



Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 09:47 AM EST

PDB ID : 7L20
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 Full wwPDB EM Validation 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

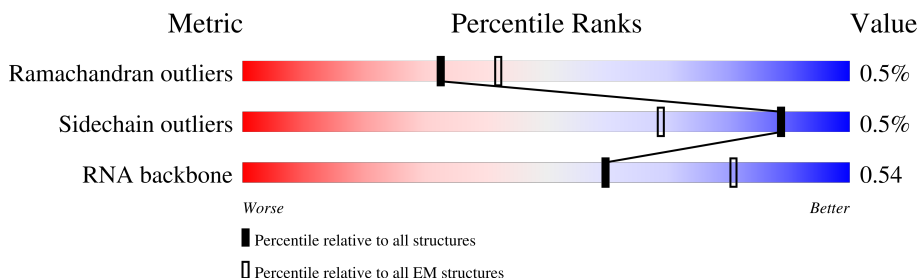
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.15 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
4	F	311	
5	H	267	
6	K	178	
7	L	145	
8	M	296	

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Mol	Chain	Length	Quality of chain
9	O	175	86% 13%
10	R	149	93% 6%
11	S	205	76% 24%
12	T	212	77% 22%
13	W	148	74% 25%
14	X	256	94% 5%
15	Y	250	70% 30%
16	Z	161	74% 25%
17	0	188	56% 43%
18	1	65	80% 20%
19	2	92	50% 50%
20	3	188	51% 49%
21	4	103	37% 63%
22	8	206	48% 52%
23	b	155	95% 5%
24	e	279	8% 76% 22%
25	g	166	79% 20%
26	i	128	73% 24%
27	j	123	74% 24%
28	m	128	34% 65%
29	o	102	91% 8%
30	q	222	10% 74% 24%
31	r	196	82% 17%
32	J	192	6% 90% 9%
33	I	261	68% 31%

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Mol	Chain	Length	Quality of chain
34	N	251	88% 12%
35	P	179	78% 20%
36	U	153	99%
37	V	216	95% 5%
38	E	348	87% 12%
39	5	423	92% 7%
40	6	380	93% 7%
41	7	338	87% 12%
42	9	137	90% 9%
43	a	142	6% 75% 24%
44	c	332	87% 13%
45	d	306	7% 83% 16%
46	f	194	11% 75% 25%
47	h	158	67% 30%
48	k	112	85% 14%
49	l	138	52% 48%
50	p	206	5% 72% 26%
51	s	439	89% 10%
52	Q	292	75% 25%
53	u	65	72% 100%
54	TA	198	6% 23% 77%
54	TB	198	13% 30% 86%
54	TC	198	16% 35% 64%
55	z	204	16% 91% 5%
56	w	696	22% 95% 5%

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
			Total	C	N	O	P		
1	A	1527	32395	14536	5844	10488	1527	0	0

- Molecule 2 is a RNA chain called tRNAval.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
27	j	93	740	460	143	135	2	0	0

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

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

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

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

- Molecule 30 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		
30	q	168	1293	801	254	233	5	0	0

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
55	z	197	1525	942	274	301	8	0	0

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

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

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
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w	?	-	GLU	deletion	UNP Q969S9
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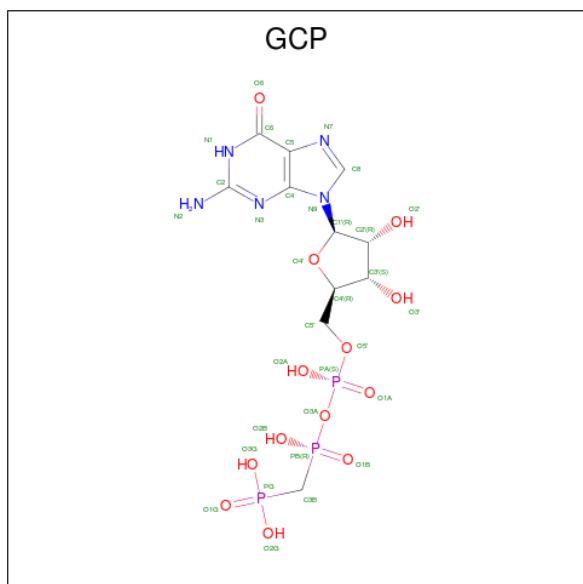
- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 59 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (three-letter code: GCP) (formula: C₁₁H₁₈N₅O₁₃P₃).

