



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 02:40 AM UTC

PDB ID : 7L20 / pdb_00007L20
EMDB ID : EMD-23121
Title : Cryo-EM structure of the human 39S mitoribosomal subunit in complex with RRFmt and EF-G2mt.
Authors : Agrawal, E.; Koripella, R.
Deposited on : 2020-12-15
Resolution : 3.15 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

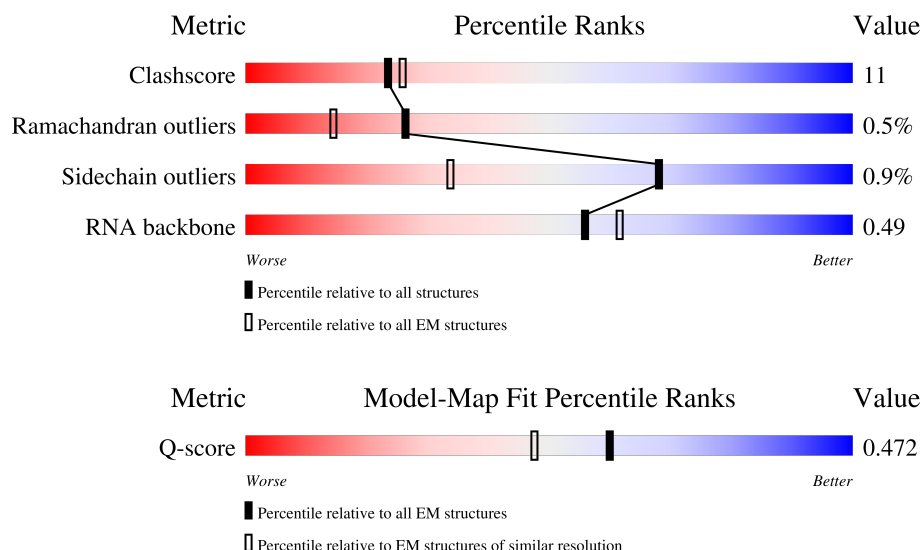
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.15 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	14486 (2.65 - 3.65)

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	A	1559	
2	B	73	
3	D	305	

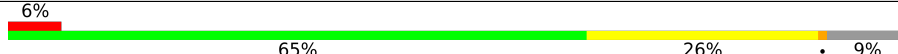
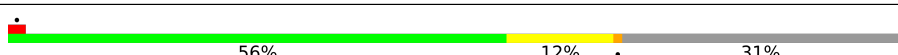
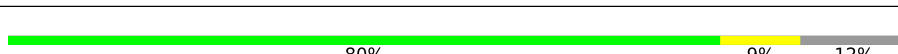
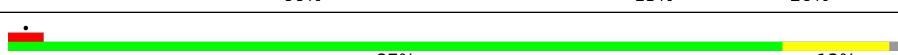
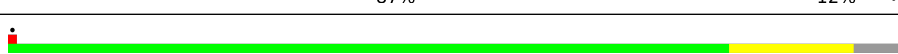
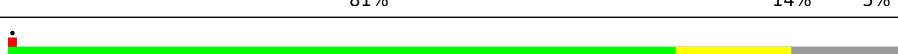
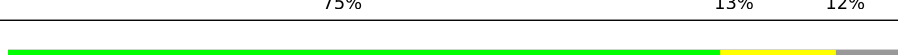
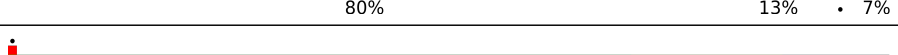
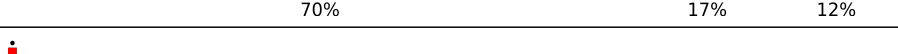
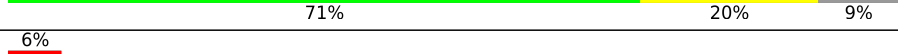
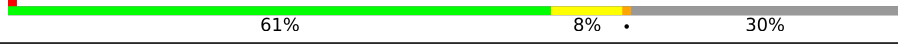
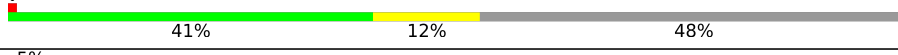
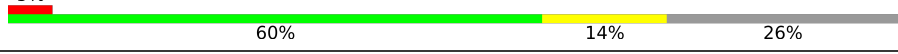
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	F	311	
5	H	267	
6	K	178	
7	L	145	
8	M	296	
9	O	175	
10	R	149	
11	S	205	
12	T	212	
13	W	148	
14	X	256	
15	Y	250	
16	Z	161	
17	0	188	
18	1	65	
19	2	92	
20	3	188	
21	4	103	
22	8	206	
23	b	155	
24	e	279	
25	g	166	
26	i	128	
27	j	123	
28	m	128	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	o	102	
30	q	222	
31	r	196	
32	J	192	
33	I	261	
34	N	251	
35	P	179	
36	U	153	
37	V	216	
38	E	348	
39	5	423	
40	6	380	
41	7	338	
42	9	137	
43	a	142	
44	c	332	
45	d	306	
46	f	194	
47	h	158	
48	k	112	
49	l	138	
50	p	206	
51	s	439	
52	Q	292	
53	u	65	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	TA	198	
54	TB	198	
54	TC	198	
55	z	204	
56	w	696	

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
59	GCP	w	801	-	-	X	-

2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 110234 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 RNA chain called 16S rRNA mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1527	Total	C	N	O	P	0	0
			32395	14536	5844	10488	1527		

- Molecule 2 is a RNA chain called tRNAval.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	56	Total	C	N	O	P	0	0
			1191	534	214	387	56		

- Molecule 3 is a protein called 39S ribosomal protein L2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	239	Total	C	N	O	S	0	0
			1866	1162	377	318	9		

- Molecule 4 is a protein called 39S ribosomal protein L4, mitochondrial.

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

- Molecule 5 is a protein called 39S ribosomal protein L9, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
5	H	98	Total	C	N	O	0	0
			806	510	156	140		

- Molecule 6 is a protein called 39S ribosomal protein L13, mitochondrial.

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

- Molecule 7 is a protein called 39S ribosomal protein L14, mitochondrial.

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

- Molecule 8 is a protein called 39S ribosomal protein L15, mitochondrial.

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

- Molecule 9 is a protein called 39S ribosomal protein L17, mitochondrial.

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

- Molecule 10 is a protein called 39S ribosomal protein L20, mitochondrial.

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

- Molecule 11 is a protein called 39S ribosomal protein L21, mitochondrial.

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

- Molecule 12 is a protein called 39S ribosomal protein L22, mitochondrial.

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

- Molecule 13 is a protein called 39S ribosomal protein L27, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	W	111	Total	C	N	O	S	0	0
			871	558	164	146	3		

- Molecule 14 is a protein called 39S ribosomal protein L28, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	X	243	Total	C	N	O	S	0	0
			2027	1310	350	362	5		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	148	ALA	THR	variant	UNP Q13084
X	149	SER	PRO	variant	UNP Q13084
X	150	GLY	LYS	variant	UNP Q13084

- Molecule 15 is a protein called 39S ribosomal protein L47, mitochondrial.

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

- Molecule 16 is a protein called 39S ribosomal protein L30, mitochondrial.

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

- Molecule 17 is a protein called 39S ribosomal protein L32, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	0	108	Total	C	N	O	S	0	0
			880	545	172	157	6		

- Molecule 18 is a protein called 39S ribosomal protein L33, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	52	Total	C	N	O	S	0	0
			433	278	83	70	2		

- Molecule 19 is a protein called 39S ribosomal protein L34, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	2	46	Total	C	N	O	S	0	0
			376	233	83	59	1		

- Molecule 20 is a protein called 39S ribosomal protein L35, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	3	95	Total	C	N	O	S	0	0
			831	539	162	127	3		

- Molecule 21 is a protein called 39S ribosomal protein L36, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	4	38	Total	C	N	O	S	0	0
			342	217	72	49	4		

- Molecule 22 is a protein called 39S ribosomal protein L40, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	8	99	Total	C	N	O	S	0	0
			836	535	144	155	2		

- Molecule 23 is a protein called 39S ribosomal protein L43, mitochondrial.

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

- Molecule 24 is a protein called 39S ribosomal protein L46, mitochondrial.

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

- Molecule 25 is a protein called 39S ribosomal protein L49, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	g	132	Total	C	N	O	S	0	0
			1096	709	191	194	2		

- Molecule 26 is a protein called 39S ribosomal protein L51, mitochondrial.

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

- Molecule 27 is a protein called cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	j	93	Total	C	N	O	S	0	0
			740	460	143	135	2		

- Molecule 28 is a protein called 39S ribosomal protein L55, mitochondrial.

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

- Molecule 29 is a protein called Ribosomal protein 63, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	o	94	Total	C	N	O	S	0	0
			797	501	165	128	3		

- Molecule 30 is a protein called Growth arrest and DNA damage-inducible proteins-interacting protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	q	168	Total	C	N	O	S	0	0
			1293	801	254	233	5		

- Molecule 31 is a protein called 39S ribosomal protein S18a, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	r	162	Total	C	N	O	S	0	0
			1322	839	252	223	8		

- Molecule 32 is a protein called 39S ribosomal protein L11, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	175	Total	C	N	O	S	0	0
			1330	847	237	244	2		

- Molecule 33 is a protein called 39S ribosomal protein L10, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	I	179	Total	C	N	O	S	0	0
			1435	925	258	242	10		

- Molecule 34 is a protein called 39S ribosomal protein L16, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	N	222	Total	C	N	O	S	0	0
			1786	1143	326	307	10		

- Molecule 35 is a protein called Mitochondrial ribosomal protein L18, isoform CRA_b.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	P	143	Total	C	N	O	S	0	0
			1165	729	223	208	5		

- Molecule 36 is a protein called 39S ribosomal protein L23, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	U	152	Total	C	N	O	S	0	0
			1222	773	233	213	3		

- Molecule 37 is a protein called 39S ribosomal protein L24, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	V	206	Total	C	N	O	S	0	0
			1682	1071	299	304	8		

- Molecule 38 is a protein called 39S ribosomal protein L3, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	E	306	Total	C	N	O	S	0	0
			2410	1547	419	433	11		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	5	393	Total	C	N	O	S	0	0
			3205	2070	559	565	11		

- Molecule 40 is a protein called 39S ribosomal protein L38, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	6	354	Total	C	N	O	S	0	0
			2948	1881	525	533	9		

- Molecule 41 is a protein called 39S ribosomal protein L39, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	7	297	Total	C	N	O	S	0	0
			2410	1540	409	443	18		

- Molecule 42 is a protein called 39S ribosomal protein L41, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	9	124	Total	C	N	O	S	0	0
			997	644	170	181	2		

- Molecule 43 is a protein called 39S ribosomal protein L42, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	a	108	Total	C	N	O	S	0	0
			896	560	162	169	5		

- Molecule 44 is a protein called 39S ribosomal protein L44, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	c	289	Total	C	N	O	S	0	0
			2322	1483	400	430	9		

- Molecule 45 is a protein called 39S ribosomal protein L45, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	d	257	Total	C	N	O	S	0	0
			2075	1326	363	372	14		

- Molecule 46 is a protein called 39S ribosomal protein L48, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	f	146	Total	C	N	O	S	0	0
			1126	714	186	222	4		

- Molecule 47 is a protein called 39S ribosomal protein L50, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	h	110	Total	C	N	O	S	0	0
			894	568	156	167	3		

- Molecule 48 is a protein called 39S ribosomal protein L53, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	k	96	Total	C	N	O	S	0	0
			743	462	143	133	5		

- Molecule 49 is a protein called 39S ribosomal protein L54, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	l	72	Total	C	N	O	S	0	0
			619	394	112	111	2		

- Molecule 50 is a protein called Peptidyl-tRNA hydrolase ICT1, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	p	152	Total	C	N	O	S	0	0
			1227	762	232	229	4		

- Molecule 51 is a protein called 39S ribosomal protein S30, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	393	Total	C	N	O	S	0	0
			3178	2036	565	563	14		

- Molecule 52 is a protein called 39S ribosomal protein L19, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Q	220	Total	C	N	O	S	0	0
			1834	1174	326	325	9		

- Molecule 53 is a protein called 39 S P-site finger.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	u	65	Total	C	N	O	0	0
			325	195	65	65		

- Molecule 54 is a protein called 39S ribosomal protein L12, mitochondrial.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	TA	45	Total	C	N	O	0	0
			345	222	54	69		
54	TB	27	Total	C	N	O	0	0
			213	137	33	43		
54	TC	71	Total	C	N	O	0	0
			352	210	71	71		

- Molecule 55 is a protein called Ribosome-recycling factor, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	197	Total	C	N	O	S	0	0
			1525	942	274	301	8		

- Molecule 56 is a protein called Ribosome-releasing factor 2, mitochondrial.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	w	696	Total	C	N	O	S	0	0
			5422	3424	932	1042	24		

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	86	LEU	THR	conflict	UNP Q969S9
w	90	VAL	ILE	conflict	UNP Q969S9
w	94	THR	SER	conflict	UNP Q969S9
w	197	ASP	MET	conflict	UNP Q969S9
w	216	ARG	LYS	conflict	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	GLY	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	LYS	deletion	UNP Q969S9
w	?	-	HIS	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9
w	?	-	GLN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	ASN	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ALA	deletion	UNP Q969S9
w	?	-	GLU	deletion	UNP Q969S9
w	?	-	ARG	deletion	UNP Q969S9

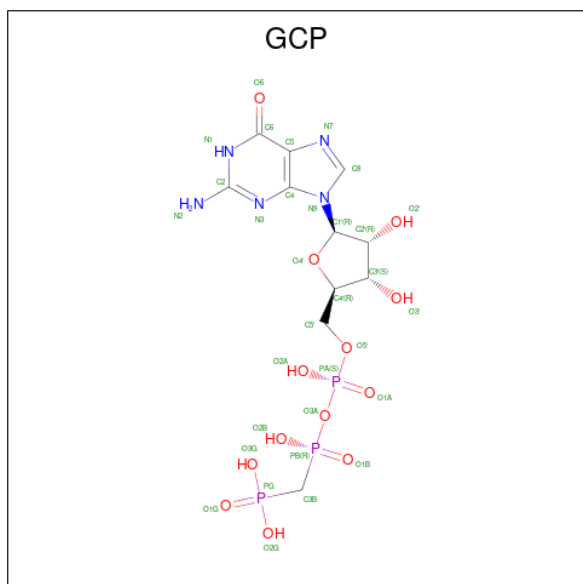
- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	A	97	Total 97	Mg 97	0
57	D	1	Total 1	Mg 1	0
57	W	1	Total 1	Mg 1	0
57	g	1	Total 1	Mg 1	0
57	E	1	Total 1	Mg 1	0
57	w	1	Total 1	Mg 1	0

- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	0	1	Total 1	Zn 1	0
58	4	1	Total 1	Zn 1	0
58	r	1	Total 1	Zn 1	0

- Molecule 59 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$).

