



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:54 PM UTC

PDB ID : 7PD3 / pdb_00007pd3
EMDB ID : EMD-13329
Title : Structure of the human mitoribosomal large subunit in complex with NSUN4.MTERF4.GTPBP7 and MALSU1.L0R8F8.mt-ACP
Authors : Chandrasekaran, V.; Desai, N.; Burton, N.O.; Yang, H.; Price, J.; Miska, E.A.; Ramakrishnan, V.
Deposited on : 2021-08-04
Resolution : 3.40 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:

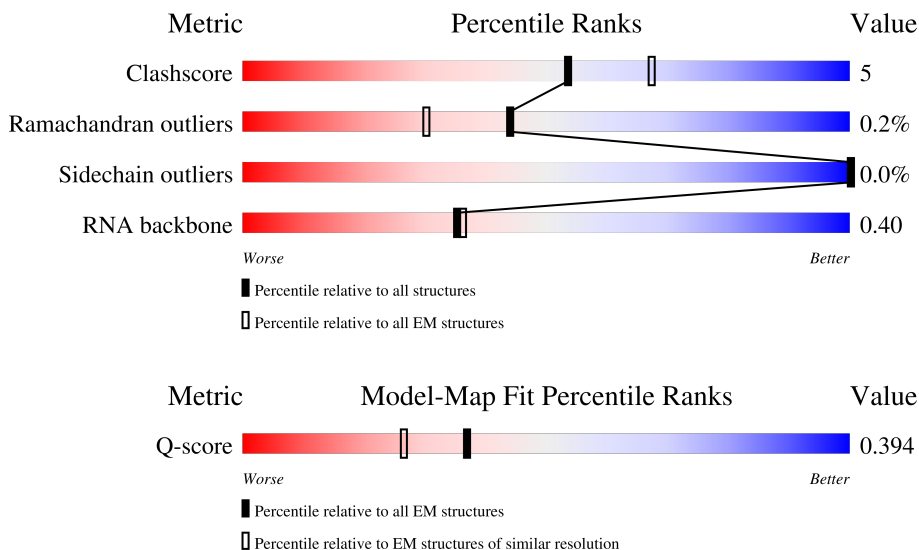
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	188	
2	1	65	
3	2	92	

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Mol	Chain	Length	Quality of chain
4	3	188	42% 9% 49%
5	4	103	28% 8% 64%
6	5	423	43% 79% 13% 7%
7	6	380	71% 73% 12% 15%
8	7	338	62% 71% 14% 15%
9	8	206	45% 39% 5% 54%
10	9	137	42% 75% 10% 15%
11	A	1737	15% 53% 27% 16%
12	B	69	91% 38% 48% 6% 7%
13	C	267	30% 27% 70%
13	H	267	25% 30% 5% 64%
14	D	305	21% 57% 13% 29%
15	E	348	19% 72% 15% 13%
16	F	311	33% 58% 22% 20%
17	G	261	56% 57% 5% 37%
18	J	192	73% 59% 14% 27%
19	K	178	17% 80% 19% 4%
20	L	145	26% 66% 13% 21%
21	M	296	44% 78% 19% 1%
22	N	251	39% 71% 9% 20%
23	O	175	17% 70% 17% 13%
24	P	180	59% 66% 13% 22%
25	Q	292	25% 61% 13% 26%
26	R	149	23% 85% 9% 6%
27	S	205	25% 64% 12% 24%

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Mol	Chain	Length	Quality of chain
28	T	206	15% 68% 13% 19%
29	U	153	41% 83% 16% ..
30	V	216	75% 80% 13% 6%
31	W	148	25% 64% 9% 26%
32	X	256	48% 86% 9% 5%
33	Y	250	23% 59% 11% 30%
34	Z	161	25% 61% 13% 25%
35	a	142	25% 53% 5% 42%
36	b	215	27% 60% 8% 31%
37	c	332	52% 70% 13% 17%
38	d	306	60% 57% 12% 31%
39	e	279	78% 62% 16% 22%
40	f	212	49% 48% 7% 45%
41	g	166	45% 66% 11% 22%
42	h	158	57% 53% 10% 37%
43	i	128	16% 60% 16% 24%
44	j	123	33% 54% 15% 31%
45	k	112	68% 57% 14% 29%
46	l	138	15% 16% 83%
47	m	128	35% 28% 7% 65%
48	o	102	35% 80% 9% 11%
49	p	206	59% 54% 7% 38%
50	q	222	77% 80% 9% 11%
51	r	196	22% 61% 14% 26%
52	s	439	31% 72% 12% 16%

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Mol	Chain	Length	Quality of chain
53	t	28	100%
54	u	234	45% 37% 10% 53%
55	v	70	99% 81% 17%
56	w	156	51% 44% 6% 49%
57	y	381	42% 56% 8% 36%
58	x	384	78% 74% 21% 5%
59	z	334	60% 83% 10% 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
11	OMG	A	2815	X	-	-	-
11	OMG	A	3040	X	-	-	-
63	SAM	x	401	X	-	X	-
64	GCP	z	401	X	-	-	-
64	GCP	z	402	X	-	-	-

2 Entry composition

There are 64 unique types of molecules in this entry. The entry contains 108075 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 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	108	880	545	172	157	6	0	0

- Molecule 2 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	1	52	433	278	83	70	2	0	0

- Molecule 3 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	45	367	227	81	58	1	0	0

- Molecule 4 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	95	831	539	162	127	3	0	0

- Molecule 5 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	37	333	212	71	47	3	0	0

- Molecule 6 is a protein called 39S ribosomal protein L37, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	392	3199	2067	558	563	11	0	0

- Molecule 7 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	324	2640	1694	470	468	8	0	0

- Molecule 8 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	7	287	2334	1495	397	425	17	0	0

- Molecule 9 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	8	94	759	477	137	143	2	0	0

- Molecule 10 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	9	117	947	614	163	168	2	0	0

- Molecule 11 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	A	1458	30973	13897	5598	10020	1458	0	0

- Molecule 12 is a RNA chain called mt-tRNAVal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	B	64	1348	607	237	441	63	0	0

- Molecule 13 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	C	80	648	421	111	112	4	0	0
13	H	95	784	498	152	134		0	0

- Molecule 14 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	D	217	Total	C	N	O	S	0	0
			1692	1046	344	294	8		

- Molecule 15 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	E	304	Total	C	N	O	S	0	0
			2396	1539	416	430	11		

- Molecule 16 is a protein called 39S ribosomal protein L4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	F	250	Total	C	N	O	S	0	0
			2013	1294	365	348	6		

- Molecule 17 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	G	165	Total	C	N	O	S	0	0
			1338	863	242	223	10		

- Molecule 18 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	J	140	Total	C	N	O	S	0	0
			1061	680	192	187	2		

- Molecule 19 is a protein called 39S ribosomal protein L13, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	K	177	Total	C	N	O	S	0	0
			1451	934	259	251	7		

- Molecule 20 is a protein called 39S ribosomal protein L14, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	L	115	Total	C	N	O	S	0	0
			889	559	171	154	5		

- Molecule 21 is a protein called 39S ribosomal protein L15, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	287	Total	C	N	O	S	0	0
			2305	1472	425	402	6		

- Molecule 22 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	200	Total	C	N	O	S	0	0
			1617	1035	298	275	9		

- Molecule 23 is a protein called 39S ribosomal protein L17, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	O	152	Total	C	N	O	S	0	0
			1245	784	239	215	7		

- Molecule 24 is a protein called 39S ribosomal protein L18, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	141	Total	C	N	O	S	0	0
			1148	719	221	203	5		

- Molecule 25 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	217	Total	C	N	O	S	0	0
			1805	1159	317	320	9		

- Molecule 26 is a protein called 39S ribosomal protein L20, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	140	Total	C	N	O	S	0	0
			1153	732	231	186	4		

- Molecule 27 is a protein called 39S ribosomal protein L21, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	156	Total	C	N	O	S	0	0
			1251	806	222	219	4		

- Molecule 28 is a protein called 39S ribosomal protein L22, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	166	Total	C	N	O	S	0	0
			1368	875	254	232	7		

- Molecule 29 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	152	Total	C	N	O	S	0	0
			1218	772	233	210	3		

- Molecule 30 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	202	Total	C	N	O	S	0	0
			1624	1032	291	293	8		

- Molecule 31 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	109	Total	C	N	O	S	0	0
			859	552	162	142	3		

- Molecule 32 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	243	Total	C	N	O	S	0	0
			2035	1317	351	362	5		

- Molecule 33 is a protein called 39S ribosomal protein L47, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	176	Total	C	N	O	S	0	0
			1517	970	291	252	4		

- Molecule 34 is a protein called 39S ribosomal protein L30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	120	Total	C	N	O	S	0	0
			978	626	183	166	3		

- Molecule 35 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	82	Total	C	N	O	S	0	0
			686	434	124	123	5		

- Molecule 36 is a protein called 39S ribosomal protein L43, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	148	Total	C	N	O	S	0	0
			1178	733	229	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	275	Total	C	N	O	S	0	0
			2217	1415	383	410	9		

- Molecule 38 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	211	Total	C	N	O	S	0	0
			1741	1123	299	309	10		

- Molecule 39 is a protein called 39S ribosomal protein L46, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	217	Total	C	N	O	S	0	0
			1762	1124	310	323	5		

- Molecule 40 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	116	Total	C	N	O	S	0	0
			915	585	152	175	3		

- Molecule 41 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	129	Total	C	N	O	S	0	0
			1067	690	185	190	2		

- Molecule 42 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	100	Total	C	N	O	S	0	0
			827	524	146	155	2		

- Molecule 43 is a protein called 39S ribosomal protein L51, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	97	Total	C	N	O	S	0	0
			827	532	165	126	4		

- Molecule 44 is a protein called 39S ribosomal protein L52, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	85	Total	C	N	O	S	0	0
			684	423	133	126	2		

- Molecule 45 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	80	Total	C	N	O	S	0	0
			627	392	116	114	5		

- Molecule 46 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	l	23	Total	C	N	O	0	0
			221	137	52	32		

- Molecule 47 is a protein called 39S ribosomal protein L55, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	45	Total	C	N	O	S	0	0
			372	232	76	62	2		

- Molecule 48 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	91	Total	C	N	O	S	0	0
			771	487	156	125	3		

- Molecule 49 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	p	127	1058	661	201	192	4	0	0

- Molecule 50 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	q	198	1625	1006	317	297	5	0	0

- Molecule 51 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	r	146	1203	764	232	199	8	0	0

- Molecule 52 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	s	370	3036	1946	542	534	14	0	0

- Molecule 53 is a protein called mL65.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
53	t	28	140	84	28	28	0	0

- Molecule 54 is a protein called Mitochondrial assembly of ribosomal large subunit protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	u	111	927	595	155	167	10	0	0

- Molecule 55 is a protein called MIEF1 upstream open reading frame protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
55	v	69	588	372	116	100	0	0

- Molecule 56 is a protein called Acyl carrier protein, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	w	79	638	410	95	128	5	0	0

- Molecule 57 is a protein called Transcription termination factor 4, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	y	245	1989	1269	344	364	12	0	0

- Molecule 58 is a protein called 5-methylcytosine rRNA methyltransferase NSUN4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	x	366	2889	1834	511	527	17	0	0

- Molecule 59 is a protein called Mitochondrial ribosome-associated GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	z	311	2443	1549	445	433	16	0	0

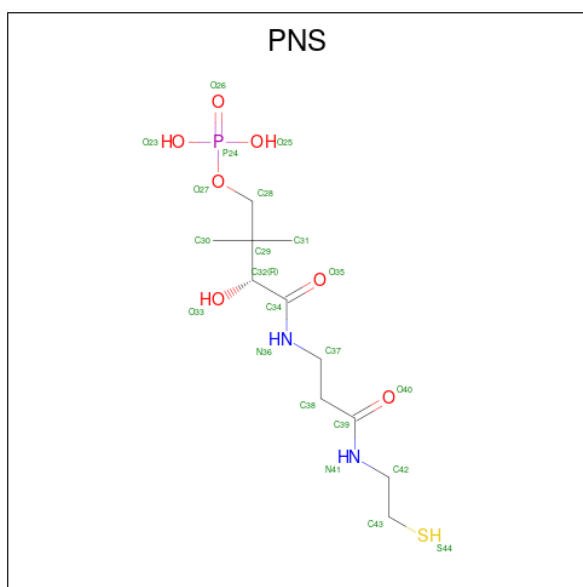
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
60	0	1	1	1	0
60	4	1	1	1	0

- Molecule 61 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

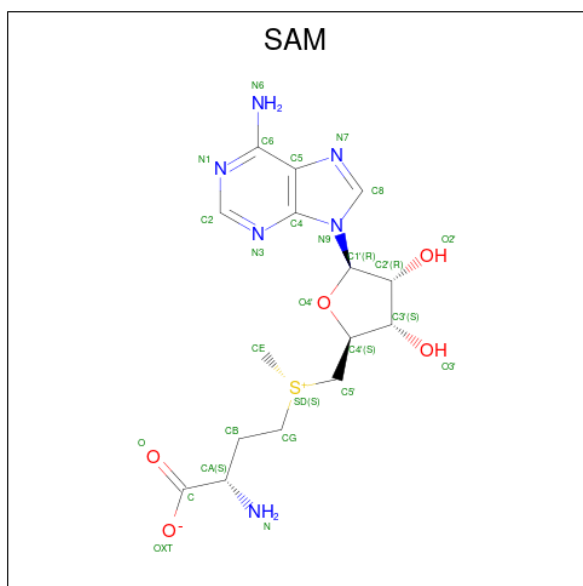
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
61	A	89	89	89	0
61	E	1	1	1	0
61	o	1	1	1	0

- Molecule 62 is 4'-PHOSPHOPANTETHEINE (CCD ID: PNS) (formula: C₁₁H₂₃N₂O₇PS).



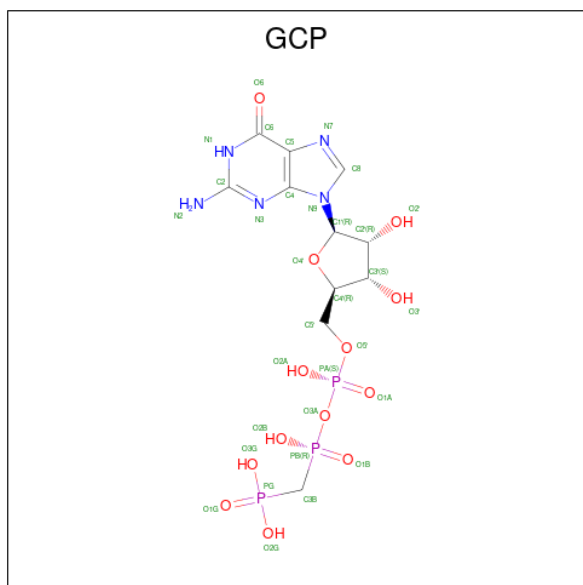
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	N	O	P		S
62	v	1	21	11	2	6	1	1	0

- Molecule 63 is S-ADENOSYLMETHIONINE (CCD ID: SAM) (formula: $C_{15}H_{22}N_6O_5S$).

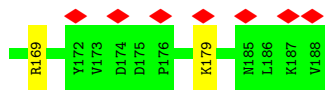


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
63	x	1	27	15	6	5	1	0

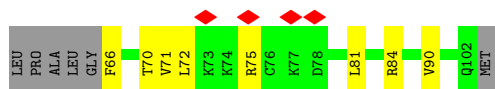
- Molecule 64 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).



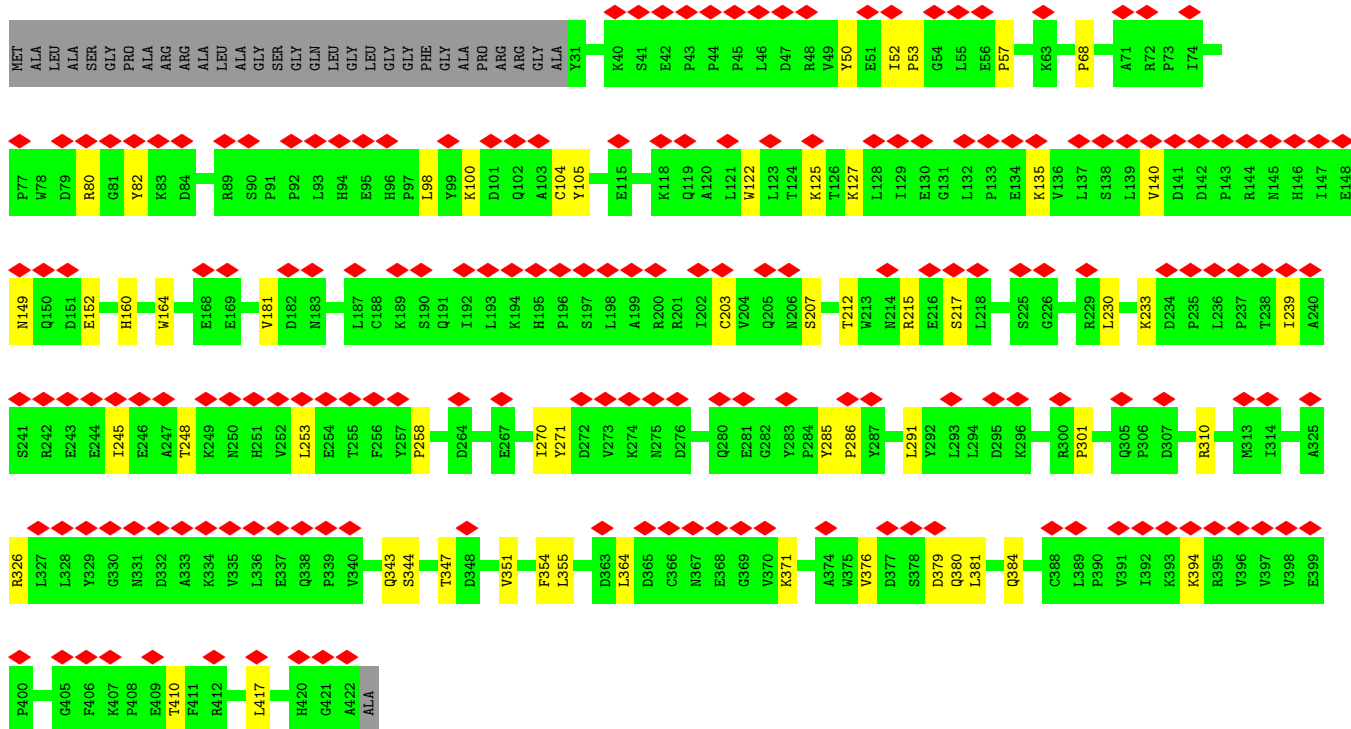
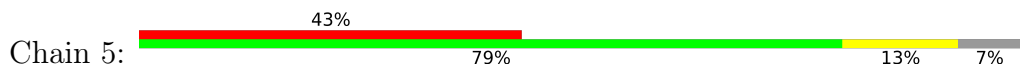
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
64	z	1	32	11	5	13	3	0
64	z	1	32	11	5	13	3	0