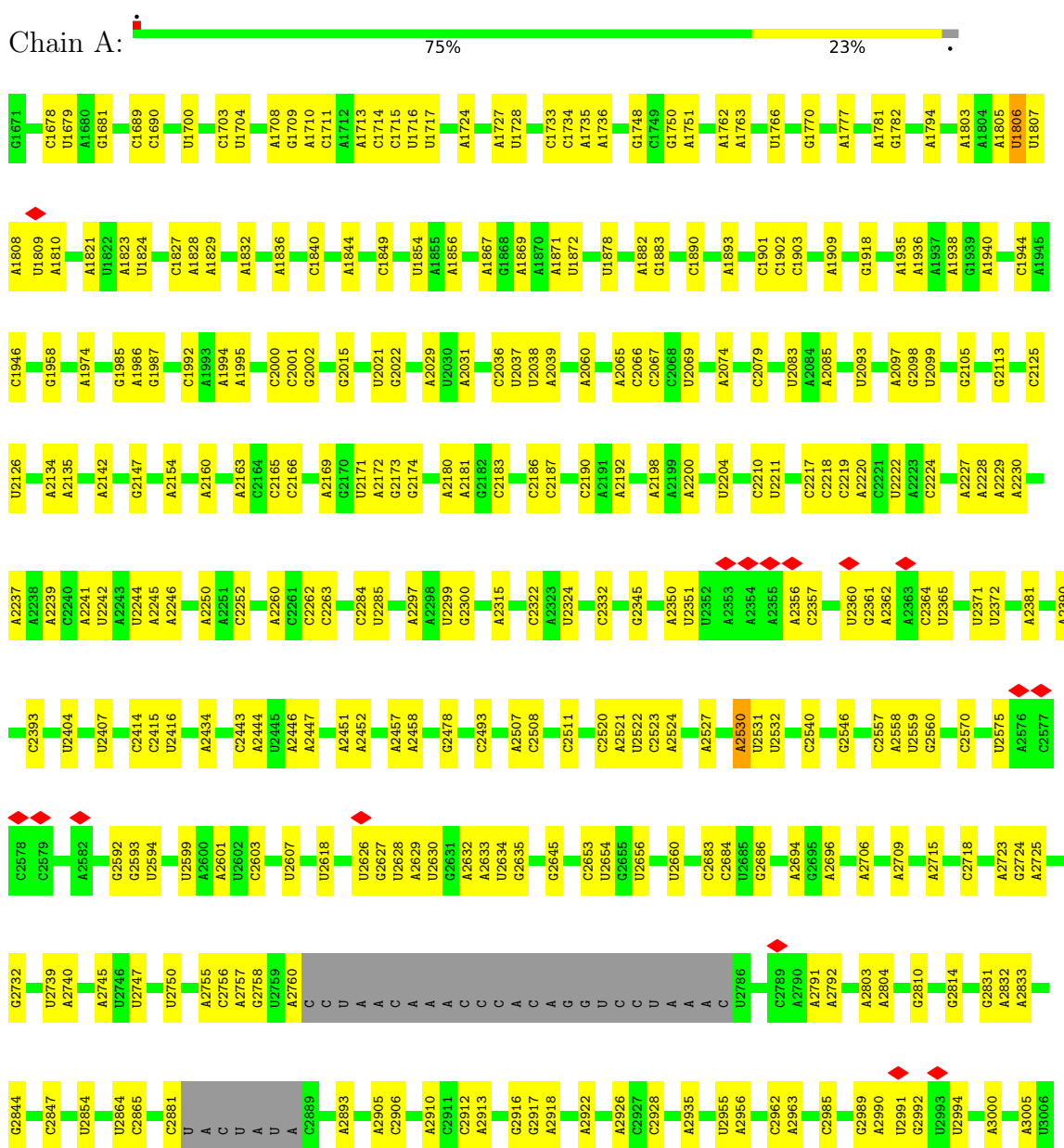


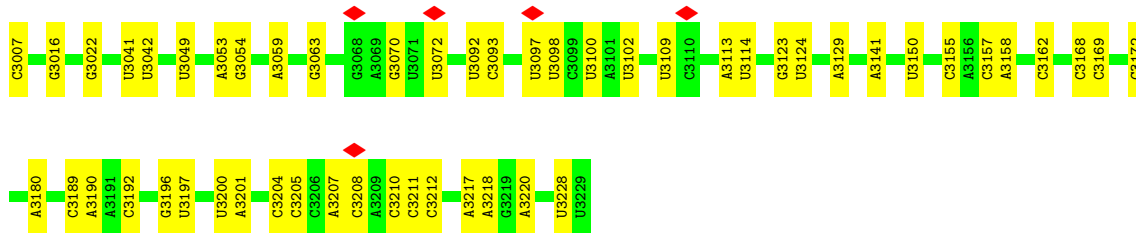
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
59	w	1	32	11	5	13	3	0

3 Residue-property plots

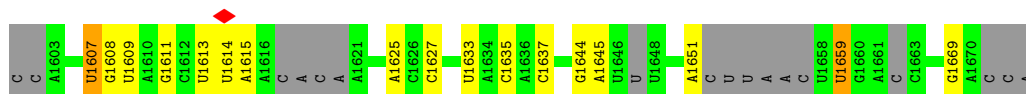
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

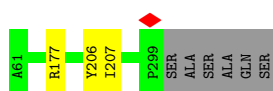
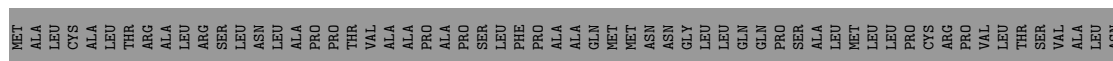
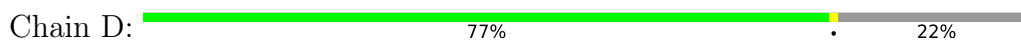




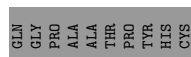
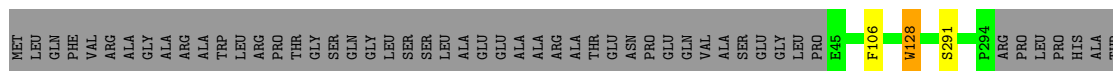
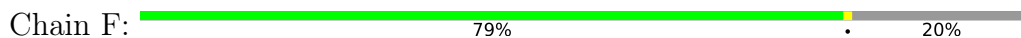
• Molecule 2: tRNAval



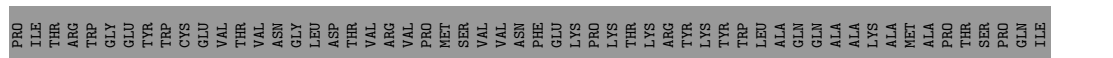
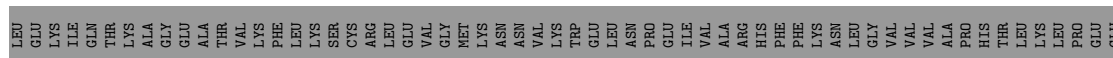
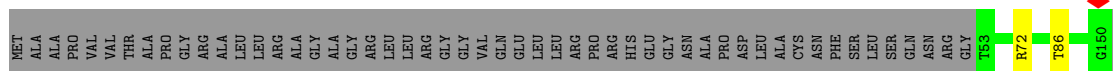
• Molecule 3: 39S ribosomal protein L2, mitochondrial



• Molecule 4: 39S ribosomal protein L4, mitochondrial

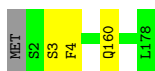


• Molecule 5: 39S ribosomal protein L9, mitochondrial

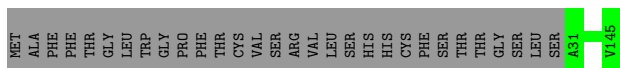
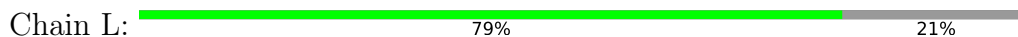