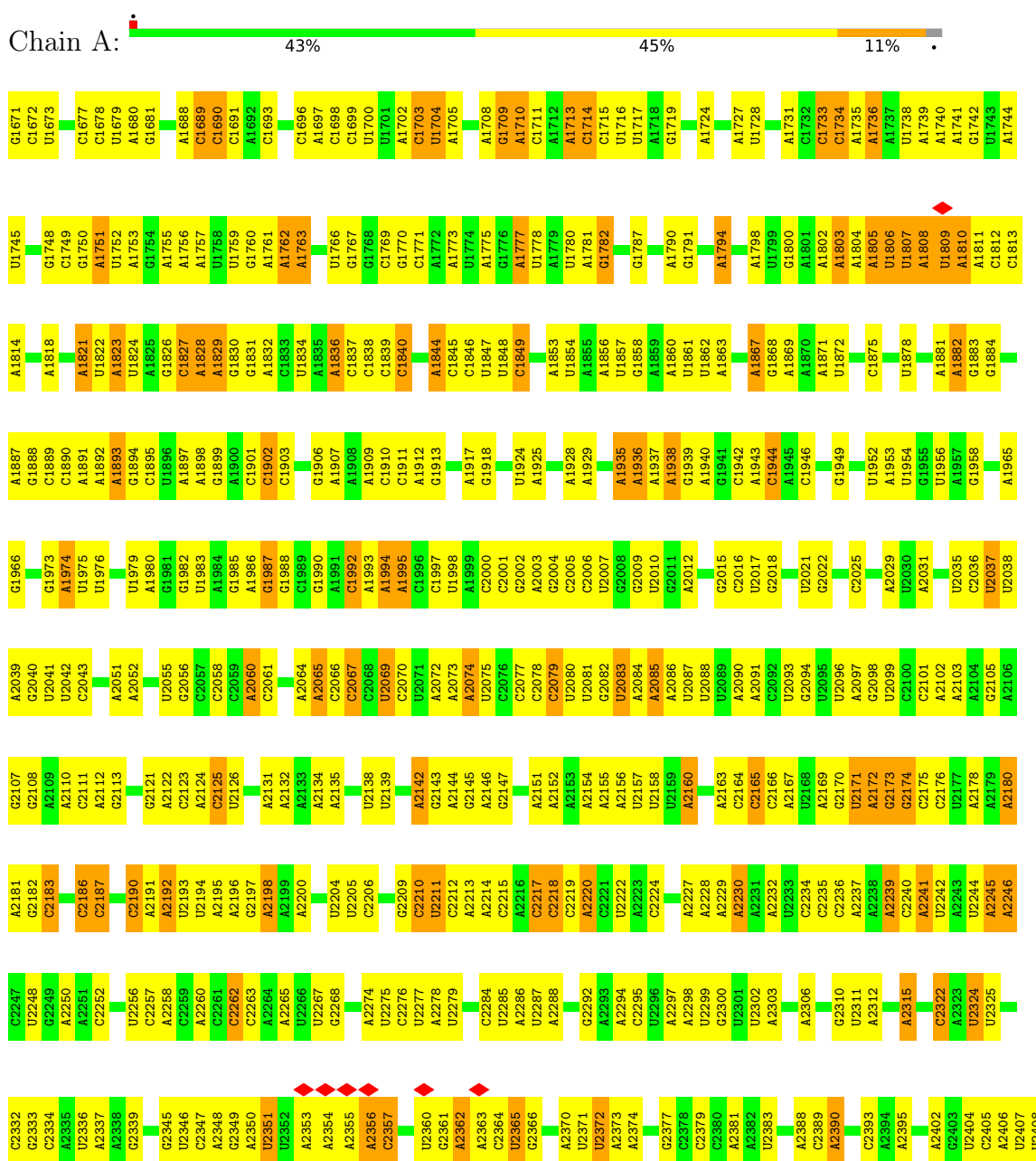


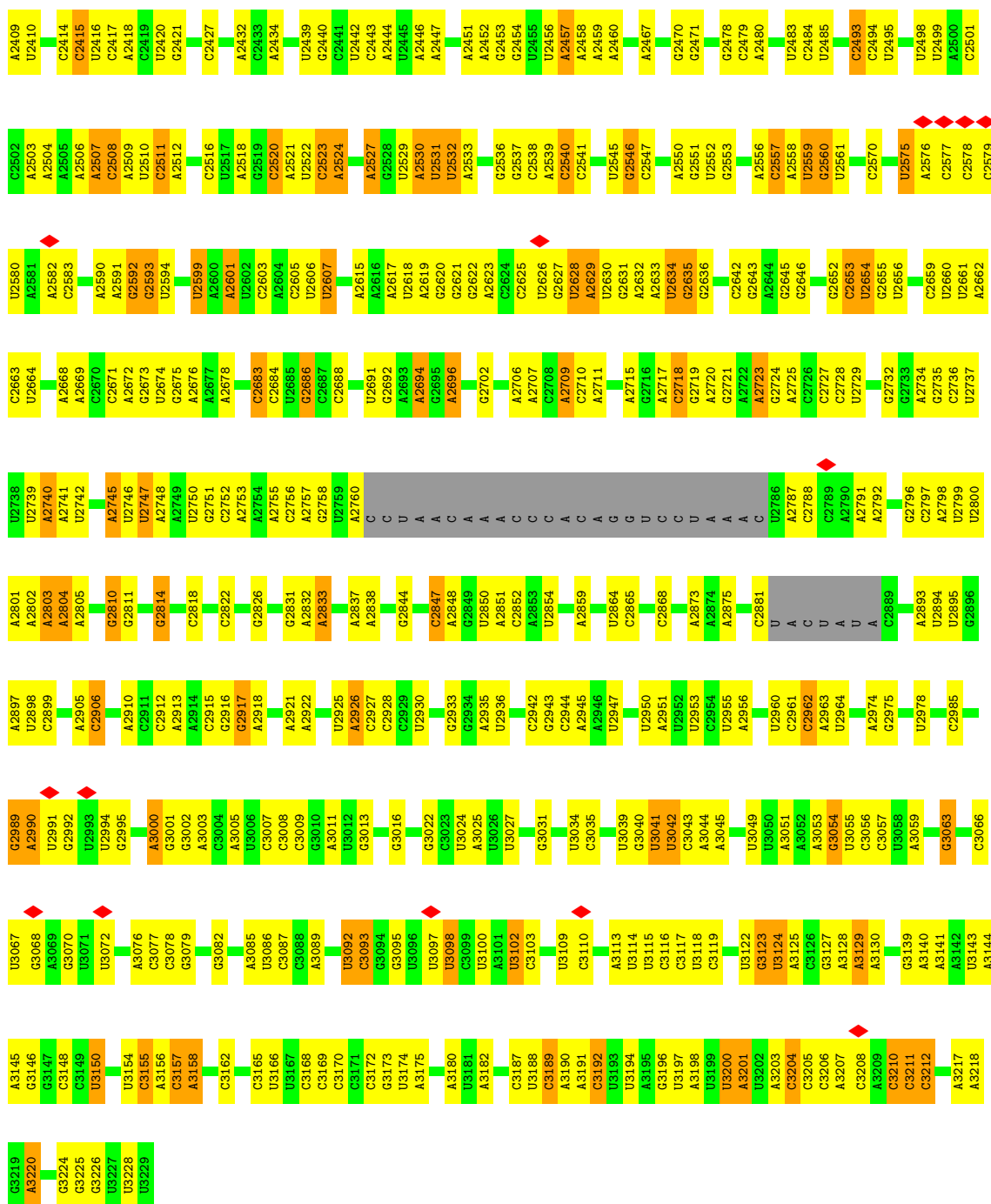
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
59	w	1	32	11	5	13	3	0

3 Residue-property plots

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

• Molecule 1: 16S rRNA mitochondrial

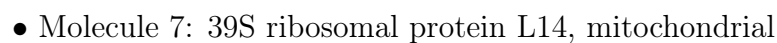
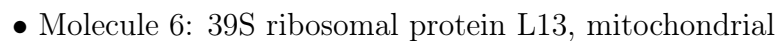


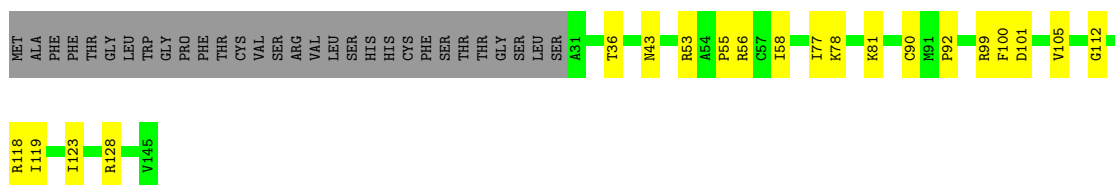


• Molecule 2: tRNAval



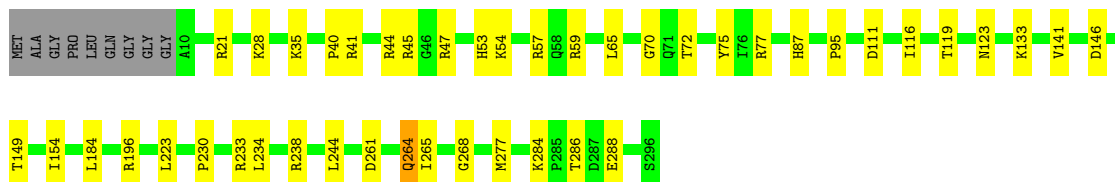
• Molecule 3: 39S ribosomal protein L2, mitochondrial





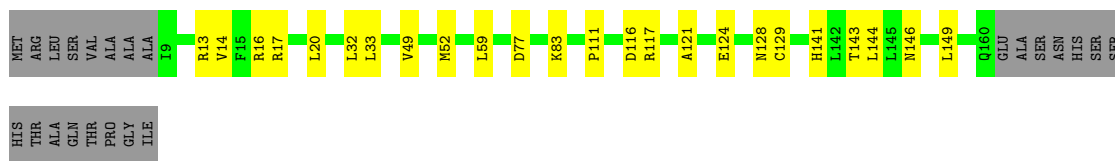
- Molecule 8: 39S ribosomal protein L15, mitochondrial

Chain M: 82% 15% .



- Molecule 9: 39S ribosomal protein L17, mitochondrial

Chain O: 73% 14% 13%



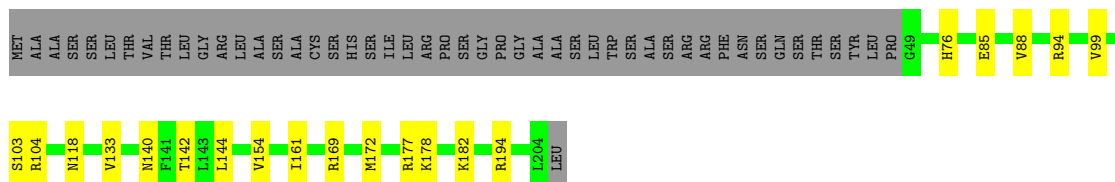
- Molecule 10: 39S ribosomal protein L20, mitochondrial

Chain R: 83% 11% 6%



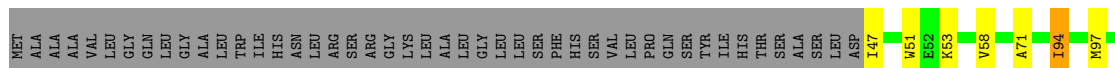
- Molecule 11: 39S ribosomal protein L21, mitochondrial

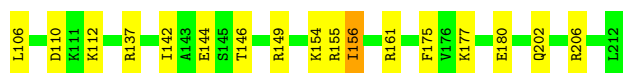
Chain S: 66% 10% 24%



- Molecule 12: 39S ribosomal protein L22, mitochondrial

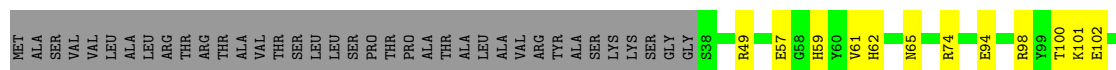
Chain T: 67% 10% 22%





- Molecule 13: 39S ribosomal protein L27, mitochondrial

Chain W: 65% 10% 25%



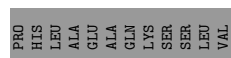
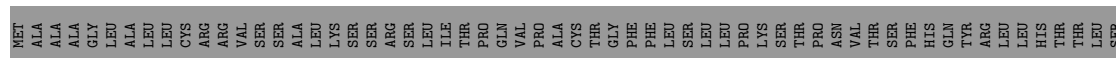
- Molecule 14: 39S ribosomal protein L28, mitochondrial

Chain X: 86% 9% 5%



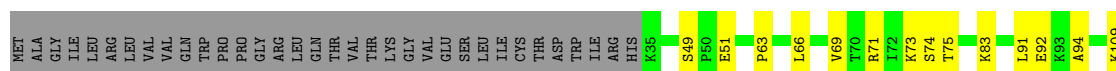
- Molecule 15: 39S ribosomal protein L47, mitochondrial