• Molecule 5: 39S ribosomal protein L36, mitochondrial

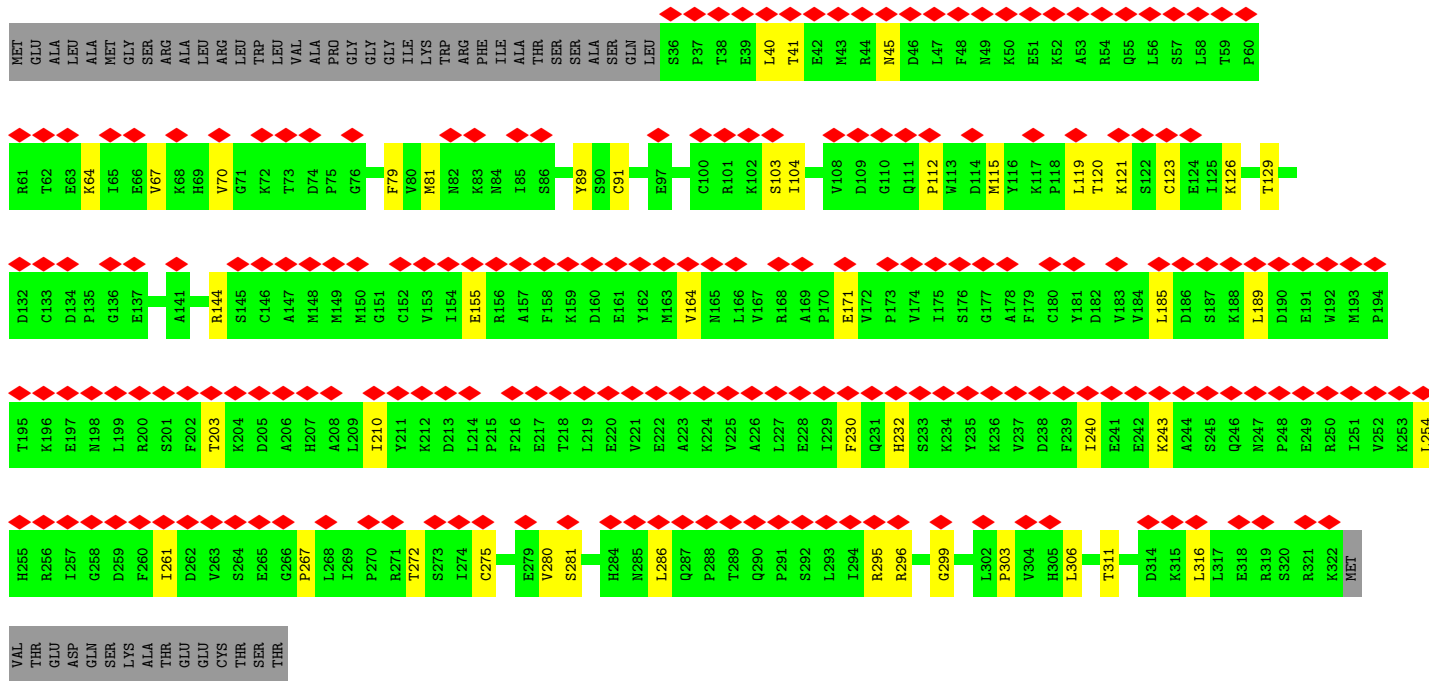


• Molecule 6: 39S ribosomal protein L37, mitochondrial

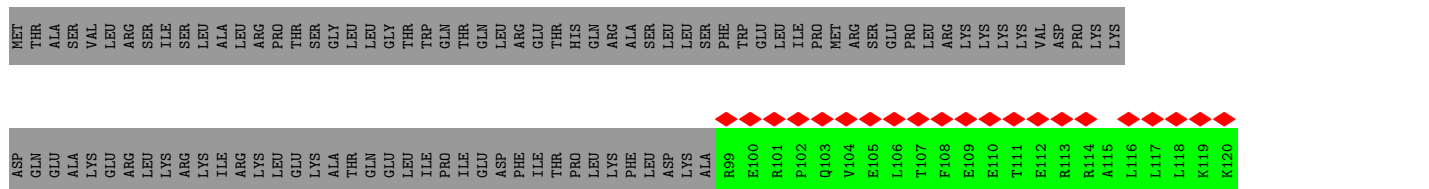
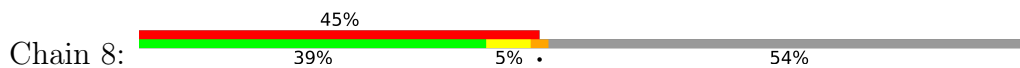


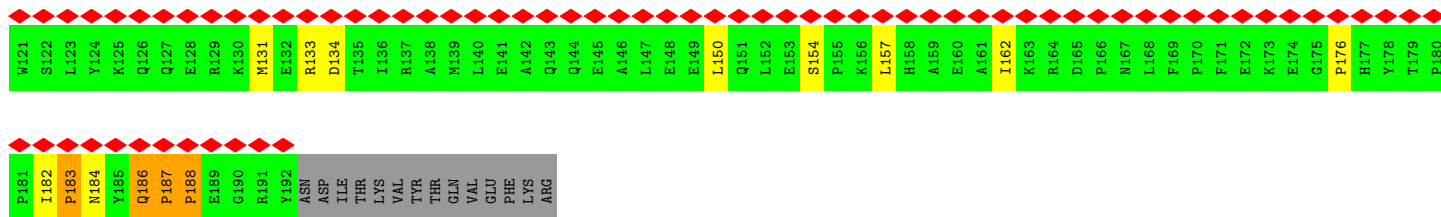


• Molecule 8: 39S ribosomal protein L39, mitochondrial

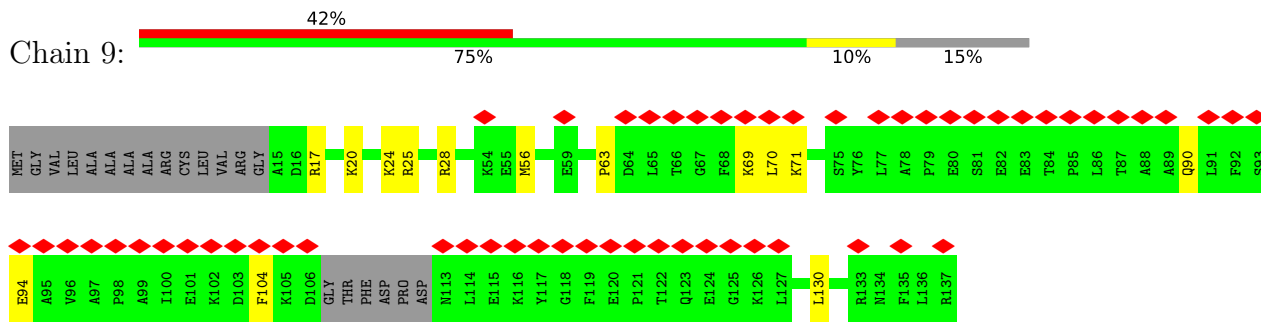


• Molecule 9: 39S ribosomal protein L40, mitochondrial

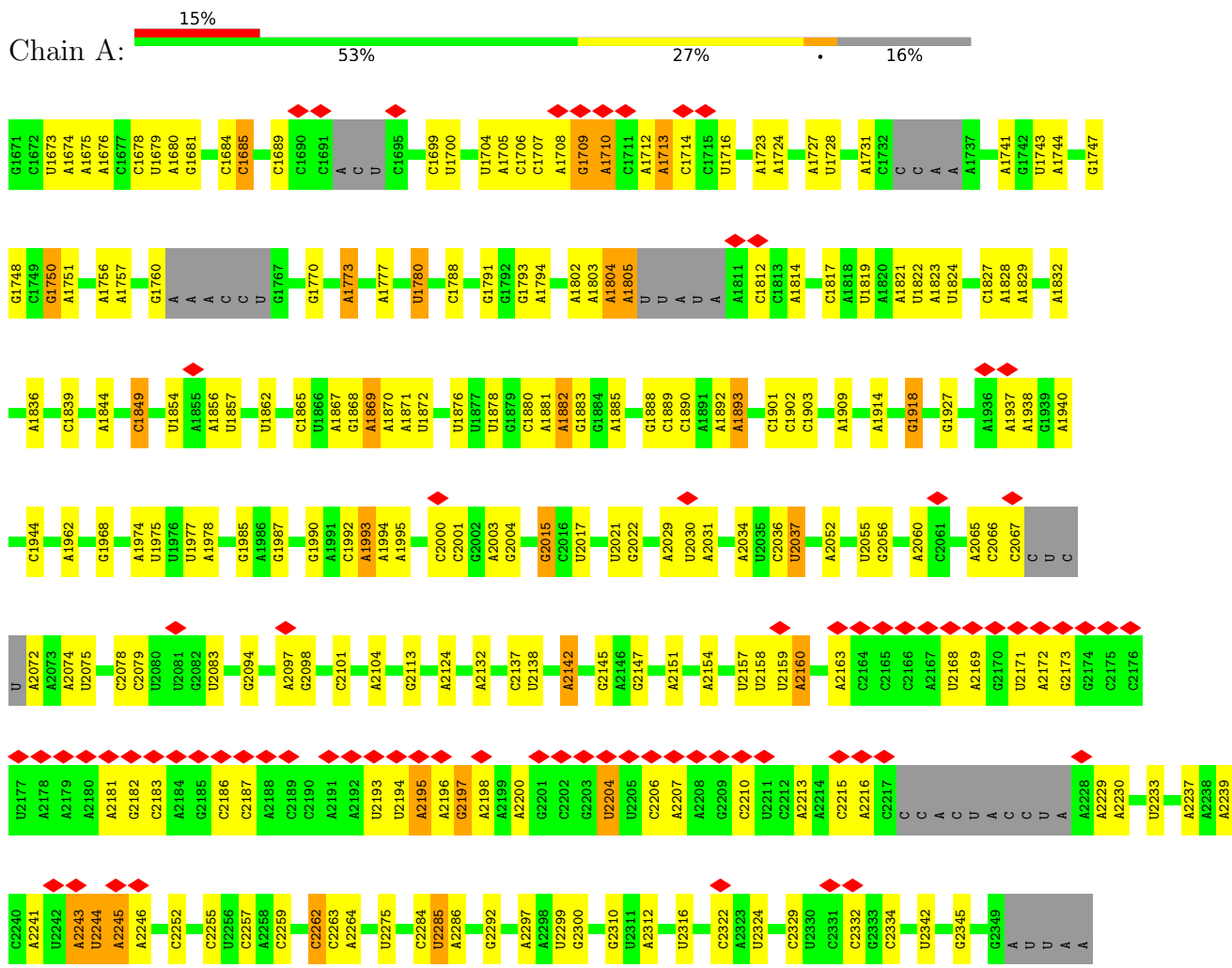


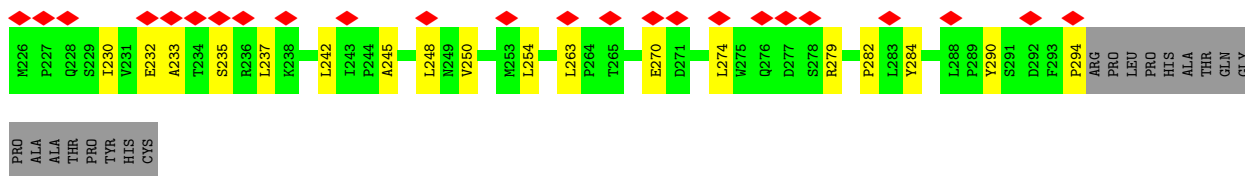


• Molecule 10: 39S ribosomal protein L41, mitochondrial

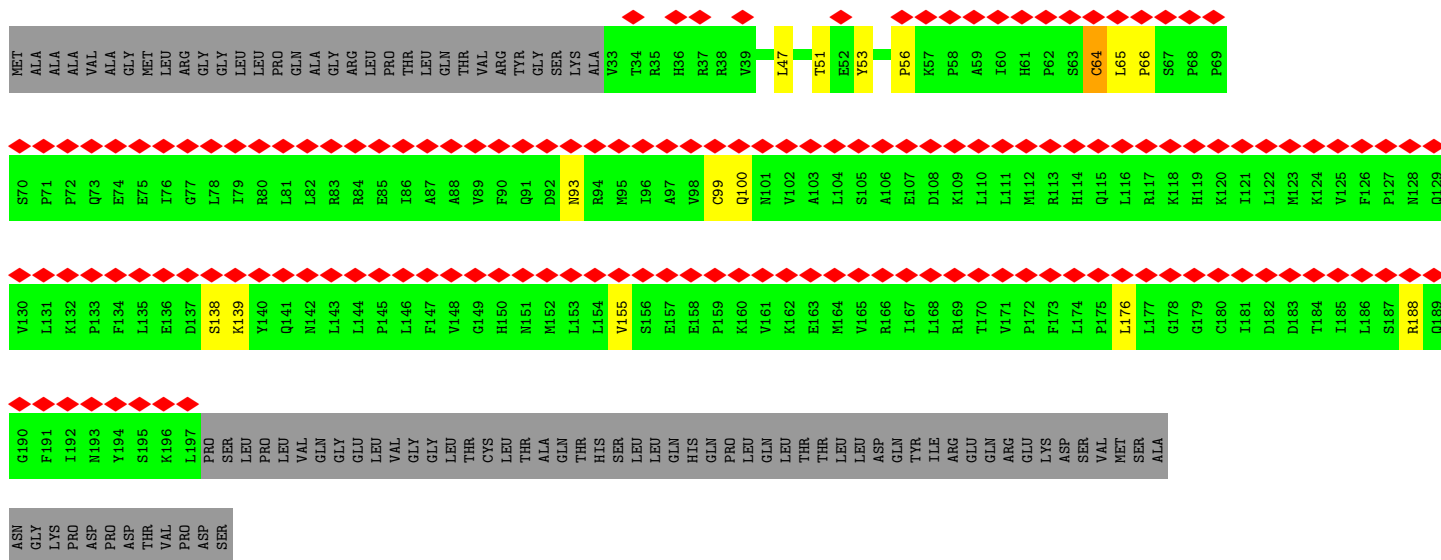


• Molecule 11: 16S rRNA

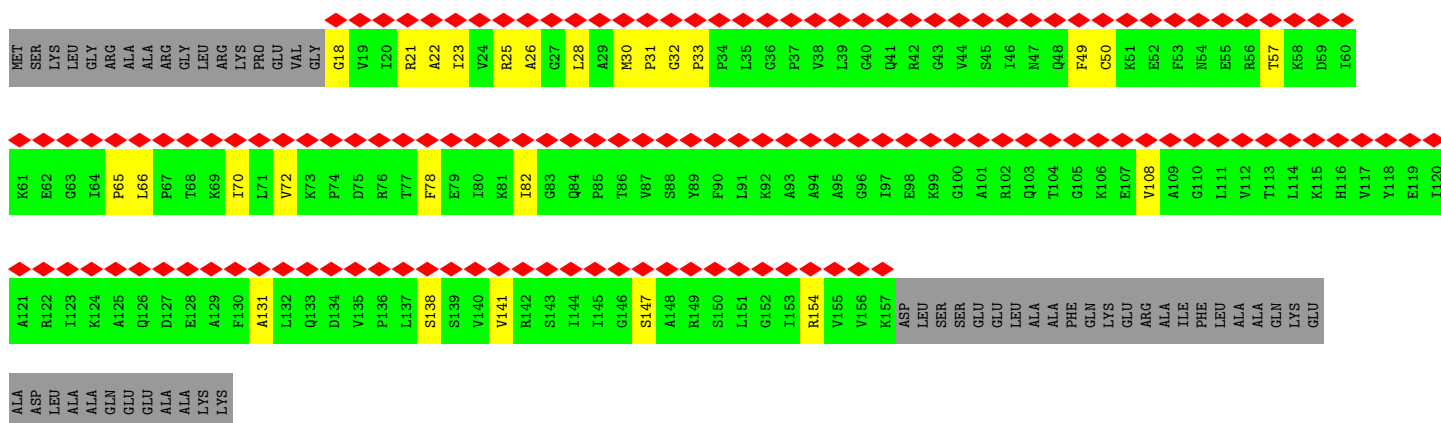




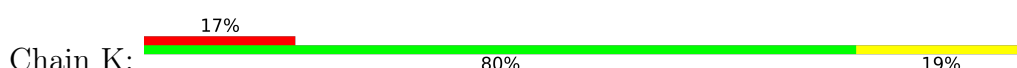
• Molecule 17: 39S ribosomal protein L10, mitochondrial