• Molecule 6: 39S ribosomal protein L13, mitochondrial

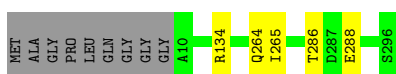




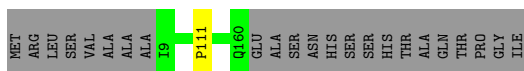
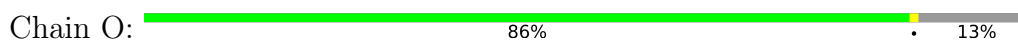
- Molecule 7: 39S ribosomal protein L14, mitochondrial



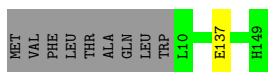
- Molecule 8: 39S ribosomal protein L15, mitochondrial



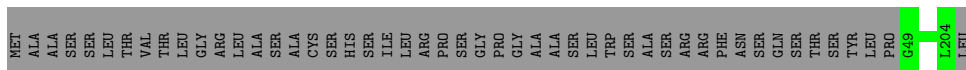
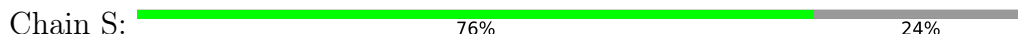
- Molecule 9: 39S ribosomal protein L17, mitochondrial



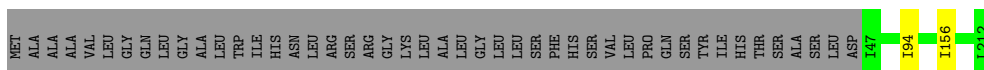
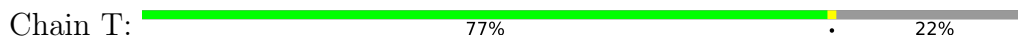
- Molecule 10: 39S ribosomal protein L20, mitochondrial



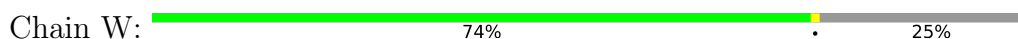
- Molecule 11: 39S ribosomal protein L21, mitochondrial

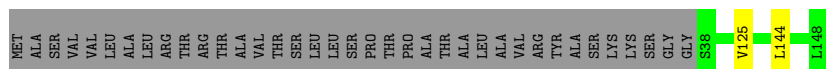


- Molecule 12: 39S ribosomal protein L22, mitochondrial



- Molecule 13: 39S ribosomal protein L27, mitochondrial

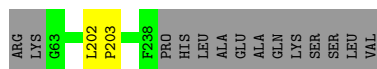




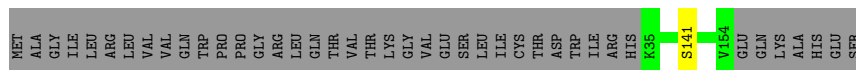
• Molecule 14: 39S ribosomal protein L28, mitochondrial



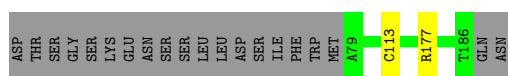
• Molecule 15: 39S ribosomal protein L47, mitochondrial



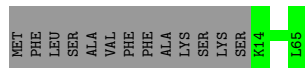
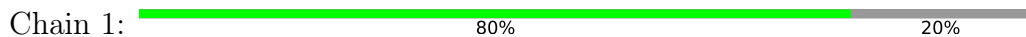
• Molecule 16: 39S ribosomal protein L30, mitochondrial



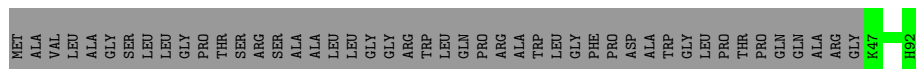
• Molecule 17: 39S ribosomal protein L32, mitochondrial

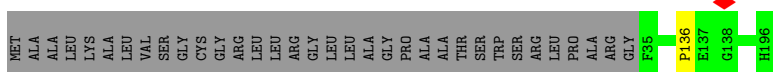
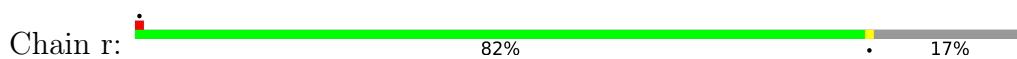


• Molecule 18: 39S ribosomal protein L33, mitochondrial

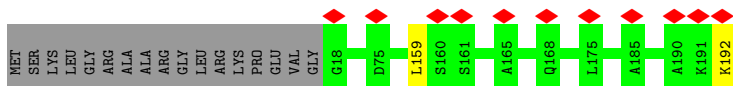
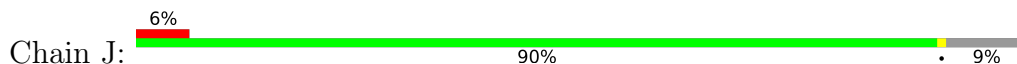


• Molecule 19: 39S ribosomal protein L34, mitochondrial

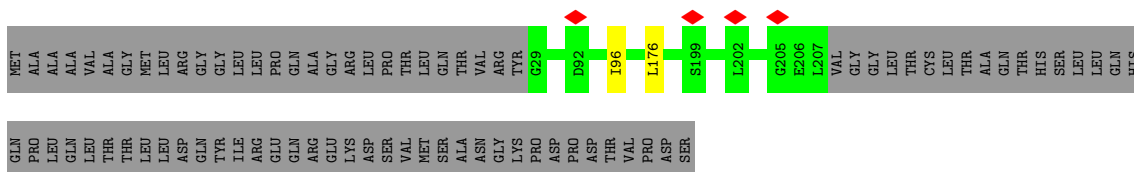




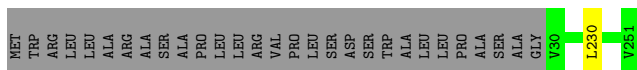
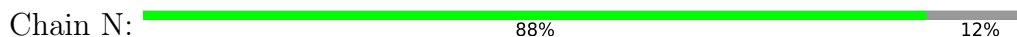
- Molecule 32: 39S ribosomal protein L11, mitochondrial