Chain Y: 58% 12% 30%



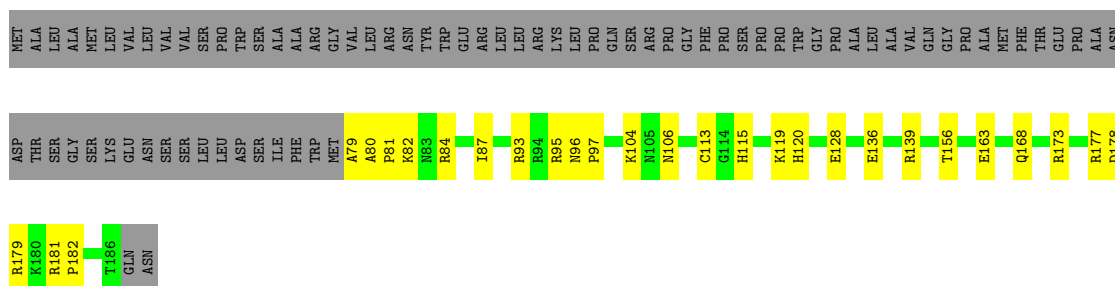
- Molecule 16: 39S ribosomal protein L30, mitochondrial

Chain Z: 62% 12% 25%



- Molecule 17: 39S ribosomal protein L32, mitochondrial

Chain 0: 43% 15% 43%



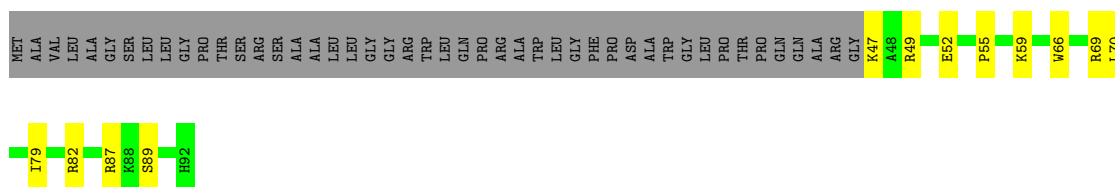
- Molecule 18: 39S ribosomal protein L33, mitochondrial

Chain 1: 66% 14% 20%



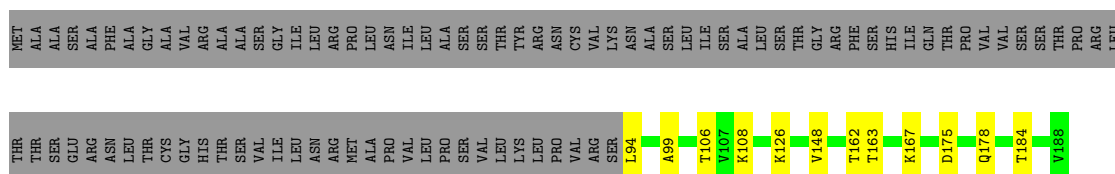
- Molecule 19: 39S ribosomal protein L34, mitochondrial

Chain 2: 37% 13% 50%



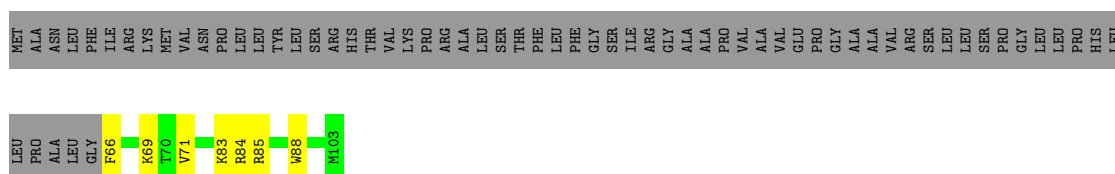
- Molecule 20: 39S ribosomal protein L35, mitochondrial

Chain 3: 44% 6% 49%



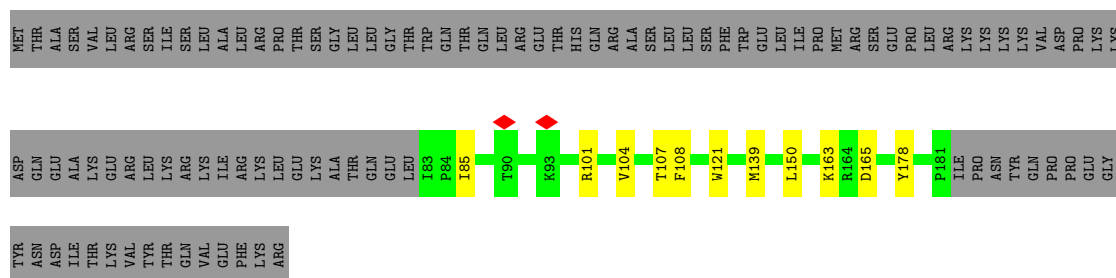
- Molecule 21: 39S ribosomal protein L36, mitochondrial

Chain 4: 30% 7% 63%



- Molecule 22: 39S ribosomal protein L40, mitochondrial

Chain 8: 43% 5% 52%

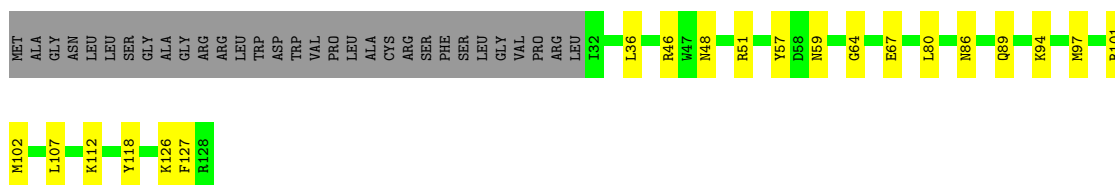


- Molecule 23: 39S ribosomal protein L43, mitochondrial

- Molecule 24: 39S ribosomal protein L46, mitochondrial

- Molecule 25: 39S ribosomal protein L49, mitochondrial

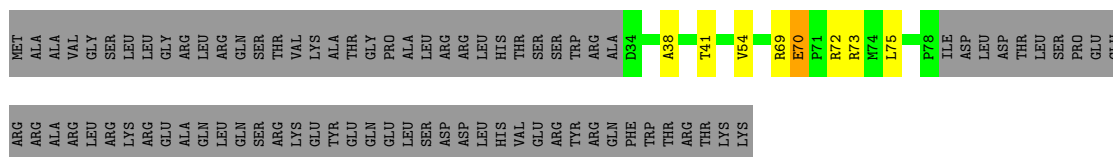
- Molecule 26: 39S ribosomal protein L51, mitochondrial



- Molecule 27: cDNA FLJ76418, highly similar to Homo sapiens mitochondrial ribosomal protein L52 (MRPL52), transcript variant 1, mRNA



- Molecule 28: 39S ribosomal protein L55, mitochondrial



- Molecule 29: Ribosomal protein 63, mitochondrial



- Molecule 30: Growth arrest and DNA damage-inducible proteins-interacting protein 1

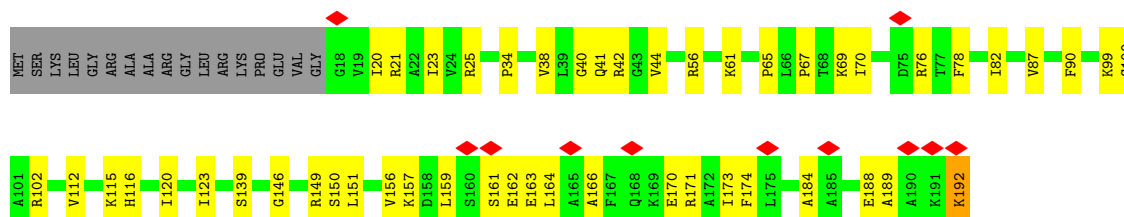


- Molecule 31: 39S ribosomal protein S18a, mitochondrial

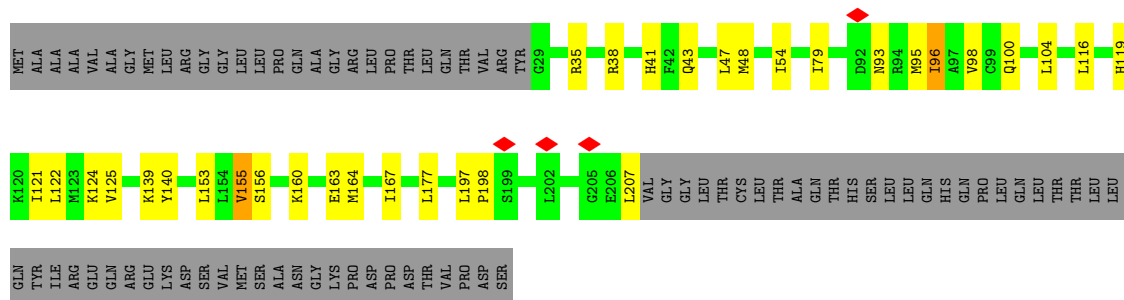




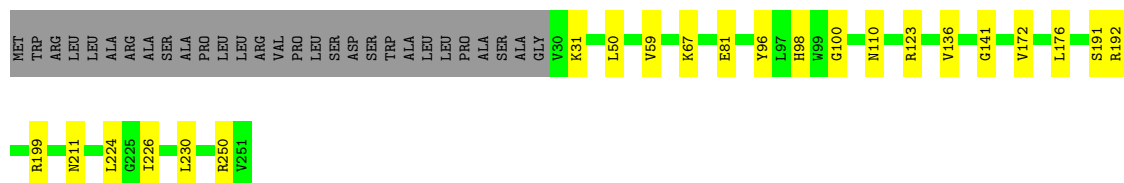
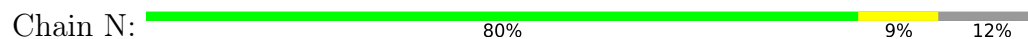
- Molecule 32: 39S ribosomal protein L11, mitochondrial



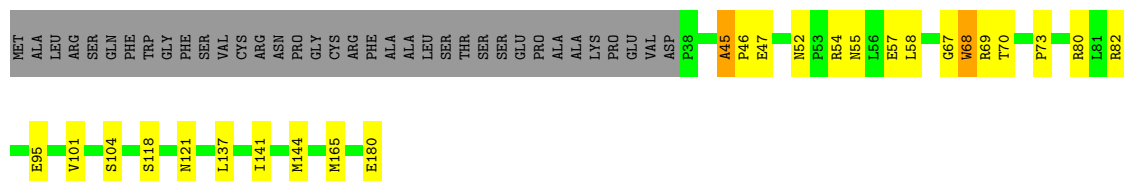
- Molecule 33: 39S ribosomal protein L10, mitochondrial



- Molecule 34: 39S ribosomal protein L16, mitochondrial



- Molecule 35: Mitochondrial ribosomal protein L18, isoform CRA_b



- Molecule 36: 39S ribosomal protein L23, mitochondrial

Chain U:  87% 12%



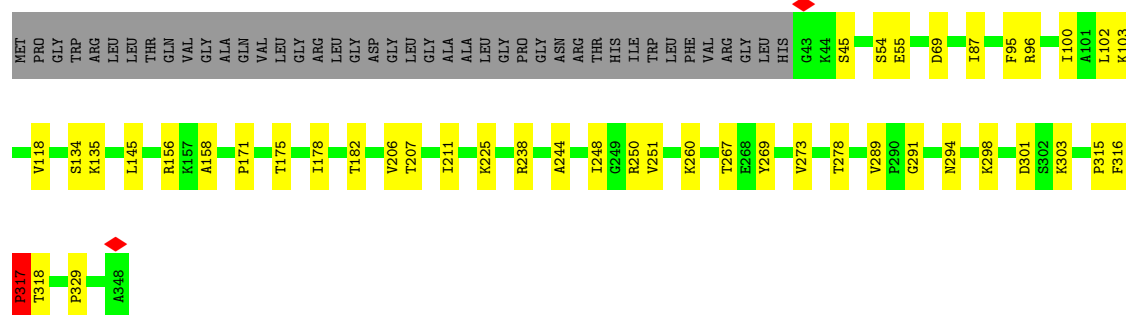
- Molecule 37: 39S ribosomal protein L24, mitochondrial

Chain V:  81% 14% 5%



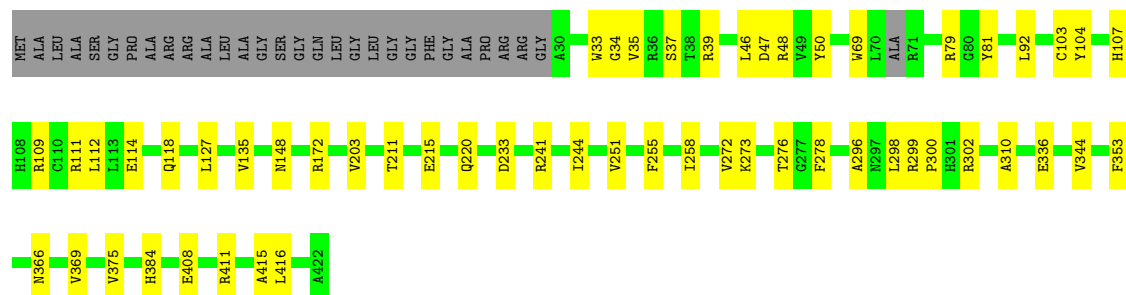
- Molecule 38: 39S ribosomal protein L3, mitochondrial

Chain E:  75% 13% 12%



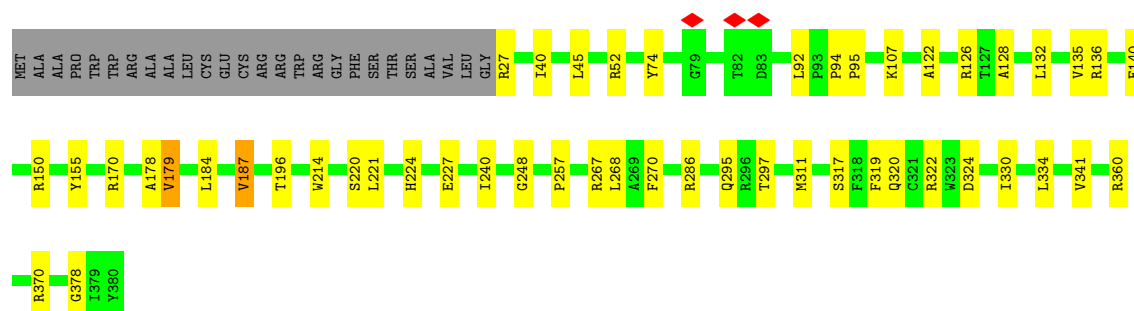
- Molecule 39: 39S ribosomal protein L37, mitochondrial

