



wwPDB EM Validation Summary Report ⓘ

Aug 4, 2026 – 06:36 PM EDT

PDB ID : 8CST / pdb_00008cst
EMDB ID : EMD-26970
Title : Human mitochondrial small subunit assembly intermediate (State E)
Authors : Harper, N.J.; Burnside, C.; Klinge, S.
Deposited on : 2022-05-13
Resolution : 2.85 Å(reported)
Based on initial models : 6AAX, 2C2N, 6RW4

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:

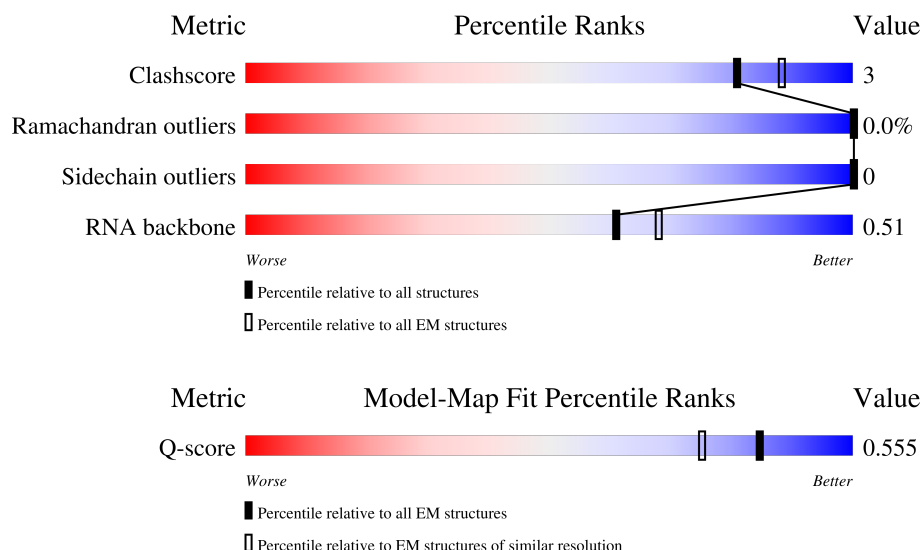
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 2.85 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	-
RNA backbone	8273	3508	-
Q-score	-	25397	11965 (2.35 - 3.35)

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	0	218	
2	1	323	
3	3	199	

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Mol	Chain	Length	Quality of chain
4	4	689	
5	6	343	
6	7	456	
7	A	955	
8	B	296	
9	C	167	
10	D	430	
11	E	125	
12	F	242	
13	G	396	
14	H	201	
15	I	194	
16	J	138	
17	K	128	
18	L	257	
19	M	137	
20	N	130	
21	O	258	
22	P	142	
23	Q	87	
24	R	360	
25	S	190	
26	T	173	
27	U	205	
28	V	414	

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Mol	Chain	Length	Quality of chain
29	W	187	9%49%48%
30	X	398	84%5%12%
31	Y	395	5%29%69%
32	Z	106	62%35%

2 Entry composition

There are 41 unique types of molecules in this entry. The entry contains 66351 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 28S ribosomal protein S34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	211	Total	C	N	O	S	0	0
			1754	1108	333	308	5		

- Molecule 2 is a protein called 28S ribosomal protein S35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	259	Total	C	N	O	S	0	0
			2098	1333	353	402	10		

- Molecule 3 is a protein called Aurora kinase A-interacting protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	70	Total	C	N	O	S	0	0
			625	401	134	89	1		

- Molecule 4 is a protein called Pentatricopeptide repeat domain-containing protein 3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	566	Total	C	N	O	S	0	0
			4585	2940	774	843	28		

- Molecule 5 is a protein called Putative ribosome-binding factor A, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	126	Total	C	N	O	S	0	0
			994	630	177	182	5		

- Molecule 6 is a protein called Methyltransferase-like protein 17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	400	Total	C	N	O	S	0	0
			3160	2017	581	546	16		

- Molecule 7 is a RNA chain called 12S mitochondrial rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	888	Total	C	N	O	P	0	0
			18866	8461	3397	6120	888		

- Molecule 8 is a protein called 28S ribosomal protein S2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	220	Total	C	N	O	S	0	0
			1789	1142	324	313	10		

- Molecule 9 is a protein called 28S ribosomal protein S24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	126	Total	C	N	O	S	0	0
			1042	679	181	177	5		

- Molecule 10 is a protein called 28S ribosomal protein S5, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	232	Total	C	N	O	S	0	0
			1838	1155	345	329	9		

- Molecule 11 is a protein called 28S ribosomal protein S6, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	108	Total	C	N	O	S	0	0
			858	539	157	158	4		

- Molecule 12 is a protein called 28S ribosomal protein S7, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	206	Total	C	N	O	S	0	0
			1696	1082	308	295	11		

- Molecule 13 is a protein called 28S ribosomal protein S9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	292	Total	C	N	O	S	0	0
			2395	1522	418	441	14		

- Molecule 14 is a protein called 28S ribosomal protein S10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	130	Total	C	N	O	S	0	0
			1064	687	177	197	3		

- Molecule 15 is a protein called 28S ribosomal protein S11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	137	Total	C	N	O	S	0	0
			1019	641	193	181	4		

- Molecule 16 is a protein called 28S ribosomal protein S12, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	J	107	Total	C	N	O	S	0	0
			829	515	167	141	6		

- Molecule 17 is a protein called 28S ribosomal protein S14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	100	Total	C	N	O	S	0	0
			847	526	177	139	5		

- Molecule 18 is a protein called 28S ribosomal protein S15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	L	161	Total	C	N	O	S	0	0
			1363	869	253	234	7		

- Molecule 19 is a protein called 28S ribosomal protein S16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	M	115	Total	C	N	O	S	0	0
			913	578	181	148	6		

- Molecule 20 is a protein called 28S ribosomal protein S17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	109	Total	C	N	O	S	0	0
			859	557	155	144	3		

- Molecule 21 is a protein called 28S ribosomal protein S18b, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	190	Total	C	N	O	S	0	0
			1570	999	291	274	6		

- Molecule 22 is a protein called 28S ribosomal protein S18c, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	96	Total	C	N	O	S	0	0
			774	498	133	135	8		

- Molecule 23 is a protein called 28S ribosomal protein S21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	86	Total	C	N	O	S	0	0
			744	460	150	126	8		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	50	ARG	CYS	variant	UNP P82921

- Molecule 24 is a protein called 28S ribosomal protein S22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	291	Total	C	N	O	S	0	0
			2382	1518	409	447	8		

- Molecule 25 is a protein called 28S ribosomal protein S23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	133	Total	C	N	O	S	0	0
			1100	709	196	194	1		

- Molecule 26 is a protein called 28S ribosomal protein S25, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	164	Total	C	N	O	S	0	0
			1344	859	234	240	11		

- Molecule 27 is a protein called 28S ribosomal protein S26, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	174	Total	C	N	O	S	0	0
			1468	905	295	264	4		

- Molecule 28 is a protein called 28S ribosomal protein S27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	359	Total	C	N	O	S	0	0
			2946	1891	491	552	12		

- Molecule 29 is a protein called 28S ribosomal protein S28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	98	Total	C	N	O	S	0	0
			775	491	138	142	4		

- Molecule 30 is a protein called 28S ribosomal protein S29, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	352	Total	C	N	O	S	0	0
			2849	1822	499	517	11		

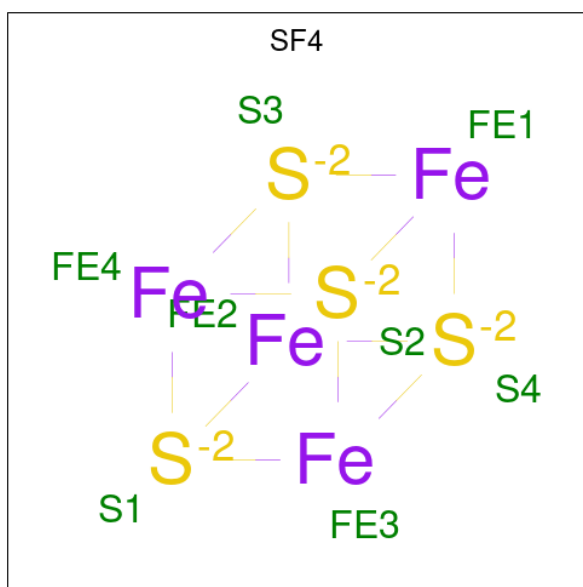
- Molecule 31 is a protein called 28S ribosomal protein S31, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	123	Total	C	N	O	S	0	0
			1043	676	175	189	3		

- Molecule 32 is a protein called 28S ribosomal protein S33, mitochondrial.

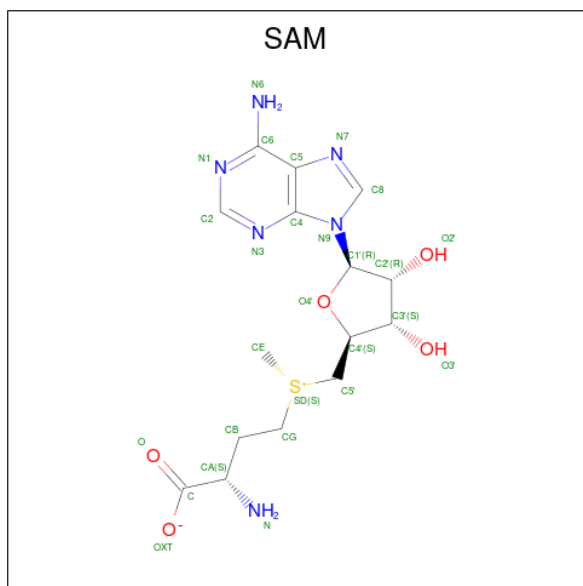
Mol	Chain	Residues	Atoms					AltConf	Trace
32	Z	69	Total	C	N	O	S	0	0
			581	377	101	100	3		

- Molecule 33 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
33	7	1	Total	Fe	S	0
			8	4	4	

- Molecule 34 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
34	7	1	Total	C	N	O	S	0
			27	15	6	5	1	

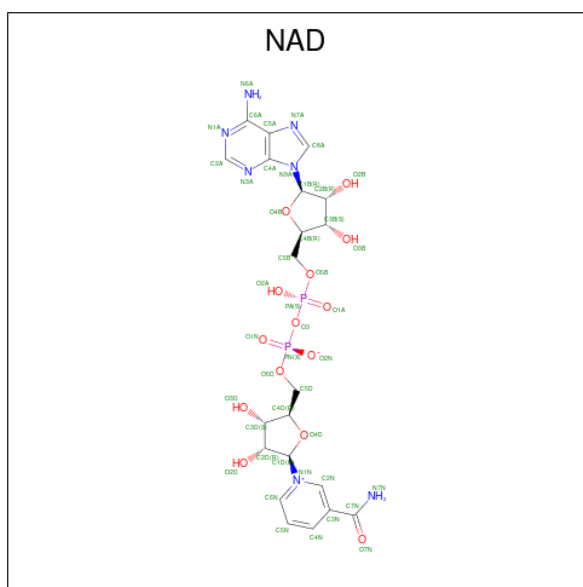
- Molecule 35 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
35	A	4	Total	K	0
			4	4	

- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	A	28	Total	Mg	0
			28	28	
36	B	1	Total	Mg	0
			1	1	
36	X	1	Total	Mg	0
			1	1	

- Molecule 37 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).

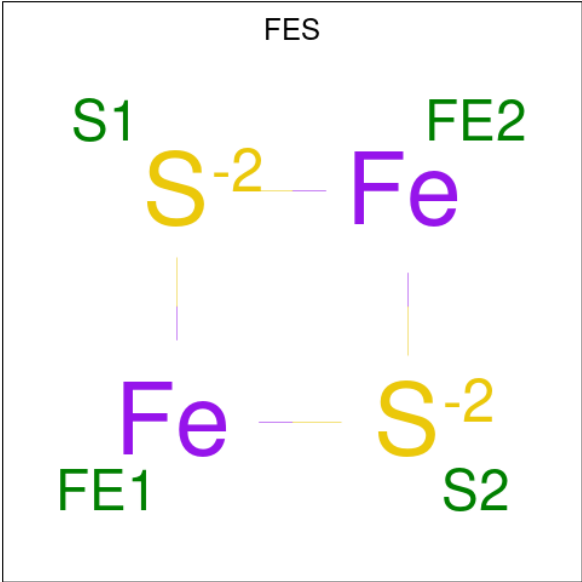


Mol	Chain	Residues	Atoms					AltConf
37	A	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

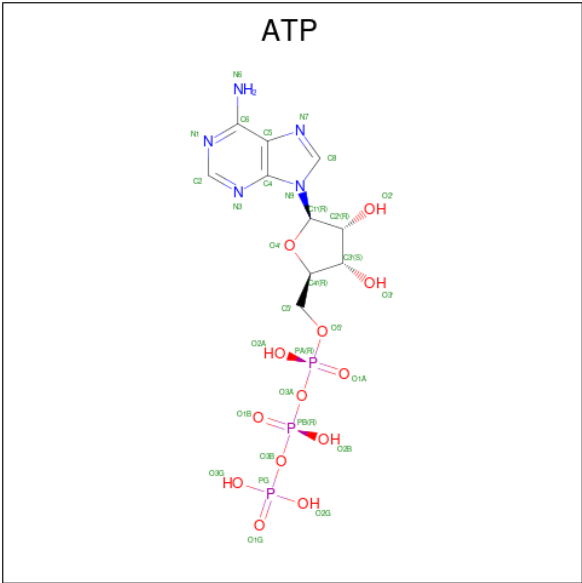
Mol	Chain	Residues	Atoms		AltConf
38	O	1	Total	Zn	0
			1	1	

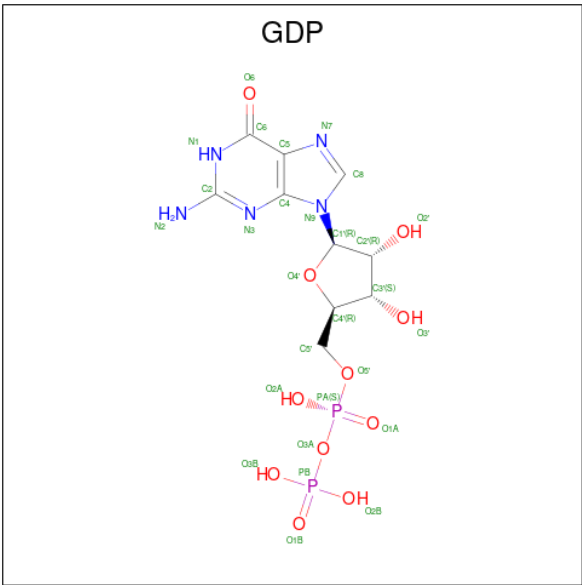
- Molecule 39 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms			AltConf
39	P	1	Total	Fe	S	0
			4	2	2	
39	T	1	Total	Fe	S	0
			4	2	2	

- Molecule 40 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



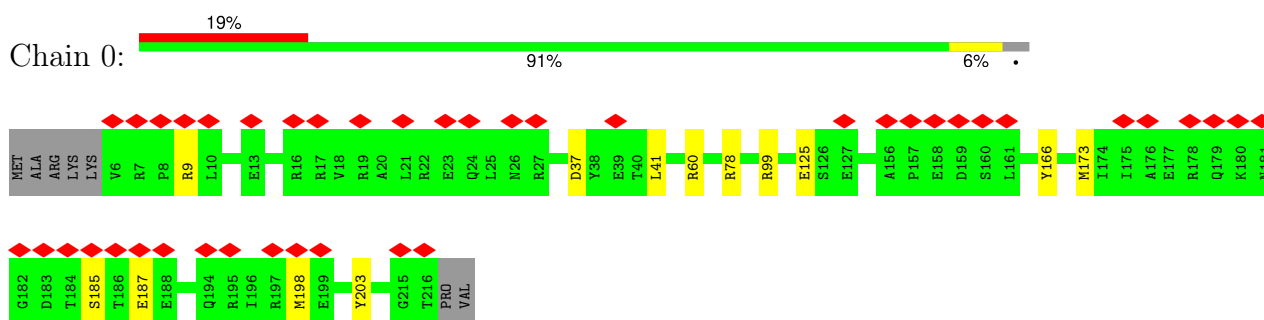


Mol	Chain	Residues	Atoms					AltConf
41	X	1	Total	C	N	O	P	0
			28	10	5	11	2	

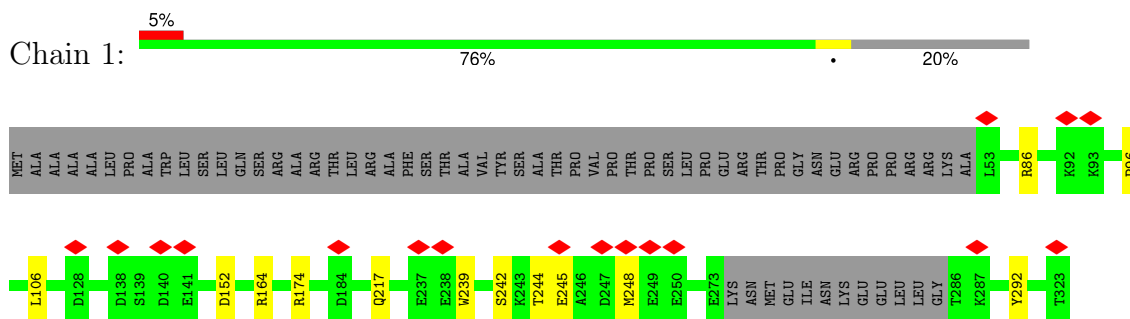
3 Residue-property plots

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.