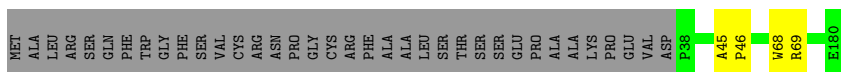
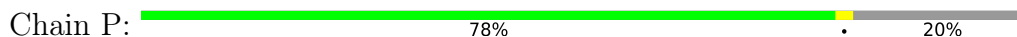
- Molecule 33: 39S ribosomal protein L10, mitochondrial



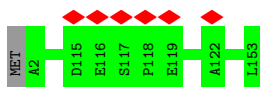
- Molecule 34: 39S ribosomal protein L16, mitochondrial



- Molecule 35: Mitochondrial ribosomal protein L18, isoform CRA_b

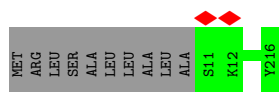


- Molecule 36: 39S ribosomal protein L23, mitochondrial

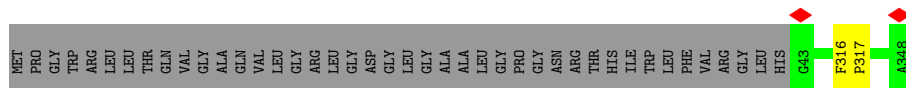
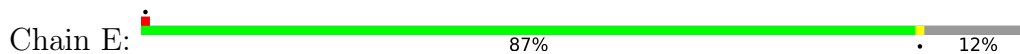


- Molecule 37: 39S ribosomal protein L24, mitochondrial

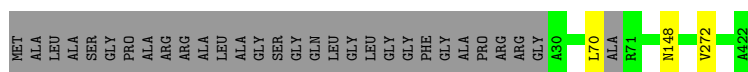




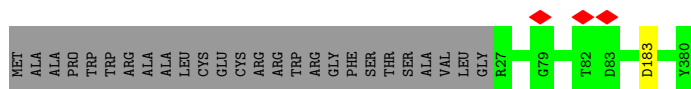
- Molecule 38: 39S ribosomal protein L3, mitochondrial



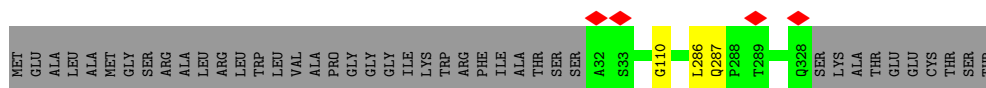
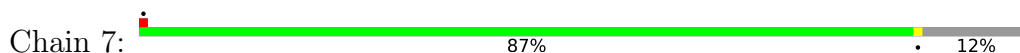
- Molecule 39: 39S ribosomal protein L37, mitochondrial



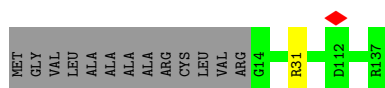
- Molecule 40: 39S ribosomal protein L38, mitochondrial



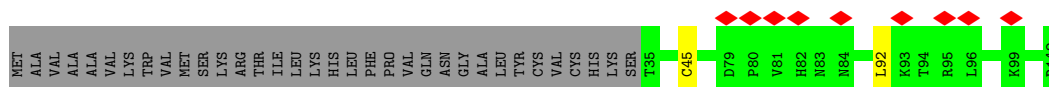
- Molecule 41: 39S ribosomal protein L39, mitochondrial



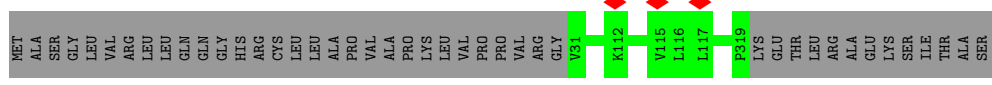
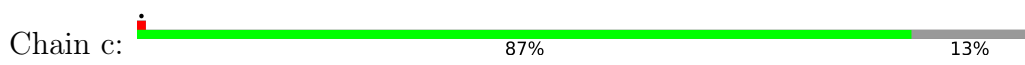
- Molecule 42: 39S ribosomal protein L41, mitochondrial



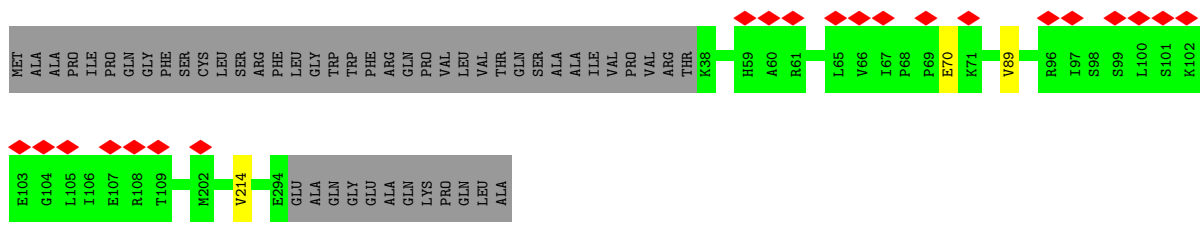
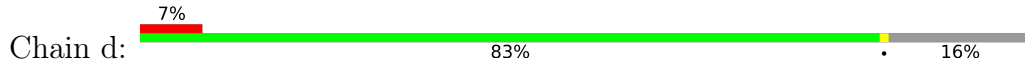
- Molecule 43: 39S ribosomal protein L42, mitochondrial



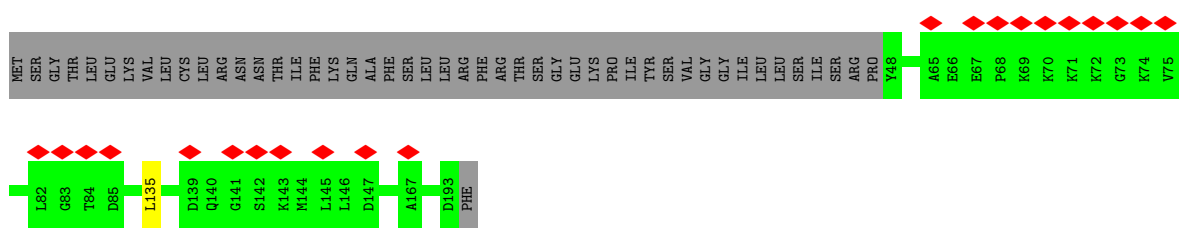
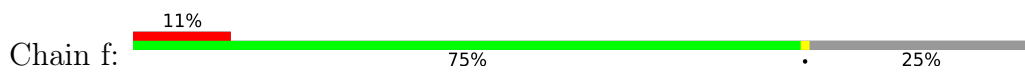
- Molecule 44: 39S ribosomal protein L44, mitochondrial