Chain 5:  80% 13% 7%

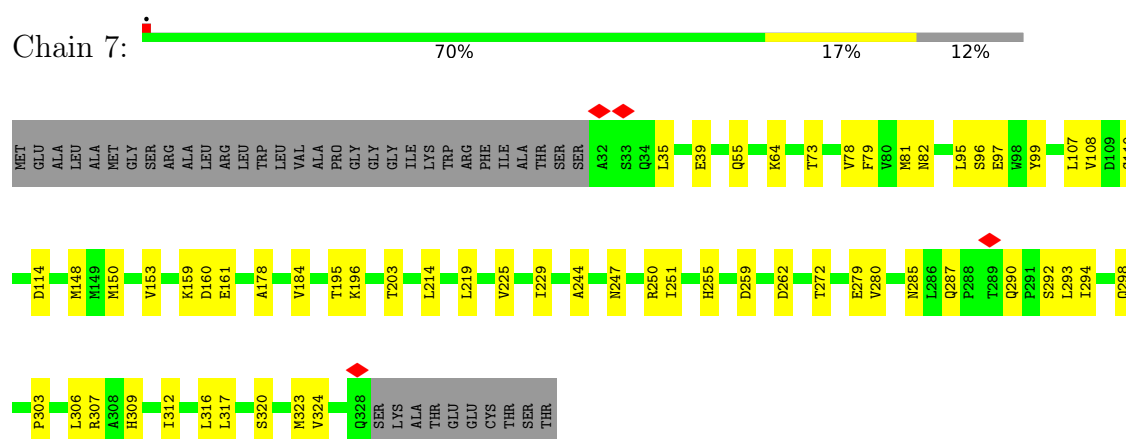


- Molecule 40: 39S ribosomal protein L38, mitochondrial

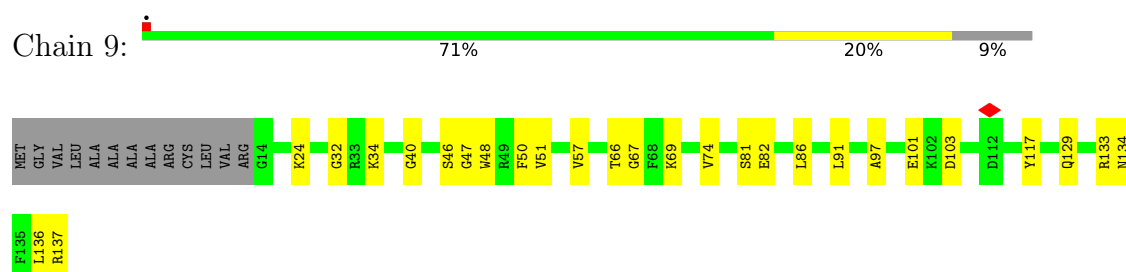
Chain 6:  80% 13% 7%



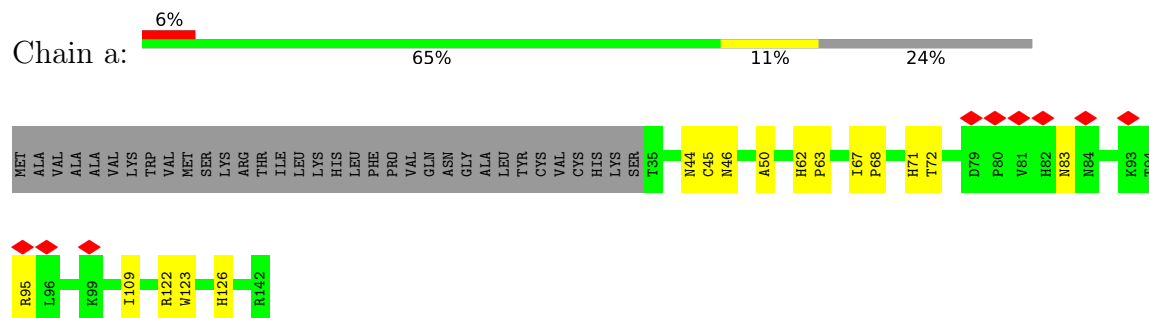
- Molecule 41: 39S ribosomal protein L39, mitochondrial



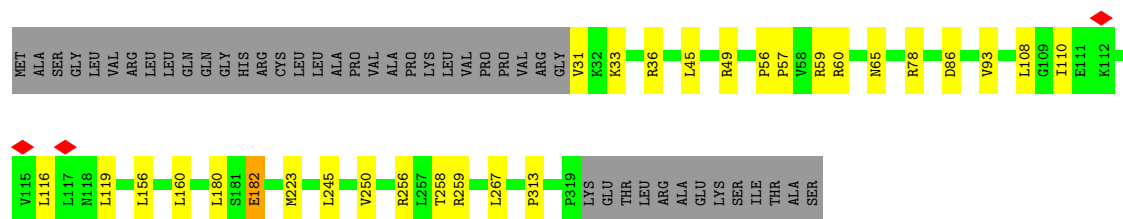
- Molecule 42: 39S ribosomal protein L41, mitochondrial



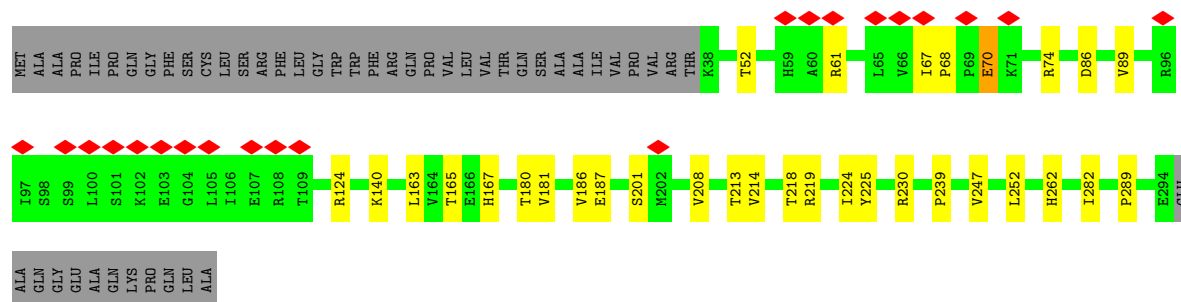
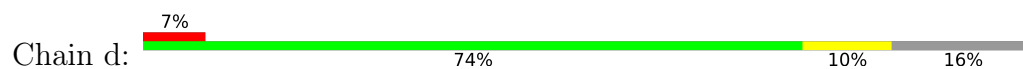
- Molecule 43: 39S ribosomal protein L42, mitochondrial



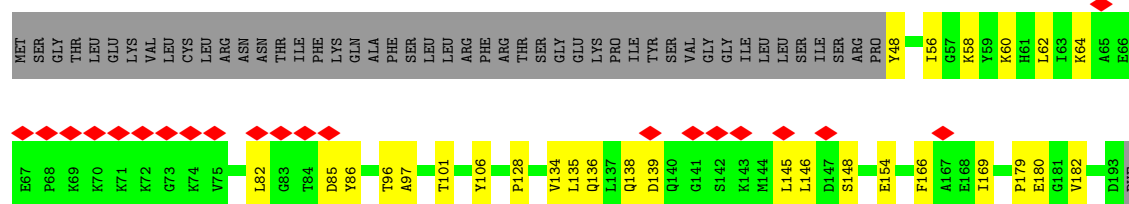
- Molecule 44: 39S ribosomal protein L44, mitochondrial



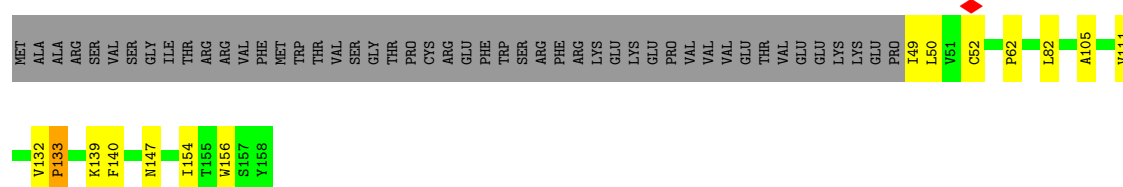
- Molecule 45: 39S ribosomal protein L45, mitochondrial



- Molecule 46: 39S ribosomal protein L48, mitochondrial



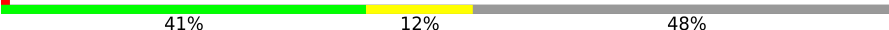
- Molecule 47: 39S ribosomal protein L50, mitochondrial



- Molecule 48: 39S ribosomal protein L53, mitochondrial



- Molecule 49: 39S ribosomal protein L54, mitochondrial

Chain l: 

MET ALA THR LYS ARG LEU PHE GLY ALA THR ARG THR TRP ALA GLY TRP TRP GLY ALA TRP GLU LEU LEU ASN PRO ALA THR SER GLY ARG LEU LEU ALA ARG ASP TYR ALA LYS LYS VAL MET LYS GLY ALA LYS SER GLY LYS GLY ALA VAL THR THR GLU LEU LYS ASP PRO ASP

VAL CYS THR ASP PRO V66 V67 L68 T69 T70 W73 G74 V75 N76 N77 Y78 K79 E80 Y92 Y97 F97 L101 G102 S114 R115 E116 I126 H129 S133 R137 LEU

- Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial

Chain p: 

MET ALA THR ARG CYS LEU ARG TRP GLY LEU SER ARG ALA GLY VAL TRP LEU LEU PRO PRO PRO ALA CYS ARG PRO ARG ALA LEU HIS LYS GLN LYS ASP GLY THR E98 Y49 P62 N63 G64 A65 K66 Q67 A68 D71 T78 I79 C82 R83 S84 S85 G86 PRO

GLY GLY GLN ASN VAL ASN K94 V95 K98 V101 H104 T107 L133 E138 L147 R155 D156 M157 E167 P168 T169 K170 E171 D172 R177 E181 N182 R185 Q190 K191 H194 S195 A196 VAL LYS THR SER ARG ARG VAL ASP MET ASP

- Molecule 51: 39S ribosomal protein S30, mitochondrial

Chain s: 

MET ALA ALA ALA ARG CYS TRP ARG PRO LEU LEU ARG GLY PRO ARG LEU SER THR HIS THR ALA ASN ALA ALA THR ALA THR THR GLU THR THR CYS GLN ASP VAL ALA THR P40 W66 T89 R81 T84 K85 Y91 Y94 D103 T112 A123 E124

P125 E126 P127 E128 N129 E130 P131 E132 P133 D138 Y156 R162 V163 H164 V171 D178 V181 L188 N192 R203 H207 L229 D234 N238 N239 C266 K267 K270 F274 N280 F299 L302 R310 L332 A349 D350 V356

A359 L374 N375 T376 L377 N391 E403 T404 I405 E406 D407 V410 K411 D416 V422 L426 E432 LYS SER GLN LEU LEU ASN

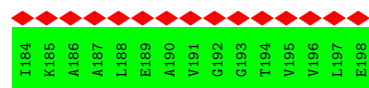
- Molecule 52: 39S ribosomal protein L19, mitochondrial

Chain Q: 

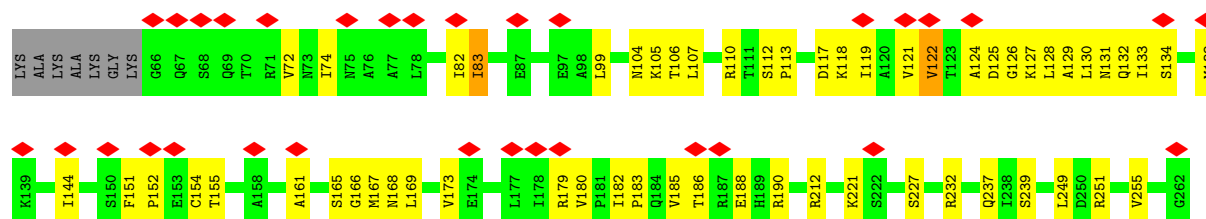
MET ALA CYS ILE ALA GLY HIS TRP ALA MET GLY LEU ARG SER PHE GLN ALA ARG LEU LEU PRO PRO PRO ALA ALA THR SER THR GLY PRO PRO GLU PRO GLY PHE GLN PRO PRO PRO PRO

VAL ILE VAL ASP LYS HIS ARG VAL VAL GLU GLU R73 L76 R84 Q85 D88 F92 R96 L100 I108 L117 T120 Y125 Q132 L151 R152 Q158 E161 L166 S186 K205 K221 P228 K231 R244 L247