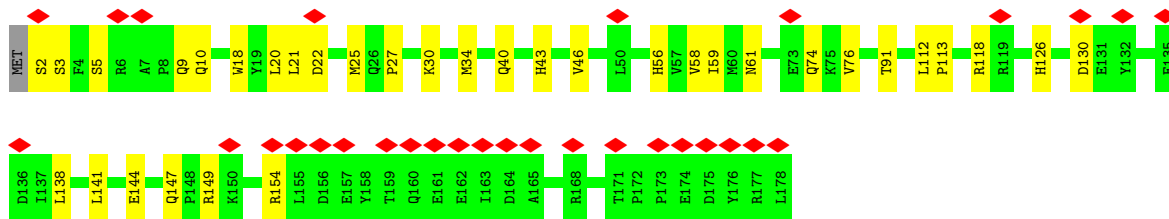


• Molecule 18: 39S ribosomal protein L11, mitochondrial

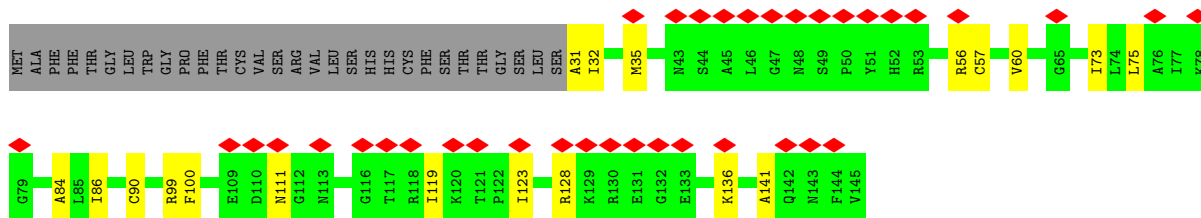


• Molecule 19: 39S ribosomal protein L13, mitochondrial

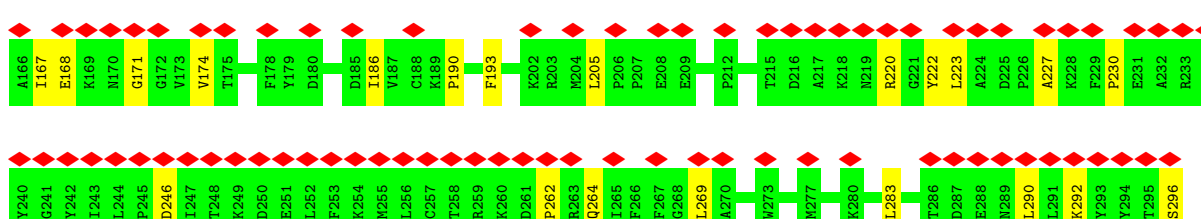
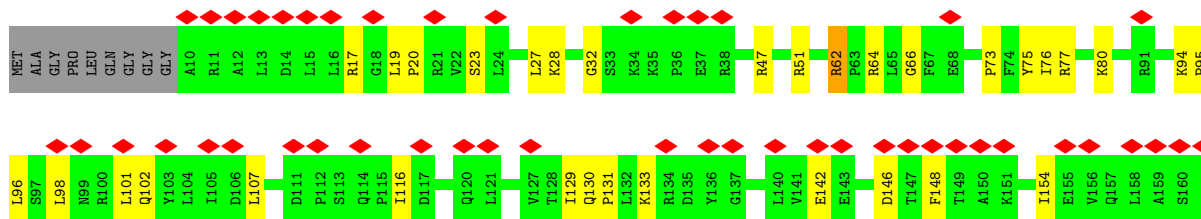
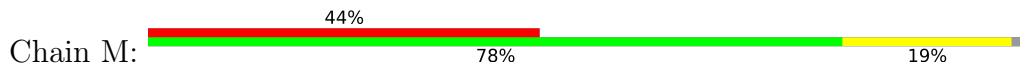




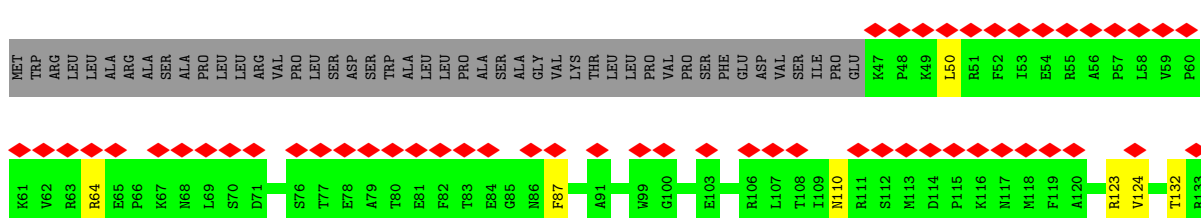
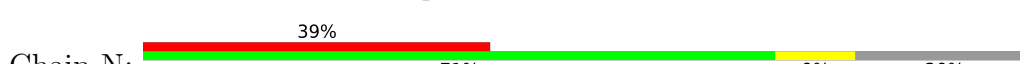
• Molecule 20: 39S ribosomal protein L14, mitochondrial



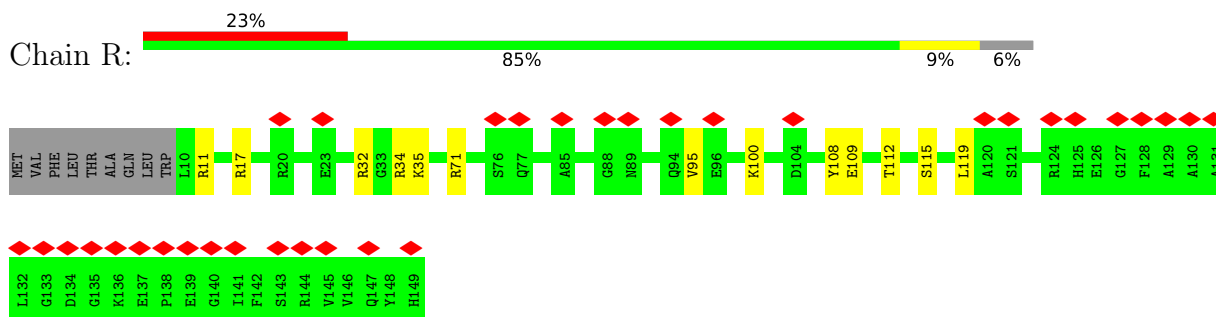
• Molecule 21: 39S ribosomal protein L15, mitochondrial



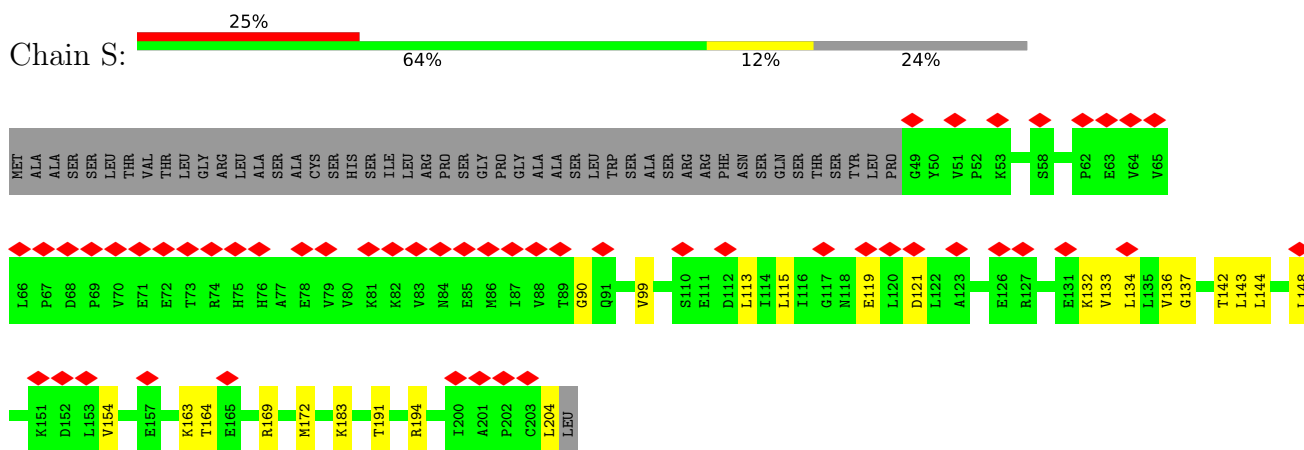
• Molecule 22: 39S ribosomal protein L16, mitochondrial



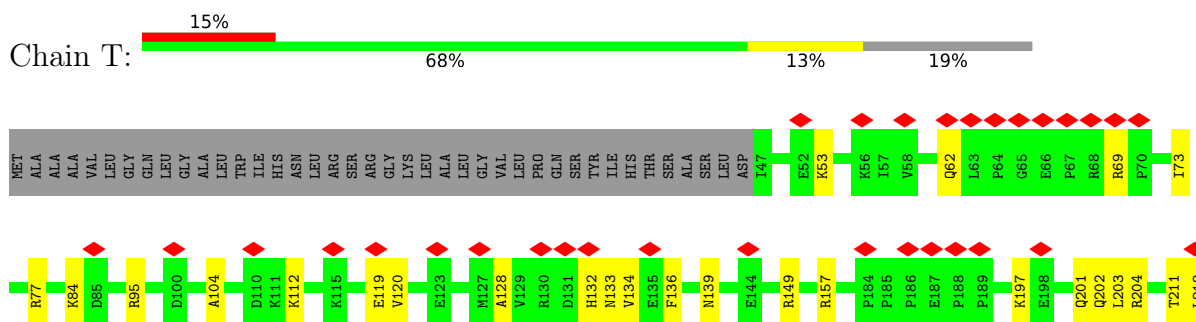
- Molecule 26: 39S ribosomal protein L20, mitochondrial



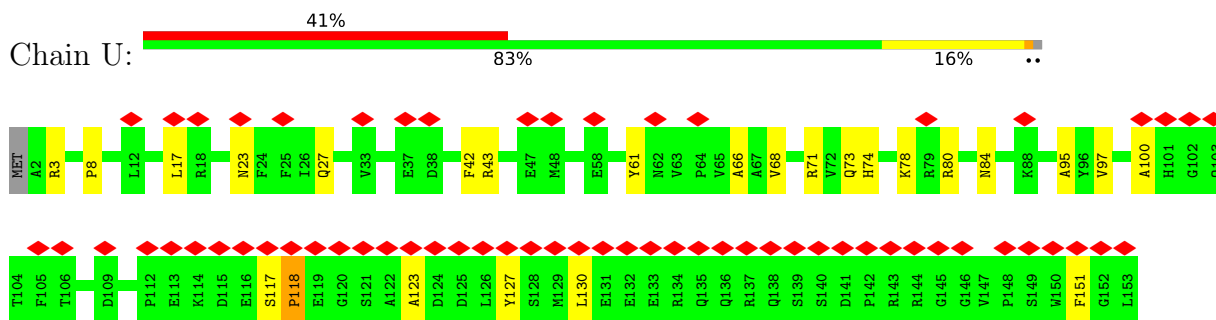
- Molecule 27: 39S ribosomal protein L21, mitochondrial



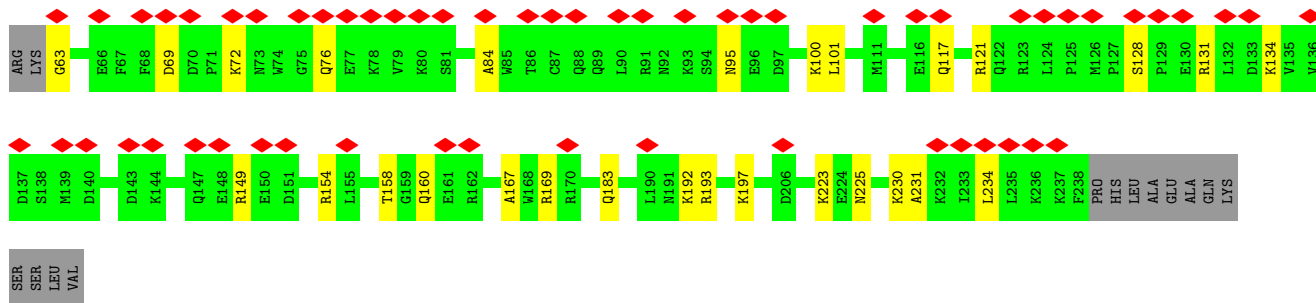
- Molecule 28: 39S ribosomal protein L22, mitochondrial



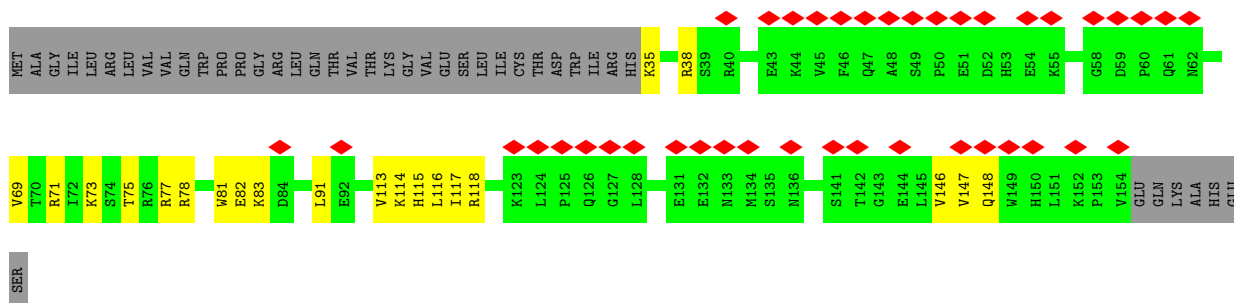
- Molecule 29: 39S ribosomal protein L23, mitochondrial



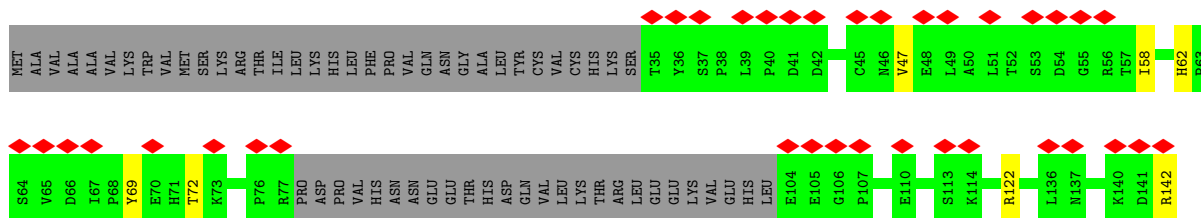
- Molecule 30: 39S ribosomal protein L24, mitochondrial



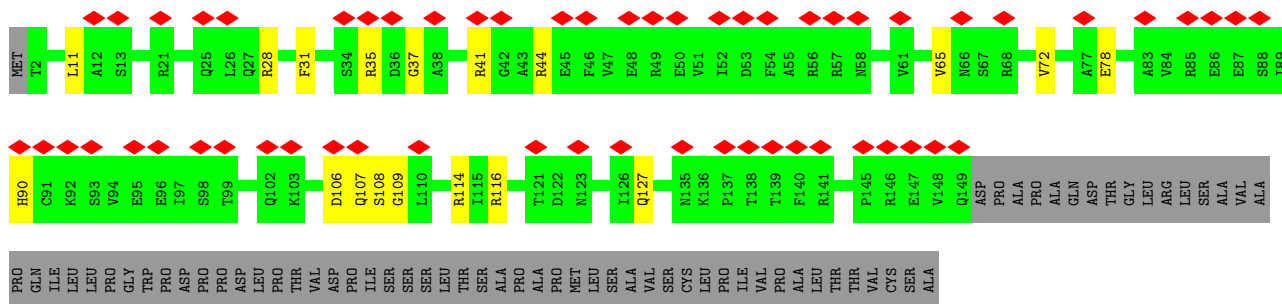
- Molecule 34: 39S ribosomal protein L30, mitochondrial



- Molecule 35: 39S ribosomal protein L42, mitochondrial



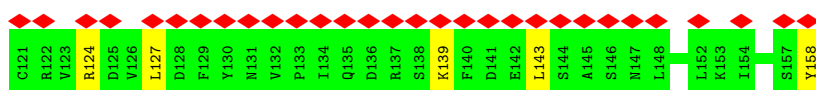
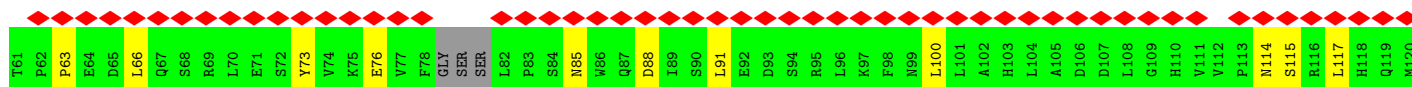
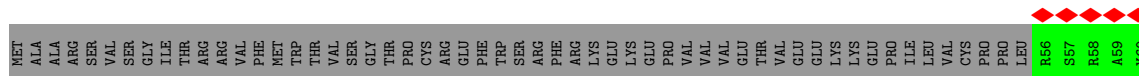
- Molecule 36: 39S ribosomal protein L43, mitochondrial



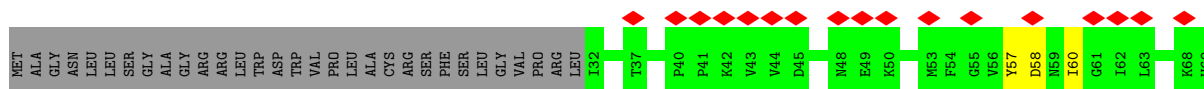
- Molecule 37: 39S ribosomal protein L44, mitochondrial



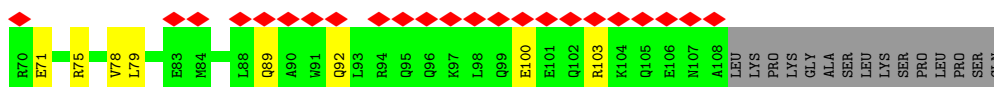
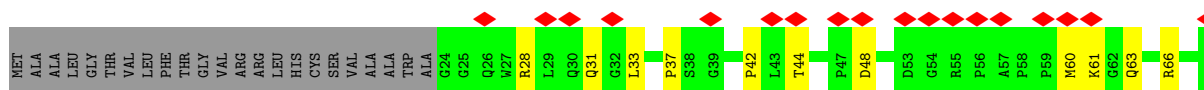
- Molecule 42: 39S ribosomal protein L50, mitochondrial



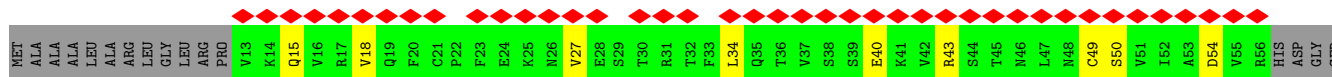
- Molecule 43: 39S ribosomal protein L51, mitochondrial

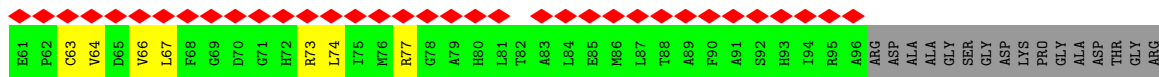


- Molecule 44: 39S ribosomal protein L52, mitochondrial

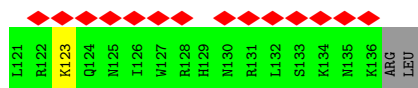
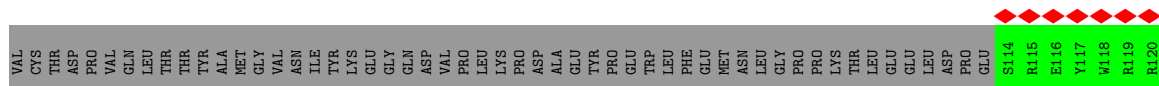
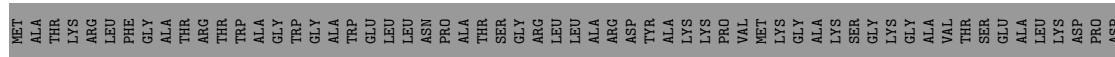


