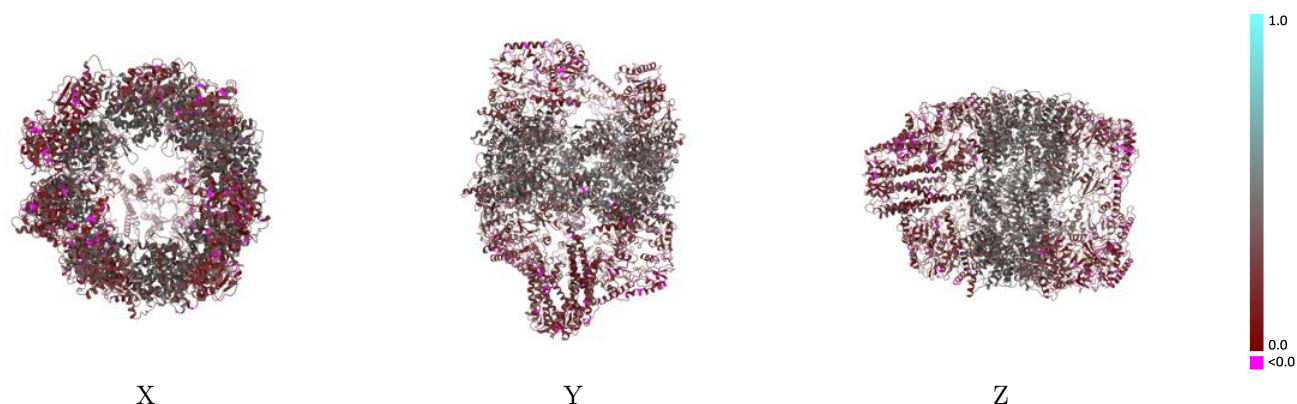
Y



Z

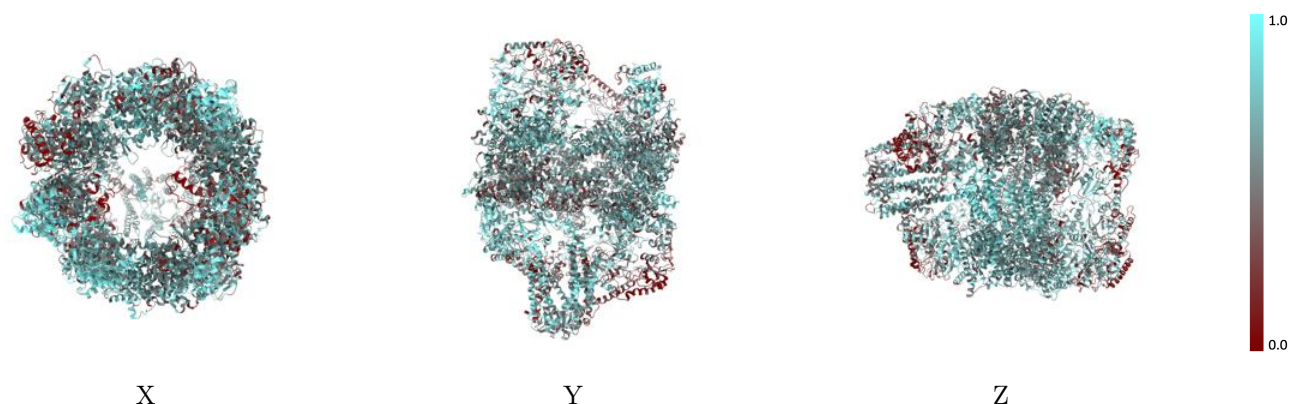
The images above show the 3D surface view of the map at the recommended contour level 0.943 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