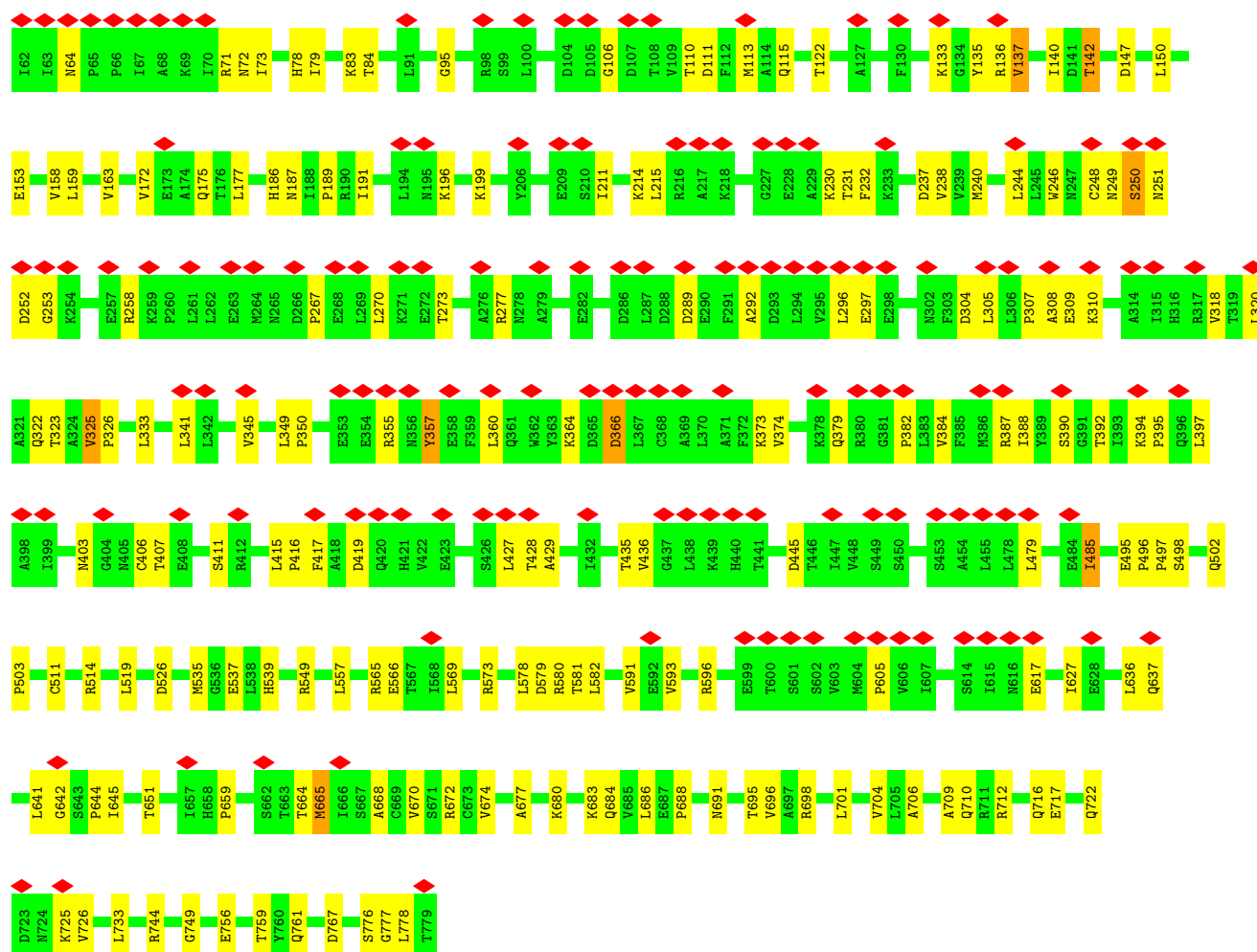
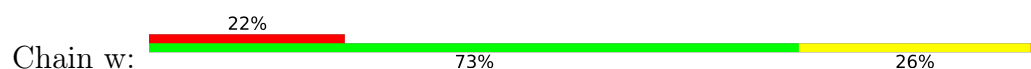
D268 N269 M270 E279 I282 K283 E285 I286 S292



• Molecule 55: Ribosome-recycling factor, mitochondrial



• Molecule 56: Ribosome-releasing factor 2, mitochondrial



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132008	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 ($e^-/\text{\AA}^2$)	71	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	DIRECT ELECTRON DE-16 (4k x 4k)	Depositor
Maximum map value	3.217	Depositor
Minimum map value	-1.964	Depositor
Average map value	-0.004	Depositor
Map value standard deviation	0.126	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	429.30002, 429.30002, 429.30002	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07325, 1.07325, 1.07325	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	A	0.11	0/36245	0.27	0/56418
2	B	0.23	0/1328	0.41	0/2056
3	D	0.34	0/1904	0.59	0/2561
4	F	0.43	0/2071	0.69	3/2817 (0.1%)
5	H	0.34	0/820	0.69	0/1102
6	K	0.45	0/1495	0.63	0/2029
7	L	0.38	0/904	0.59	2/1218 (0.2%)
8	M	0.41	0/2359	0.70	0/3185
9	O	0.41	0/1269	0.66	0/1708
10	R	0.43	0/1174	0.67	0/1572
11	S	0.42	0/1276	0.62	0/1729
12	T	0.40	0/1402	0.59	1/1886 (0.1%)
13	W	0.42	0/893	0.62	0/1204
14	X	0.33	0/2081	0.64	2/2812 (0.1%)
15	Y	0.38	0/1552	0.57	0/2079
16	Z	0.41	0/1003	0.61	0/1354
17	0	0.38	0/895	0.69	0/1201
18	1	0.33	0/438	0.58	0/583
19	2	0.45	0/382	0.60	0/507
20	3	0.44	0/852	0.57	0/1136
21	4	0.44	0/350	0.60	0/461
22	8	0.26	0/855	0.56	0/1152
23	b	0.39	0/1202	0.60	0/1626
24	e	0.30	0/1797	0.67	0/2422
25	g	0.41	0/1132	0.63	2/1543 (0.1%)
26	i	0.42	0/849	0.69	2/1135 (0.2%)
27	j	0.36	0/755	0.57	0/1016
28	m	0.25	0/379	0.57	0/510
29	o	0.39	0/818	0.70	0/1097
30	q	0.29	0/1323	0.62	0/1794
31	r	0.41	0/1362	0.62	0/1846
32	J	0.40	2/1348 (0.1%)	0.63	0/1813

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.32	0/1467	0.69	0/1984
34	N	0.39	1/1833 (0.1%)	0.54	0/2468
35	P	0.34	0/1191	0.69	2/1611 (0.1%)
36	U	0.36	0/1252	0.54	0/1697
37	V	0.31	0/1727	0.57	0/2341
38	E	0.38	0/2479	0.59	2/3360 (0.1%)
39	5	0.33	0/3300	0.57	0/4495
40	6	0.32	0/3043	0.58	2/4140 (0.0%)
41	7	0.31	0/2467	0.56	2/3337 (0.1%)
42	9	0.33	0/1025	0.58	0/1379
43	a	0.34	0/923	0.57	0/1254
44	c	0.33	0/2371	0.57	0/3205
45	d	0.30	0/2132	0.63	0/2887
46	f	0.28	0/1144	0.62	0/1551
47	h	0.30	0/917	0.59	0/1249
48	k	0.29	0/754	0.65	1/1017 (0.1%)
49	l	0.27	0/636	0.50	0/860
50	p	0.30	0/1246	0.60	0/1675
51	s	0.39	1/3262 (0.0%)	0.58	1/4435 (0.0%)
52	Q	0.35	0/1875	0.53	0/2523
54	TA	0.22	0/349	0.62	0/475
54	TB	0.26	0/212	0.57	0/286
54	TC	0.08	0/351	0.18	0/488
55	z	0.17	0/1534	0.41	0/2063
56	w	0.16	0/5511	0.43	0/7479
All	All	0.29	4/115514 (0.0%)	0.50	22/163831 (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
3	D	0	1
5	H	0	1
6	K	0	1
8	M	0	2
10	R	0	1
12	T	0	1
16	Z	0	1
17	0	0	1
26	i	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
27	j	0	1
28	m	0	1
30	q	0	1
35	P	0	2
38	E	0	1
41	7	0	1
45	d	0	1
47	h	0	3
50	p	0	2
51	s	0	2
56	w	0	1
All	All	0	26

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
32	J	188	GLU	C-N	8.19	1.45	1.34
34	N	230	LEU	C-N	-7.97	1.19	1.33
51	s	164	HIS	CE1-NE2	7.26	1.39	1.32
32	J	184	ALA	C-N	-6.68	1.25	1.33

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	L	112	GLY	CA-C-N	5.83	132.20	121.70
7	L	112	GLY	C-N-CA	5.83	132.20	121.70
4	F	221	LEU	CA-C-N	5.83	132.67	121.54
4	F	221	LEU	C-N-CA	5.83	132.67	121.54
14	X	126	THR	CA-C-N	5.72	128.30	120.35

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	206	TYR	Peptide
5	H	86	THR	Peptide
6	K	3	SER	Peptide
8	M	264	GLN	Peptide
8	M	286	THR	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32395	0	16443	1157	0
2	B	1191	0	607	6	0
3	D	1866	0	1927	44	0
4	F	2013	0	2044	30	0
5	H	806	0	849	24	0
6	K	1451	0	1448	29	0
7	L	889	0	941	19	0
8	M	2305	0	2378	43	0
9	O	1245	0	1283	22	0
10	R	1153	0	1214	19	0
11	S	1251	0	1322	20	0
12	T	1368	0	1410	26	0
13	W	871	0	898	22	0
14	X	2027	0	2040	17	0
15	Y	1517	0	1561	34	0
16	Z	978	0	1030	12	0
17	0	880	0	902	37	0
18	1	433	0	475	7	0
19	2	376	0	406	20	0
20	3	831	0	883	10	0
21	4	342	0	361	10	0
22	8	836	0	844	10	0
23	b	1178	0	1180	23	0
24	e	1762	0	1767	35	0
25	g	1096	0	1081	23	0
26	i	827	0	857	32	0
27	j	740	0	741	10	0
28	m	372	0	387	7	0
29	o	797	0	804	31	0
30	q	1293	0	1176	18	0
31	r	1322	0	1349	45	0
32	J	1330	0	1405	80	0
33	I	1435	0	1519	47	0
34	N	1786	0	1817	31	0
35	P	1165	0	1162	18	0
36	U	1222	0	1187	15	0
37	V	1682	0	1692	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	E	2410	0	2418	60	0
39	5	3205	0	3201	50	0
40	6	2948	0	2841	38	0
41	7	2410	0	2415	33	0
42	9	997	0	987	29	0
43	a	896	0	847	14	0
44	c	2322	0	2338	30	0
45	d	2075	0	2037	21	0
46	f	1126	0	1106	23	0
47	h	894	0	881	7	0
48	k	743	0	758	28	0
49	l	619	0	611	21	0
50	p	1227	0	1239	20	0
51	s	3178	0	3124	46	0
52	Q	1834	0	1872	27	0
53	u	325	0	75	2	0
54	TA	345	0	363	173	0
54	TB	213	0	234	134	0
54	TC	352	0	169	7	0
55	z	1525	0	1599	213	0
56	w	5422	0	5495	262	0
57	A	97	0	0	0	0
57	D	1	0	0	0	0
57	E	1	0	0	0	0
57	W	1	0	0	0	0
57	g	1	0	0	0	0
57	w	1	0	0	0	0
58	0	1	0	0	0	0
58	4	1	0	0	0	0
58	r	1	0	0	0	0
59	w	32	0	14	13	0
All	All	110234	0	94014	2232	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 11.

The worst 5 of 2232 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)
1:A:2172:A:H2'	32:J:23:ILE:CD1	1.26	1.62
54:TA:68:VAL:CG2	54:TB:85:LEU:HD23	1.21	1.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:z:138:MET:HE1	56:w:636:LEU:CD2	1.08	1.55
48:k:57:HIS:CB	54:TA:53:LEU:HD13	1.37	1.55
48:k:57:HIS:HB3	54:TA:53:LEU:CD1	1.42	1.48

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	
3	D	237/305 (78%)	227 (96%)	9 (4%)	1 (0%)	30	59
4	F	248/311 (80%)	226 (91%)	20 (8%)	2 (1%)	16	46
5	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
6	K	175/178 (98%)	153 (87%)	20 (11%)	2 (1%)	11	39
7	L	113/145 (78%)	102 (90%)	11 (10%)	0	100	100
8	M	285/296 (96%)	248 (87%)	35 (12%)	2 (1%)	18	49
9	O	150/175 (86%)	133 (89%)	16 (11%)	1 (1%)	18	49
10	R	138/149 (93%)	130 (94%)	8 (6%)	0	100	100
11	S	154/205 (75%)	143 (93%)	11 (7%)	0	100	100
12	T	164/212 (77%)	156 (95%)	8 (5%)	0	100	100
13	W	109/148 (74%)	102 (94%)	7 (6%)	0	100	100
14	X	241/256 (94%)	221 (92%)	20 (8%)	0	100	100
15	Y	174/250 (70%)	165 (95%)	7 (4%)	2 (1%)	11	39
16	Z	118/161 (73%)	110 (93%)	8 (7%)	0	100	100
17	0	106/188 (56%)	92 (87%)	14 (13%)	0	100	100
18	1	50/65 (77%)	45 (90%)	5 (10%)	0	100	100
19	2	44/92 (48%)	43 (98%)	1 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	3	93/188 (50%)	89 (96%)	4 (4%)	0	100	100
21	4	36/103 (35%)	34 (94%)	2 (6%)	0	100	100
22	8	97/206 (47%)	95 (98%)	2 (2%)	0	100	100
23	b	146/155 (94%)	135 (92%)	11 (8%)	0	100	100
24	e	211/279 (76%)	203 (96%)	8 (4%)	0	100	100
25	g	130/166 (78%)	122 (94%)	8 (6%)	0	100	100
26	i	95/128 (74%)	88 (93%)	7 (7%)	0	100	100
27	j	91/123 (74%)	84 (92%)	6 (7%)	1 (1%)	11	39
28	m	43/128 (34%)	37 (86%)	6 (14%)	0	100	100
29	o	92/102 (90%)	85 (92%)	7 (8%)	0	100	100
30	q	164/222 (74%)	153 (93%)	8 (5%)	3 (2%)	6	29
31	r	160/196 (82%)	148 (92%)	11 (7%)	1 (1%)	21	52
32	J	173/192 (90%)	163 (94%)	10 (6%)	0	100	100
33	I	177/261 (68%)	167 (94%)	10 (6%)	0	100	100
34	N	220/251 (88%)	215 (98%)	5 (2%)	0	100	100
35	P	141/179 (79%)	131 (93%)	8 (6%)	2 (1%)	9	34
36	U	150/153 (98%)	141 (94%)	9 (6%)	0	100	100
37	V	204/216 (94%)	194 (95%)	10 (5%)	0	100	100
38	E	304/348 (87%)	283 (93%)	20 (7%)	1 (0%)	36	64
39	5	391/423 (92%)	375 (96%)	16 (4%)	0	100	100
40	6	352/380 (93%)	328 (93%)	24 (7%)	0	100	100
41	7	295/338 (87%)	276 (94%)	18 (6%)	1 (0%)	36	64
42	9	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
43	a	106/142 (75%)	101 (95%)	5 (5%)	0	100	100
44	c	287/332 (86%)	269 (94%)	18 (6%)	0	100	100
45	d	255/306 (83%)	235 (92%)	20 (8%)	0	100	100
46	f	144/194 (74%)	135 (94%)	9 (6%)	0	100	100
47	h	108/158 (68%)	98 (91%)	9 (8%)	1 (1%)	14	43
48	k	94/112 (84%)	88 (94%)	6 (6%)	0	100	100
49	l	70/138 (51%)	63 (90%)	7 (10%)	0	100	100
50	p	148/206 (72%)	139 (94%)	8 (5%)	1 (1%)	18	49