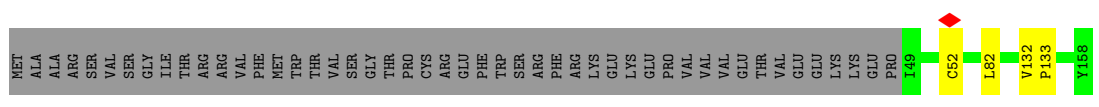
• Molecule 45: 39S ribosomal protein L45, mitochondrial



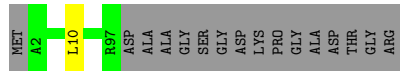
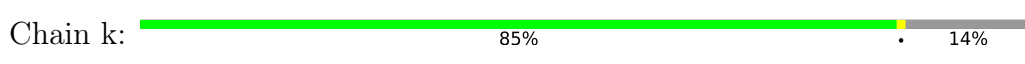
• Molecule 46: 39S ribosomal protein L48, mitochondrial



• Molecule 47: 39S ribosomal protein L50, mitochondrial

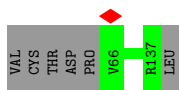


• Molecule 48: 39S ribosomal protein L53, mitochondrial

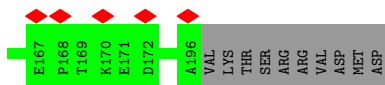
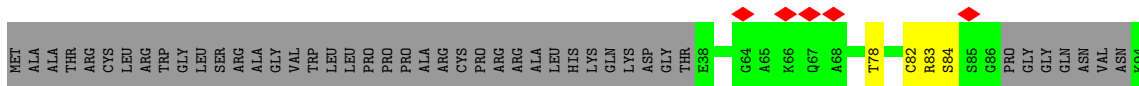
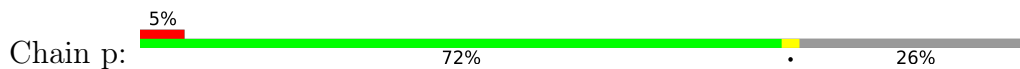


• Molecule 49: 39S ribosomal protein L54, mitochondrial

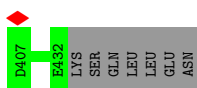
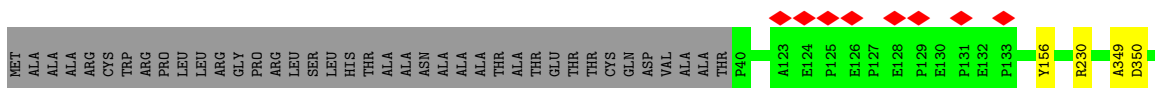
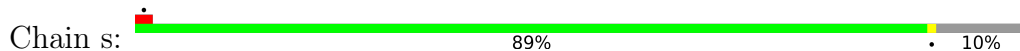




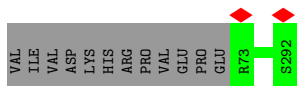
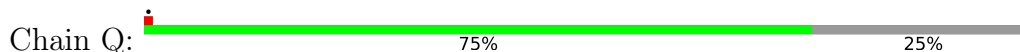
• Molecule 50: Peptidyl-tRNA hydrolase ICT1, mitochondrial



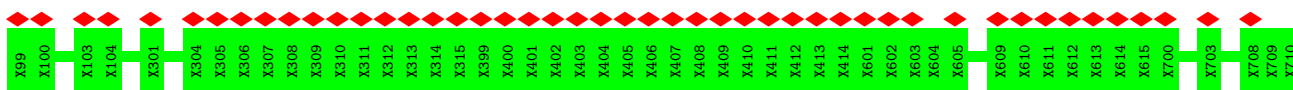
• Molecule 51: 39S ribosomal protein S30, mitochondrial