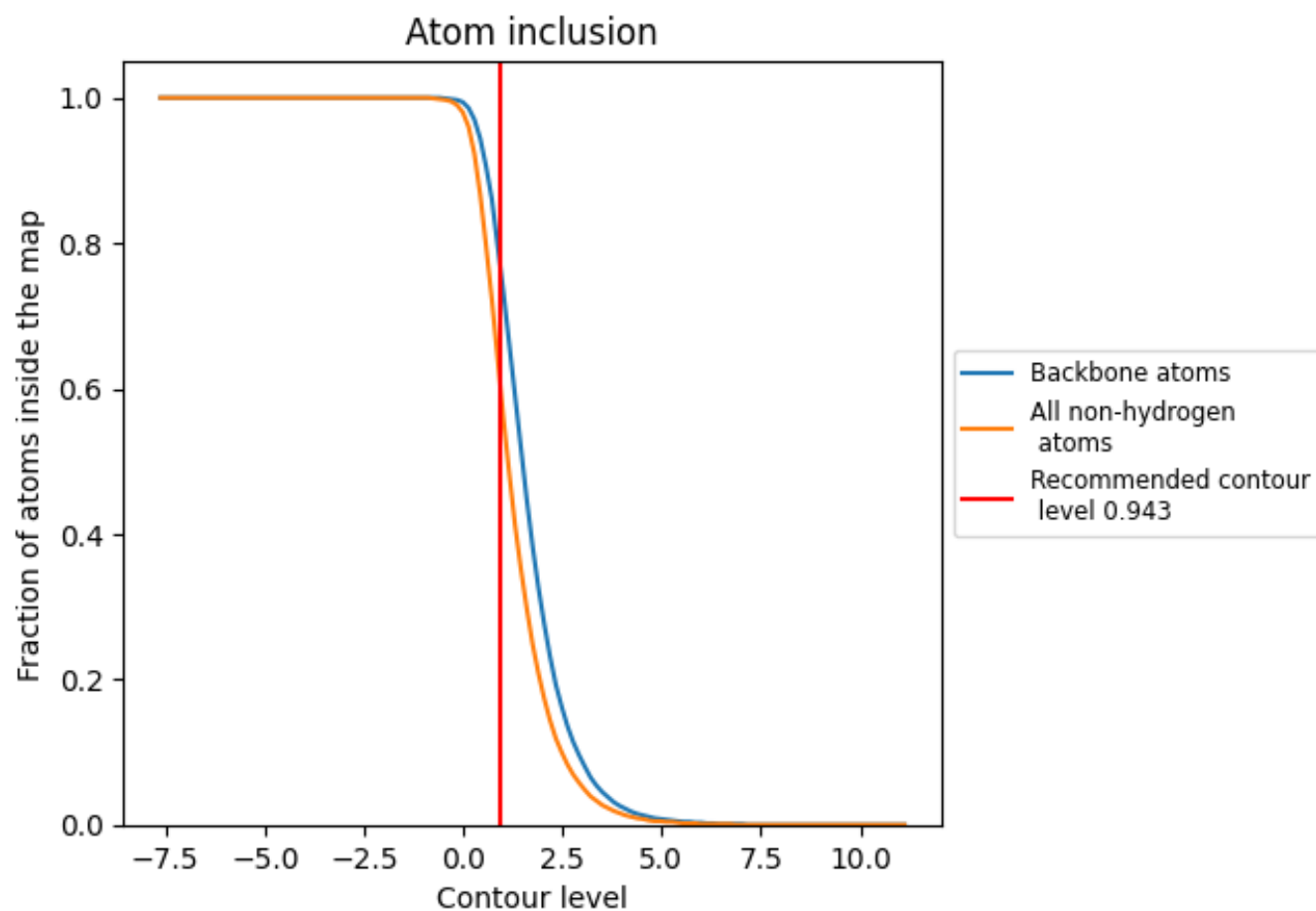
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.943).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 60% 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 (0.943) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5980	 0.3020
1	 0.6210	 0.2070
2	 0.5150	 0.2520
3	 0.7030	 0.2300
4	 0.6210	 0.2110
5	 0.5870	 0.2020
6	 0.6670	 0.1780
A	 0.5600	 0.3060
B	 0.5440	 0.2970
C	 0.5200	 0.2900
D	 0.6580	 0.3150
E	 0.6120	 0.2960
F	 0.5590	 0.3300
G	 0.6570	 0.3030
H	 0.5600	 0.3370
I	 0.6230	 0.3000
J	 0.6330	 0.2930
K	 0.5880	 0.2820
L	 0.6630	 0.3070
M	 0.5130	 0.2970
N	 0.6710	 0.3480
O	 0.6380	 0.3080
P	 0.5310	 0.3480