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	s	391/439 (89%)	361 (92%)	29 (7%)	1 (0%)	36	64
52	Q	218/292 (75%)	209 (96%)	9 (4%)	0	100	100
54	TA	43/198 (22%)	35 (81%)	8 (19%)	0	100	100
54	TB	25/198 (13%)	24 (96%)	1 (4%)	0	100	100
54	TC	69/198 (35%)	59 (86%)	9 (13%)	1 (1%)	9	34
55	z	195/204 (96%)	164 (84%)	23 (12%)	8 (4%)	2	14
56	w	692/696 (99%)	583 (84%)	93 (13%)	16 (2%)	5	24
All	All	9334/12090 (77%)	8605 (92%)	682 (7%)	47 (0%)	26	55

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
30	q	43	GLU
35	P	69	ARG
6	K	160	GLN
38	E	317	PRO
55	z	106	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	
3	D	193/245 (79%)	192 (100%)	1 (0%)	81	82
4	F	217/262 (83%)	216 (100%)	1 (0%)	81	82
5	H	88/228 (39%)	88 (100%)	0	100	100
6	K	155/156 (99%)	155 (100%)	0	100	100
7	L	98/124 (79%)	97 (99%)	1 (1%)	68	76
8	M	245/249 (98%)	244 (100%)	1 (0%)	84	84
9	O	133/150 (89%)	132 (99%)	1 (1%)	73	78
10	R	118/126 (94%)	118 (100%)	0	100	100
11	S	141/180 (78%)	141 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	T	146/182 (80%)	143 (98%)	3 (2%)	47	67
13	W	91/119 (76%)	90 (99%)	1 (1%)	65	75
14	X	217/227 (96%)	216 (100%)	1 (0%)	81	82
15	Y	159/223 (71%)	158 (99%)	1 (1%)	78	81
16	Z	111/147 (76%)	110 (99%)	1 (1%)	70	77
17	0	97/164 (59%)	97 (100%)	0	100	100
18	1	49/60 (82%)	49 (100%)	0	100	100
19	2	40/72 (56%)	40 (100%)	0	100	100
20	3	88/166 (53%)	88 (100%)	0	100	100
21	4	37/89 (42%)	37 (100%)	0	100	100
22	8	91/190 (48%)	90 (99%)	1 (1%)	65	75
23	b	130/135 (96%)	130 (100%)	0	100	100
24	e	188/236 (80%)	187 (100%)	1 (0%)	81	82
25	g	122/148 (82%)	120 (98%)	2 (2%)	55	71
26	i	86/110 (78%)	84 (98%)	2 (2%)	44	66
27	j	74/97 (76%)	74 (100%)	0	100	100
28	m	40/113 (35%)	40 (100%)	0	100	100
29	o	80/87 (92%)	80 (100%)	0	100	100
30	q	113/178 (64%)	112 (99%)	1 (1%)	70	77
31	r	147/169 (87%)	145 (99%)	2 (1%)	59	73
32	J	138/150 (92%)	136 (99%)	2 (1%)	59	73
33	I	164/232 (71%)	160 (98%)	4 (2%)	43	66
34	N	189/211 (90%)	188 (100%)	1 (0%)	81	82
35	P	125/154 (81%)	125 (100%)	0	100	100
36	U	125/135 (93%)	125 (100%)	0	100	100
37	V	184/191 (96%)	180 (98%)	4 (2%)	45	67
38	E	260/290 (90%)	257 (99%)	3 (1%)	63	74
39	5	353/368 (96%)	348 (99%)	5 (1%)	59	73
40	6	313/332 (94%)	311 (99%)	2 (1%)	78	81
41	7	272/303 (90%)	271 (100%)	1 (0%)	84	84
42	9	104/112 (93%)	103 (99%)	1 (1%)	68	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
43	a	101/133 (76%)	101 (100%)	0	100	100
44	c	253/288 (88%)	252 (100%)	1 (0%)	84	84
45	d	224/274 (82%)	222 (99%)	2 (1%)	70	77
46	f	122/173 (70%)	122 (100%)	0	100	100
47	h	104/148 (70%)	104 (100%)	0	100	100
48	k	81/90 (90%)	80 (99%)	1 (1%)	63	74
49	l	67/116 (58%)	67 (100%)	0	100	100
50	p	134/181 (74%)	133 (99%)	1 (1%)	76	80
51	s	336/381 (88%)	335 (100%)	1 (0%)	86	85
52	Q	202/256 (79%)	202 (100%)	0	100	100
54	TA	39/158 (25%)	39 (100%)	0	100	100
54	TB	26/158 (16%)	25 (96%)	1 (4%)	29	58
55	z	175/179 (98%)	171 (98%)	4 (2%)	44	66
56	w	604/604 (100%)	588 (97%)	16 (3%)	40	64
All	All	8189/10249 (80%)	8118 (99%)	71 (1%)	68	77

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	w	232	PHE
56	w	305	LEU
56	w	428	THR
33	I	104	LEU
33	I	96	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
41	7	45	ASN
51	s	87	GLN
44	c	69	HIS
45	d	207	ASN
51	s	387	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1522/1559 (97%)	349 (22%)	28 (1%)
2	B	51/73 (69%)	13 (25%)	1 (1%)
All	All	1573/1632 (96%)	362 (23%)	29 (1%)

5 of 362 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	1678	C
1	A	1679	U
1	A	1681	G
1	A	1689	C
1	A	1690	C

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2245	A
1	A	3196	G
1	A	2507	A
1	A	3041	U
1	A	2457	A

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 106 ligands modelled in this entry, 105 are monoatomic - leaving 1 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
59	GCP	w	801	57,56	32,34,34	1.70	6 (18%)	49,54,54	1.90	10 (20%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	GCP	w	801	57,56	-	5/19/38/38	0/3/3/3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	w	801	GCP	PG-O1G	5.63	1.61	1.50
59	w	801	GCP	C5-C4	3.18	1.47	1.38
59	w	801	GCP	PG-O3G	3.07	1.61	1.55
59	w	801	GCP	PG-O2G	-2.58	1.49	1.55
59	w	801	GCP	C4-N9	-2.30	1.32	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	w	801	GCP	PB-O3A-PA	-5.88	113.17	132.37
59	w	801	GCP	C2-N3-C4	4.95	120.82	112.30
59	w	801	GCP	C5-C4-N3	-4.77	120.79	128.39
59	w	801	GCP	C6-C5-N7	4.20	137.93	130.29
59	w	801	GCP	N9-C4-N3	3.37	132.69	125.95

There are no chirality outliers.

All (5) torsion outliers are listed below:

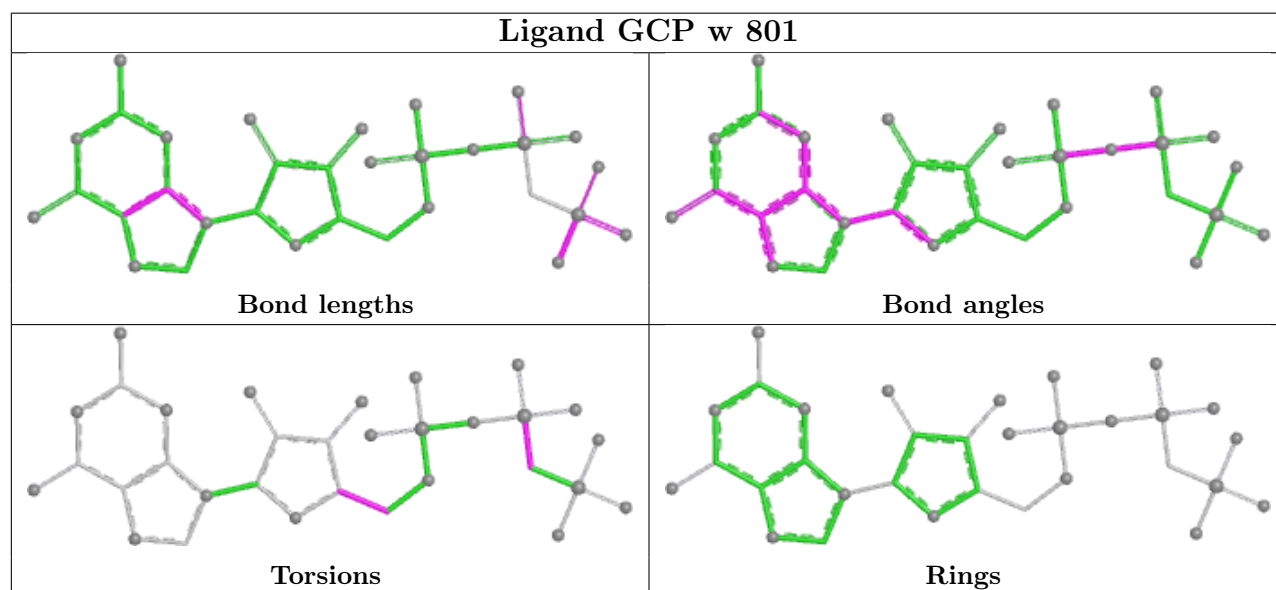
Mol	Chain	Res	Type	Atoms
59	w	801	GCP	PG-C3B-PB-O1B
59	w	801	GCP	PG-C3B-PB-O3A
59	w	801	GCP	O4'-C4'-C5'-O5'
59	w	801	GCP	C3'-C4'-C5'-O5'
59	w	801	GCP	PG-C3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	w	801	GCP	13	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
53	u	4
56	w	1
1	A	1

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
34	N	1

The worst 5 of 7 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	414:UNK	C	601:UNK	N	50.84
1	u	106:UNK	C	301:UNK	N	32.66
1	u	315:UNK	C	399:UNK	N	23.91
1	u	615:UNK	C	700:UNK	N	15.49
1	w	455:LEU	C	478:LEU	N	11.53

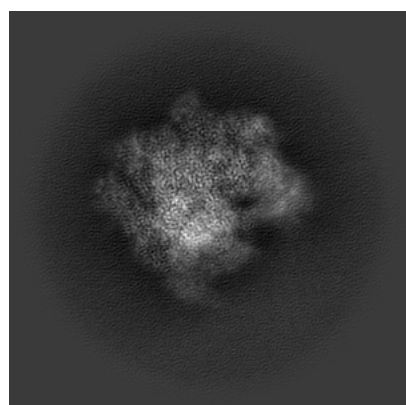
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23121. These allow visual inspection of the internal detail of the map and identification of artifacts.

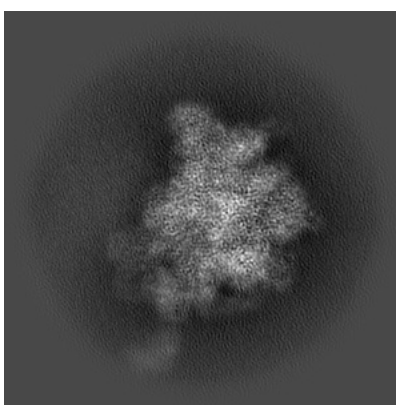
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

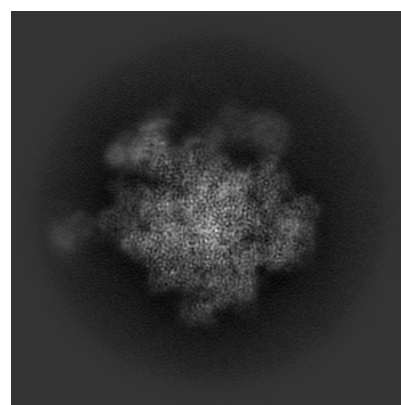
6.1.1 Primary map



X



Y

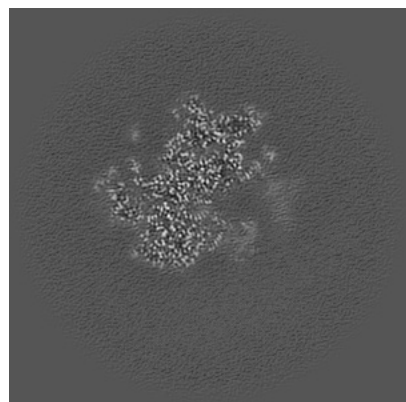


Z

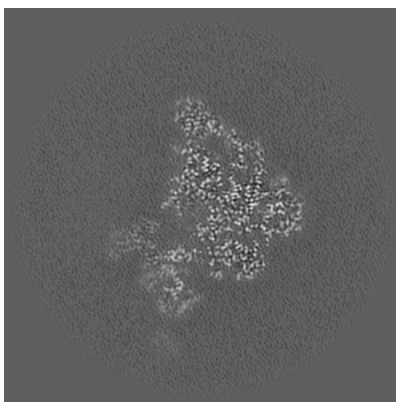
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