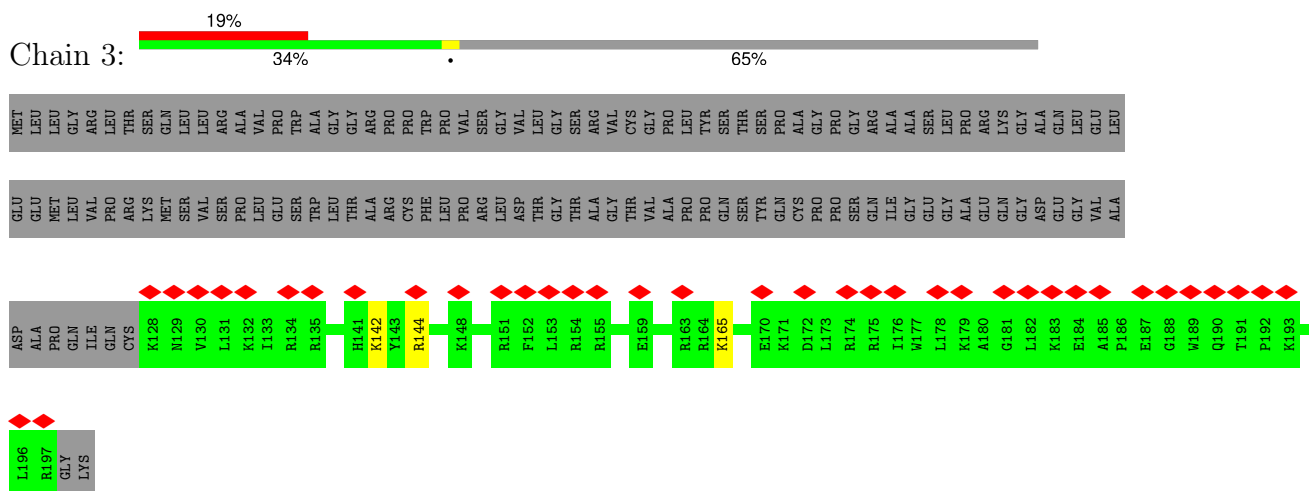
- Molecule 1: 28S ribosomal protein S34, mitochondrial



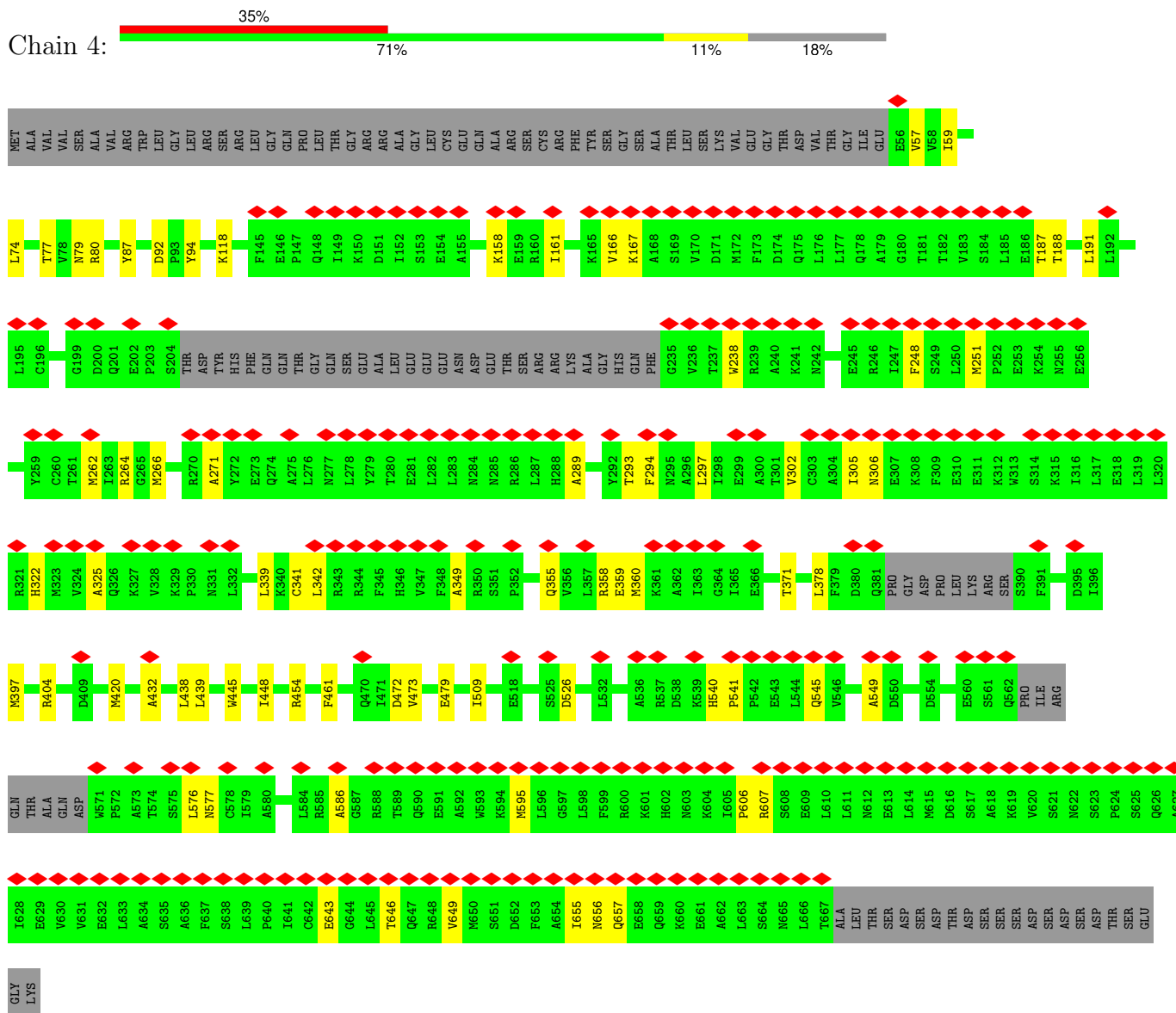
- Molecule 2: 28S ribosomal protein S35, mitochondrial



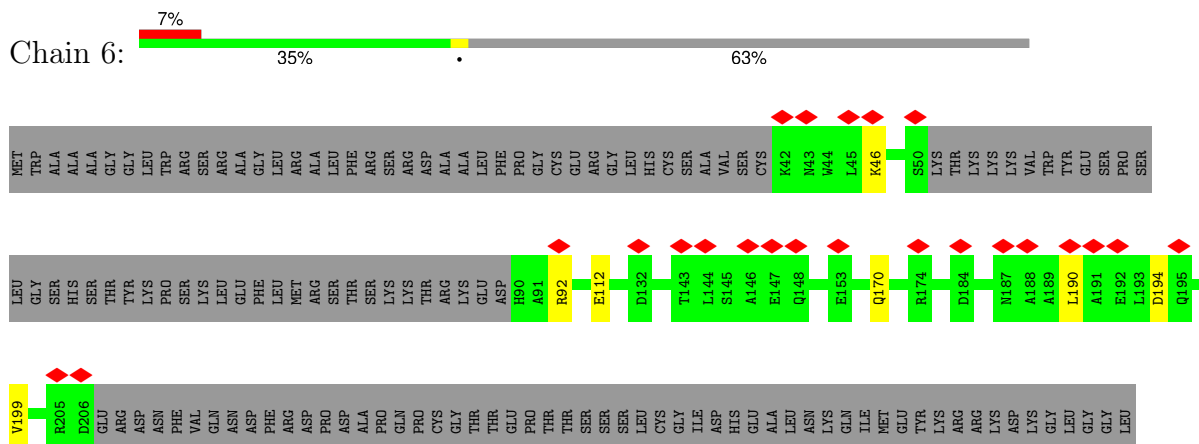
- Molecule 3: Aurora kinase A-interacting protein



- Chain 4:

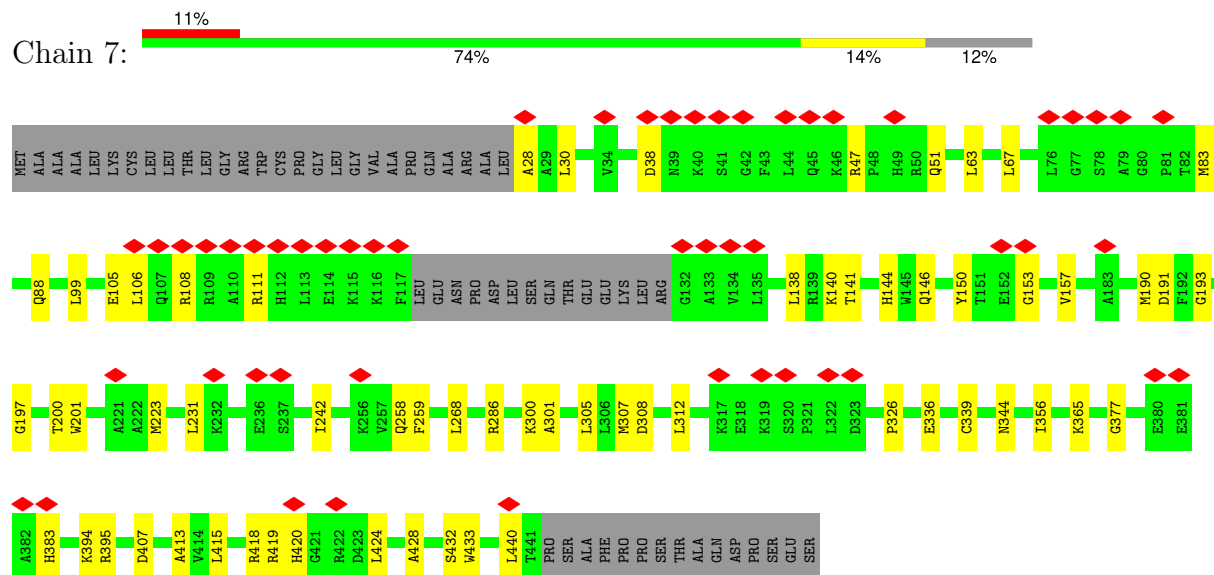


- Chain 6:

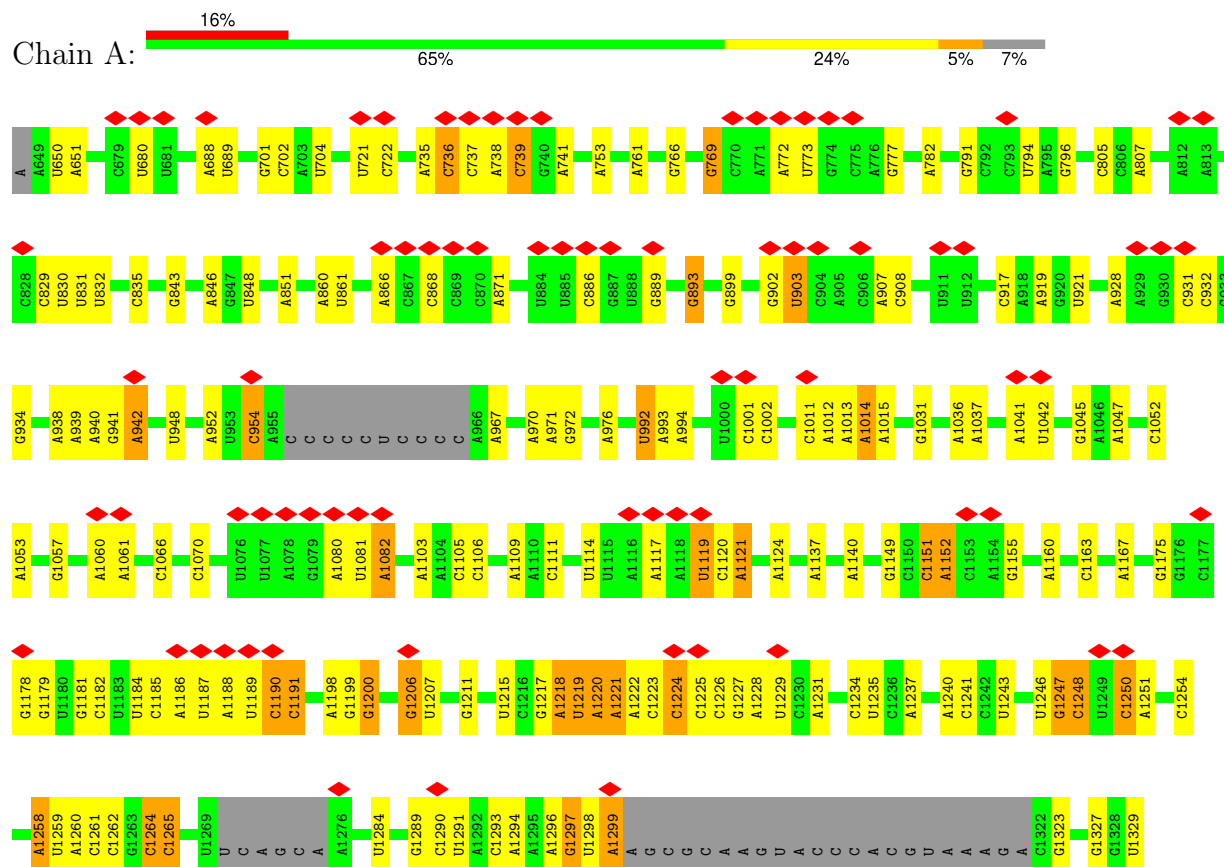


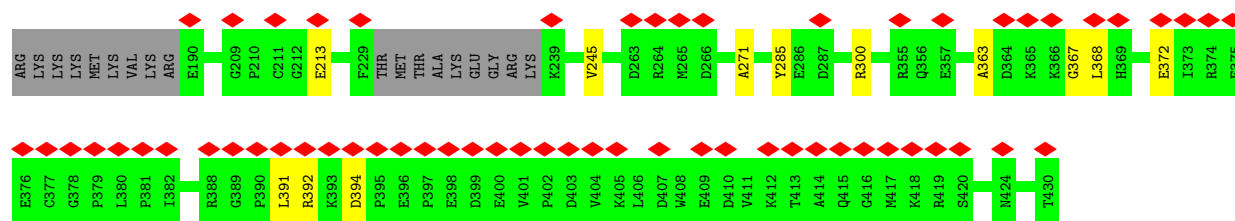
VAL	TRP	GLN	GLY	VAL	GLN	VAL	ALA	GLU	THR	THR	THR	GLY	ASP	GLY	MET	LYS	LYS	LYS	ARG	LYS	ARG	ALA	LYS	PRO	ARG	LEU	GLU	GLN	GLN	SER	SER	SER	LYS	LYS	TYR	SER	SER	GLY	GLU	GLU	VAL	GLU	ASP	ASP	LEU	LEU	VAL	GLY	GLY	ALA	PRO	PRO	GLU	TYR	GLU	GLU	CYS	VAL	ALA	ASP	THR	THR	GLU	GLU
LEU	GLU	ALA	GLU	ARG	GLY	GLY	ALA	GLU	THR	THR	THR	GLY	ASP	GLY	HIS	LYS	SER	CYS	GLY	ALA	SER	ARG	ALA	GLU	LEU	GLN	ARG	ALA	A28	A29	L30	V34	D38	R39	R40	S41	G42	F43	L44	Q45	K46	R47	P48	H49	R50	Q51	L63	L67	L76	G77	S78	A79	G80	P81	T82	M83								