- Molecule 45: 39S ribosomal protein L53, mitochondrial

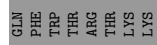
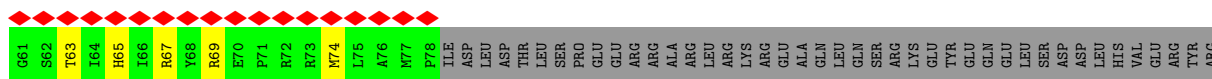
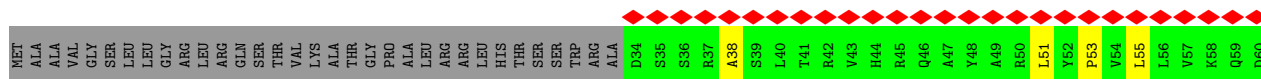




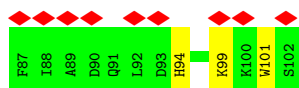
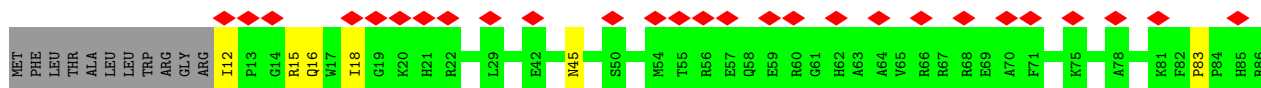
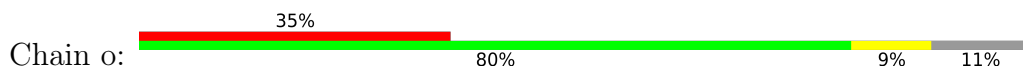
• Molecule 46: 39S ribosomal protein L54, mitochondrial



• Molecule 47: 39S ribosomal protein L55, mitochondrial

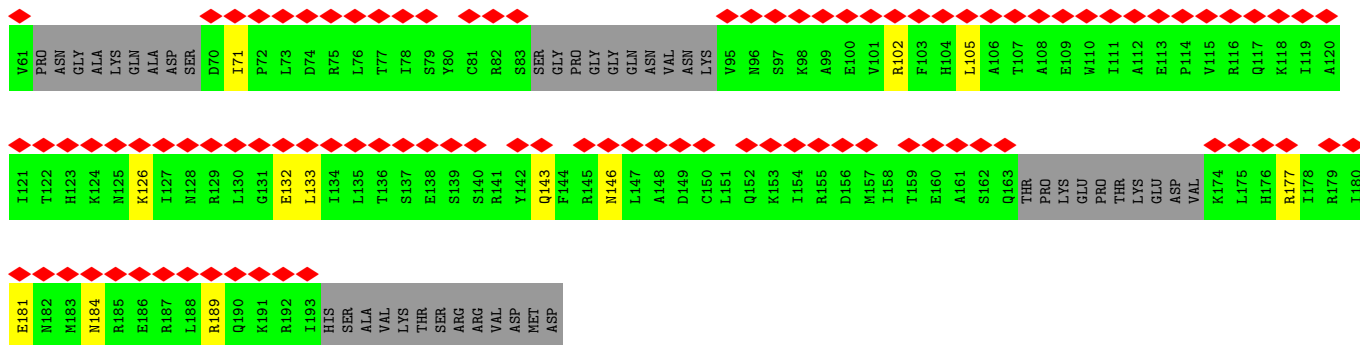


• Molecule 48: Ribosomal protein 63, mitochondrial

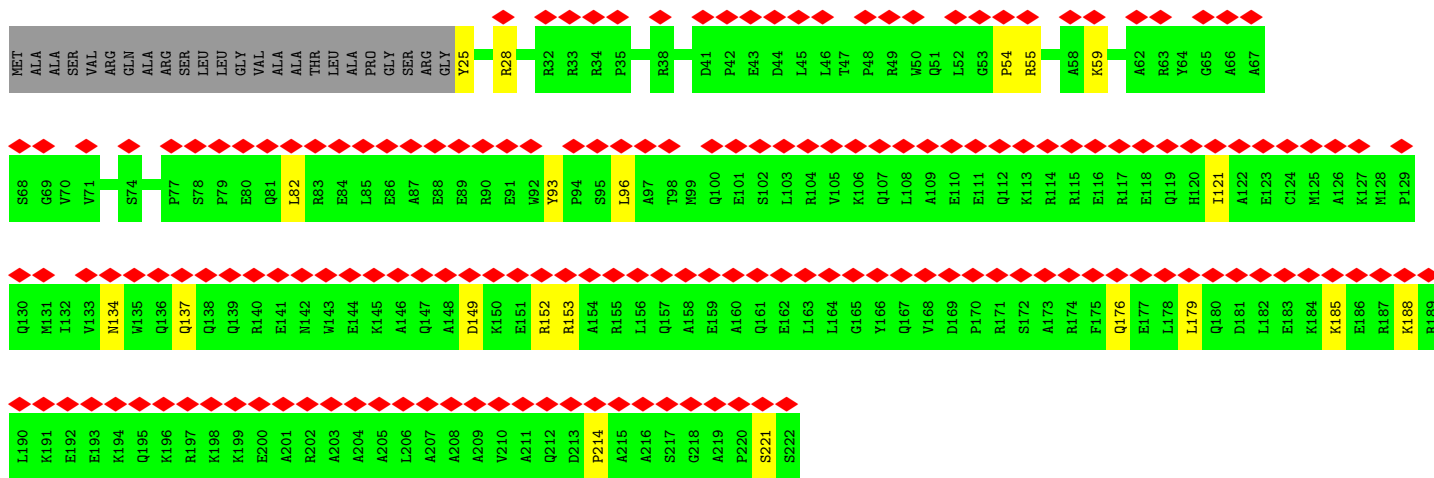
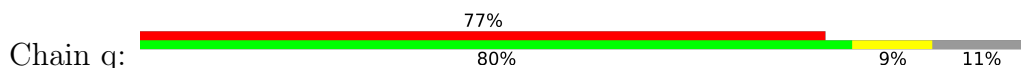


• Molecule 49: Peptidyl-tRNA hydrolase ICT1, mitochondrial

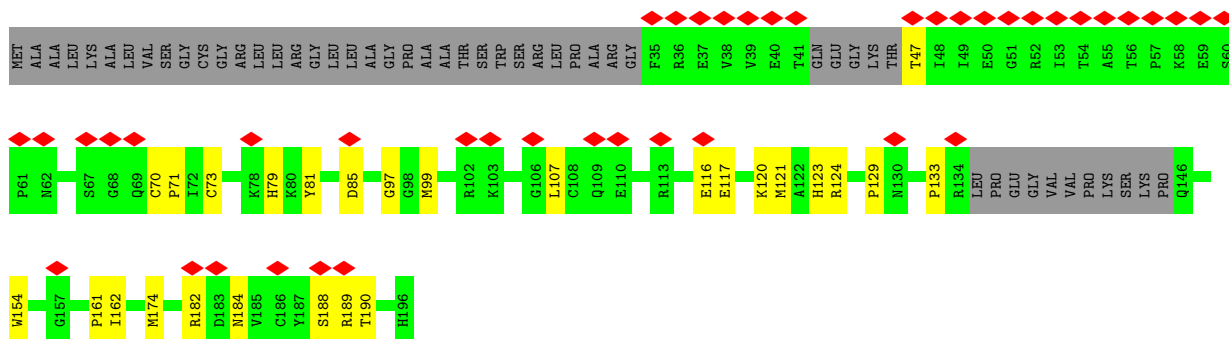




• Molecule 50: Growth arrest and DNA damage-inducible proteins-interacting protein 1

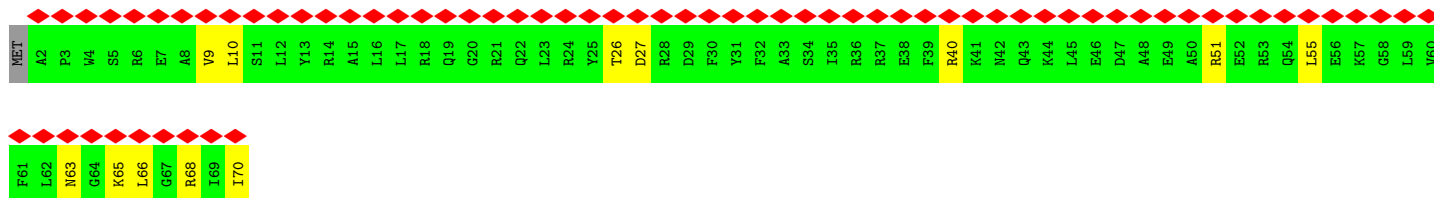


• Molecule 51: 39S ribosomal protein S18a, mitochondrial

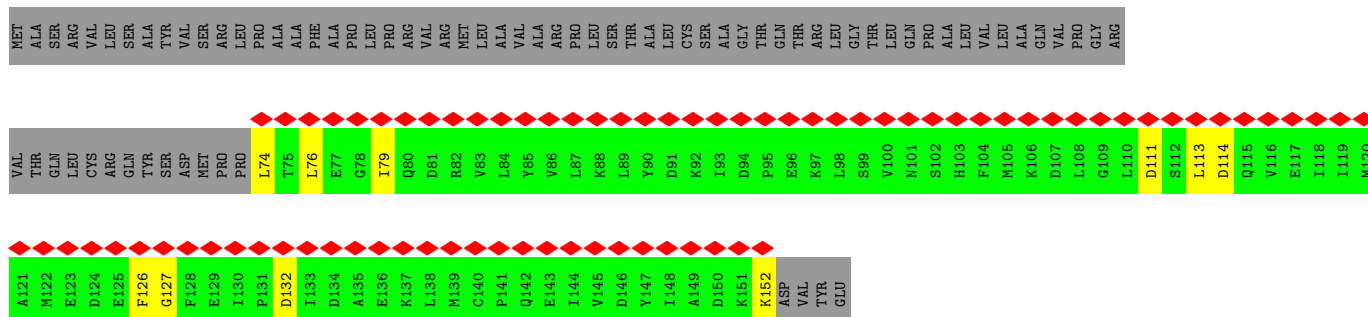
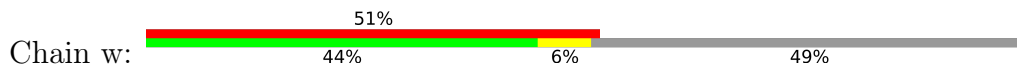


• Molecule 52: 39S ribosomal protein S30, mitochondrial

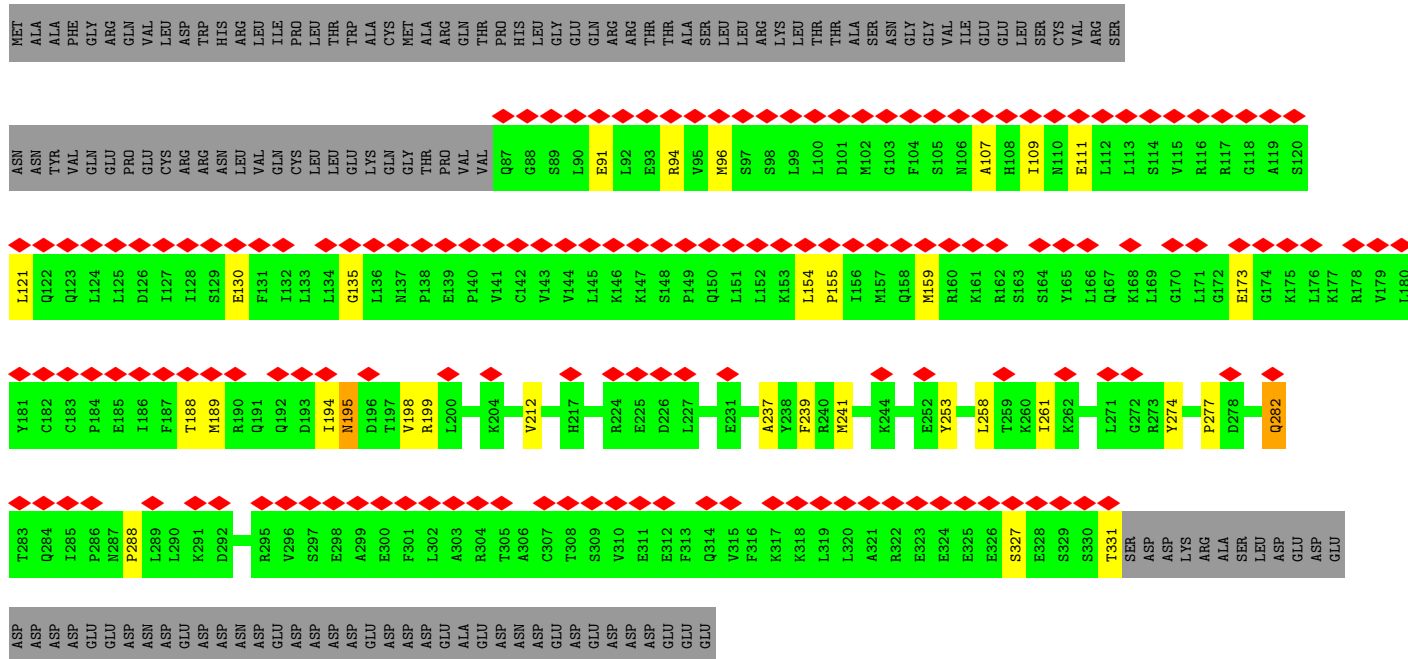
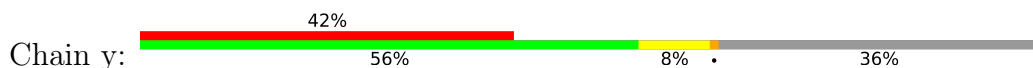




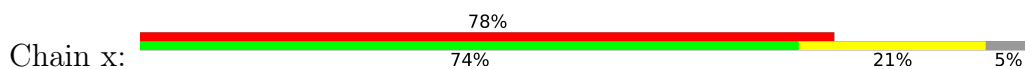
• Molecule 56: Acyl carrier protein, mitochondrial

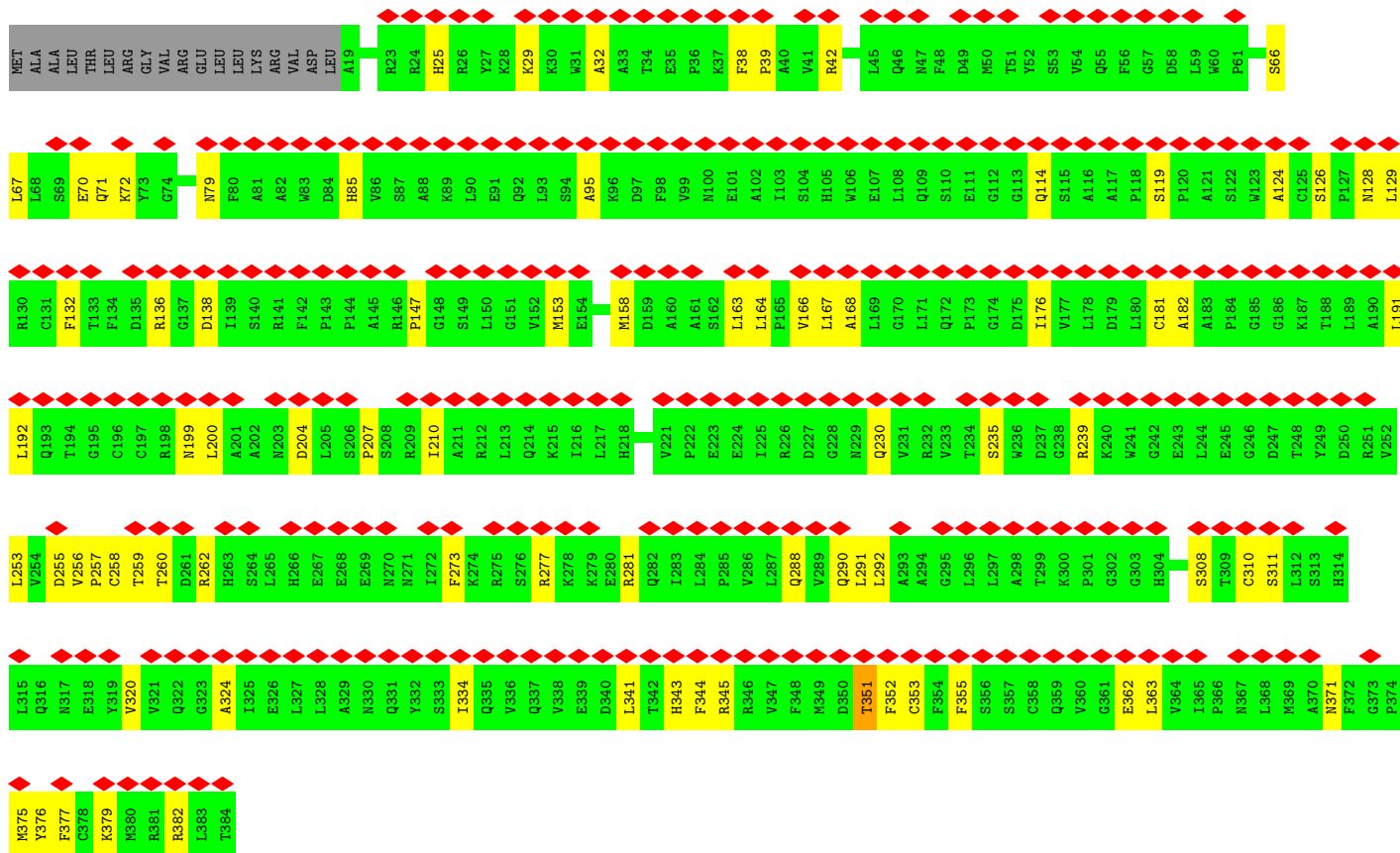


• Molecule 57: Transcription termination factor 4, mitochondrial

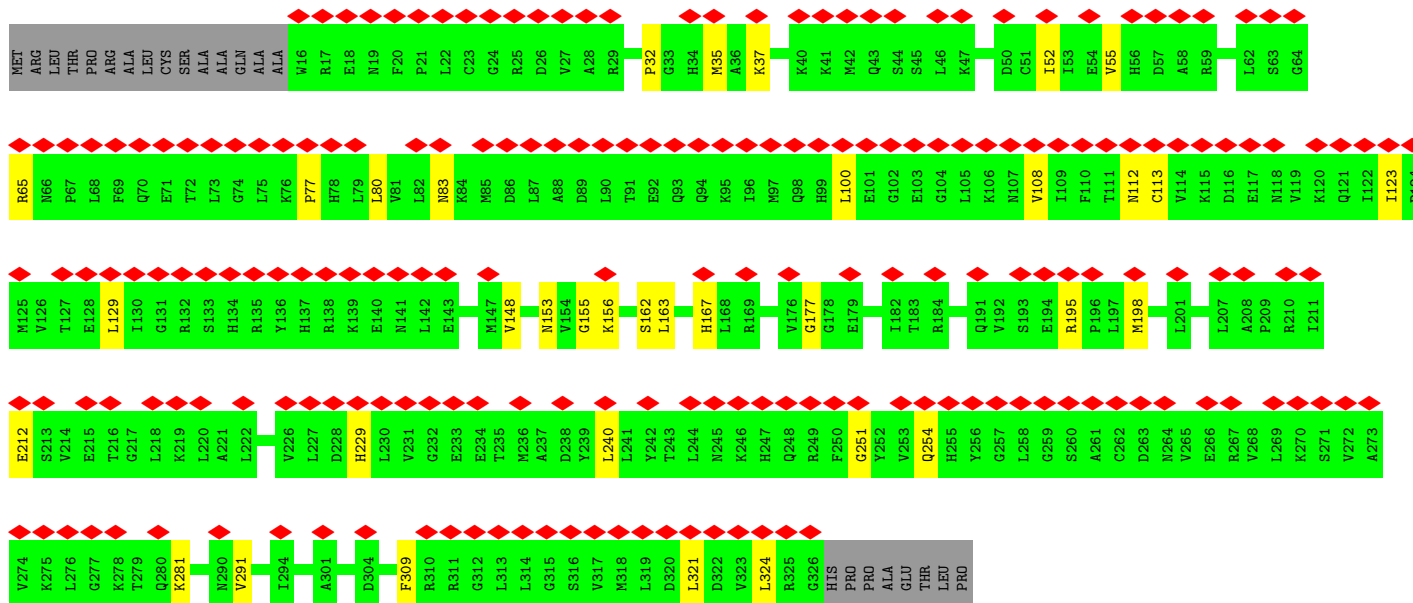
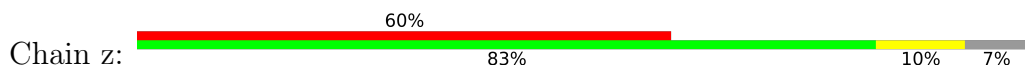