• Molecule 52: 39S ribosomal protein L19, mitochondrial

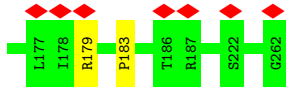


• Molecule 53: 39 S P-site finger

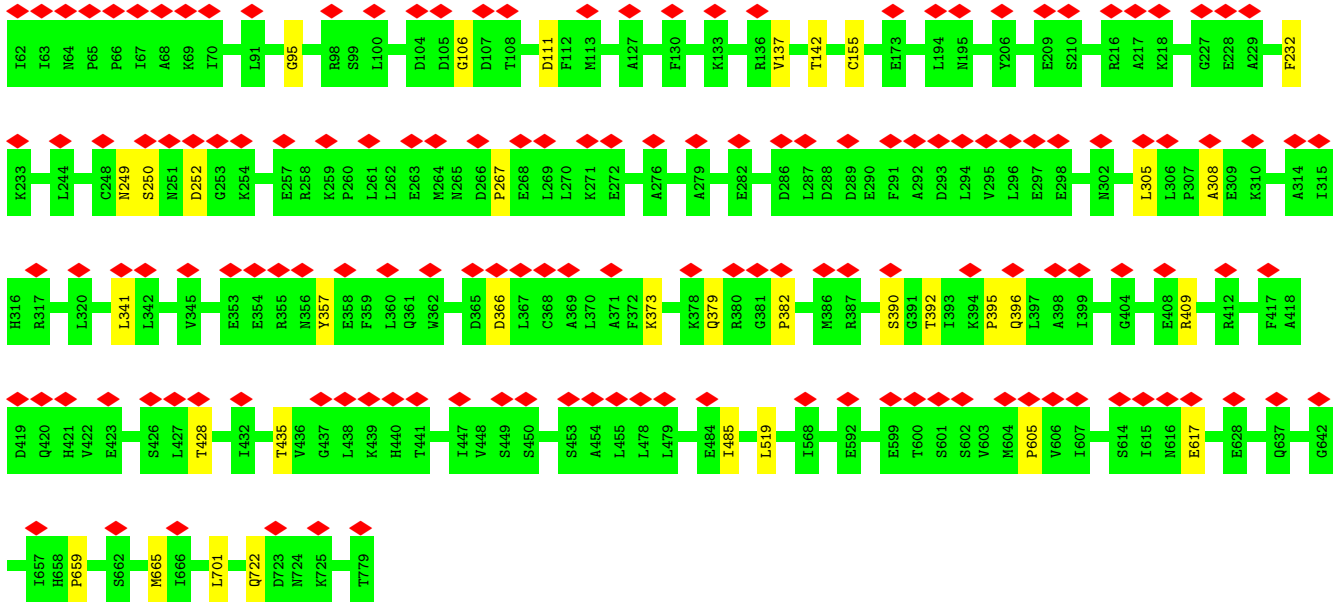


• Molecule 54: 39S ribosomal protein L12, mitochondrial





- 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.18	0/36245	0.77	3/56418 (0.0%)
2	B	0.45	0/1328	1.17	12/2056 (0.6%)
3	D	0.40	0/1904	0.57	0/2561
4	F	0.47	0/2071	0.66	1/2817 (0.0%)
5	H	0.38	0/820	0.70	1/1102 (0.1%)
6	K	0.48	0/1495	0.58	0/2029
7	L	0.42	0/904	0.59	0/1218
8	M	0.45	0/2359	0.62	0/3185
9	O	0.46	0/1269	0.63	0/1708
10	R	0.49	0/1174	0.59	0/1572
11	S	0.43	0/1276	0.62	0/1729
12	T	0.46	0/1402	0.55	0/1886
13	W	0.53	0/893	0.61	0/1204
14	X	0.39	0/2081	0.55	0/2812
15	Y	0.42	0/1552	0.52	0/2079
16	Z	0.44	0/1003	0.60	0/1354
17	0	0.42	0/895	0.61	0/1201
18	1	0.38	0/438	0.60	0/583
19	2	0.49	0/382	0.61	0/507
20	3	0.50	0/852	0.55	0/1136
21	4	0.51	0/350	0.61	0/461
22	8	0.33	0/855	0.56	0/1152
23	b	0.43	0/1202	0.56	0/1626
24	e	0.34	0/1797	0.70	3/2422 (0.1%)
25	g	0.46	0/1132	0.62	0/1543
26	i	0.48	0/849	0.66	1/1135 (0.1%)
27	j	0.44	0/755	0.53	0/1016
28	m	0.29	0/379	0.59	0/510
29	o	0.44	0/818	0.64	1/1097 (0.1%)
30	q	0.34	0/1323	0.55	0/1794
31	r	0.46	0/1362	0.60	0/1846
32	J	0.38	0/1348	0.62	1/1813 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	I	0.36	0/1467	0.66	1/1984 (0.1%)
34	N	0.44	1/1833 (0.1%)	0.52	0/2468
35	P	0.40	0/1191	0.60	0/1611
36	U	0.42	0/1252	0.52	0/1697
37	V	0.39	0/1727	0.57	0/2341
38	E	0.44	0/2479	0.58	0/3360
39	5	0.38	0/3300	0.58	2/4495 (0.0%)
40	6	0.39	0/3043	0.54	0/4140
41	7	0.39	0/2467	0.55	1/3337 (0.0%)
42	9	0.41	0/1025	0.57	0/1379
43	a	0.44	1/923 (0.1%)	0.52	1/1254 (0.1%)
44	c	0.39	0/2371	0.54	0/3205
45	d	0.36	0/2132	0.59	0/2887
46	f	0.34	0/1144	0.68	1/1551 (0.1%)
47	h	0.34	0/917	0.56	0/1249
48	k	0.33	0/754	0.65	1/1017 (0.1%)
49	l	0.33	0/636	0.54	0/860
50	p	0.34	0/1246	0.54	0/1675
51	s	0.42	0/3262	0.55	0/4435
52	Q	0.40	0/1875	0.54	0/2523
54	TA	0.27	0/349	0.52	0/475
54	TB	0.28	0/212	0.57	0/286
54	TC	0.23	0/351	0.40	0/488
55	z	0.23	0/1534	0.39	0/2063
56	w	0.24	0/5511	0.44	0/7479
All	All	0.35	2/115514 (0.0%)	0.66	30/163831 (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 (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	N	230	LEU	C-N	-6.33	1.19	1.34
43	a	45	CYS	CB-SG	-5.81	1.72	1.81

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	f	135	LEU	CA-CB-CG	7.00	131.39	115.30
2	B	1633	U	N1-C2-O2	6.91	127.63	122.80
24	e	83	LEU	CA-CB-CG	6.83	131.01	115.30
29	o	93	ASP	CB-CG-OD2	6.53	124.17	118.30
33	I	176	LEU	CA-CB-CG	6.23	129.62	115.30
32	J	159	LEU	CA-CB-CG	6.21	129.58	115.30
2	B	1633	U	N3-C2-O2	-6.21	117.86	122.20
48	k	10	LEU	CA-CB-CG	6.01	129.13	115.30
2	B	1635	C	N1-C2-O2	5.96	122.47	118.90
39	5	70	LEU	CB-CG-CD1	-5.92	100.94	111.00
24	e	173	LEU	CA-CB-CG	5.87	128.79	115.30
2	B	1607	U	P-O3'-C3'	5.79	126.64	119.70
2	B	1637	C	N1-C2-O2	5.70	122.32	118.90
2	B	1607	U	C2-N1-C1'	5.69	124.53	117.70
24	e	160	LEU	CA-CB-CG	5.61	128.19	115.30
1	A	2530	A	OP2-P-O3'	5.51	117.32	105.20
4	F	128	TRP	CA-CB-CG	5.38	123.93	113.70
5	H	72	ARG	NE-CZ-NH1	5.38	122.99	120.30
2	B	1659	U	N1-C2-O2	5.37	126.56	122.80
43	a	92	LEU	CA-CB-CG	5.32	127.53	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1627	C	C6-N1-C2	-5.31	118.18	120.30
2	B	1635	C	C2-N1-C1'	5.28	124.61	118.80
41	7	286	LEU	CA-CB-CG	5.21	127.29	115.30
2	B	1659	U	N3-C2-O2	-5.15	118.59	122.20
2	B	1607	U	N1-C2-O2	5.13	126.39	122.80
39	5	70	LEU	CA-CB-CG	5.11	127.06	115.30
1	A	1806	U	P-O3'-C3'	5.04	125.75	119.70
1	A	2530	A	P-O3'-C3'	5.03	125.74	119.70
26	i	80	LEU	CA-CB-CG	5.02	126.84	115.30
2	B	1633	U	C2-N1-C1'	5.01	123.71	117.70