• Molecule 6: Methyltransferase-like protein 17, mitochondrial

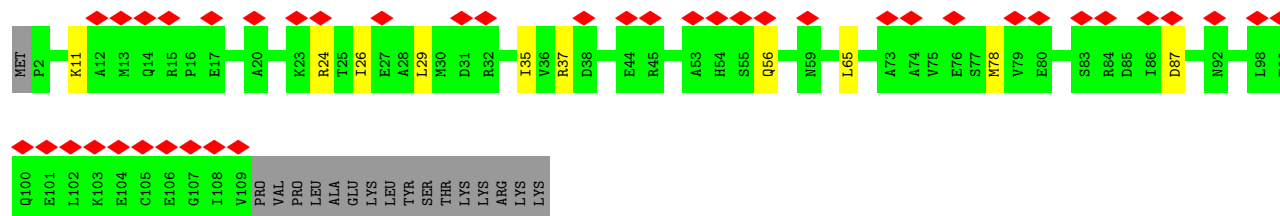
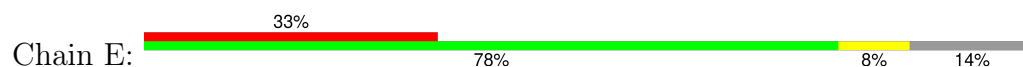


• Molecule 7: 12S mitochondrial rRNA

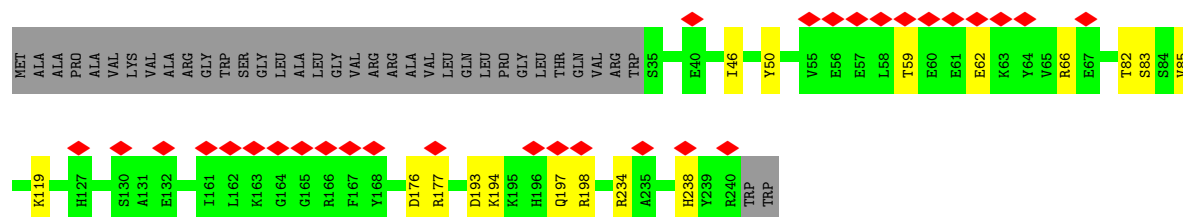
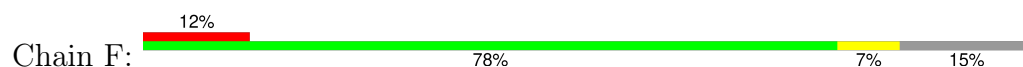




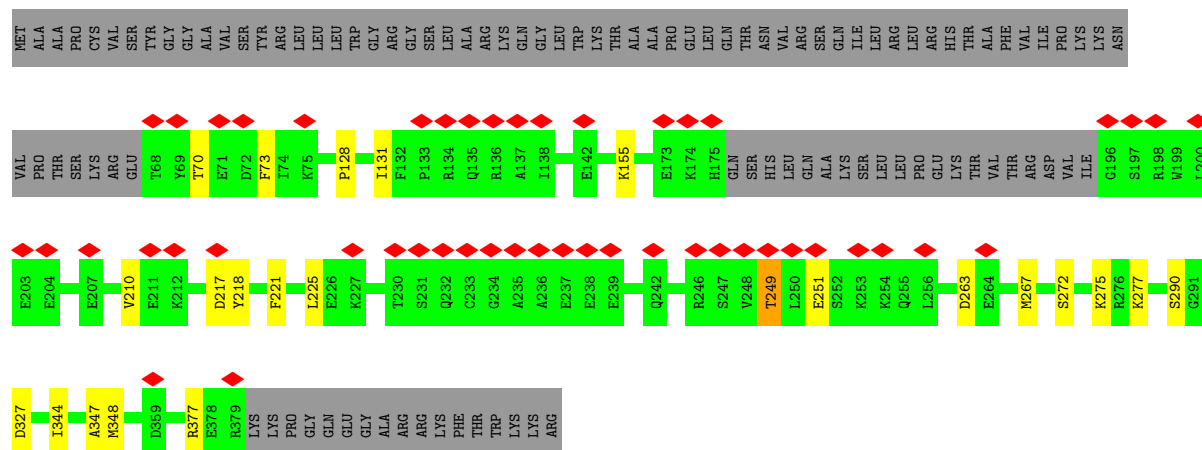
- Molecule 11: 28S ribosomal protein S6, mitochondrial



- Molecule 12: 28S ribosomal protein S7, mitochondrial

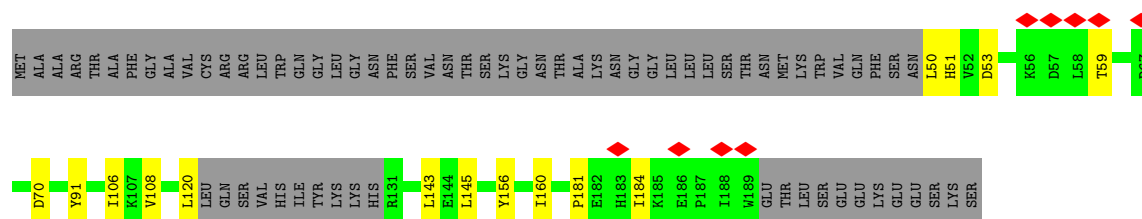


- Molecule 13: 28S ribosomal protein S9, mitochondrial



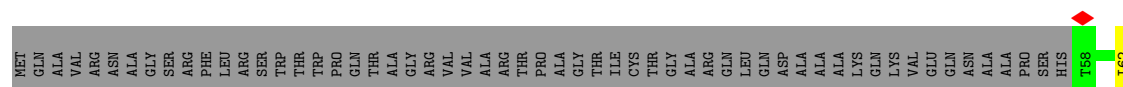
- Molecule 14: 28S ribosomal protein S10, mitochondrial





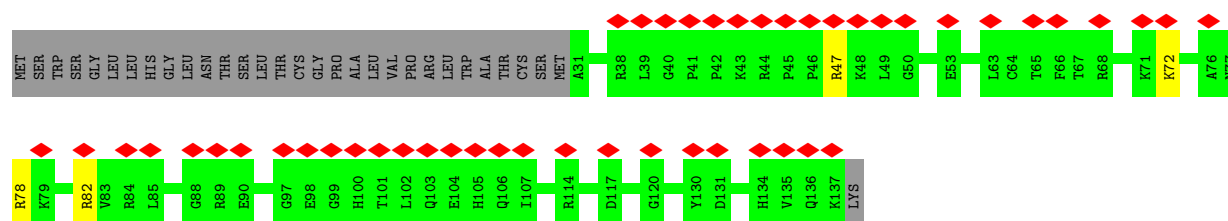
- Molecule 15: 28S ribosomal protein S11, mitochondrial

Chain I: 69% 29%



- Molecule 16: 28S ribosomal protein S12, mitochondrial

Chain J: 35% 75% 22%



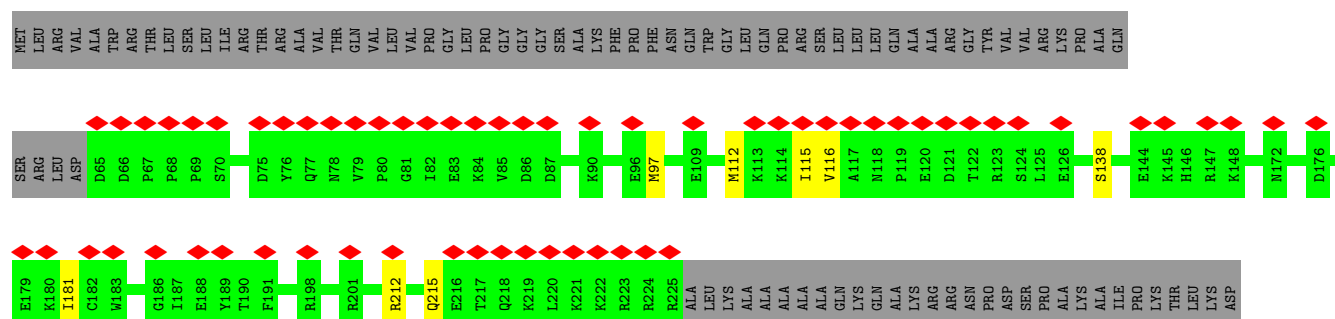
- Molecule 17: 28S ribosomal protein S14, mitochondrial

Chain K: 67% 11% 22%



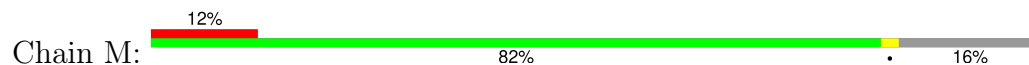
- Molecule 18: 28S ribosomal protein S15, mitochondrial

Chain L: 24% 60% 37%

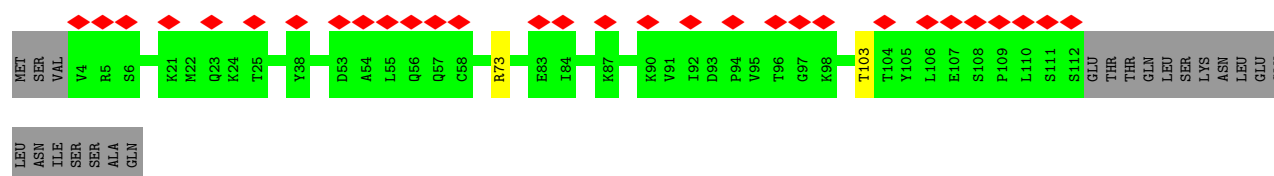
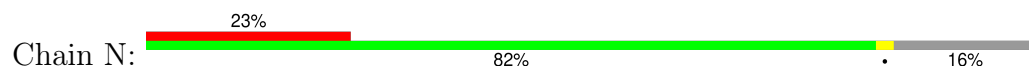


SER
GLN

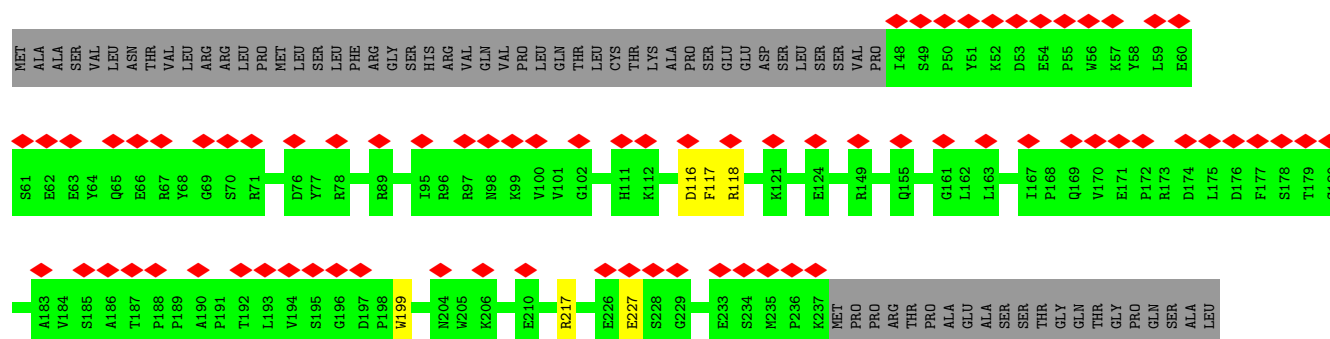
- Molecule 19: 28S ribosomal protein S16, mitochondrial



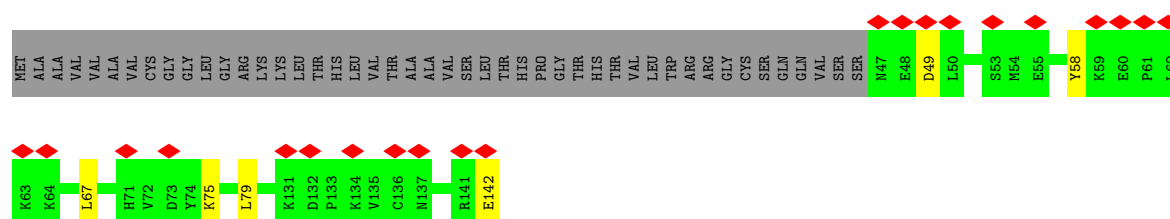
- Molecule 20: 28S ribosomal protein S17, mitochondrial



- Molecule 21: 28S ribosomal protein S18b, mitochondrial

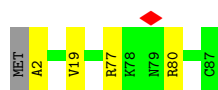


- Molecule 22: 28S ribosomal protein S18c, mitochondrial



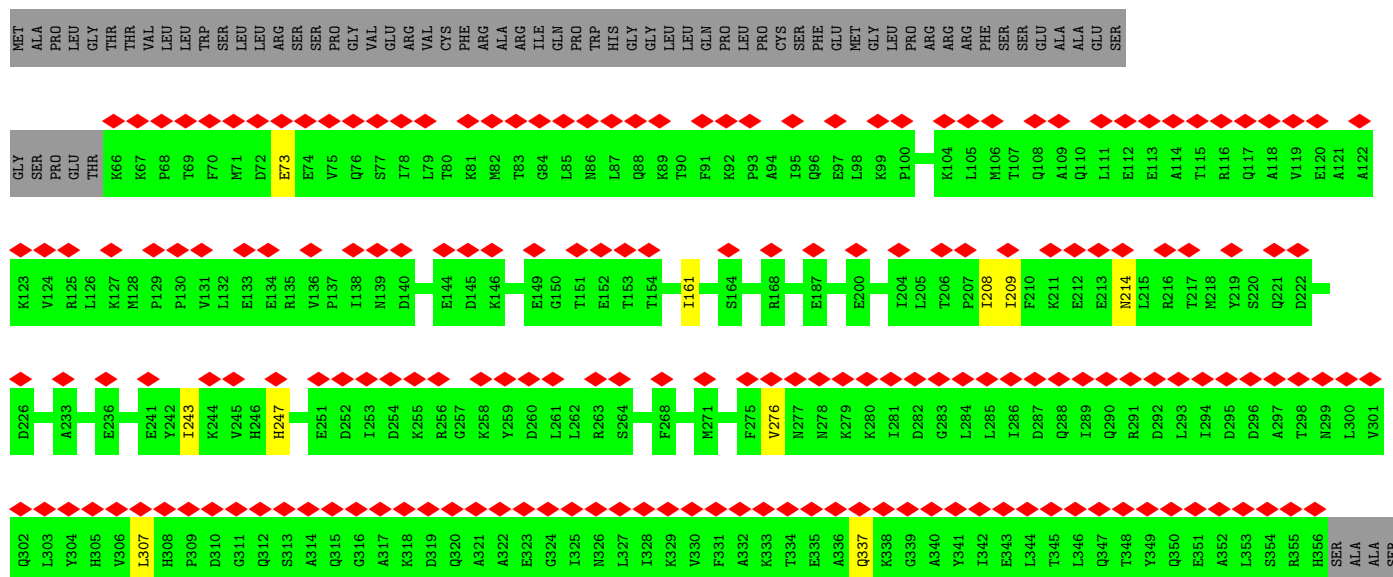
- Molecule 23: 28S ribosomal protein S21, mitochondrial