• Molecule 58: 5-methylcytosine rRNA methyltransferase NSUN4





● Molecule 59: Mitochondrial ribosome-associated GTPase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66340	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 ($e^-/\text{\AA}^2$)	1.1	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.723	Depositor
Minimum map value	-0.325	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.15	Depositor
Map size (Å)	532.48, 532.48, 532.48	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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: GCP, SAM, PSU, MG, OMU, ZN, PNS, OMG

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	0.32	0/895	0.70	0/1201
2	1	0.21	0/438	0.55	0/583
3	2	0.25	0/373	0.65	0/496
4	3	0.29	0/852	0.60	0/1136
5	4	0.29	0/341	0.62	0/451
6	5	0.32	1/3294 (0.0%)	0.68	3/4488 (0.1%)
7	6	0.27	0/2726	0.60	0/3715
8	7	0.27	0/2391	0.64	0/3234
9	8	0.27	0/774	0.77	5/1043 (0.5%)
10	9	0.27	0/972	0.62	0/1306
11	A	0.19	0/34547	0.35	1/53754 (0.0%)
12	B	3.02	7/1504 (0.5%)	0.48	1/2333 (0.0%)
13	C	0.23	0/665	0.64	0/905
13	H	0.24	0/798	0.65	0/1073
14	D	0.38	0/1723	0.84	1/2317 (0.0%)
15	E	0.30	0/2465	0.65	0/3344
16	F	0.34	0/2071	0.70	4/2817 (0.1%)
17	G	0.27	0/1368	0.65	1/1849 (0.1%)
18	J	0.28	0/1077	0.72	2/1452 (0.1%)
19	K	0.35	1/1495 (0.1%)	0.85	3/2029 (0.1%)
20	L	0.33	0/904	0.80	2/1218 (0.2%)
21	M	0.31	0/2359	0.83	6/3185 (0.2%)
22	N	0.30	0/1658	0.67	0/2229
23	O	0.48	1/1269 (0.1%)	0.88	6/1708 (0.4%)
24	P	0.35	0/1173	0.76	1/1588 (0.1%)
25	Q	0.30	0/1846	0.72	2/2487 (0.1%)
26	R	0.25	0/1174	0.61	0/1572
27	S	0.32	0/1276	0.66	0/1729
28	T	0.30	0/1402	0.65	2/1886 (0.1%)
29	U	0.27	0/1248	0.68	1/1692 (0.1%)
30	V	0.27	0/1666	0.68	2/2260 (0.1%)
31	W	0.31	0/881	0.69	1/1188 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	X	0.31	0/2090	0.70	0/2825
33	Y	0.27	0/1552	0.63	0/2079
34	Z	0.29	0/1003	0.63	0/1354
35	a	0.28	0/709	0.72	0/963
36	b	0.34	0/1202	0.68	0/1626
37	c	0.31	0/2264	0.72	3/3059 (0.1%)
38	d	0.29	0/1790	0.65	0/2423
39	e	0.23	0/1797	0.58	0/2422
40	f	0.26	0/931	0.61	0/1259
41	g	0.30	0/1102	0.70	0/1503
42	h	0.28	0/847	0.58	0/1150
43	i	0.33	0/849	0.68	0/1135
44	j	0.28	0/698	0.62	0/940
45	k	0.22	0/635	0.74	1/855 (0.1%)
46	l	0.13	0/226	0.45	0/299
47	m	0.38	0/379	0.88	1/510 (0.2%)
48	o	0.27	0/792	0.70	0/1064
49	p	0.20	0/1071	0.53	1/1433 (0.1%)
50	q	0.18	0/1661	0.50	0/2236
51	r	0.37	0/1238	0.81	2/1676 (0.1%)
52	s	0.30	0/3114	0.66	1/4225 (0.0%)
54	u	0.23	0/949	0.68	2/1281 (0.2%)
55	v	0.17	0/597	0.49	0/796
56	w	0.21	0/647	0.61	2/871 (0.2%)
57	y	0.29	0/2020	0.65	1/2714 (0.0%)
58	x	0.32	0/2958	0.76	4/4014 (0.1%)
59	z	0.30	0/2484	0.74	0/3349
All	All	0.44	10/113230 (0.0%)	0.59	62/160329 (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
11	A	5	0
14	D	0	3
17	G	0	1
21	M	0	1
25	Q	0	1
41	g	0	1
51	r	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
58	x	0	1
59	z	0	1
All	All	5	10

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	1625	A	P-OP2	71.52	2.92	1.49
12	B	1635	C	C2-N3	39.98	2.15	1.35
12	B	1635	C	N1-C2	39.83	2.19	1.40
12	B	1635	C	N3-C4	38.92	2.11	1.33
12	B	1635	C	N1-C6	37.71	2.12	1.37

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	O	22	PRO	N-CD-CG	-14.56	81.36	103.20
19	K	43	HIS	CA-C-N	13.57	140.48	121.61
19	K	43	HIS	C-N-CA	13.57	140.48	121.61
12	B	1624	C	OP1-P-O3'	-9.53	79.41	108.00
9	8	187	PRO	N-CA-CB	8.45	111.28	103.08

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	2815	OMG	C4',C3'
11	A	3040	OMG	C1',C2',C4'

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
14	D	122	PHE	Peptide
14	D	206	TYR	Peptide
14	D	208	ARG	Sidechain
17	G	64	CYS	Peptide
21	M	62	ARG	Sidechain

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	0	880	0	904	15	0
2	1	433	0	475	9	0
3	2	367	0	393	3	0
4	3	831	0	883	11	0
5	4	333	0	352	8	0
6	5	3199	0	3196	37	0
7	6	2640	0	2464	32	0
8	7	2334	0	2343	30	0
9	8	759	0	725	7	0
10	9	947	0	949	13	0
11	A	30973	0	15733	169	0
12	B	1348	0	691	23	0
13	C	648	0	657	3	0
13	H	784	0	832	10	0
14	D	1692	0	1732	24	0
15	E	2396	0	2402	33	0
16	F	2013	0	2044	51	0
17	G	1338	0	1416	11	0
18	J	1061	0	1141	14	0
19	K	1451	0	1447	20	0
20	L	889	0	941	14	0
21	M	2305	0	2378	41	0
22	N	1617	0	1645	17	0
23	O	1245	0	1283	21	0
24	P	1148	0	1148	17	0
25	Q	1805	0	1841	23	0
26	R	1153	0	1214	13	0
27	S	1251	0	1322	18	0
28	T	1368	0	1410	21	0
29	U	1218	0	1187	17	0
30	V	1624	0	1606	18	0
31	W	859	0	888	9	0
32	X	2035	0	2054	18	0
33	Y	1517	0	1561	23	0
34	Z	978	0	1030	16	0
35	a	686	0	658	7	0
36	b	1178	0	1180	16	0
37	c	2217	0	2220	26	0
38	d	1741	0	1727	28	0
39	e	1762	0	1767	28	0
40	f	915	0	917	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
41	g	1067	0	1056	15	0
42	h	827	0	806	11	0
43	i	827	0	857	18	0
44	j	684	0	673	11	0
45	k	627	0	636	10	0
46	l	221	0	227	1	0
47	m	372	0	387	6	0
48	o	771	0	775	10	0
49	p	1058	0	1083	12	0
50	q	1625	0	1619	17	0
51	r	1203	0	1219	20	0
52	s	3036	0	3022	30	0
53	t	140	0	30	0	0
54	u	927	0	921	16	0
55	v	588	0	604	11	0
56	w	638	0	637	9	0
57	y	1989	0	2074	20	0
58	x	2889	0	2862	79	0
59	z	2443	0	2547	26	0
60	0	1	0	0	0	0
60	4	1	0	0	0	0
61	A	89	0	0	0	0
61	E	1	0	0	0	0
61	o	1	0	0	0	0
62	v	21	0	21	1	0
63	x	27	0	16	34	0
64	z	64	0	26	7	0
All	All	108075	0	92854	1000	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 5.

The worst 5 of 1000 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)
58:x:257:PRO:HG3	63:x:401:SAM:C8	1.04	1.52
58:x:257:PRO:CG	63:x:401:SAM:H8	1.34	1.50
12:B:1635:C:C6	12:B:1635:C:C5	2.02	1.47
58:x:257:PRO:CG	63:x:401:SAM:C8	1.87	1.44
58:x:255:ASP:OD2	63:x:401:SAM:CB	1.71	1.38

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	106/188 (56%)	101 (95%)	5 (5%)	0	100	100
2	1	50/65 (77%)	50 (100%)	0	0	100	100
3	2	43/92 (47%)	42 (98%)	0	1 (2%)	5	23
4	3	93/188 (50%)	93 (100%)	0	0	100	100
5	4	35/103 (34%)	35 (100%)	0	0	100	100
6	5	390/423 (92%)	367 (94%)	22 (6%)	1 (0%)	36	65
7	6	316/380 (83%)	305 (96%)	11 (4%)	0	100	100
8	7	285/338 (84%)	262 (92%)	23 (8%)	0	100	100
9	8	92/206 (45%)	77 (84%)	9 (10%)	6 (6%)	1	6
10	9	113/137 (82%)	104 (92%)	9 (8%)	0	100	100
13	C	78/267 (29%)	68 (87%)	8 (10%)	2 (3%)	4	21
13	H	93/267 (35%)	90 (97%)	3 (3%)	0	100	100
14	D	215/305 (70%)	186 (86%)	28 (13%)	1 (0%)	24	54
15	E	302/348 (87%)	286 (95%)	15 (5%)	1 (0%)	36	65
16	F	248/311 (80%)	234 (94%)	14 (6%)	0	100	100
17	G	163/261 (62%)	155 (95%)	8 (5%)	0	100	100
18	J	138/192 (72%)	120 (87%)	17 (12%)	1 (1%)	18	47
19	K	175/178 (98%)	167 (95%)	8 (5%)	0	100	100
20	L	113/145 (78%)	104 (92%)	9 (8%)	0	100	100
21	M	285/296 (96%)	270 (95%)	15 (5%)	0	100	100
22	N	196/251 (78%)	189 (96%)	7 (4%)	0	100	100
23	O	150/175 (86%)	144 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	P	139/180 (77%)	133 (96%)	6 (4%)	0	100	100
25	Q	215/292 (74%)	200 (93%)	15 (7%)	0	100	100
26	R	138/149 (93%)	136 (99%)	2 (1%)	0	100	100
27	S	154/205 (75%)	146 (95%)	8 (5%)	0	100	100
28	T	164/206 (80%)	158 (96%)	6 (4%)	0	100	100
29	U	150/153 (98%)	137 (91%)	11 (7%)	2 (1%)	9	33
30	V	200/216 (93%)	192 (96%)	7 (4%)	1 (0%)	24	54
31	W	107/148 (72%)	107 (100%)	0	0	100	100
32	X	241/256 (94%)	228 (95%)	13 (5%)	0	100	100
33	Y	174/250 (70%)	170 (98%)	4 (2%)	0	100	100
34	Z	118/161 (73%)	113 (96%)	5 (4%)	0	100	100
35	a	78/142 (55%)	74 (95%)	4 (5%)	0	100	100
36	b	146/215 (68%)	134 (92%)	12 (8%)	0	100	100
37	c	271/332 (82%)	264 (97%)	7 (3%)	0	100	100
38	d	203/306 (66%)	194 (96%)	9 (4%)	0	100	100
39	e	211/279 (76%)	196 (93%)	15 (7%)	0	100	100
40	f	110/212 (52%)	97 (88%)	13 (12%)	0	100	100
41	g	127/166 (76%)	118 (93%)	9 (7%)	0	100	100
42	h	96/158 (61%)	92 (96%)	4 (4%)	0	100	100
43	i	95/128 (74%)	91 (96%)	4 (4%)	0	100	100
44	j	83/123 (68%)	80 (96%)	3 (4%)	0	100	100
45	k	76/112 (68%)	73 (96%)	3 (4%)	0	100	100
46	l	21/138 (15%)	21 (100%)	0	0	100	100
47	m	43/128 (34%)	35 (81%)	8 (19%)	0	100	100
48	o	89/102 (87%)	82 (92%)	7 (8%)	0	100	100
49	p	119/206 (58%)	117 (98%)	2 (2%)	0	100	100
50	q	196/222 (88%)	195 (100%)	1 (0%)	0	100	100
51	r	140/196 (71%)	134 (96%)	6 (4%)	0	100	100
52	s	366/439 (83%)	354 (97%)	12 (3%)	0	100	100
54	u	109/234 (47%)	102 (94%)	6 (6%)	1 (1%)	14	42
55	v	67/70 (96%)	66 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	w	77/156 (49%)	69 (90%)	8 (10%)	0	100	100
57	y	243/381 (64%)	228 (94%)	14 (6%)	1 (0%)	30	59
58	x	364/384 (95%)	326 (90%)	37 (10%)	1 (0%)	36	65
59	z	309/334 (92%)	275 (89%)	33 (11%)	1 (0%)	36	65
All	All	9118/12495 (73%)	8586 (94%)	512 (6%)	20 (0%)	44	71

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	2	52	GLU
6	5	217	SER
9	8	182	ILE
9	8	184	ASN
9	8	186	GLN

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	97/164 (59%)	97 (100%)	0	100	100
2	1	49/60 (82%)	49 (100%)	0	100	100
3	2	39/72 (54%)	39 (100%)	0	100	100
4	3	88/166 (53%)	88 (100%)	0	100	100
5	4	36/89 (40%)	36 (100%)	0	100	100
6	5	353/368 (96%)	353 (100%)	0	100	100
7	6	265/332 (80%)	265 (100%)	0	100	100
8	7	263/303 (87%)	263 (100%)	0	100	100
9	8	76/190 (40%)	76 (100%)	0	100	100
10	9	99/112 (88%)	99 (100%)	0	100	100
13	C	73/228 (32%)	73 (100%)	0	100	100
13	H	86/228 (38%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	D	175/245 (71%)	175 (100%)	0	100	100
15	E	259/290 (89%)	259 (100%)	0	100	100
16	F	217/262 (83%)	217 (100%)	0	100	100
17	G	153/232 (66%)	153 (100%)	0	100	100
18	J	113/150 (75%)	113 (100%)	0	100	100
19	K	155/156 (99%)	155 (100%)	0	100	100
20	L	98/124 (79%)	98 (100%)	0	100	100
21	M	245/249 (98%)	245 (100%)	0	100	100
22	N	169/211 (80%)	169 (100%)	0	100	100
23	O	133/150 (89%)	133 (100%)	0	100	100
24	P	123/155 (79%)	123 (100%)	0	100	100
25	Q	199/256 (78%)	199 (100%)	0	100	100
26	R	118/126 (94%)	118 (100%)	0	100	100
27	S	141/180 (78%)	141 (100%)	0	100	100
28	T	146/176 (83%)	146 (100%)	0	100	100
29	U	124/135 (92%)	124 (100%)	0	100	100
30	V	172/191 (90%)	172 (100%)	0	100	100
31	W	89/119 (75%)	89 (100%)	0	100	100
32	X	219/229 (96%)	219 (100%)	0	100	100
33	Y	159/223 (71%)	159 (100%)	0	100	100
34	Z	111/147 (76%)	111 (100%)	0	100	100
35	a	78/133 (59%)	78 (100%)	0	100	100
36	b	130/186 (70%)	130 (100%)	0	100	100
37	c	241/288 (84%)	241 (100%)	0	100	100
38	d	193/274 (70%)	193 (100%)	0	100	100
39	e	188/236 (80%)	188 (100%)	0	100	100
40	f	101/188 (54%)	101 (100%)	0	100	100
41	g	119/148 (80%)	119 (100%)	0	100	100
42	h	95/148 (64%)	95 (100%)	0	100	100
43	i	86/110 (78%)	86 (100%)	0	100	100
44	j	68/97 (70%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	k	71/90 (79%)	71 (100%)	0	100	100
46	l	23/116 (20%)	23 (100%)	0	100	100
47	m	40/113 (35%)	40 (100%)	0	100	100
48	o	78/87 (90%)	78 (100%)	0	100	100
49	p	117/181 (65%)	117 (100%)	0	100	100
50	q	163/178 (92%)	163 (100%)	0	100	100
51	r	133/169 (79%)	133 (100%)	0	100	100
52	s	326/381 (86%)	326 (100%)	0	100	100
54	u	105/200 (52%)	105 (100%)	0	100	100
55	v	59/60 (98%)	59 (100%)	0	100	100
56	w	73/136 (54%)	73 (100%)	0	100	100
57	y	227/350 (65%)	226 (100%)	1 (0%)	84	83
58	x	313/328 (95%)	313 (100%)	0	100	100
59	z	270/287 (94%)	270 (100%)	0	100	100
All	All	8139/10802 (75%)	8138 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
57	y	195	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
40	f	112	ASN
52	s	387	ASN
44	j	105	GLN
50	q	176	GLN
57	y	195	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1443/1737 (83%)	376 (26%)	22 (1%)
12	B	61/69 (88%)	31 (50%)	2 (3%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	1504/1806 (83%)	407 (27%)	24 (1%)