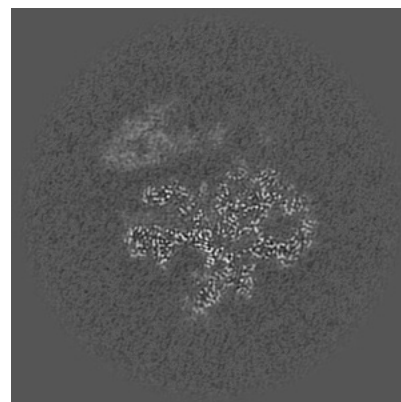
6.2.1 Primary map



X Index: 200



Y Index: 200

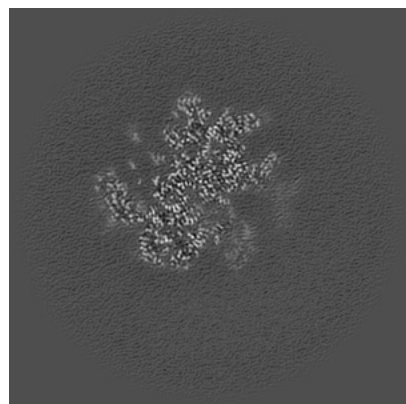


Z Index: 200

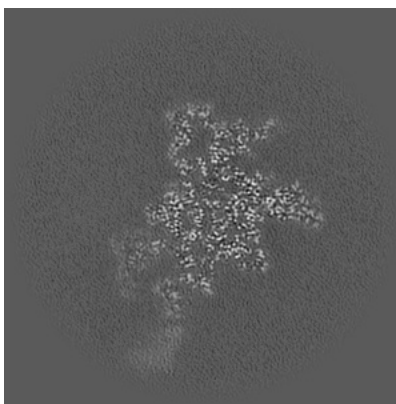
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

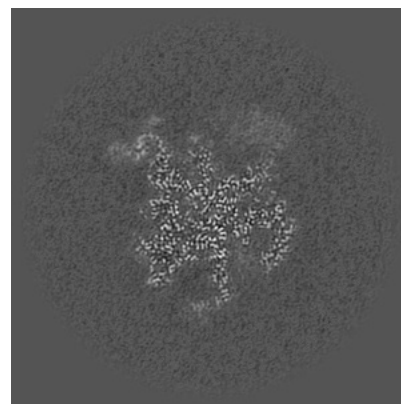
6.3.1 Primary map



X Index: 195



Y Index: 179

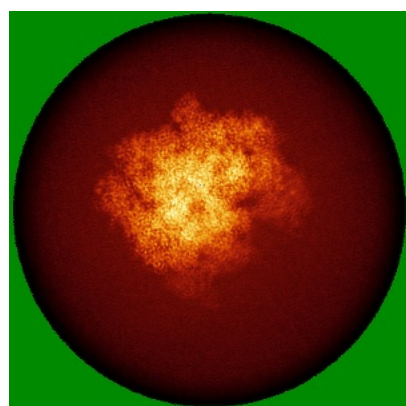


Z Index: 232

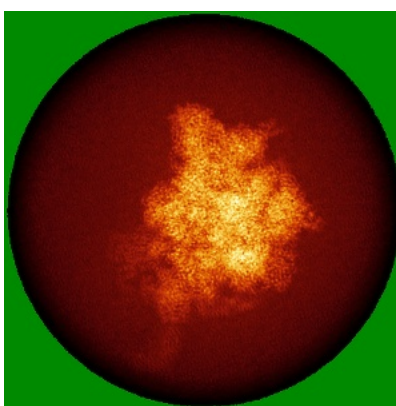
The images above show the largest variance slices of the map in three orthogonal directions.

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

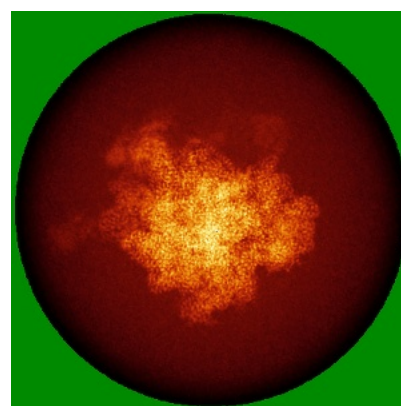
6.4.1 Primary map



X



Y

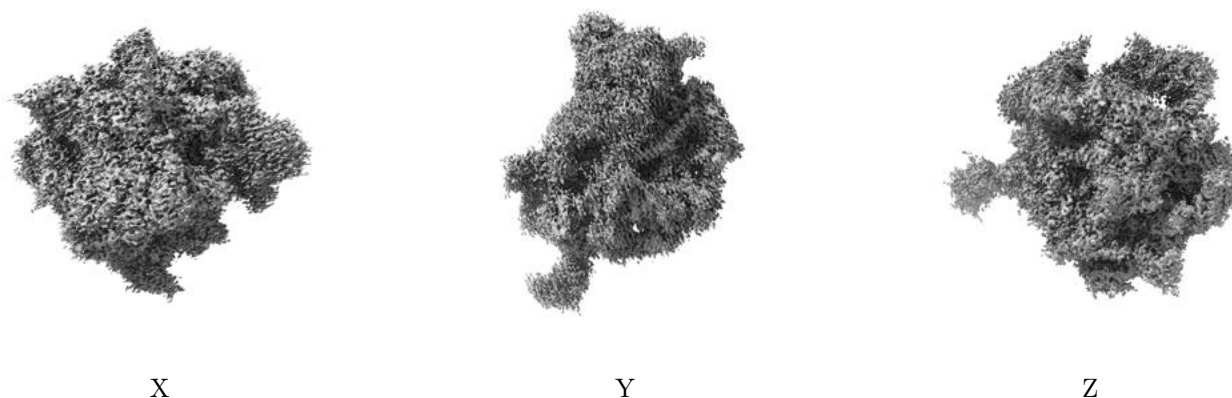


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

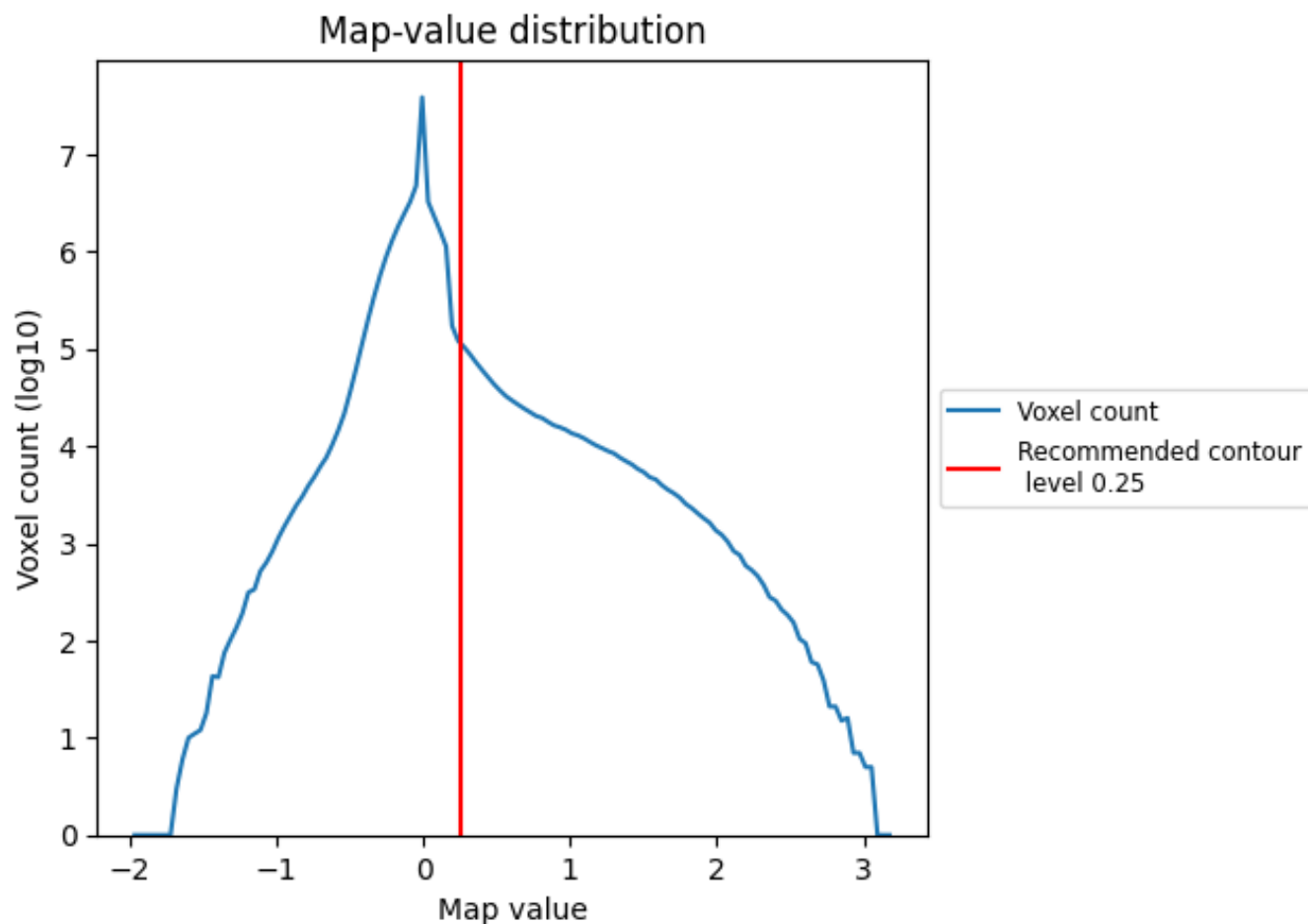
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

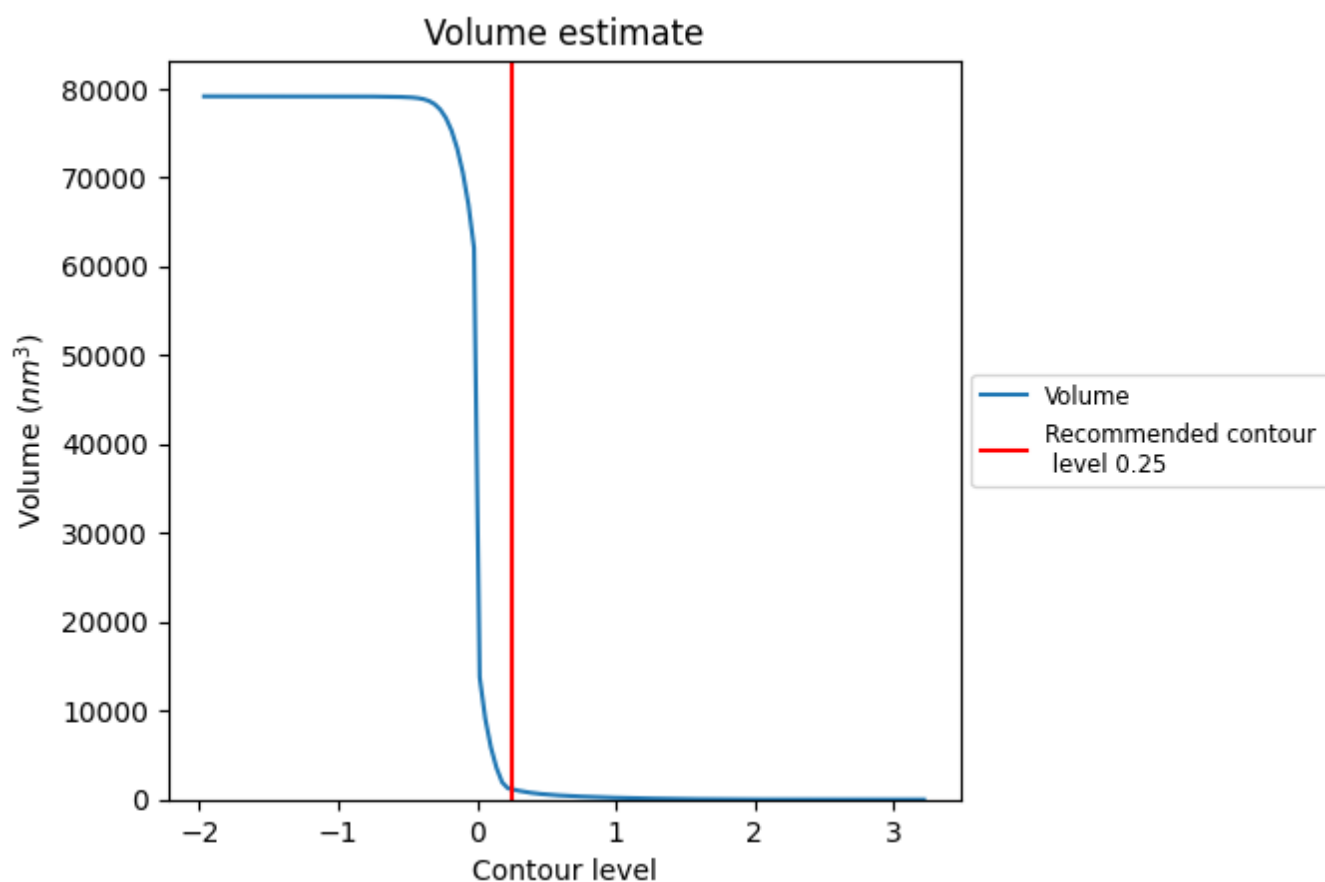
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