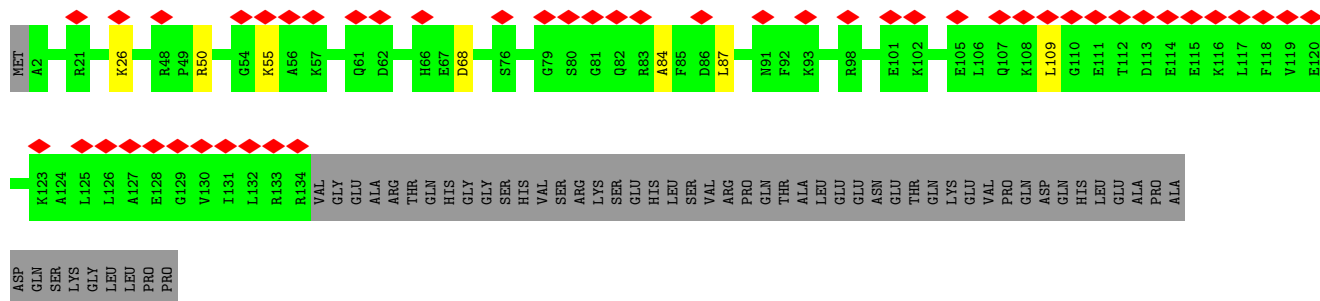
- Molecule 24: 28S ribosomal protein S22, mitochondrial

Chain R: 52% 78% 19%



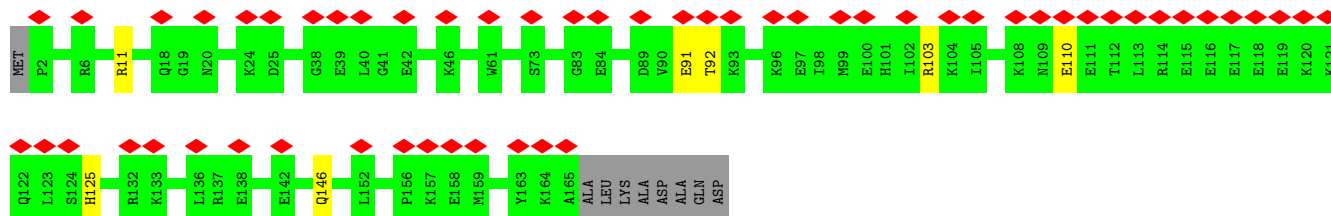
- Molecule 25: 28S ribosomal protein S23, mitochondrial

Chain S: 25% 66% 30%

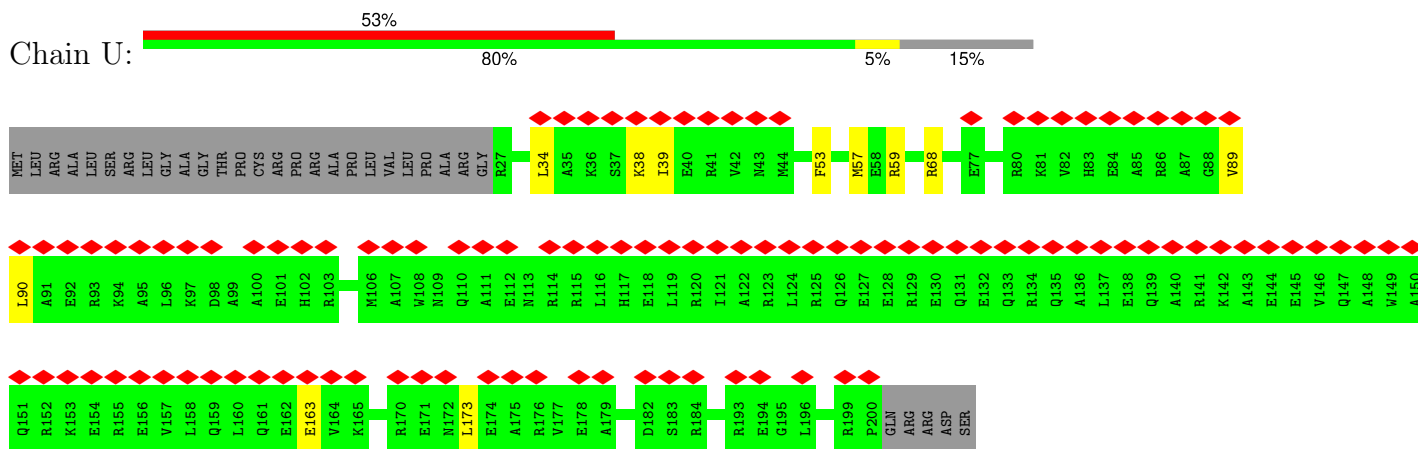


- Molecule 26: 28S ribosomal protein S25, mitochondrial

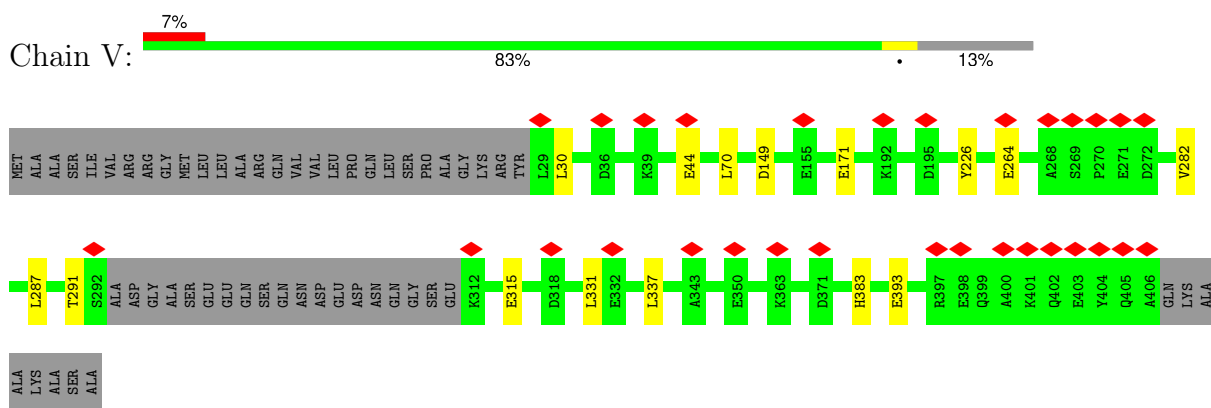
Chain T: 32% 91% 5%



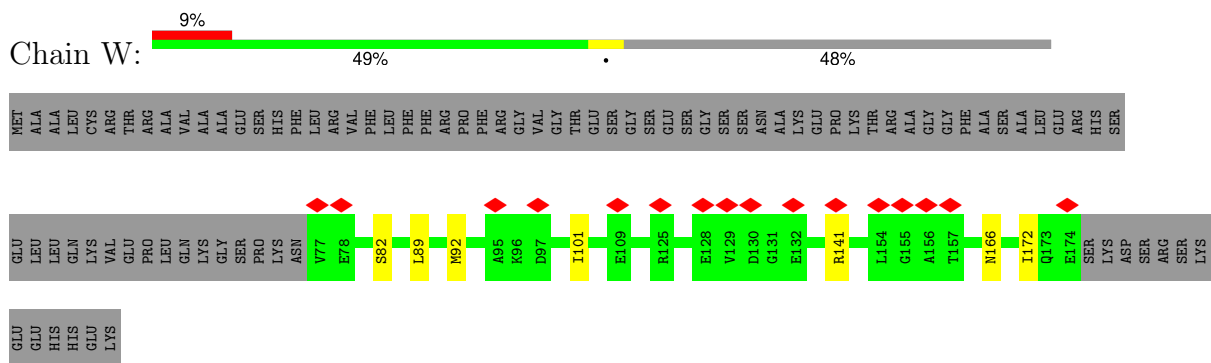
- Molecule 27: 28S ribosomal protein S26, mitochondrial



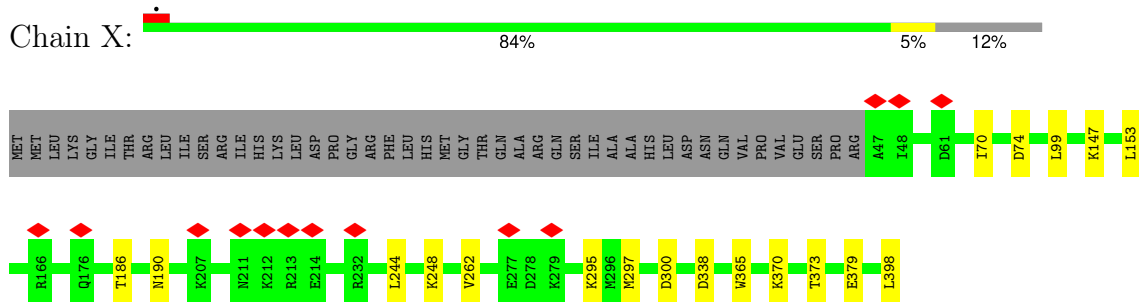
- Molecule 28: 28S ribosomal protein S27, mitochondrial

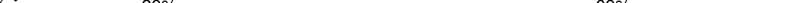


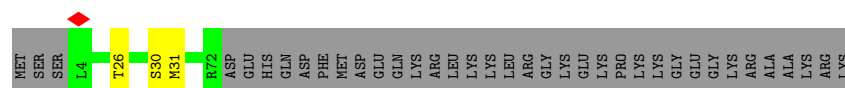
- Molecule 29: 28S ribosomal protein S28, mitochondrial



- Molecule 30: 28S ribosomal protein S29, mitochondrial



- Chain Y:  5% 29% 69%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	39864	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	64000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	45.140	Depositor
Minimum map value	-17.779	Depositor
Average map value	0.035	Depositor
Map value standard deviation	1.235	Depositor
Recommended contour level	7.66	Depositor
Map size ($\text{\AA}$)	424.80002, 424.80002, 424.80002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.062, 1.062, 1.062	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: ATP, K, MA6, FES, GDP, MG, ZN, AYA, SAM, SF4, NAD

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	0	0.17	0/1800	0.33	0/2440
2	1	0.20	0/2143	0.35	0/2902
3	3	0.15	0/636	0.38	0/839
4	4	0.21	1/4686 (0.0%)	0.40	2/6335 (0.0%)
5	6	0.16	0/1012	0.34	0/1371
6	7	0.20	0/3250	0.40	0/4411
7	A	0.15	0/21046	0.30	0/32755
8	B	0.17	0/1832	0.36	0/2480
9	C	0.23	0/1074	0.41	0/1456
10	D	0.16	0/1877	0.34	0/2523
11	E	0.15	0/872	0.35	0/1177
12	F	0.17	0/1734	0.37	0/2327
13	G	0.18	0/2446	0.36	0/3283
14	H	0.21	0/1086	0.37	0/1473
15	I	0.19	0/1039	0.38	0/1400
16	J	0.14	0/845	0.33	0/1137
17	K	0.16	0/863	0.30	0/1159
18	L	0.14	0/1387	0.30	0/1853
19	M	0.15	0/934	0.33	0/1255
20	N	0.15	0/877	0.32	0/1187
21	O	0.14	0/1624	0.32	0/2210
22	P	0.15	0/791	0.31	0/1062
23	Q	0.16	0/748	0.29	0/994
24	R	0.14	0/2429	0.30	0/3280
25	S	0.16	0/1127	0.31	0/1518
26	T	0.14	0/1375	0.32	0/1847
27	U	0.16	0/1490	0.33	0/1999
28	V	0.18	0/3007	0.34	0/4062
29	W	0.16	0/787	0.29	0/1060
30	X	0.20	0/2921	0.35	0/3954
31	Y	0.19	0/1073	0.36	0/1444
32	Z	0.17	0/596	0.36	0/801

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.17	1/69407 (0.0%)	0.33	2/97994 (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
4	4	0	1
16	J	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	4	606	PRO	CG-CD	-5.26	1.32	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	4	606	PRO	N-CD-CG	-7.14	92.49	103.20
4	4	606	PRO	CA-N-CD	-6.49	102.92	112.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	4	264	ARG	Sidechain
16	J	72	LYS	Peptide

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	0	1754	0	1754	12	0
2	1	2098	0	2115	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	625	0	699	3	0
4	4	4585	0	4595	53	0
5	6	994	0	1004	7	0
6	7	3160	0	3171	42	0
7	A	18866	0	9583	83	0
8	B	1789	0	1781	7	0
9	C	1042	0	1033	8	0
10	D	1838	0	1858	8	0
11	E	858	0	871	7	0
12	F	1696	0	1749	14	0
13	G	2395	0	2364	15	0
14	H	1064	0	1089	12	0
15	I	1019	0	1059	3	0
16	J	829	0	874	3	0
17	K	847	0	875	12	0
18	L	1363	0	1442	5	0
19	M	913	0	943	4	0
20	N	859	0	922	2	0
21	O	1570	0	1533	4	0
22	P	774	0	801	5	0
23	Q	744	0	758	3	0
24	R	2382	0	2405	8	0
25	S	1100	0	1103	8	0
26	T	1344	0	1359	5	0
27	U	1468	0	1478	8	0
28	V	2946	0	2942	9	0
29	W	775	0	791	7	0
30	X	2849	0	2843	12	0
31	Y	1043	0	996	11	0
32	Z	581	0	590	3	0
33	7	8	0	0	0	0
34	7	27	0	22	2	0
35	A	4	0	0	0	0
36	A	28	0	0	0	0
36	B	1	0	0	0	0
36	X	1	0	0	0	0
37	A	44	0	26	1	0
38	O	1	0	0	0	0
39	P	4	0	0	0	0
39	T	4	0	0	0	0
40	X	31	0	12	0	0
41	X	28	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	66351	0	57452	311	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 3.

The worst 5 of 311 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)
7:A:1199:G:H21	7:A:1423:A:N6	1.62	0.97
7:A:1199:G:N2	7:A:1423:A:H62	1.64	0.96
6:7:30:LEU:HD21	6:7:415:LEU:HD21	1.53	0.91
7:A:1013:A:O2'	7:A:1014:A:O5'	1.94	0.84
7:A:1247:G:N2	7:A:1250:C:O2	2.14	0.80

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	0	209/218 (96%)	207 (99%)	2 (1%)	0	100	100
2	1	255/323 (79%)	252 (99%)	3 (1%)	0	100	100
3	3	68/199 (34%)	68 (100%)	0	0	100	100
4	4	558/689 (81%)	552 (99%)	6 (1%)	0	100	100
5	6	122/343 (36%)	119 (98%)	3 (2%)	0	100	100
6	7	396/456 (87%)	389 (98%)	7 (2%)	0	100	100
8	B	218/296 (74%)	217 (100%)	1 (0%)	0	100	100
9	C	122/167 (73%)	119 (98%)	3 (2%)	0	100	100
10	D	228/430 (53%)	224 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	E	106/125 (85%)	104 (98%)	2 (2%)	0	100	100
12	F	204/242 (84%)	202 (99%)	2 (1%)	0	100	100
13	G	288/396 (73%)	286 (99%)	1 (0%)	1 (0%)	36	54
14	H	126/201 (63%)	124 (98%)	2 (2%)	0	100	100
15	I	135/194 (70%)	130 (96%)	5 (4%)	0	100	100
16	J	105/138 (76%)	101 (96%)	4 (4%)	0	100	100
17	K	98/128 (77%)	97 (99%)	1 (1%)	0	100	100
18	L	159/257 (62%)	157 (99%)	2 (1%)	0	100	100
19	M	113/137 (82%)	113 (100%)	0	0	100	100
20	N	107/130 (82%)	106 (99%)	1 (1%)	0	100	100
21	O	188/258 (73%)	185 (98%)	3 (2%)	0	100	100
22	P	94/142 (66%)	94 (100%)	0	0	100	100
23	Q	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
24	R	289/360 (80%)	285 (99%)	4 (1%)	0	100	100
25	S	131/190 (69%)	130 (99%)	1 (1%)	0	100	100
26	T	162/173 (94%)	161 (99%)	1 (1%)	0	100	100
27	U	172/205 (84%)	172 (100%)	0	0	100	100
28	V	355/414 (86%)	348 (98%)	7 (2%)	0	100	100
29	W	96/187 (51%)	95 (99%)	1 (1%)	0	100	100
30	X	350/398 (88%)	342 (98%)	8 (2%)	0	100	100
31	Y	119/395 (30%)	118 (99%)	1 (1%)	0	100	100
32	Z	67/106 (63%)	65 (97%)	2 (3%)	0	100	100
All	All	5724/7984 (72%)	5645 (99%)	78 (1%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	G	249	THR