5 of 407 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	1674	A
11	A	1675	A
11	A	1676	A
11	A	1679	U
11	A	1680	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	2631	G
11	A	2816	G
11	A	2815	OMG
11	A	2818	C
11	A	2243	A

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 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
11	OMG	A	2815	11	23,26,27	2.40	6 (26%)	32,38,41	2.99	16 (50%)
11	PSU	A	3067	11	18,21,22	2.05	8 (44%)	21,30,33	2.02	4 (19%)
11	OMG	A	3040	11	23,26,27	2.39	5 (21%)	32,38,41	3.22	15 (46%)
11	OMU	A	3039	11	19,22,23	2.57	6 (31%)	25,31,34	2.01	6 (24%)

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
11	OMG	A	2815	11	2/2/5/5	1/9/27/28	0/3/3/3
11	PSU	A	3067	11	-	1/7/25/26	0/2/2/2
11	OMG	A	3040	11	3/3/5/5	4/9/27/28	0/3/3/3
11	OMU	A	3039	11	-	6/9/27/28	0/2/2/2

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	3039	OMU	O4-C4	9.20	1.42	1.24
11	A	2815	OMG	O6-C6	8.97	1.40	1.23
11	A	3040	OMG	O6-C6	8.95	1.40	1.23
11	A	3040	OMG	C2-N2	4.92	1.45	1.34
11	A	2815	OMG	C2-N2	4.88	1.45	1.34

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	3040	OMG	O2'-C2'-C1'	7.65	123.52	108.99
11	A	3040	OMG	C2'-C1'-N9	7.00	127.53	114.24
11	A	2815	OMG	O2'-C2'-C1'	6.58	121.48	108.99
11	A	2815	OMG	C2'-C1'-N9	6.36	126.30	114.24
11	A	3067	PSU	N1-C2-N3	6.23	121.74	115.17

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
11	A	2815	OMG	C4'
11	A	2815	OMG	C3'
11	A	3040	OMG	C1'
11	A	3040	OMG	C2'
11	A	3040	OMG	C4'

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	2815	OMG	C4'-C5'-O5'-P
11	A	3039	OMU	C2'-C1'-N1-C2
11	A	3039	OMU	C2'-C1'-N1-C6
11	A	3040	OMG	C1'-C2'-O2'-CM2
11	A	3040	OMG	C3'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	3067	PSU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 97 ligands modelled in this entry, 93 are monoatomic - leaving 4 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	$\# Z > 2$
64	GCP	z	402	-	32,34,34	3.55	13 (40%)	49,54,54	1.79	9 (18%)
64	GCP	z	401	-	32,34,34	3.43	14 (43%)	49,54,54	2.08	15 (30%)
62	PNS	v	101	-	14,20,21	2.17	4 (28%)	18,26,29	1.25	1 (5%)
63	SAM	x	401	-	27,29,29	0.48	0	34,42,42	0.68	0

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
64	GCP	z	402	-	2/2/7/7	5/19/38/38	0/3/3/3
62	PNS	v	101	-	-	8/24/26/27	-
64	GCP	z	401	-	1/1/7/7	7/19/38/38	0/3/3/3
63	SAM	x	401	-	1/1/7/7	9/17/33/33	0/3/3/3

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	z	402	GCP	O6-C6	8.81	1.40	1.23
64	z	401	GCP	O6-C6	8.72	1.40	1.23
64	z	402	GCP	C3'-C4'	-8.52	1.31	1.53
64	z	401	GCP	C3'-C4'	-8.32	1.31	1.53
64	z	402	GCP	O4'-C4'	7.71	1.62	1.45

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	z	402	GCP	C5-C4-N3	-6.26	118.42	128.39
64	z	401	GCP	C5-C4-N3	-6.03	118.80	128.39
64	z	402	GCP	C2-N3-C4	5.63	122.00	112.30
64	z	401	GCP	C2-N3-C4	5.49	121.76	112.30
64	z	401	GCP	N9-C4-N3	4.45	134.86	125.95

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
63	x	401	SAM	CA
64	z	401	GCP	C2'
64	z	402	GCP	C2'
64	z	402	GCP	C4'

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	v	101	PNS	C28-C29-C32-O33
62	v	101	PNS	C28-C29-C32-C34
62	v	101	PNS	C31-C29-C32-O33
62	v	101	PNS	C31-C29-C32-C34
63	x	401	SAM	C4'-C5'-SD-CE

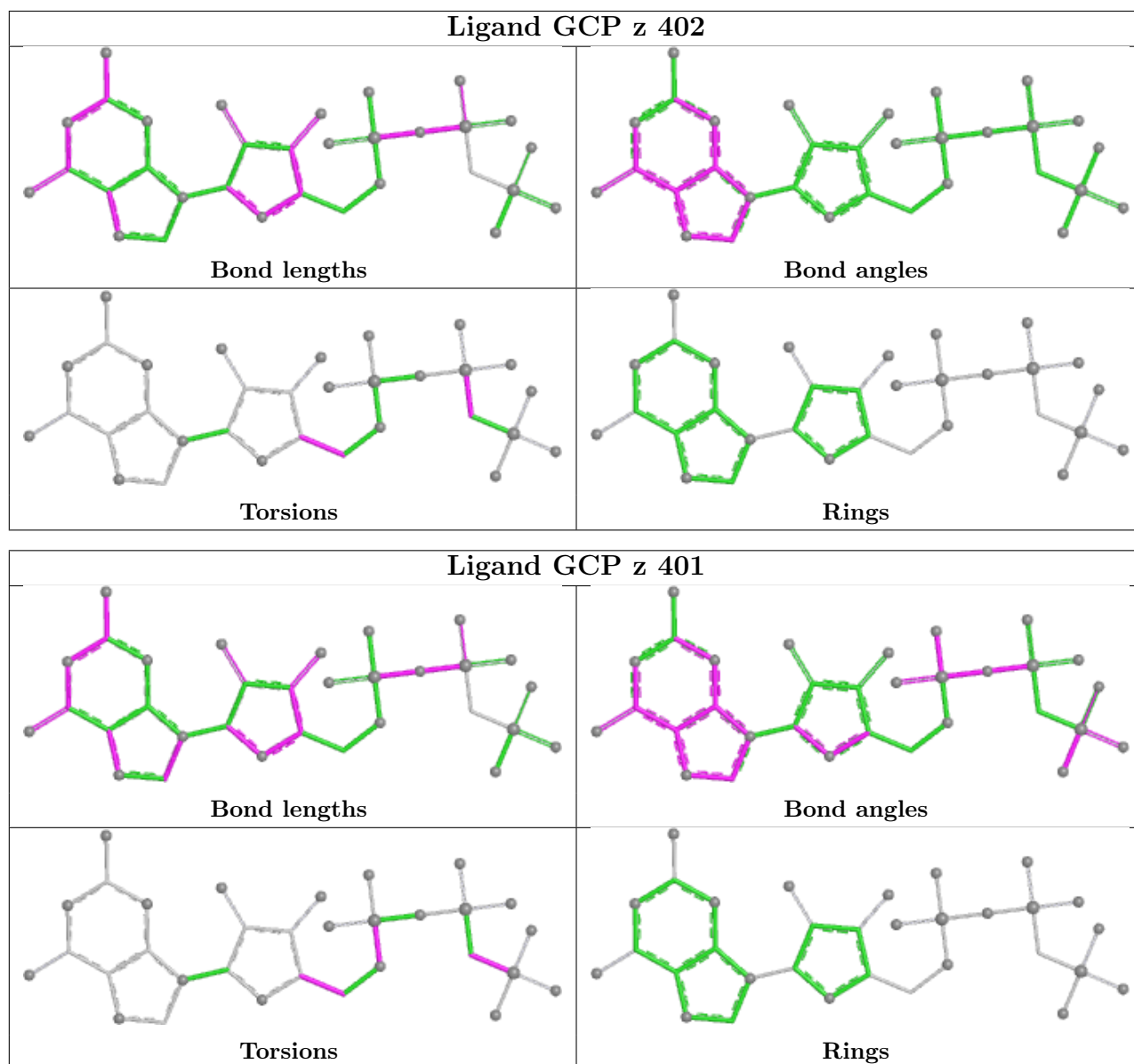
There are no ring outliers.

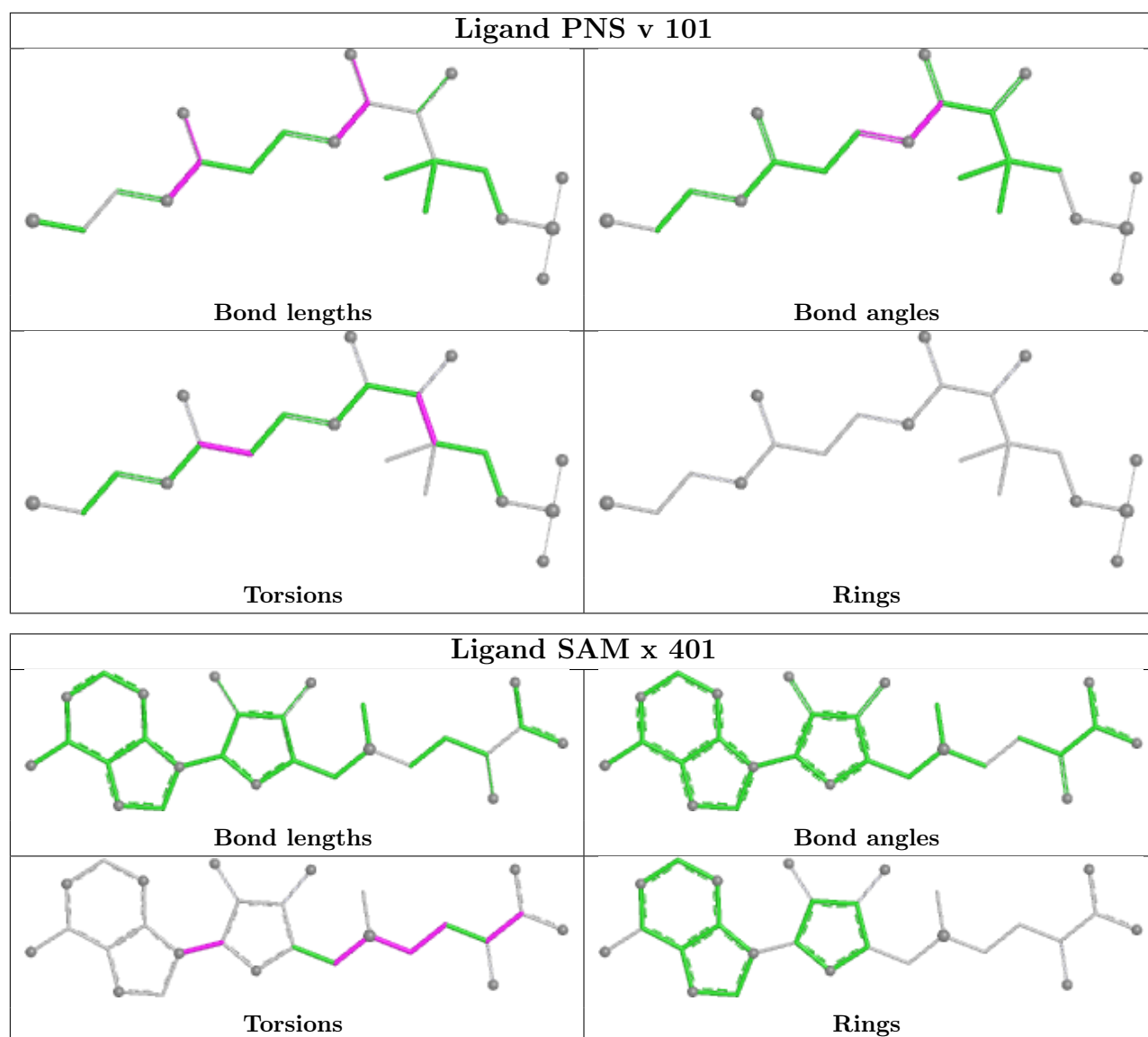
4 monomers are involved in 42 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
64	z	402	GCP	2	0
64	z	401	GCP	6	0
62	v	101	PNS	1	0
63	x	401	SAM	34	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 [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
11	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	3390:A	O3'	3391:C	P	21.25
1	A	3383:G	O3'	3384:A	P	15.46
1	A	3299:U	O3'	3300:A	P	11.65

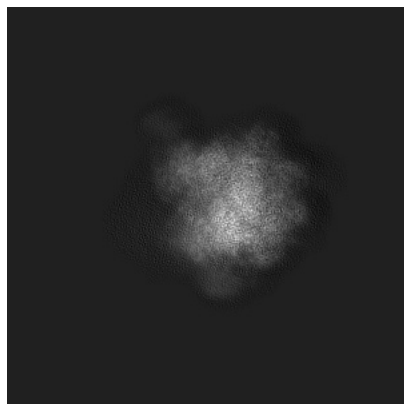
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13329. These allow visual inspection of the internal detail of the map and identification of artifacts.

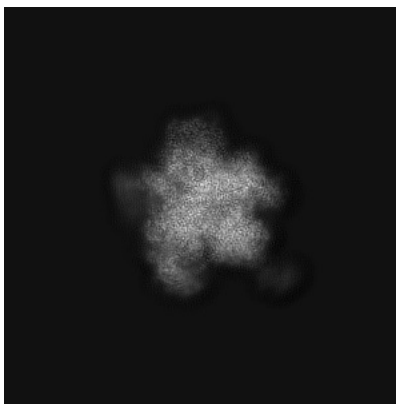
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

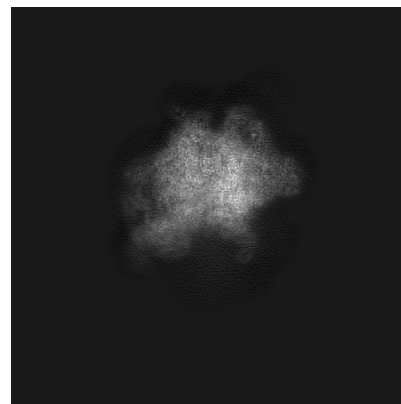
6.1.1 Primary map



X

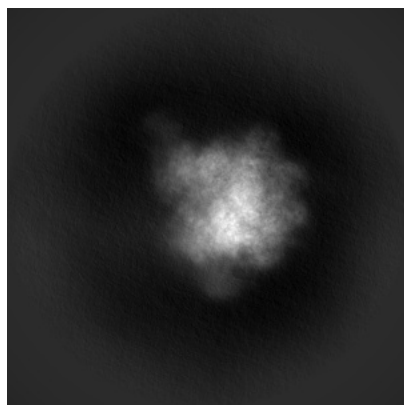


Y

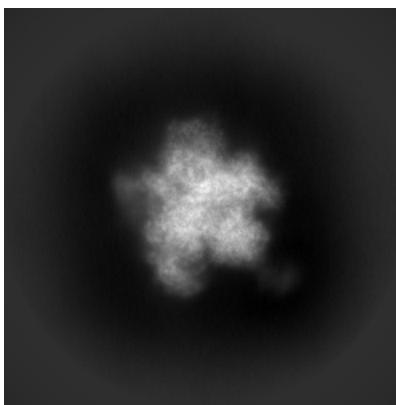


Z

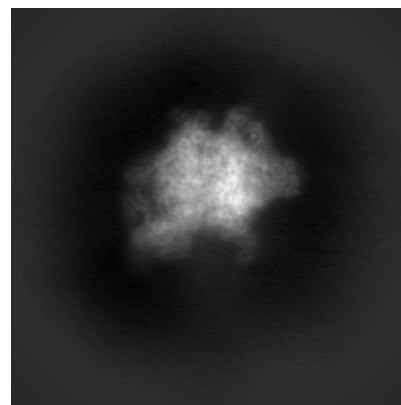
6.1.2 Raw map



X



Y

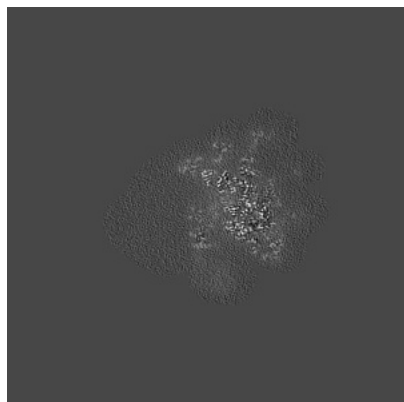


Z

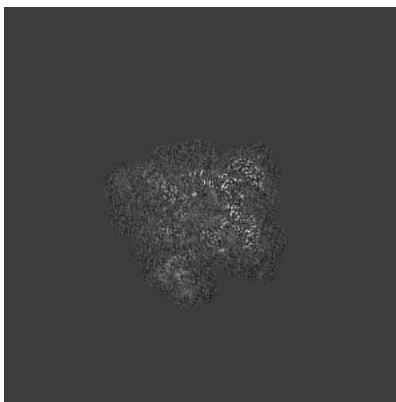
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