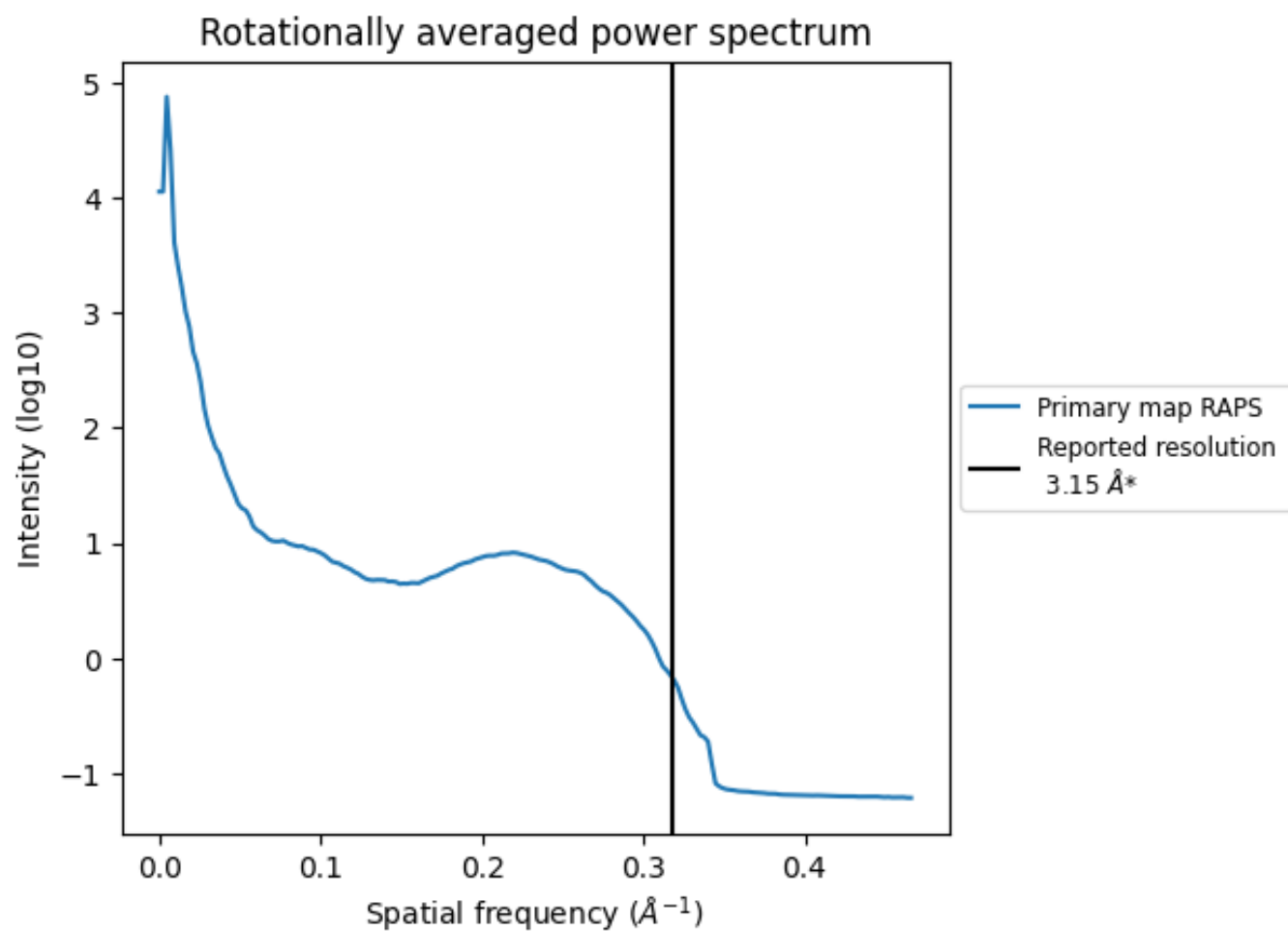
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1170 nm^3 ; this corresponds to an approximate mass of 1057 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 0.317 $\text{\AA}^{-1}$

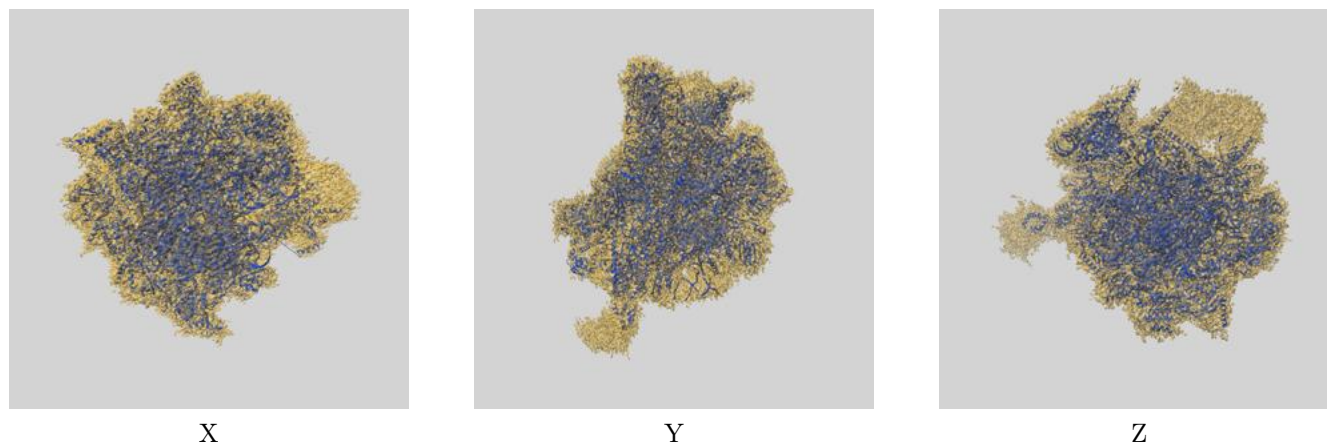
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

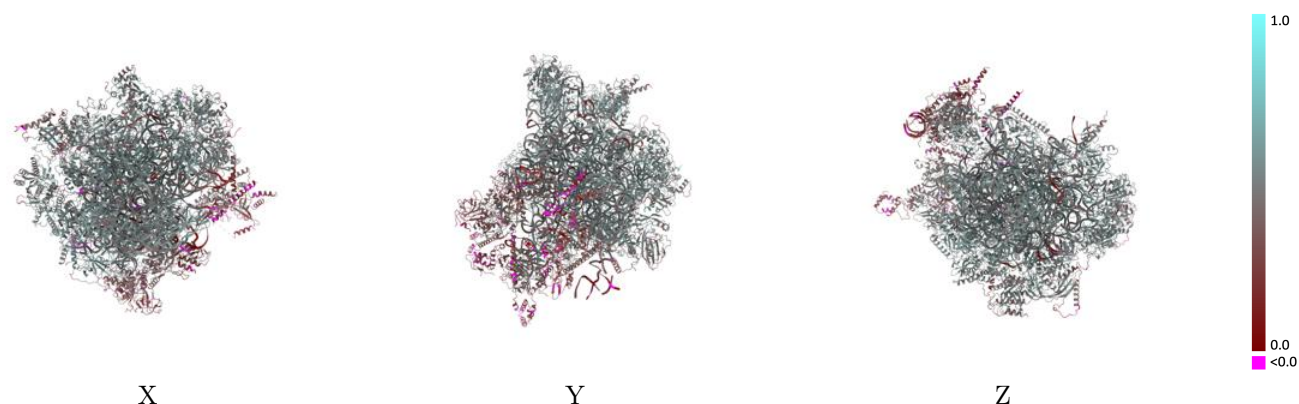
This section contains information regarding the fit between EMDB map EMD-23121 and PDB model 7L20. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



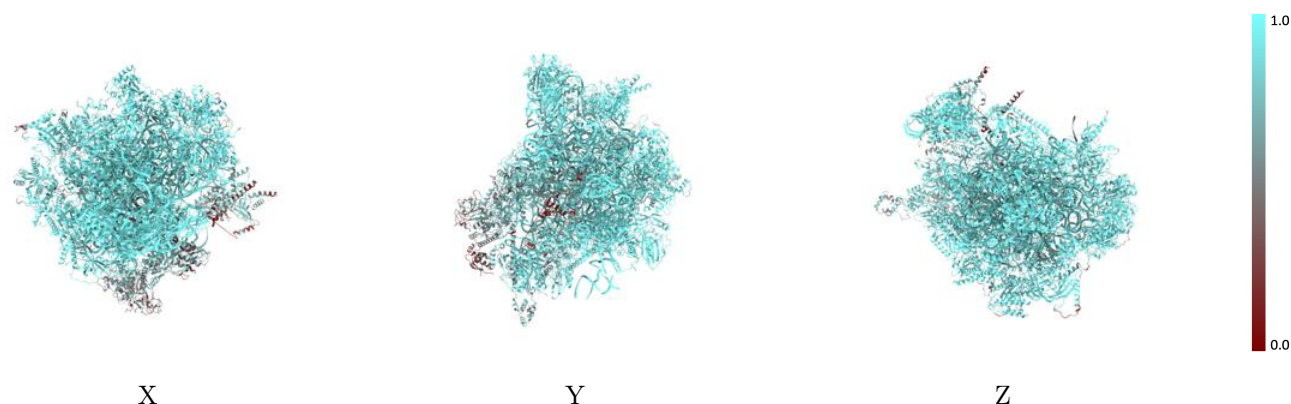
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



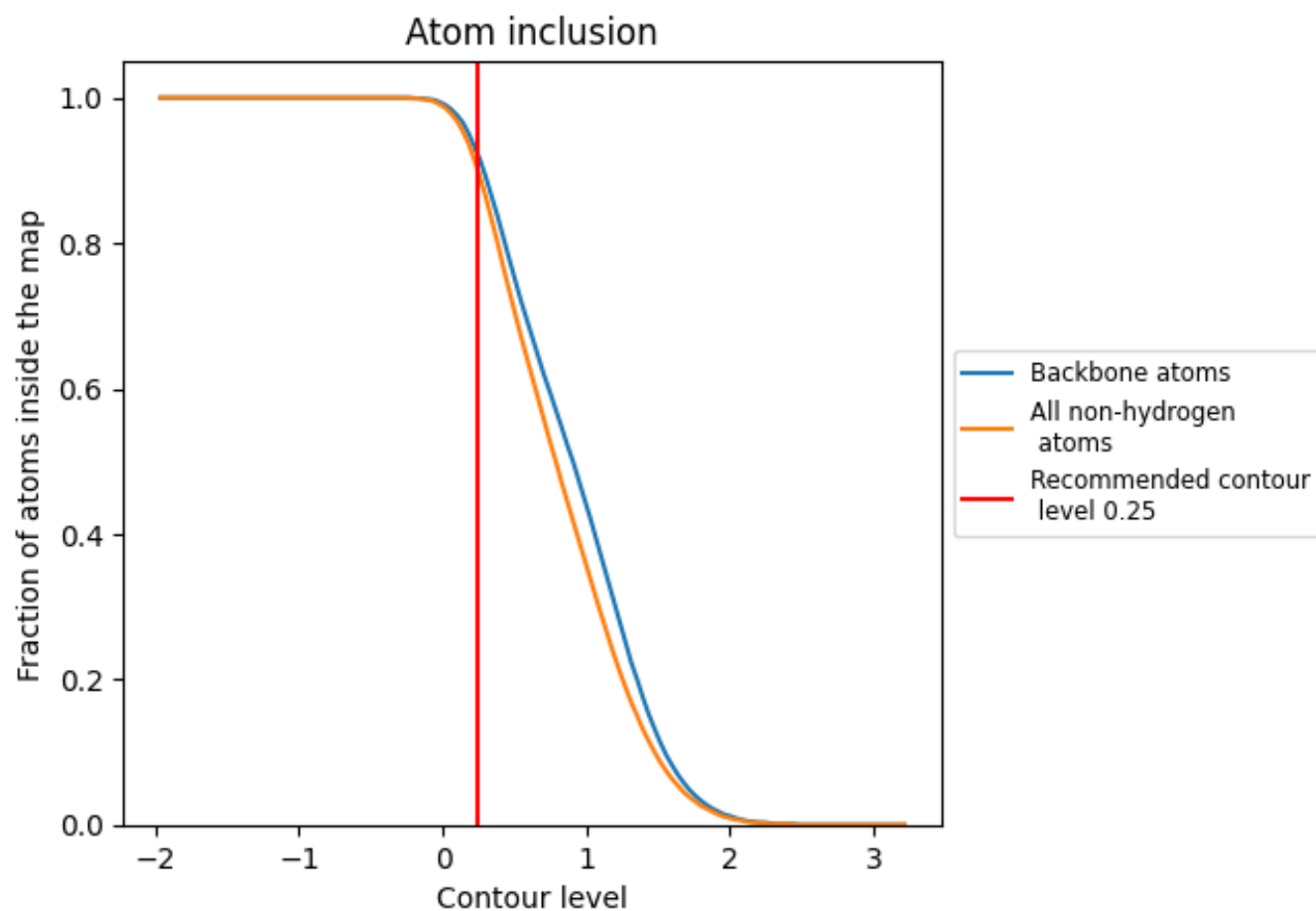
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8980	 0.4720
0	 0.9450	 0.5340
1	 0.9330	 0.5240
2	 0.9610	 0.5740
3	 0.9550	 0.5720
4	 0.9730	 0.5740
5	 0.9530	 0.5150
6	 0.9350	 0.4680
7	 0.9250	 0.4850
8	 0.7820	 0.3180
9	 0.9510	 0.5210
A	 0.9310	 0.4740
B	 0.9370	 0.3360
D	 0.9580	 0.5400
E	 0.9530	 0.5470
F	 0.9550	 0.5400
H	 0.9280	 0.4970
I	 0.8800	 0.4210
J	 0.7820	 0.3140
K	 0.9640	 0.5510
L	 0.9520	 0.5370
M	 0.9580	 0.5410
N	 0.9430	 0.5450
O	 0.9500	 0.5410
P	 0.9520	 0.5080
Q	 0.9480	 0.5380
R	 0.9370	 0.5510
S	 0.9570	 0.5510
T	 0.9480	 0.5530
TA	 0.6080	 0.1640
TB	 0.6010	 0.1610
TC	 0.2590	 0.1400
U	 0.9180	 0.5120
V	 0.9120	 0.4810
W	 0.9380	 0.5500



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
X	 0.9380	 0.5250
Y	 0.9510	 0.5320
Z	 0.9510	 0.5530
a	 0.8710	 0.4760
b	 0.9560	 0.5480
c	 0.9280	 0.5070
d	 0.8630	 0.4480
e	 0.7420	 0.2390
f	 0.7580	 0.3490
g	 0.9330	 0.5230
h	 0.9190	 0.4730
i	 0.9500	 0.5560
j	 0.9110	 0.5070
k	 0.9160	 0.4430
l	 0.8680	 0.4000
m	 0.8500	 0.3360
o	 0.9400	 0.5430
p	 0.8530	 0.4360
q	 0.8350	 0.4010
r	 0.9550	 0.5280
s	 0.9370	 0.5180
u	 0.3170	 0.0710
w	 0.5880	 0.2990
z	 0.6480	 0.3260