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	184/190 (97%)	184 (100%)	0	100	100
2	1	239/291 (82%)	239 (100%)	0	100	100
3	3	65/166 (39%)	65 (100%)	0	100	100
4	4	506/609 (83%)	506 (100%)	0	100	100
5	6	107/288 (37%)	107 (100%)	0	100	100
6	7	340/385 (88%)	340 (100%)	0	100	100
8	B	194/249 (78%)	194 (100%)	0	100	100
9	C	111/143 (78%)	111 (100%)	0	100	100
10	D	196/357 (55%)	196 (100%)	0	100	100
11	E	91/107 (85%)	91 (100%)	0	100	100
12	F	183/209 (88%)	183 (100%)	0	100	100
13	G	254/342 (74%)	254 (100%)	0	100	100
14	H	120/180 (67%)	120 (100%)	0	100	100
15	I	105/147 (71%)	105 (100%)	0	100	100
16	J	92/118 (78%)	92 (100%)	0	100	100
17	K	90/113 (80%)	90 (100%)	0	100	100
18	L	151/226 (67%)	151 (100%)	0	100	100
19	M	94/113 (83%)	94 (100%)	0	100	100
20	N	95/115 (83%)	95 (100%)	0	100	100
21	O	171/230 (74%)	171 (100%)	0	100	100
22	P	87/123 (71%)	87 (100%)	0	100	100
23	Q	78/79 (99%)	78 (100%)	0	100	100
24	R	261/318 (82%)	261 (100%)	0	100	100
25	S	115/164 (70%)	115 (100%)	0	100	100
26	T	151/157 (96%)	151 (100%)	0	100	100
27	U	150/174 (86%)	150 (100%)	0	100	100
28	V	323/364 (89%)	323 (100%)	0	100	100
29	W	85/158 (54%)	85 (100%)	0	100	100
30	X	311/351 (89%)	311 (100%)	0	100	100
31	Y	113/357 (32%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Z	63/95 (66%)	63 (100%)	0	100	100
All	All	5125/6918 (74%)	5125 (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 52 such sidechains are listed below:

Mol	Chain	Res	Type
15	I	129	GLN
24	R	76	GLN
30	X	367	GLN
15	I	146	HIS
21	O	169	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	A	882/955 (92%)	204 (23%)	4 (0%)

5 of 204 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	650	U
7	A	651	A
7	A	680	U
7	A	688	A
7	A	689	U

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1151	C
7	A	1219	U
7	A	1354	A
7	A	1434	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
7	MA6	A	1583	7	23,26,27	2.41	6 (26%)	33,38,41	3.67	14 (42%)
23	AYA	Q	2	23	6,7,8	1.28	1 (16%)	6,8,10	1.16	1 (16%)
7	MA6	A	1584	7	23,26,27	2.43	6 (26%)	33,38,41	3.72	13 (39%)

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
7	MA6	A	1583	7	-	2/11/29/30	0/3/3/3
23	AYA	Q	2	23	-	1/5/6/8	-
7	MA6	A	1584	7	-	0/11/29/30	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1584	MA6	C5-N7	7.15	1.52	1.39
7	A	1583	MA6	C5-N7	7.08	1.52	1.39
7	A	1584	MA6	C8-N9	-5.87	1.27	1.37
7	A	1583	MA6	C8-N9	-5.76	1.27	1.37
7	A	1584	MA6	C4-N9	-4.20	1.29	1.37

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	1584	MA6	C4-N9-C8	14.93	121.41	105.74
7	A	1583	MA6	C4-N9-C8	14.55	121.01	105.74
7	A	1583	MA6	C4-C5-N7	-6.16	103.54	110.58
7	A	1584	MA6	C4-C5-N7	-6.15	103.55	110.58
7	A	1584	MA6	N9-C8-N7	-5.55	106.06	113.94

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	Q	2	AYA	O-C-CA-CB
7	A	1583	MA6	O4'-C4'-C5'-O5'
7	A	1583	MA6	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 35 are monoatomic - leaving 7 for Mogul analysis.

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
37	NAD	A	1733	36	46,48,48	3.05	18 (39%)	64,73,73	2.70	17 (26%)
34	SAM	7	502	-	27,29,29	1.08	5 (18%)	34,42,42	1.99	8 (23%)
39	FES	T	201	19,26	0,4,4	-	-	-		
39	FES	P	201	22,11	0,4,4	-	-	-		
40	ATP	X	501	36	32,33,33	0.58	0	48,52,52	0.71	1 (2%)
33	SF4	7	501	6	0,12,12	-	-	-		
41	GDP	X	503	-	29,30,30	3.28	10 (34%)	45,47,47	2.32	14 (31%)

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
37	NAD	A	1733	36	-	1/30/62/62	0/5/5/5
34	SAM	7	502	-	-	4/17/33/33	0/3/3/3
39	FES	T	201	19,26	-	-	0/1/1/1
40	ATP	X	501	36	-	3/22/38/38	0/3/3/3
39	FES	P	201	22,11	-	-	0/1/1/1
33	SF4	7	501	6	-	-	0/6/5/5
41	GDP	X	503	-	-	7/16/32/32	0/3/3/3

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	X	503	GDP	O6-C6	9.76	1.42	1.23
41	X	503	GDP	C2-N1	7.67	1.56	1.37
41	X	503	GDP	PA-O3A	7.25	1.67	1.59
37	A	1733	NAD	C7N-N7N	7.23	1.46	1.33
37	A	1733	NAD	C5A-N7A	6.97	1.51	1.39

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	A	1733	NAD	C4A-N9A-C8A	13.45	119.86	105.74
41	X	503	GDP	N9-C8-N7	-6.82	100.75	113.40
41	X	503	GDP	C8-N7-C5	6.79	116.36	104.26
37	A	1733	NAD	N3A-C4A-N9A	6.66	138.50	127.17
37	A	1733	NAD	C5A-C4A-N3A	-6.27	118.09	126.72

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	7	502	SAM	CB-CG-SD-CE
40	X	501	ATP	PB-O3B-PG-O2G
41	X	503	GDP	PA-O3A-PB-O3B
41	X	503	GDP	C5'-O5'-PA-O3A
41	X	503	GDP	C5'-O5'-PA-O1A

There are no ring outliers.

3 monomers are involved in 4 short contacts:

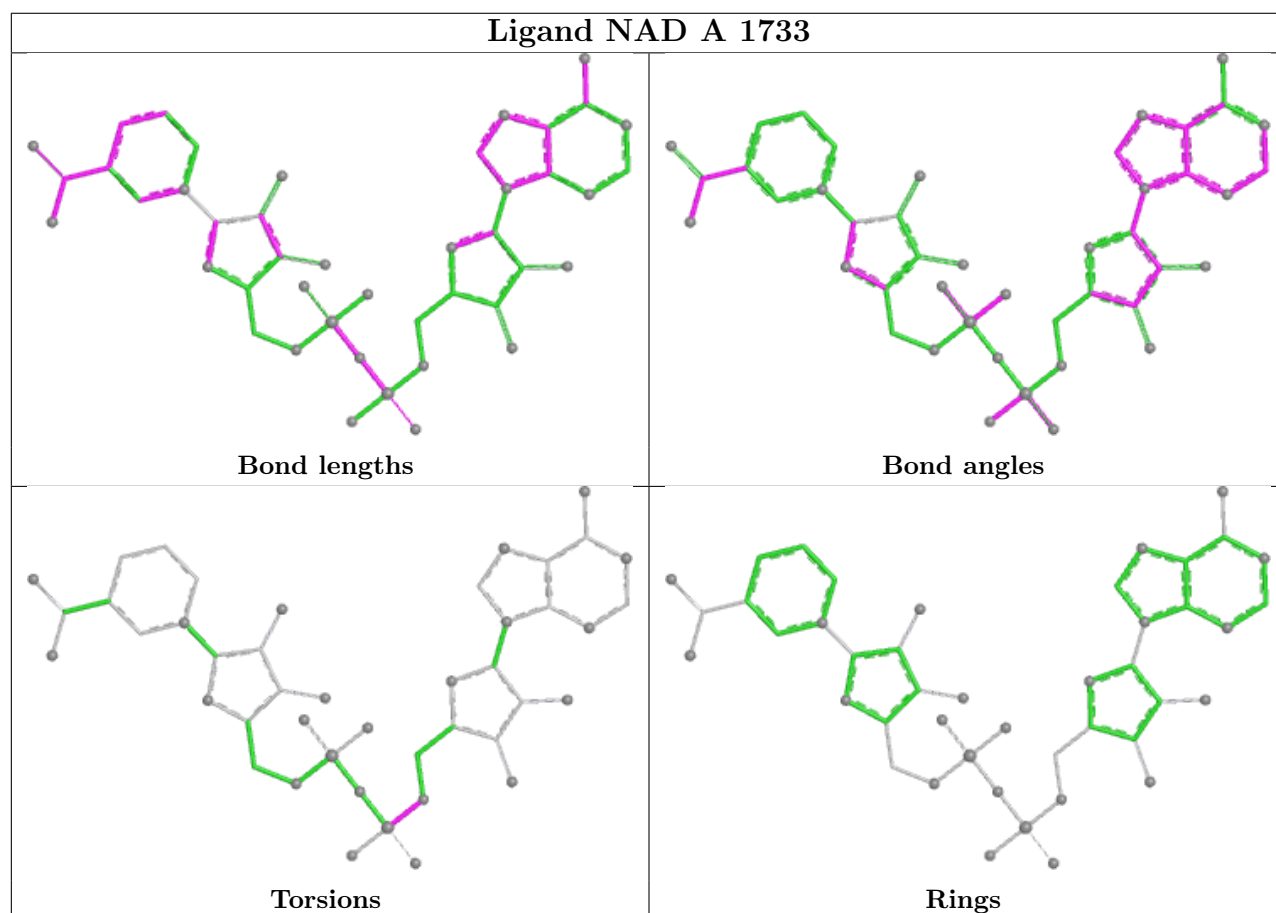
Mol	Chain	Res	Type	Clashes	Symm-Clashes
37	A	1733	NAD	1	0

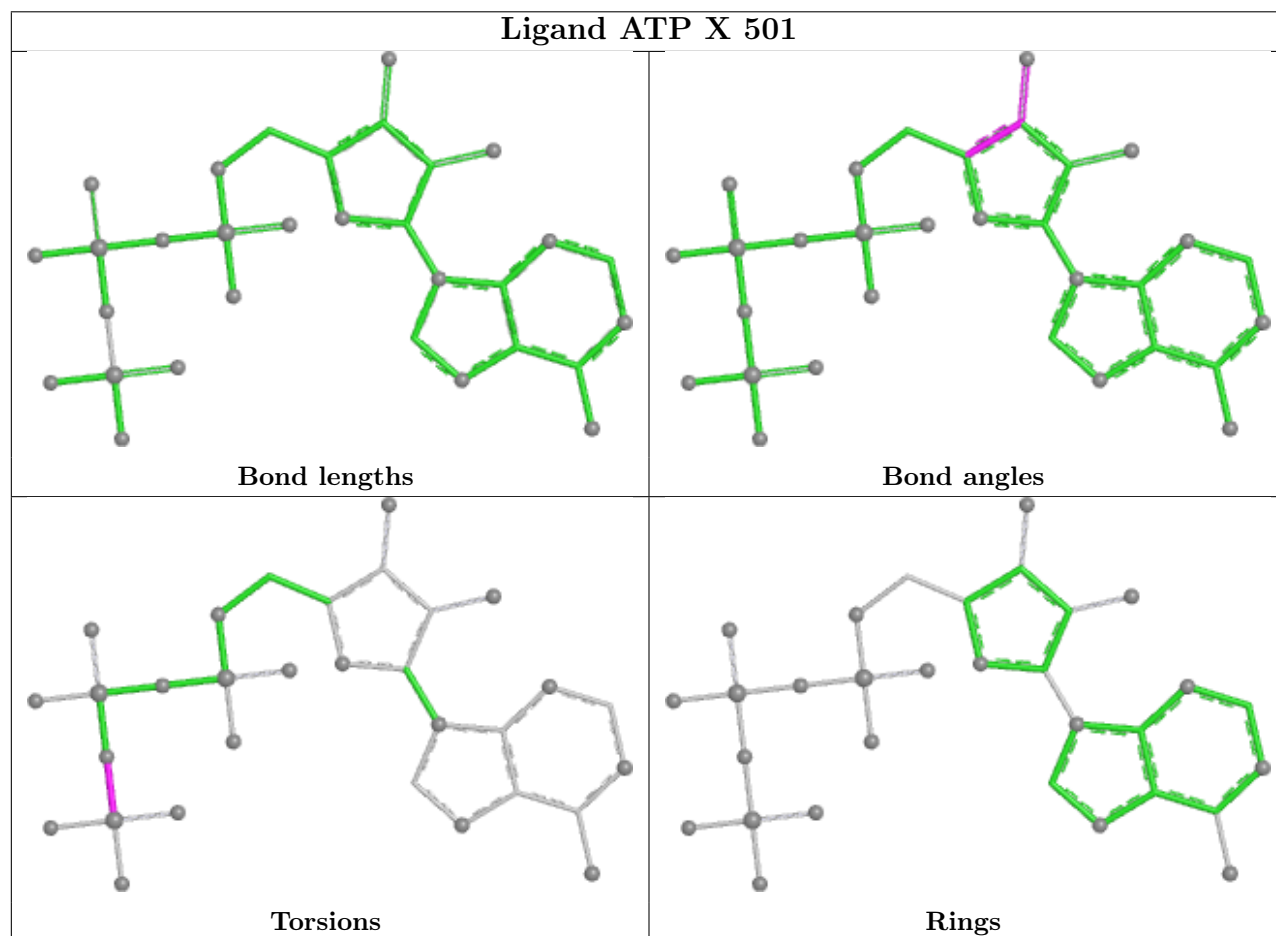
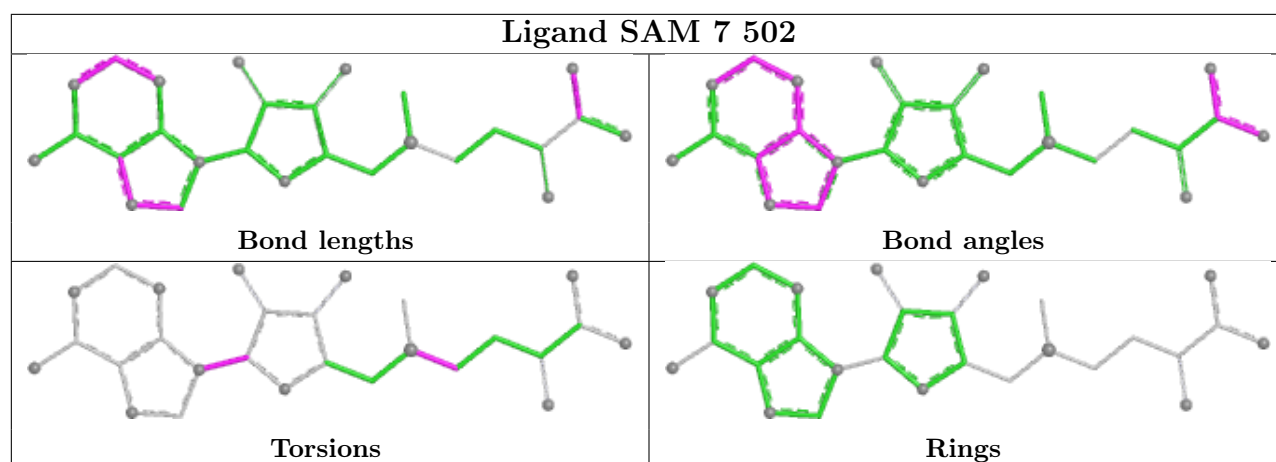
Continued on next page...