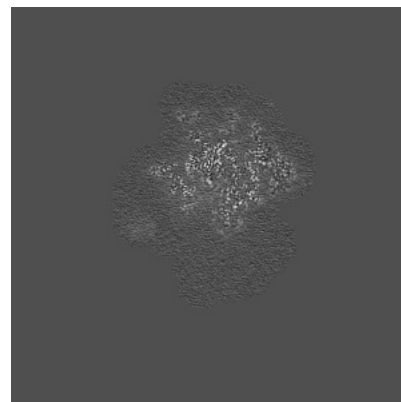
6.2.1 Primary map



X Index: 256

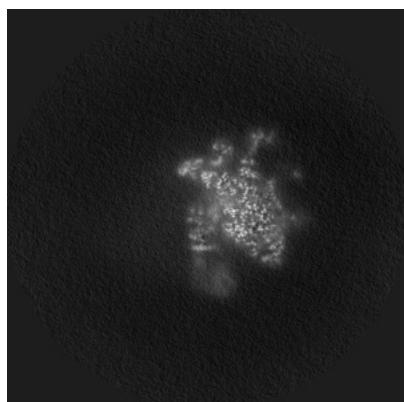


Y Index: 256

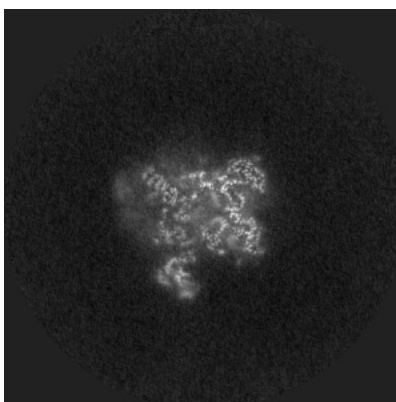


Z Index: 256

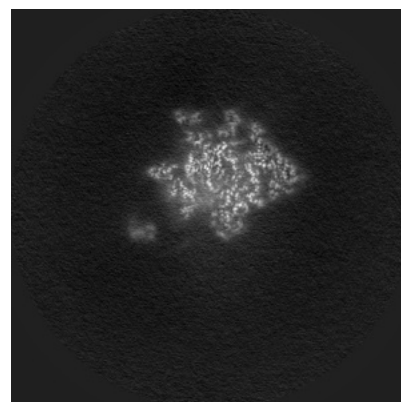
6.2.2 Raw map



X Index: 256



Y Index: 256

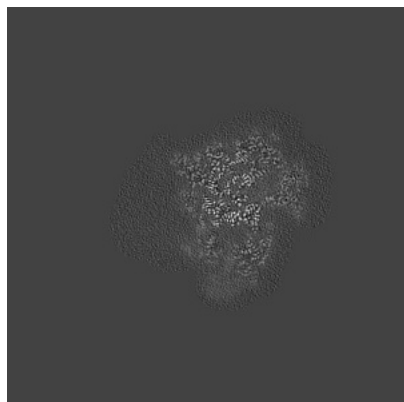


Z Index: 256

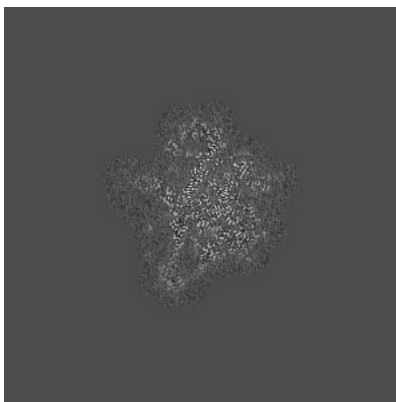
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

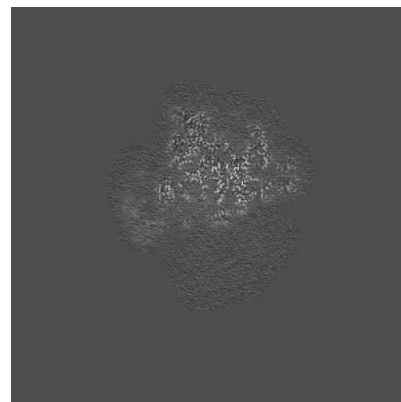
6.3.1 Primary map



X Index: 286

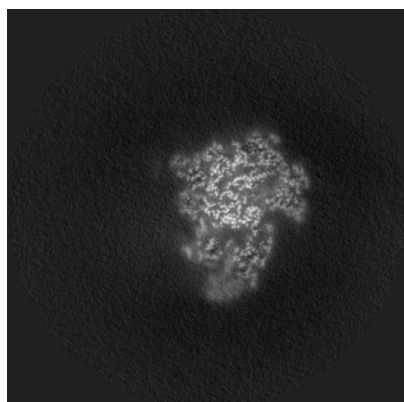


Y Index: 304

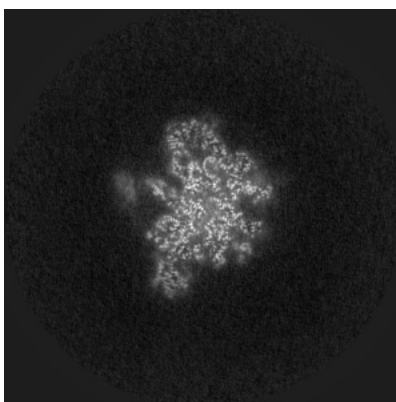


Z Index: 240

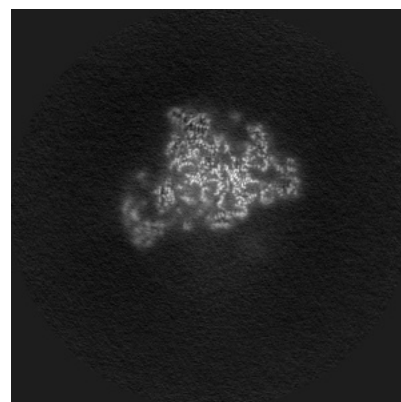
6.3.2 Raw map



X Index: 285



Y Index: 291

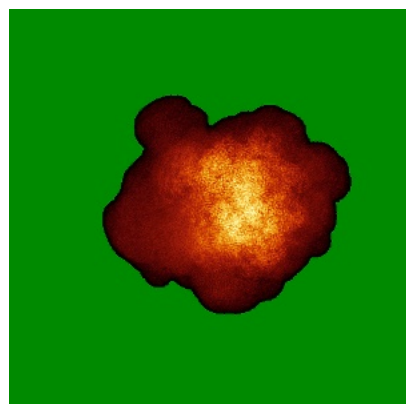


Z Index: 240

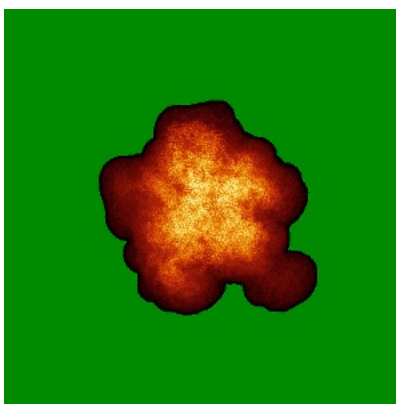
The images above show the largest variance slices of the map in three orthogonal directions.

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

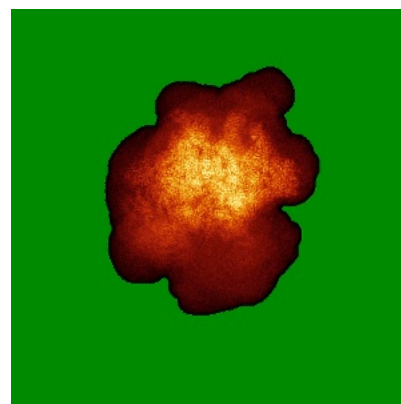
6.4.1 Primary map



X

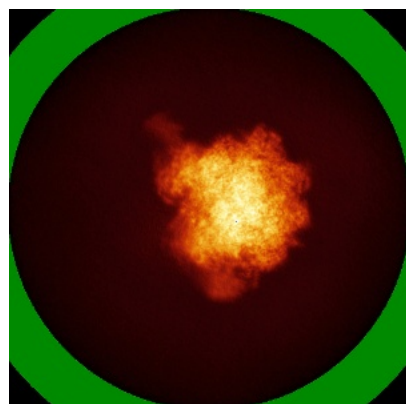


Y

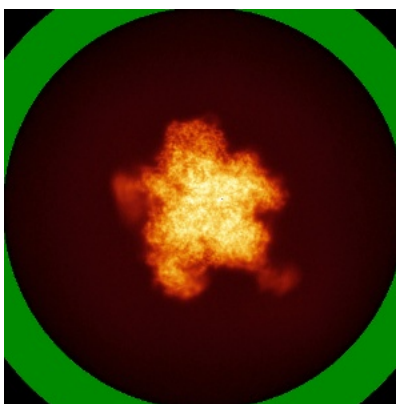


Z

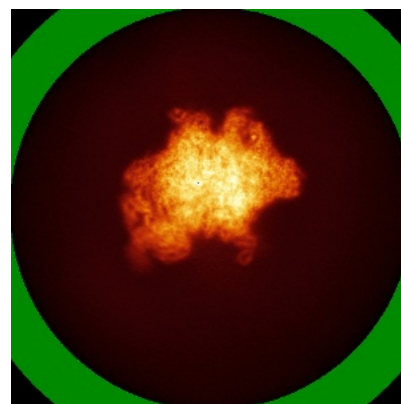
6.4.2 Raw map



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](#)

This section was not generated.

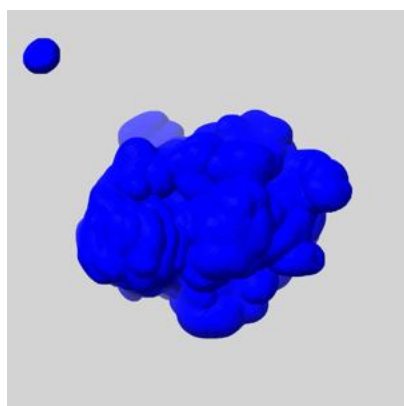
6.6 Mask visualisation [i](#)

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

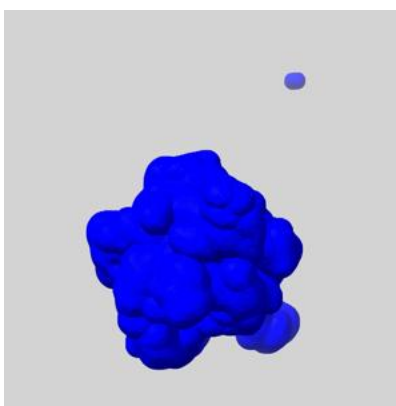
A mask typically either:

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

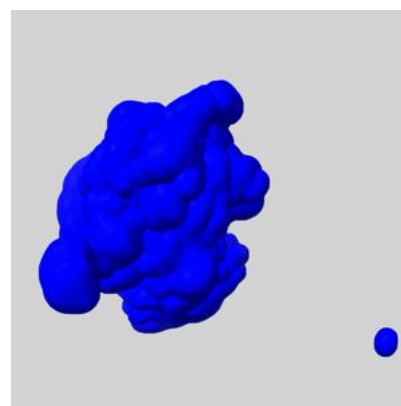
6.6.1 emd_13329_msk_1.map [i](#)



X



Y

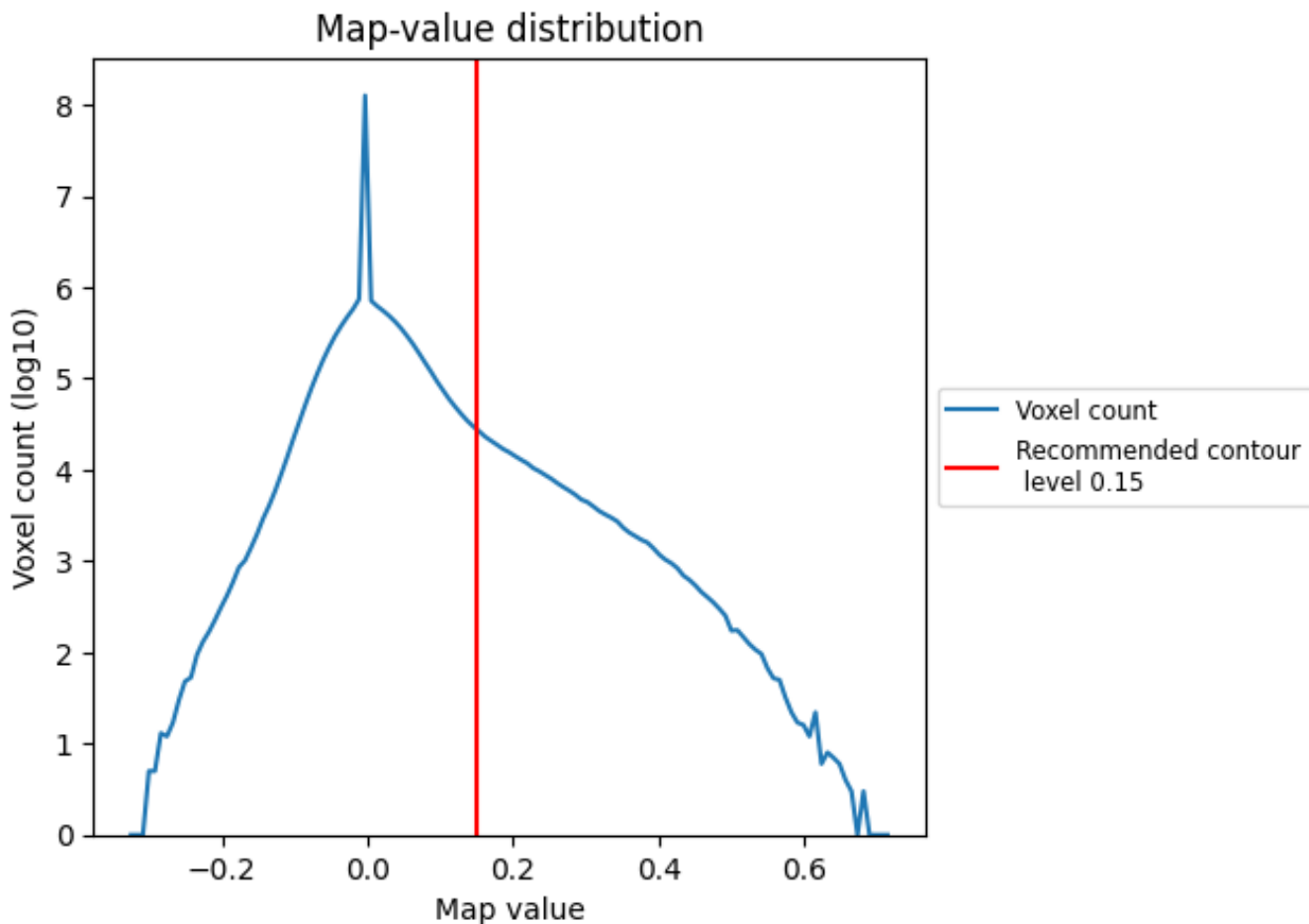


Z

7 Map analysis [i](#)

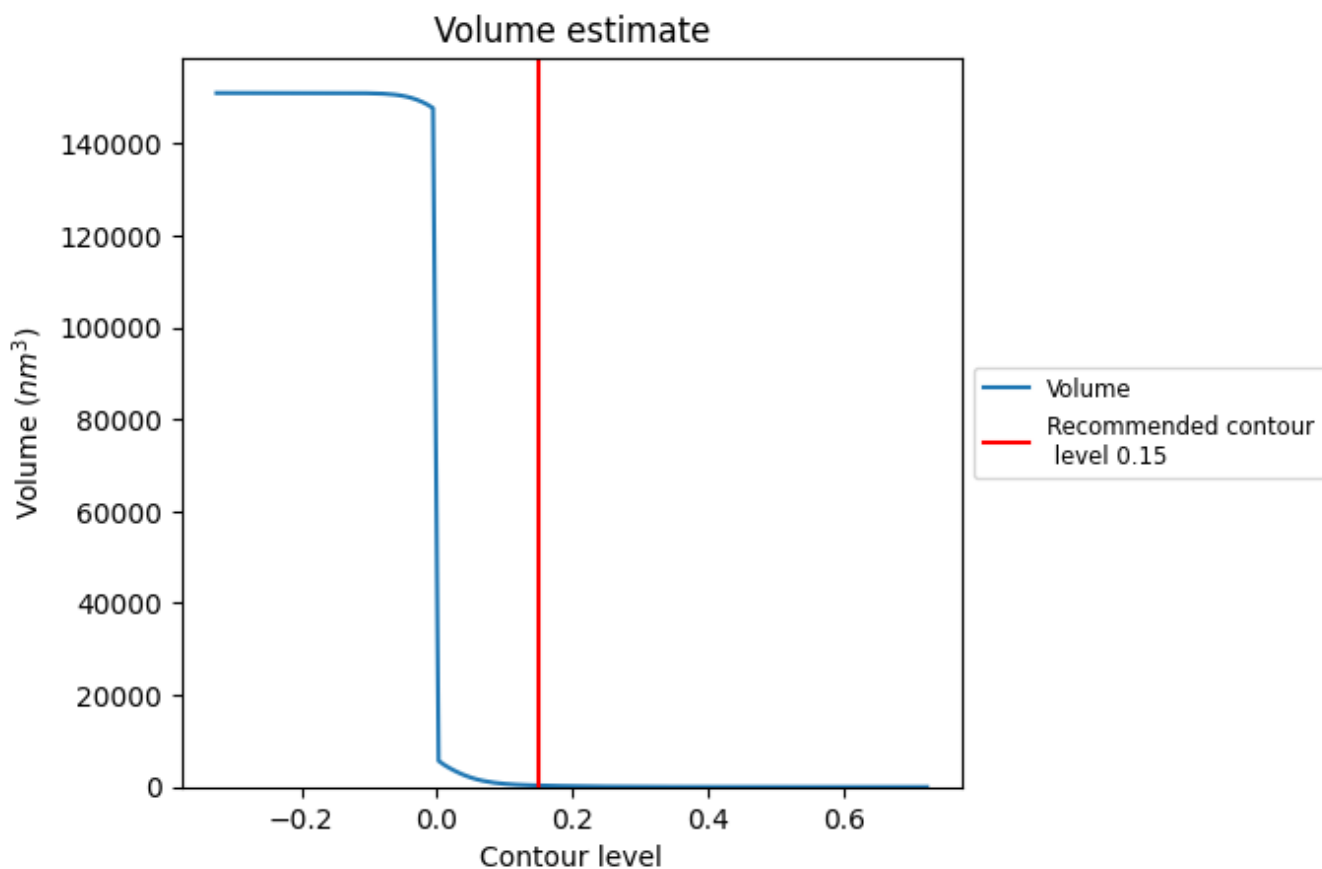
This section contains the results of statistical analysis of the map.

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.