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	0	177	ARG	Peptide
41	7	287	GLN	Peptide
3	D	206	TYR	Peptide
38	E	316	PHE	Peptide
5	H	86	THR	Peptide
6	K	3	SER	Peptide
8	M	264	GLN	Peptide
8	M	286	THR	Peptide
35	P	45	ALA	Peptide
35	P	68	TRP	Peptide
10	R	137	GLU	Peptide
12	T	94	ILE	Peptide
16	Z	141	SER	Peptide
45	d	70	GLU	Peptide
47	h	132	VAL	Peptide
47	h	52	CYS	Peptide
47	h	82	LEU	Peptide
26	i	57	TYR	Peptide
27	j	110	LYS	Peptide
28	m	70	GLU	Peptide
50	p	82	CYS	Peptide
50	p	83	ARG	Peptide
30	q	78	SER	Peptide
51	s	156	TYR	Peptide
51	s	349	ALA	Peptide
56	w	142	THR	Mainchain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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%)	34	68
4	F	248/311 (80%)	226 (91%)	20 (8%)	2 (1%)	19	55
5	H	96/267 (36%)	88 (92%)	8 (8%)	0	100	100
6	K	175/178 (98%)	153 (87%)	20 (11%)	2 (1%)	14	48
7	L	113/145 (78%)	102 (90%)	11 (10%)	0	100	100
8	M	285/296 (96%)	248 (87%)	35 (12%)	2 (1%)	22	59
9	O	150/175 (86%)	133 (89%)	16 (11%)	1 (1%)	22	59
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%)	14	48
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	14	48
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%)	8	37
31	r	160/196 (82%)	148 (92%)	11 (7%)	1 (1%)	25	62
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%)	11	43
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%)	41	73
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%)	41	73
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%)	17	53
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%)	22	59
51	s	391/439 (89%)	361 (92%)	29 (7%)	1 (0%)	41	73
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	TC	69/198 (35%)	59 (86%)	9 (13%)	1 (1%)	11	43
55	z	195/204 (96%)	164 (84%)	23 (12%)	8 (4%)	3	18
56	w	692/696 (99%)	583 (84%)	93 (13%)	16 (2%)	6	31
All	All	9334/12090 (77%)	8605 (92%)	682 (7%)	47 (0%)	32	65

All (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
55	z	183	PRO
56	w	111	ASP
56	w	379	GLN
56	w	605	PRO
4	F	291	SER
8	M	288	GLU
30	q	42	PRO
50	p	84	SER
56	w	250	SER
56	w	366	ASP
56	w	373	LYS
3	D	207	ILE
6	K	4	PHE
27	j	35	ALA
30	q	79	PRO
51	s	350	ASP
54	TC	169	PRO
55	z	168	ASN
56	w	249	ASN
56	w	252	ASP
8	M	265	ILE
15	Y	203	PRO
55	z	112	SER
55	z	165	SER
56	w	308	ALA
56	w	390	SER
41	7	110	GLY
55	z	166	GLY

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Mol	Chain	Res	Type
55	z	167	MET
56	w	95	GLY
56	w	106	GLY
56	w	485	ILE
56	w	722	GLN
47	h	133	PRO
9	O	111	PRO
31	r	136	PRO
35	P	46	PRO
55	z	152	PRO
4	F	128	TRP
15	Y	202	LEU
56	w	395	PRO
56	w	659	PRO

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	
3	D	193/245 (79%)	192 (100%)	1 (0%)	88	95
4	F	217/262 (83%)	216 (100%)	1 (0%)	88	95
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%)	98 (100%)	0	100	100
8	M	245/249 (98%)	244 (100%)	1 (0%)	91	96
9	O	133/150 (89%)	133 (100%)	0	100	100
10	R	118/126 (94%)	118 (100%)	0	100	100
11	S	141/180 (78%)	141 (100%)	0	100	100
12	T	146/182 (80%)	145 (99%)	1 (1%)	84	93
13	W	91/119 (76%)	89 (98%)	2 (2%)	52	77
14	X	217/227 (96%)	214 (99%)	3 (1%)	67	85
15	Y	159/223 (71%)	159 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	Z	111/147 (76%)	111 (100%)	0	100	100
17	0	97/164 (59%)	96 (99%)	1 (1%)	76	89
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%)	91 (100%)	0	100	100
23	b	130/135 (96%)	130 (100%)	0	100	100
24	e	188/236 (80%)	187 (100%)	1 (0%)	88	95
25	g	122/148 (82%)	121 (99%)	1 (1%)	81	92
26	i	86/110 (78%)	85 (99%)	1 (1%)	71	87
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%)	113 (100%)	0	100	100
31	r	147/169 (87%)	147 (100%)	0	100	100
32	J	138/150 (92%)	137 (99%)	1 (1%)	84	93
33	I	164/232 (71%)	163 (99%)	1 (1%)	86	94
34	N	189/211 (90%)	189 (100%)	0	100	100
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%)	184 (100%)	0	100	100
38	E	260/290 (90%)	260 (100%)	0	100	100
39	5	353/368 (96%)	351 (99%)	2 (1%)	86	94
40	6	313/332 (94%)	312 (100%)	1 (0%)	92	97
41	7	272/303 (90%)	272 (100%)	0	100	100
42	9	104/112 (93%)	103 (99%)	1 (1%)	76	89
43	a	101/133 (76%)	101 (100%)	0	100	100
44	c	253/288 (88%)	253 (100%)	0	100	100
45	d	224/274 (82%)	222 (99%)	2 (1%)	78	91
46	f	122/173 (70%)	122 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	h	104/148 (70%)	104 (100%)	0	100	100
48	k	81/90 (90%)	81 (100%)	0	100	100
49	l	67/116 (58%)	67 (100%)	0	100	100
50	p	134/181 (74%)	133 (99%)	1 (1%)	84	93
51	s	336/381 (88%)	335 (100%)	1 (0%)	92	97
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%)	33	65
55	z	175/179 (98%)	172 (98%)	3 (2%)	60	82
56	w	604/604 (100%)	587 (97%)	17 (3%)	43	73
All	All	8189/10249 (80%)	8145 (100%)	44 (0%)	89	95