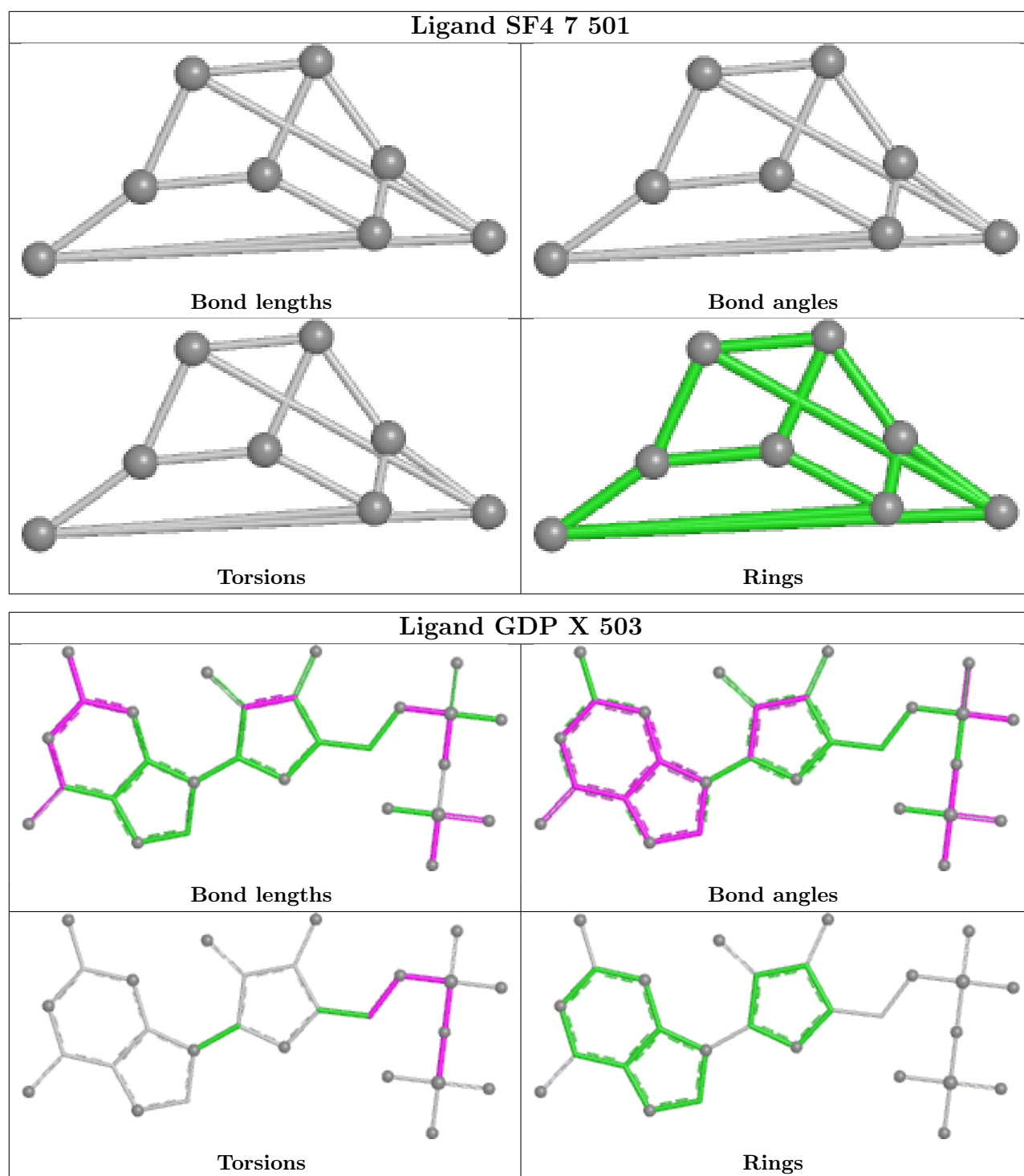
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
34	7	502	SAM	2	0
41	X	503	GDP	1	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.

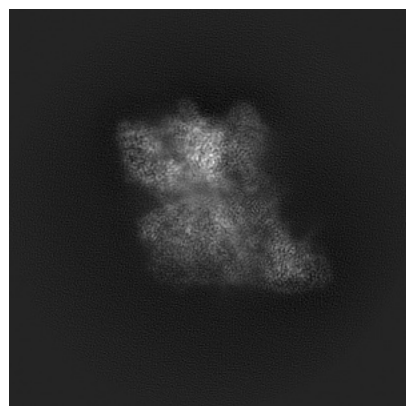
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26970. These allow visual inspection of the internal detail of the map and identification of artifacts.

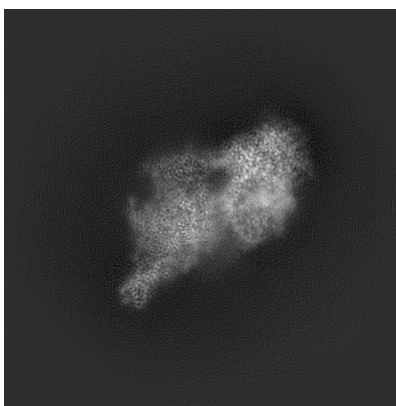
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

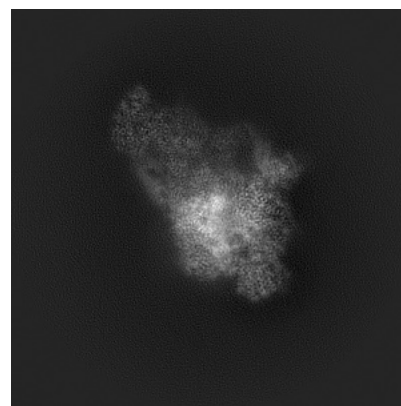
6.1.1 Primary map



X

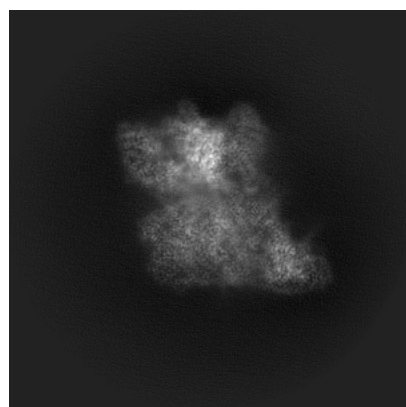


Y

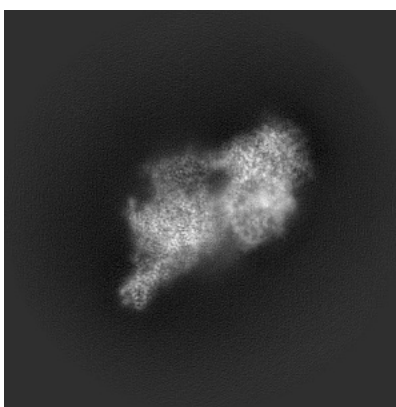


Z

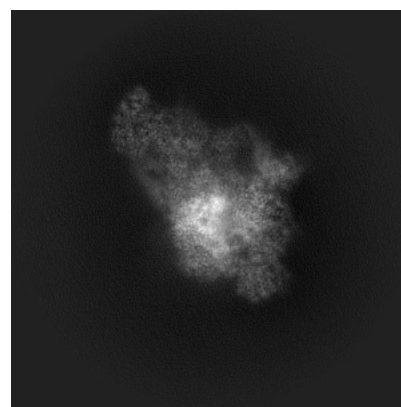
6.1.2 Raw map



X



Y

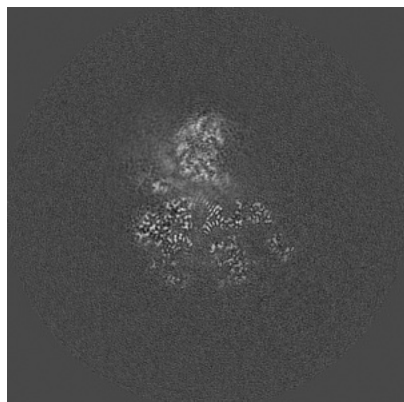


Z

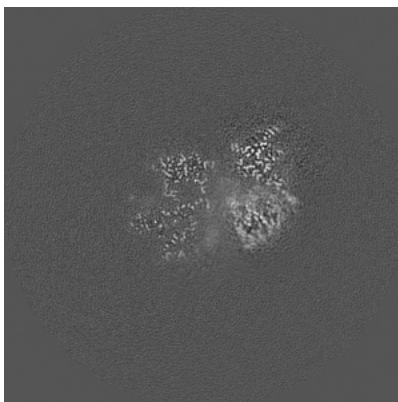
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

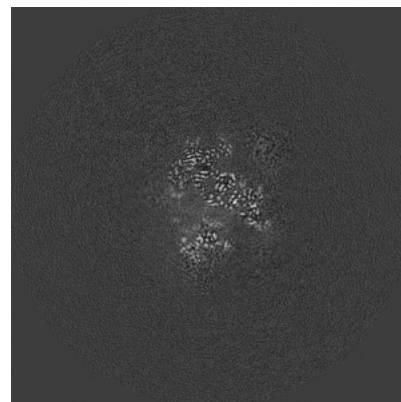
6.2.1 Primary map



X Index: 200

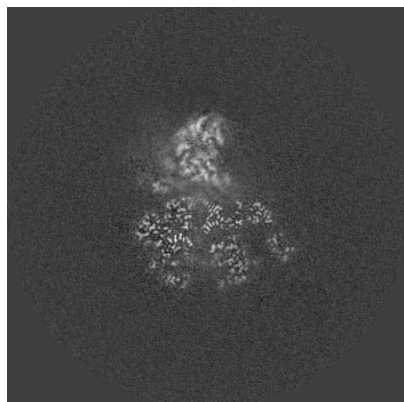


Y Index: 200

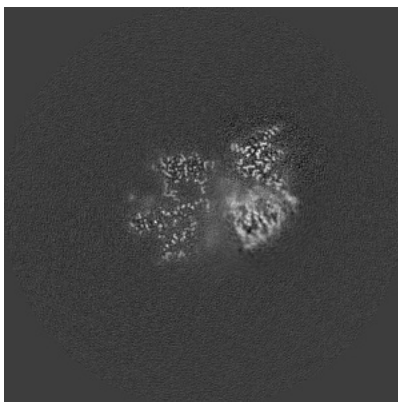


Z Index: 200

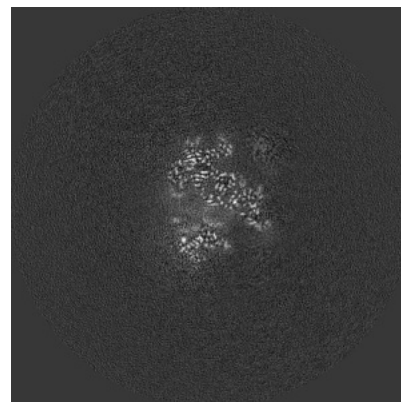
6.2.2 Raw map



X Index: 200



Y Index: 200

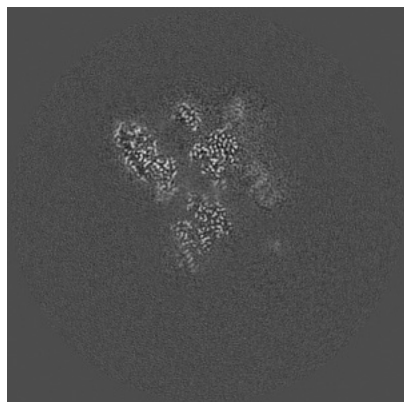


Z Index: 200

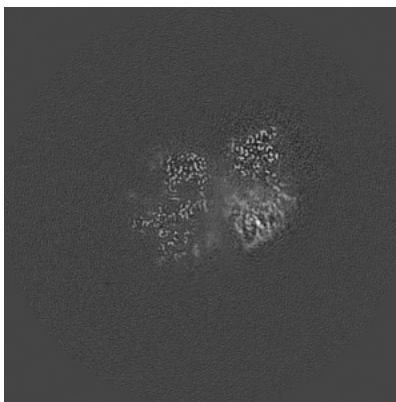
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

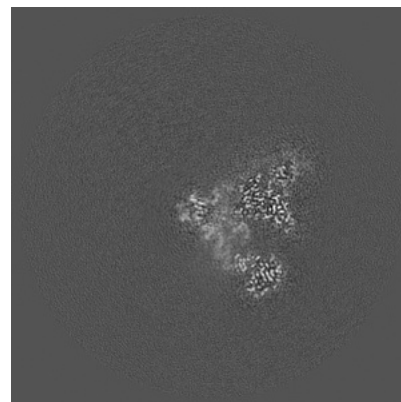
6.3.1 Primary map



X Index: 245

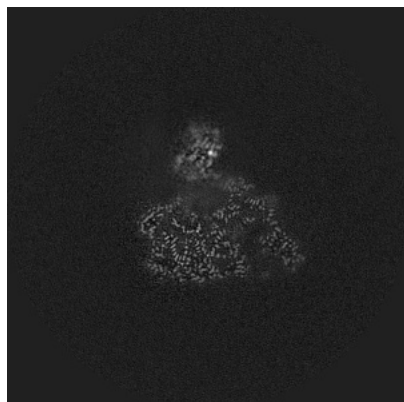


Y Index: 202

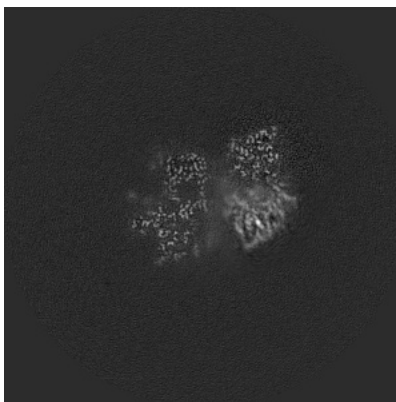


Z Index: 261

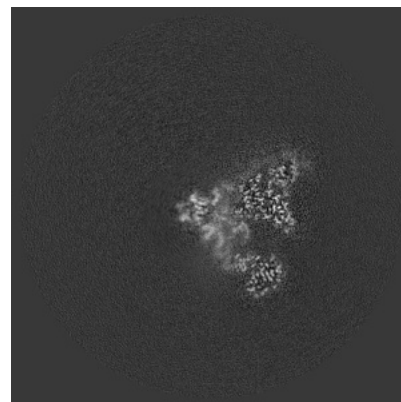
6.3.2 Raw map



X Index: 185



Y Index: 202

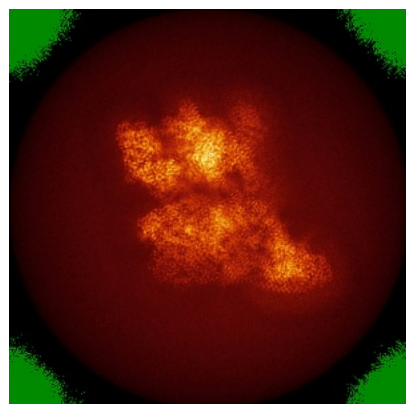


Z Index: 261

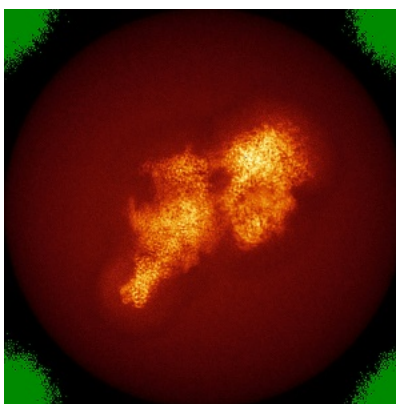
The images above show the largest variance slices of the map in three orthogonal directions.