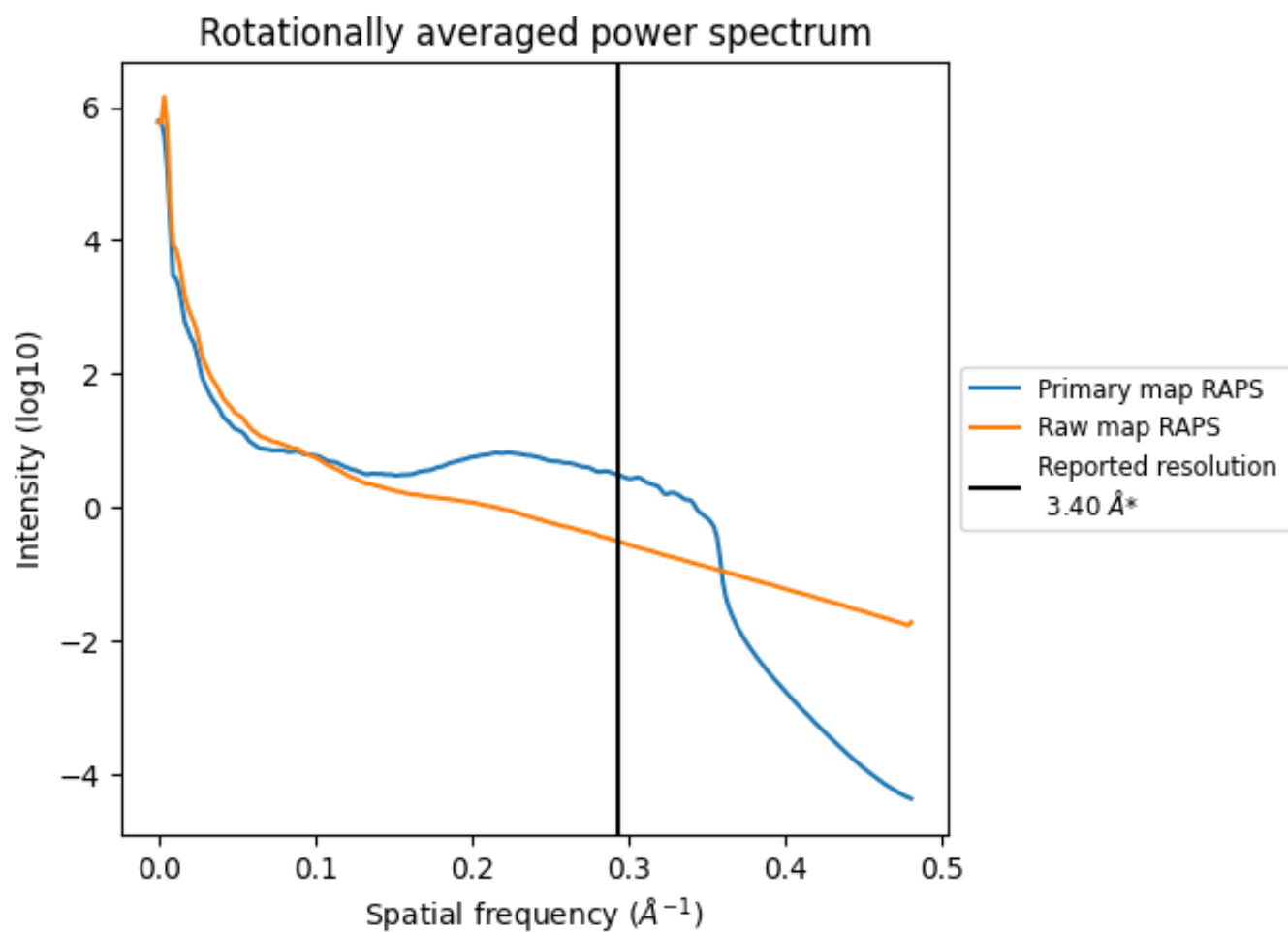
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 315 nm^3 ; this corresponds to an approximate mass of 284 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

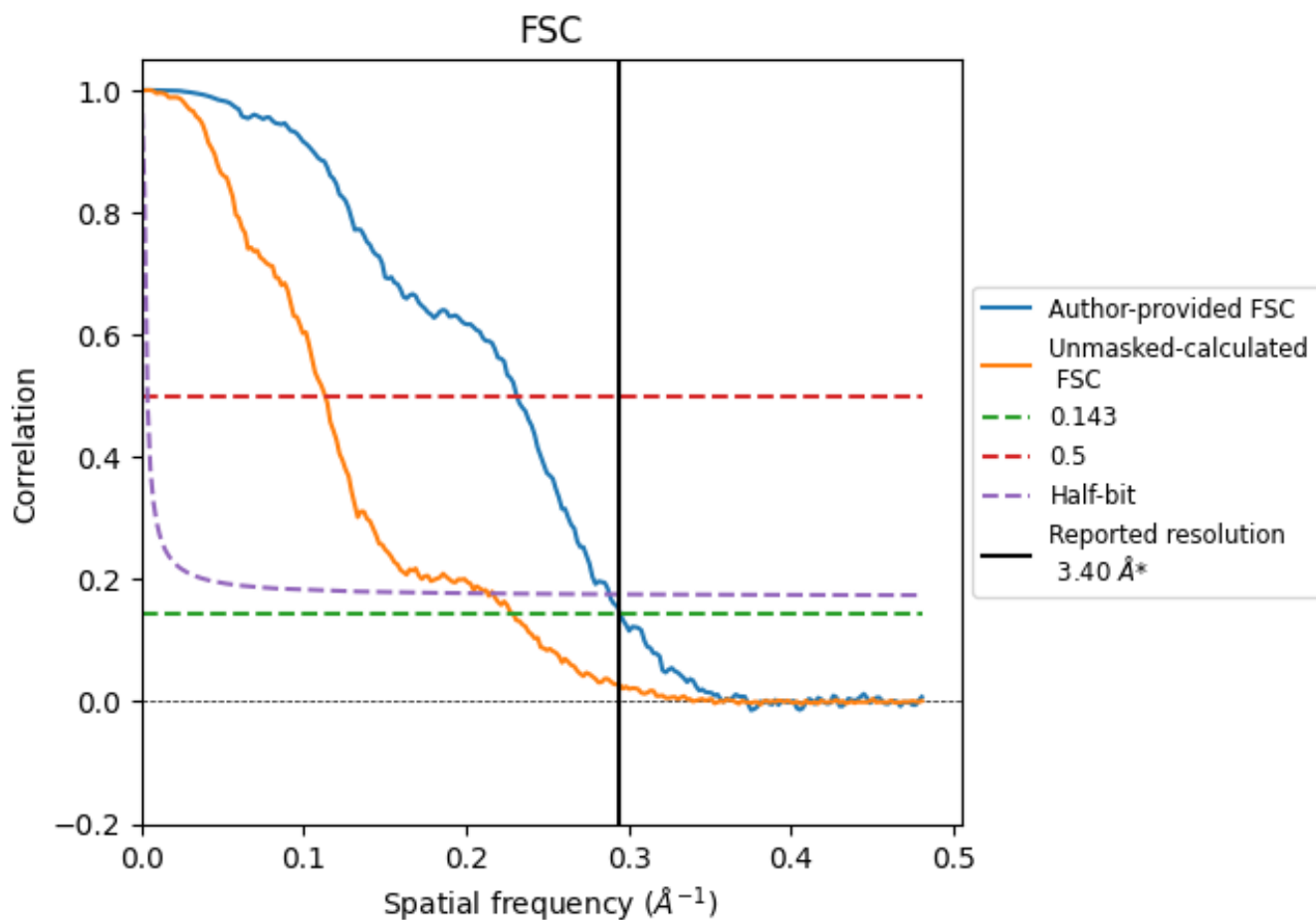


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

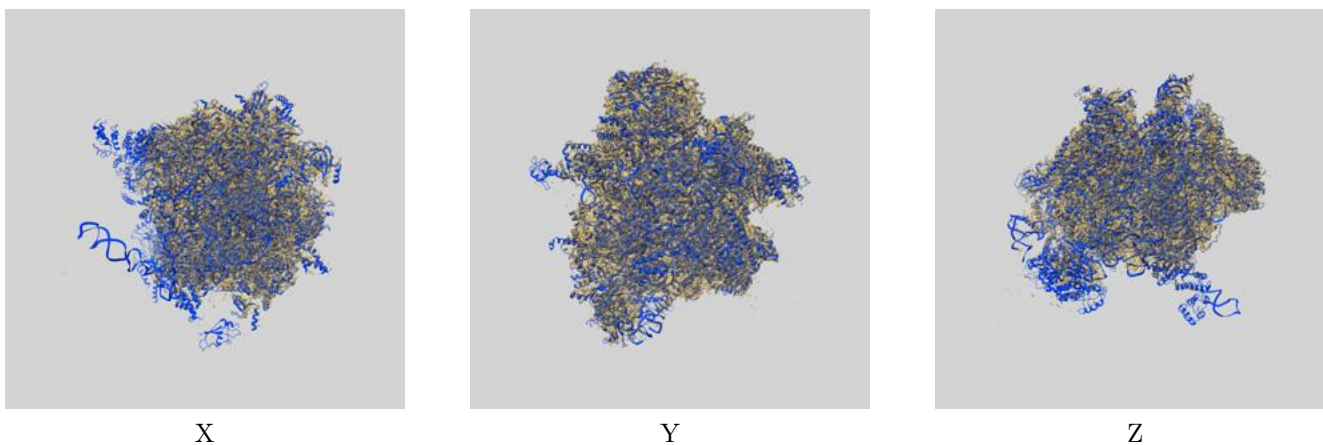
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	4.32	3.47
Unmasked-calculated*	4.36	8.83	4.69

*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 4.36 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

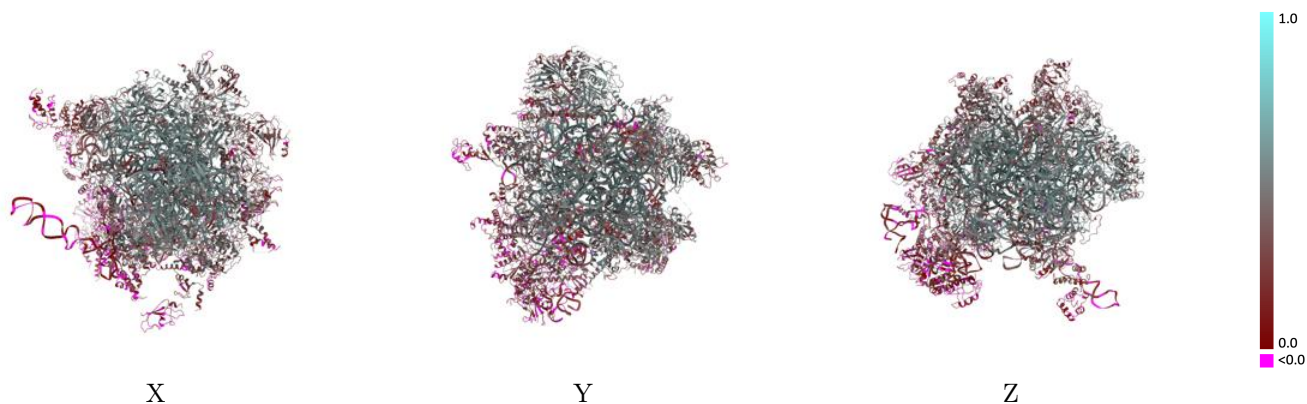
This section contains information regarding the fit between EMDB map EMD-13329 and PDB model 7PD3. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



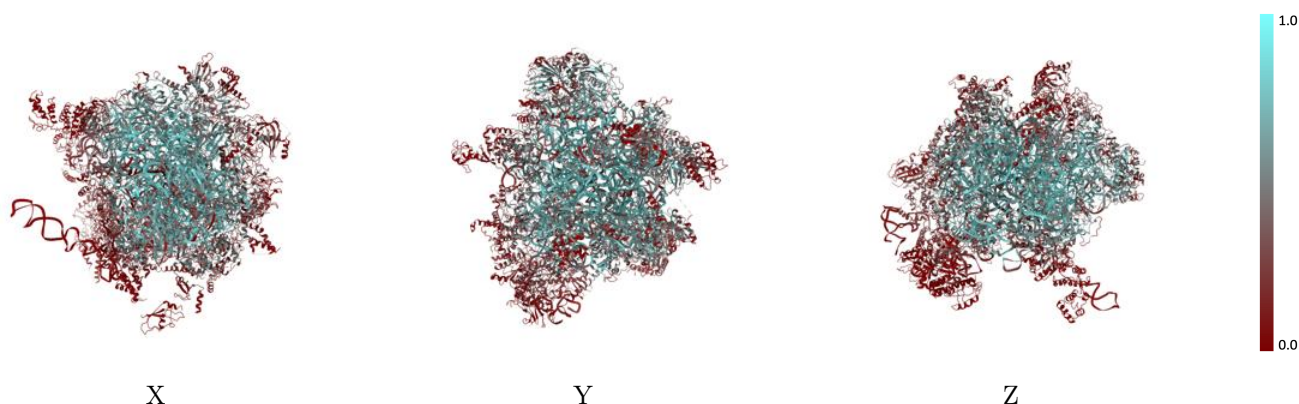
The images above show the 3D surface view of the map at the recommended contour level 0.15 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



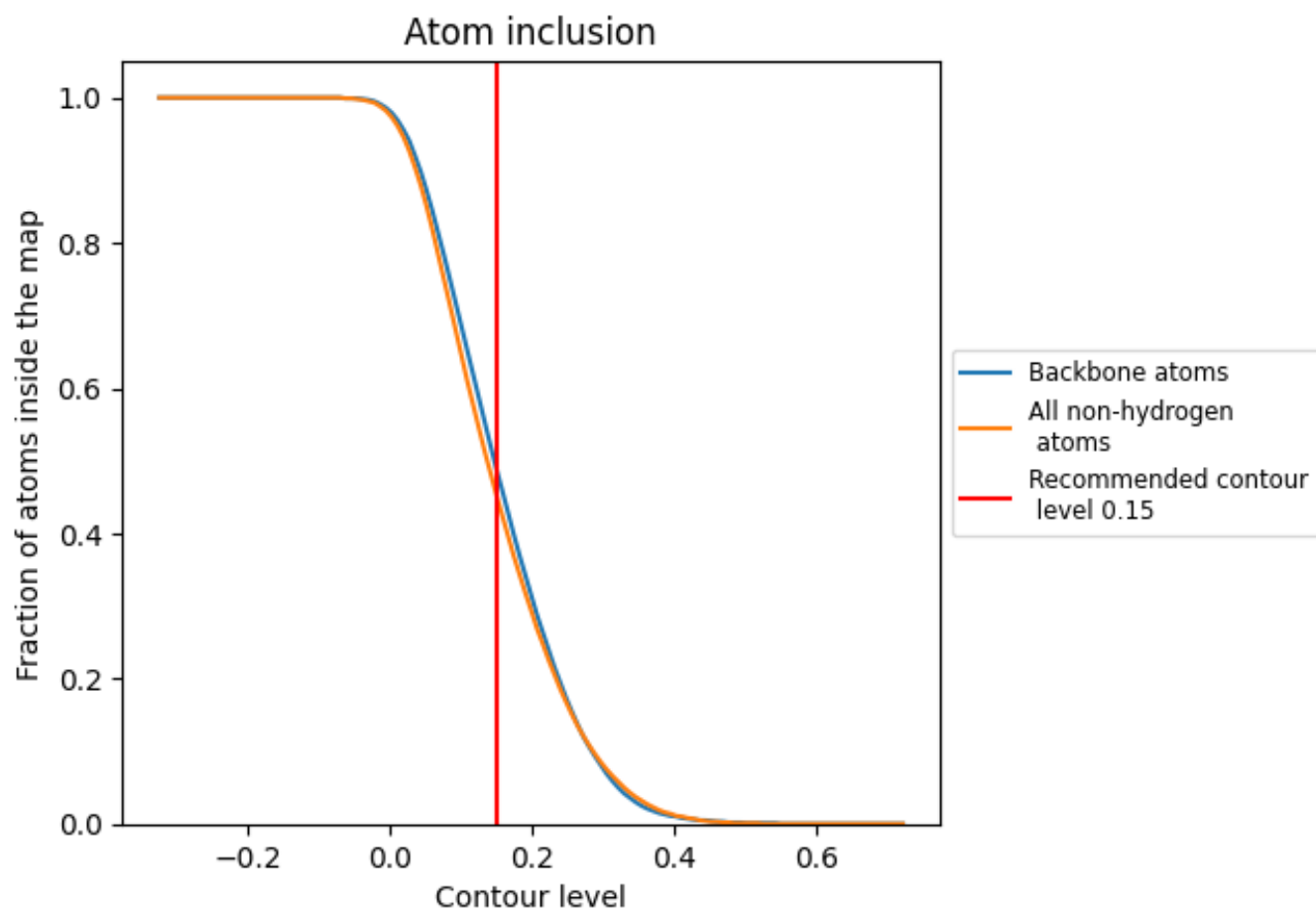
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.15).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 49% of all backbone atoms, 45% 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 (0.15) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4530	 0.3940
0	 0.4700	 0.4540
1	 0.4090	 0.3450
2	 0.7920	 0.5740
3	 0.6970	 0.5170
4	 0.6630	 0.5020
5	 0.4340	 0.4320
6	 0.1970	 0.2300
7	 0.2710	 0.3720
8	 0.0150	 0.1150
9	 0.3970	 0.4020
A	 0.6810	 0.4870
B	 0.0850	 0.0760
C	 0.0000	 0.0800
D	 0.5610	 0.4640
E	 0.5880	 0.5090
F	 0.4920	 0.3980
G	 0.1230	 0.2610
H	 0.2780	 0.3450
J	 0.0230	 0.1270
K	 0.6210	 0.4960
L	 0.5140	 0.4630
M	 0.4450	 0.3600
N	 0.4210	 0.4090
O	 0.6060	 0.5050
P	 0.2560	 0.2330
Q	 0.4930	 0.4680
R	 0.6070	 0.4720
S	 0.5160	 0.4470
T	 0.6200	 0.4990
U	 0.4750	 0.4460
V	 0.2210	 0.3090
W	 0.5490	 0.4580
X	 0.4000	 0.3780
Y	 0.5200	 0.4550



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Chain	Atom inclusion	Q-score
Z	 0.5010	 0.4380
a	 0.4990	 0.4620
b	 0.4940	 0.4110
c	 0.3350	 0.3890
d	 0.1740	 0.2970
e	 0.0040	 0.0830
f	 0.1060	 0.1740
g	 0.3540	 0.3140
h	 0.1340	 0.2180
i	 0.6530	 0.4910
j	 0.3900	 0.3370
k	 0.1140	 0.2240
l	 0.1990	 0.2890
m	 0.0000	 0.0580
o	 0.4740	 0.4140
p	 0.1250	 0.1890
q	 0.1320	 0.1760
r	 0.5410	 0.4520
s	 0.5100	 0.4700
t	 0.0000	 0.2160
u	 0.1440	 0.3250
v	 0.0330	 0.2480
w	 0.0000	 0.1020
x	 0.2020	 0.2730
y	 0.2960	 0.3400
z	 0.2960	 0.3550