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

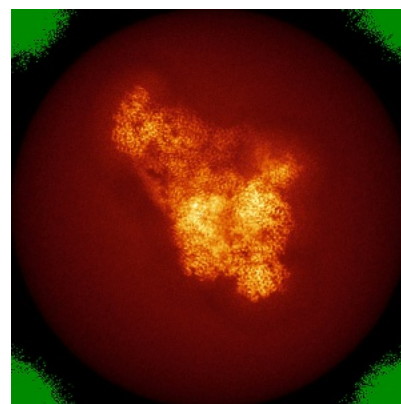
6.4.1 Primary map



X

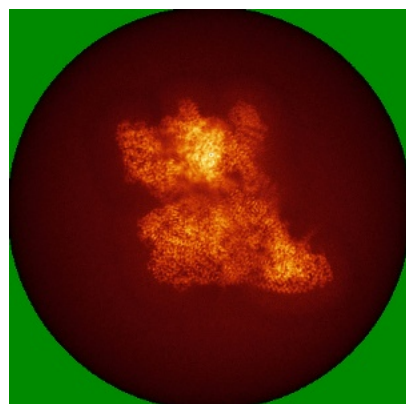


Y

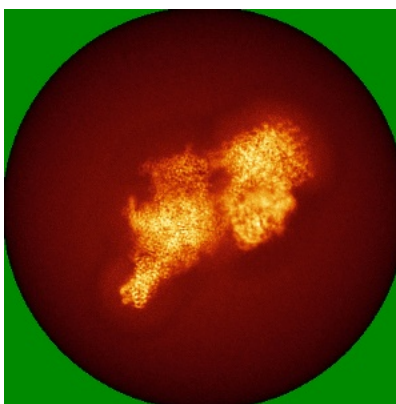


Z

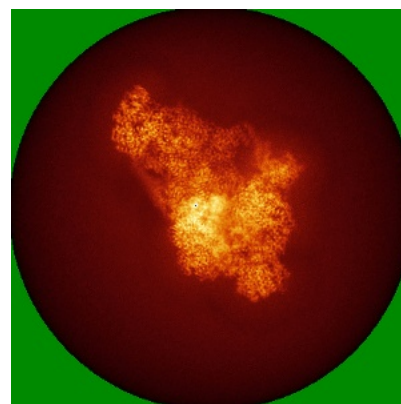
6.4.2 Raw map



X



Y

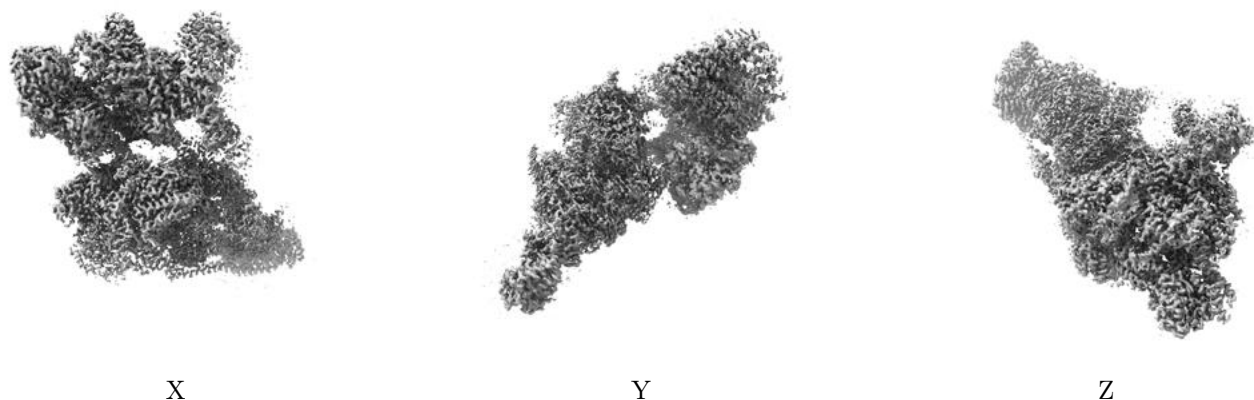


Z

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.

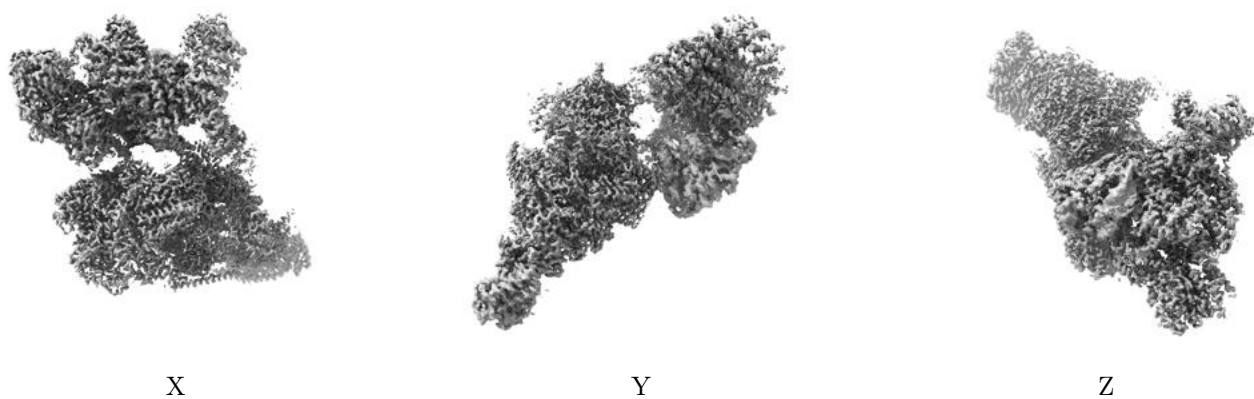
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 7.66. 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.

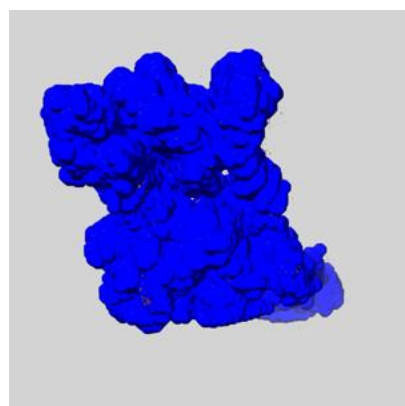
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

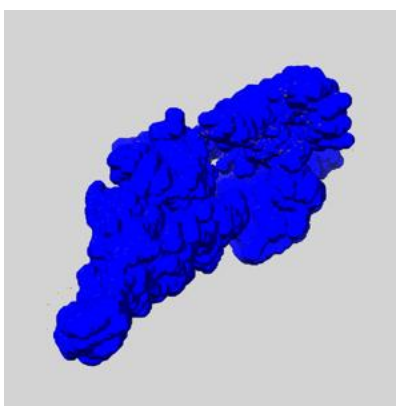
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

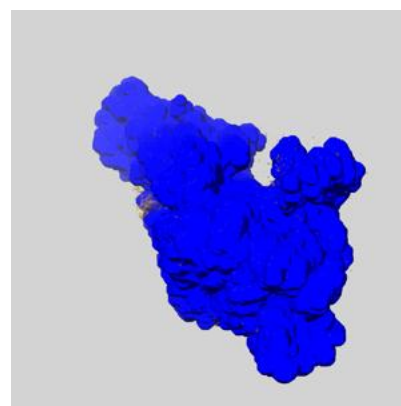
6.6.1 emd_26970_msk_1.map [i](#)



X



Y

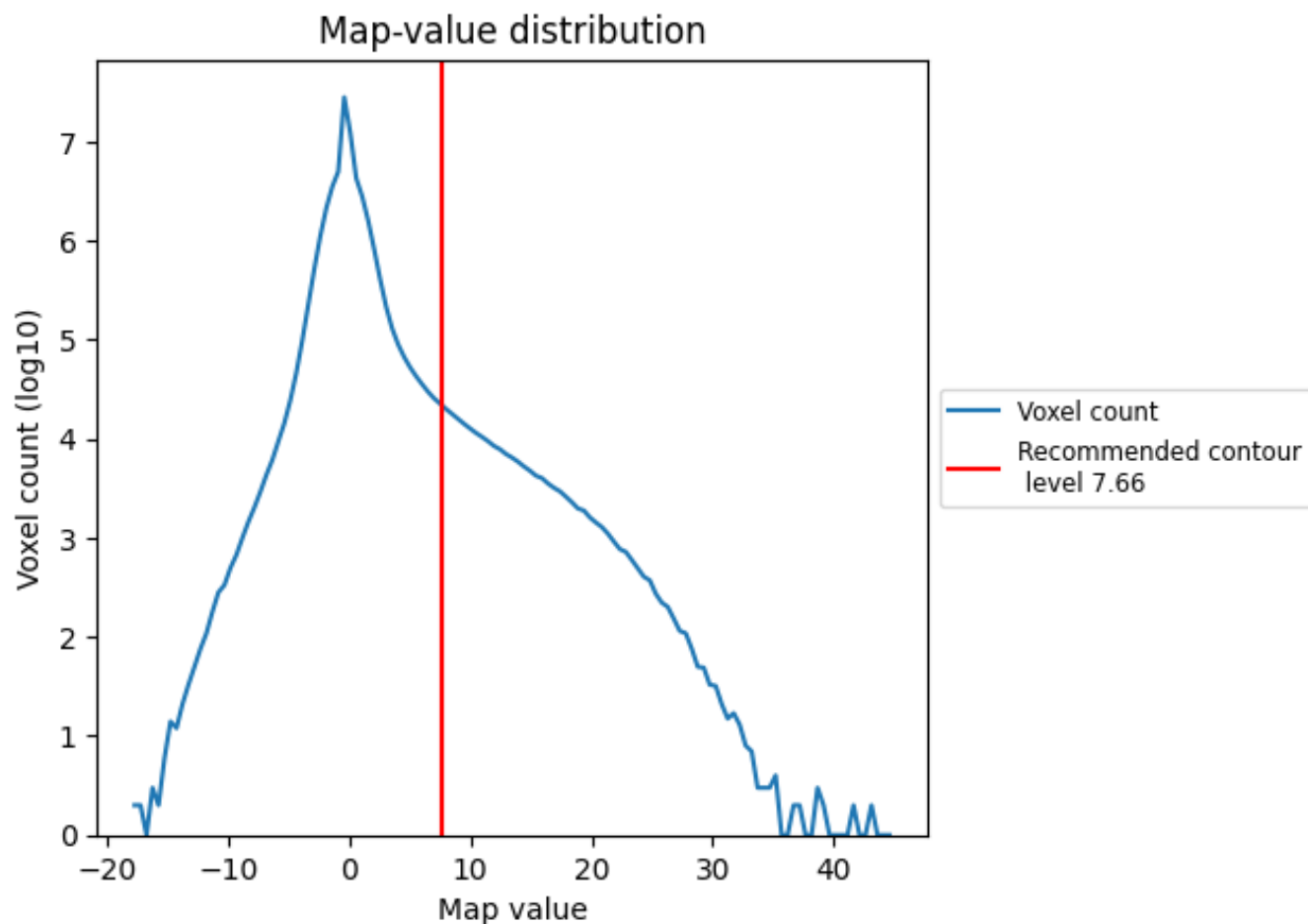


Z

7 Map analysis [i](#)

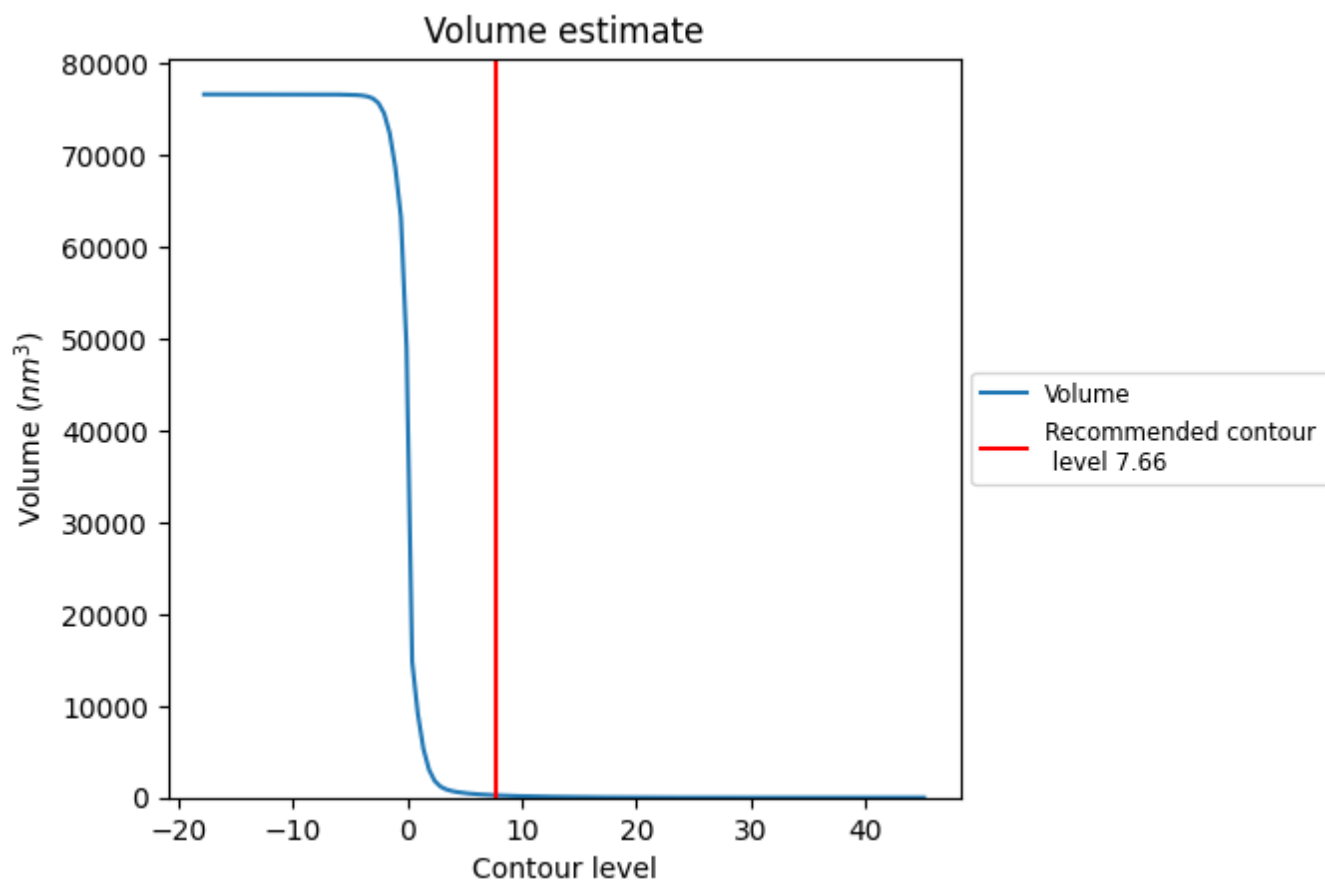
This section contains the results of statistical analysis of the map.

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.

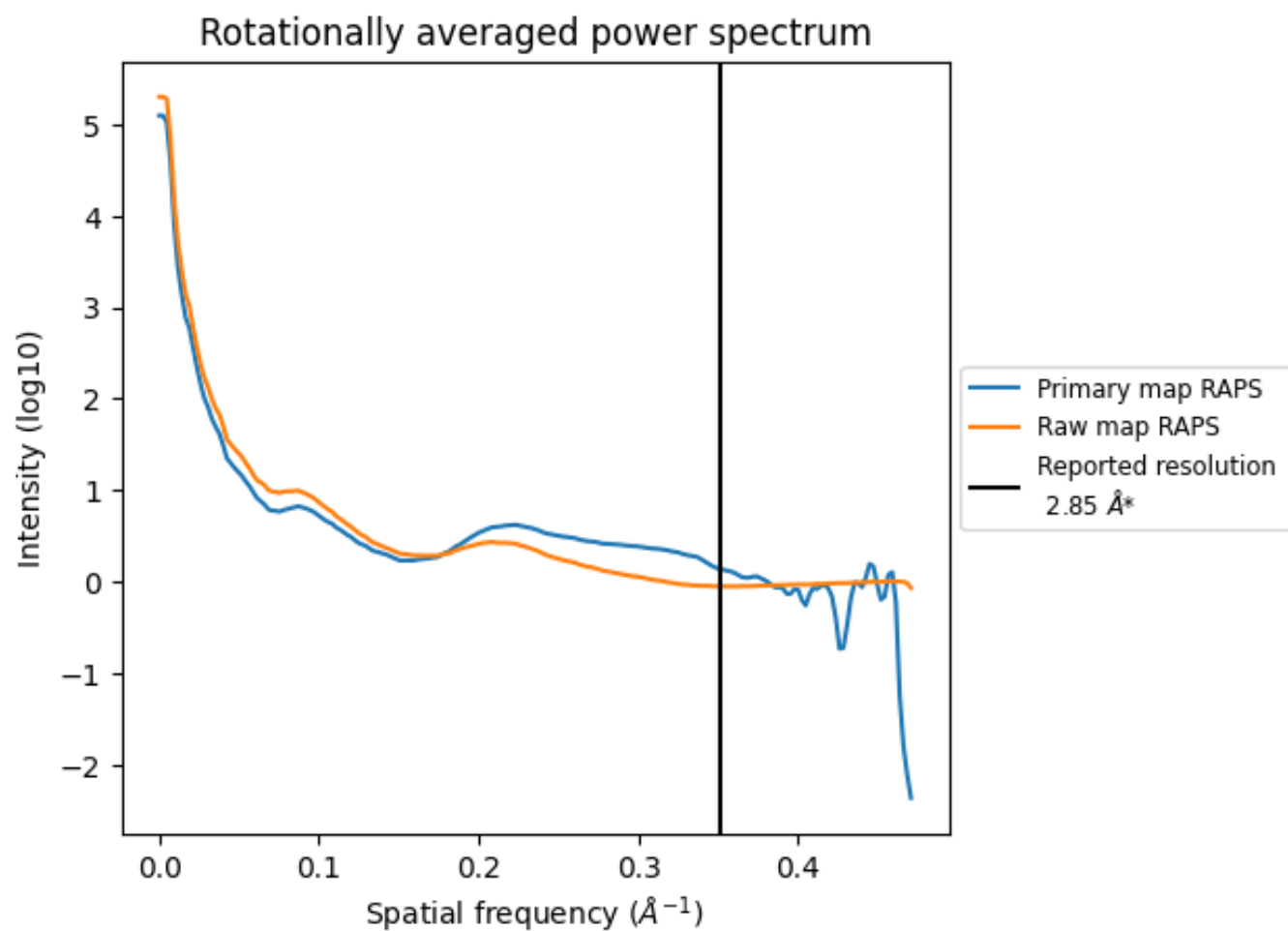
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 252 nm³; this corresponds to an approximate mass of 228 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 ⓘ

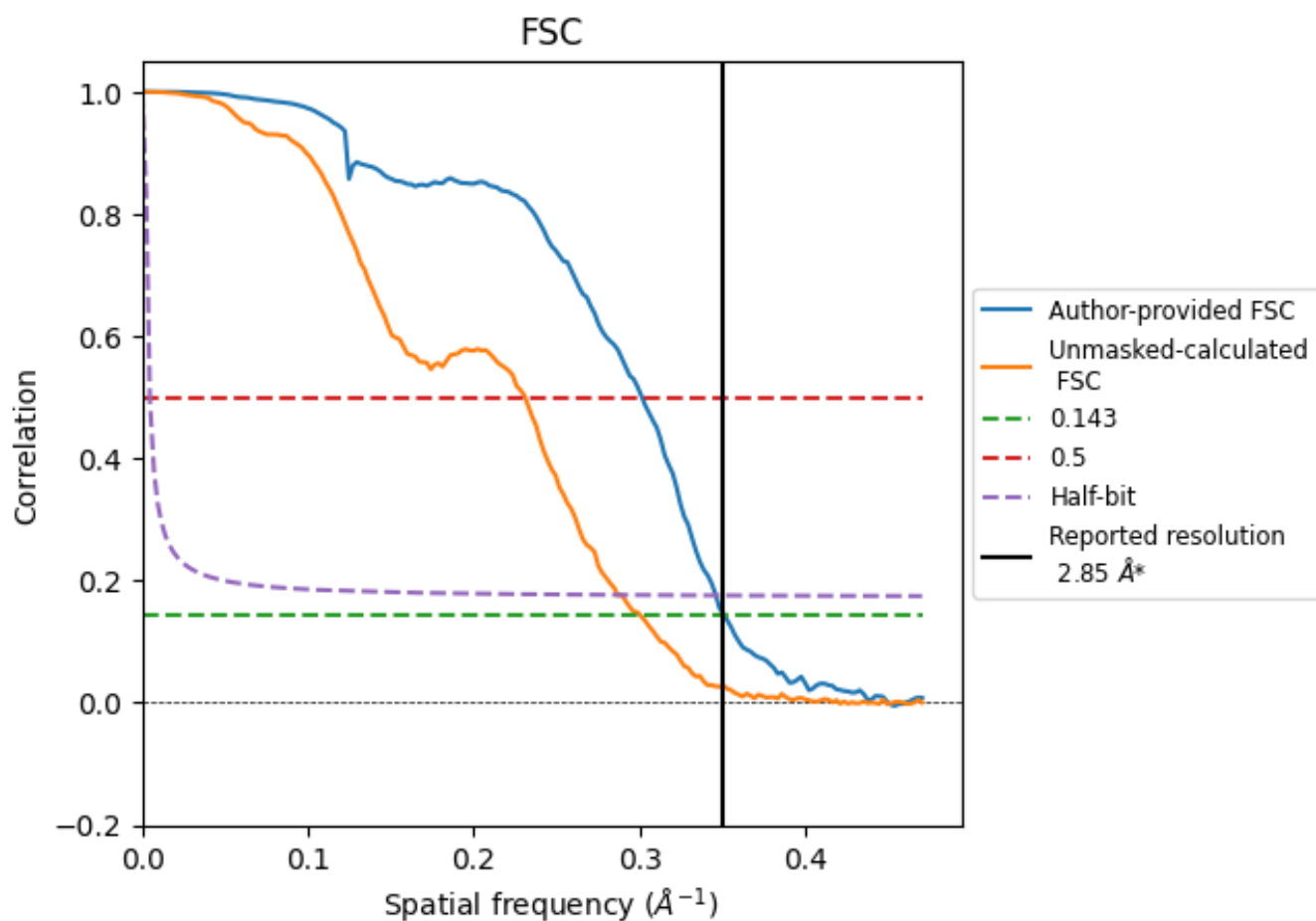


*Reported resolution corresponds to spatial frequency of 0.351 Å⁻¹

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 $0.351 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

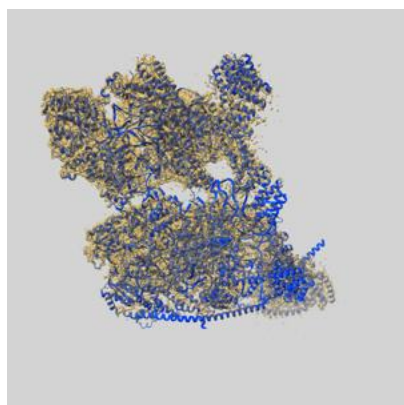
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.85	-	-
Author-provided FSC curve	2.85	3.31	2.89
Unmasked-calculated*	3.33	4.33	3.48

*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 3.33 differs from the reported value 2.85 by more than 10 %

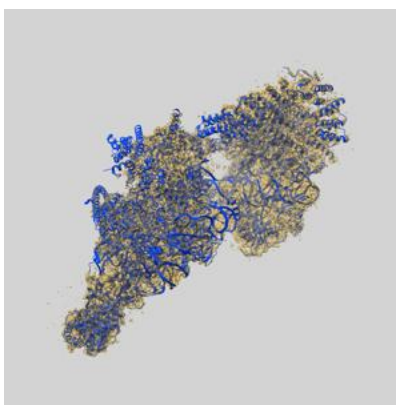
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26970 and PDB model 8CST. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

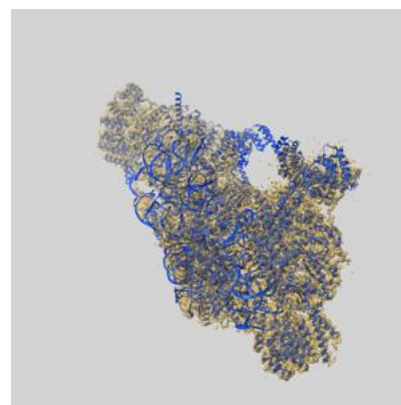
9.1 Map-model overlay [i](#)



X



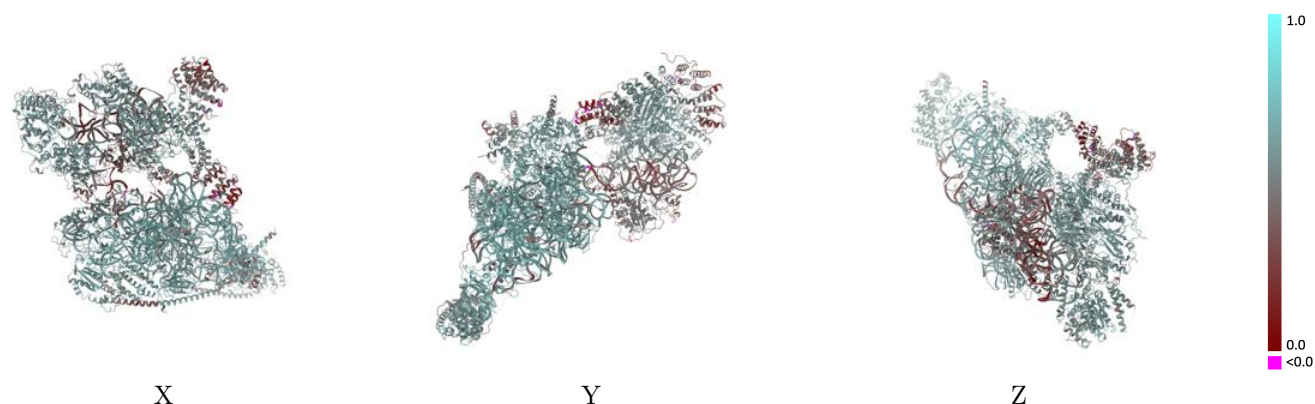
Y



Z

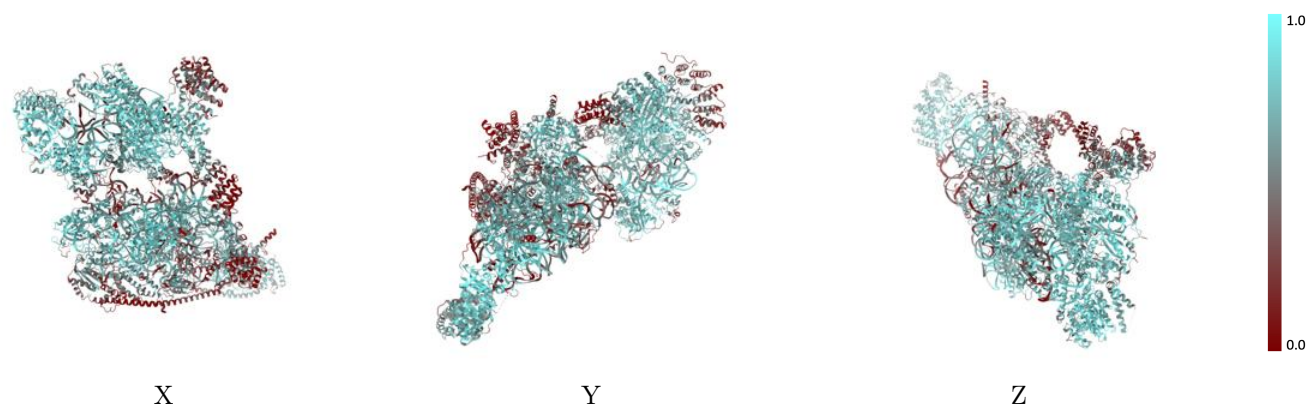
The images above show the 3D surface view of the map at the recommended contour level 7.66 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



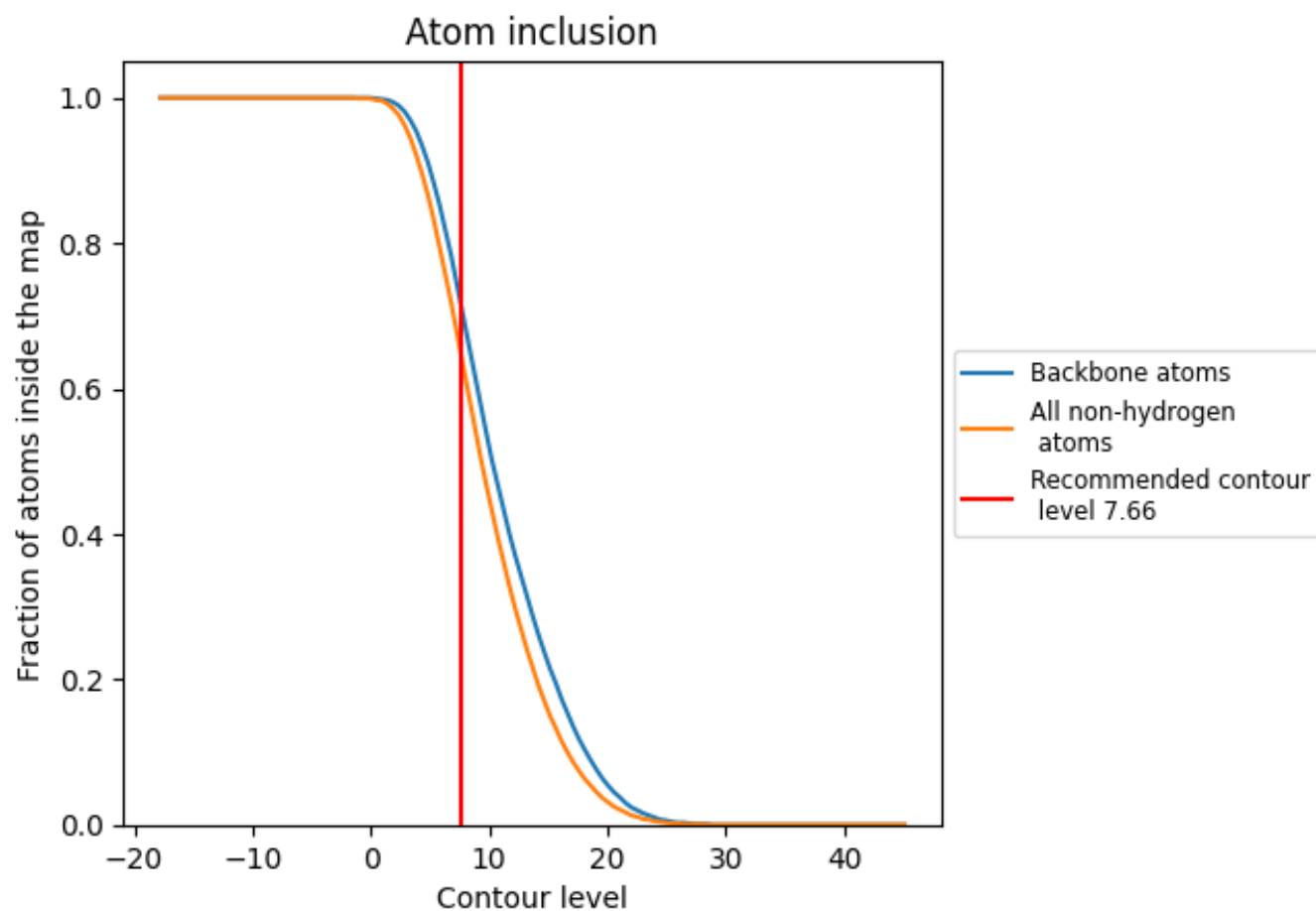
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7.66).

9.4 Atom inclusion [i](#)



At the recommended contour level, 71% of all backbone atoms, 64% 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 (7.66) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6440	 0.5550
0	 0.7030	 0.6050
1	 0.7630	 0.5690
3	 0.3780	 0.5800
4	 0.4770	 0.4270
6	 0.6880	 0.5540
7	 0.7130	 0.4110
A	 0.6910	 0.5370
B	 0.7960	 0.6320
C	 0.8210	 0.5830
D	 0.6010	 0.6190
E	 0.4750	 0.6170
F	 0.7000	 0.5180
G	 0.6670	 0.5520
H	 0.7730	 0.5800
I	 0.7720	 0.5800
J	 0.4130	 0.6050
K	 0.8010	 0.5820
L	 0.4980	 0.6210
M	 0.6660	 0.6480
N	 0.5570	 0.6430
O	 0.4980	 0.6250
P	 0.6050	 0.6310
Q	 0.7910	 0.6150
R	 0.3260	 0.5820
S	 0.5400	 0.5760
T	 0.5100	 0.6340
U	 0.3380	 0.5690
V	 0.7070	 0.5800
W	 0.6450	 0.6080
X	 0.8040	 0.5770
Y	 0.6700	 0.5370
Z	 0.7430	 0.5680