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	177	ARG
4	F	106	PHE
8	M	134	ARG
12	T	156	ILE
13	W	125	VAL
13	W	144	LEU
14	X	64	ASP
14	X	173	ASP
14	X	238	LEU
17	0	113	CYS
24	e	258	ASP
25	g	77	ASP
26	i	59	ASN
32	J	192	LYS
33	I	96	ILE
39	5	148	ASN
39	5	272	VAL
40	6	183	ASP
42	9	31	ARG
45	d	89	VAL
45	d	214	VAL
50	p	78	THR
51	s	230	ARG

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Mol	Chain	Res	Type
54	TB	86	LEU
55	z	107	LEU
55	z	154	CYS
55	z	179	ARG
56	w	137	VAL
56	w	155	CYS
56	w	232	PHE
56	w	267	PRO
56	w	305	LEU
56	w	341	LEU
56	w	357	TYR
56	w	382	PRO
56	w	392	THR
56	w	396	GLN
56	w	409	ARG
56	w	428	THR
56	w	435	THR
56	w	519	LEU
56	w	617	GLU
56	w	665	MET
56	w	701	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (125) such sidechains are listed below:

Mol	Chain	Res	Type
3	D	165	ASN
3	D	194	ASN
3	D	195	ASN
4	F	74	GLN
4	F	97	HIS
4	F	103	GLN
5	H	88	HIS
5	H	136	ASN
6	K	26	GLN
6	K	48	HIS
6	K	56	HIS
6	K	64	HIS
7	L	72	GLN
7	L	80	GLN
7	L	104	ASN
8	M	26	ASN
8	M	87	HIS

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Mol	Chain	Res	Type
8	M	92	GLN
8	M	120	GLN
8	M	198	GLN
9	O	128	ASN
9	O	141	HIS
9	O	160	GLN
10	R	30	HIS
10	R	125	HIS
11	S	118	ASN
11	S	140	ASN
12	T	201	GLN
13	W	110	ASN
14	X	215	GLN
15	Y	88	GLN
15	Y	99	HIS
16	Z	67	HIS
17	0	118	GLN
17	0	168	GLN
20	3	154	GLN
23	b	25	GLN
23	b	123	ASN
24	e	126	GLN
24	e	175	GLN
24	e	198	ASN
24	e	212	HIS
24	e	245	GLN
24	e	248	ASN
24	e	251	HIS
24	e	271	GLN
25	g	73	GLN
25	g	102	HIS
26	i	89	GLN
27	j	30	GLN
27	j	36	ASN
27	j	63	GLN
29	o	16	GLN
29	o	58	GLN
29	o	85	HIS
30	q	142	ASN
30	q	157	GLN
31	r	184	ASN
32	J	41	GLN

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Mol	Chain	Res	Type
33	I	41	HIS
33	I	150	HIS
33	I	189	GLN
33	I	193	ASN
34	N	98	HIS
34	N	110	ASN
34	N	181	HIS
37	V	73	GLN
38	E	57	ASN
38	E	128	HIS
38	E	280	HIS
38	E	281	ASN
38	E	294	ASN
39	5	65	HIS
39	5	118	GLN
39	5	149	GLN
39	5	301	HIS
40	6	224	HIS
40	6	234	HIS
40	6	239	ASN
40	6	275	GLN
40	6	320	GLN
41	7	247	ASN
41	7	298	GLN
43	a	62	HIS
43	a	121	HIS
43	a	126	HIS
44	c	82	ASN
44	c	94	ASN
44	c	128	GLN
44	c	204	GLN
44	c	249	ASN
45	d	59	HIS
45	d	154	ASN
45	d	161	HIS
45	d	193	HIS
45	d	251	GLN
46	f	108	GLN
46	f	138	GLN
47	h	103	HIS
49	l	67	GLN
49	l	124	GLN

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Mol	Chain	Res	Type
50	p	104	HIS
51	s	87	GLN
51	s	207	HIS
51	s	240	GLN
51	s	391	ASN
51	s	408	ASN
52	Q	172	GLN
52	Q	212	ASN
55	z	131	ASN
55	z	252	HIS
56	w	72	ASN
56	w	78	HIS
56	w	115	GLN
56	w	182	GLN
56	w	187	ASN
56	w	278	ASN
56	w	283	GLN
56	w	312	GLN
56	w	403	ASN
56	w	420	GLN
56	w	507	HIS
56	w	714	ASN
56	w	716	GLN
56	w	766	GLN

5.3.3 RNA [i](#)

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%)

All (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
1	A	1700	U

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Mol	Chain	Res	Type
1	A	1704	U
1	A	1708	A
1	A	1709	G
1	A	1710	A
1	A	1711	C
1	A	1713	A
1	A	1714	C
1	A	1715	C
1	A	1716	U
1	A	1717	U
1	A	1724	A
1	A	1727	A
1	A	1728	U
1	A	1733	C
1	A	1734	C
1	A	1735	A
1	A	1736	A
1	A	1748	G
1	A	1750	G
1	A	1751	A
1	A	1762	A
1	A	1763	A
1	A	1766	U
1	A	1770	G
1	A	1777	A
1	A	1781	A
1	A	1782	G
1	A	1794	A
1	A	1803	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1809	U
1	A	1810	A
1	A	1821	A
1	A	1823	A
1	A	1824	U
1	A	1827	C
1	A	1828	A
1	A	1829	A
1	A	1832	A

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Mol	Chain	Res	Type
1	A	1836	A
1	A	1840	C
1	A	1844	A
1	A	1849	C
1	A	1854	U
1	A	1856	A
1	A	1867	A
1	A	1869	A
1	A	1871	A
1	A	1872	U
1	A	1878	U
1	A	1882	A
1	A	1883	G
1	A	1890	C
1	A	1893	A
1	A	1901	C
1	A	1902	C
1	A	1903	C
1	A	1909	A
1	A	1918	G
1	A	1935	A
1	A	1936	A
1	A	1938	A
1	A	1940	A
1	A	1944	C
1	A	1946	C
1	A	1958	G
1	A	1974	A
1	A	1985	G
1	A	1986	A
1	A	1987	G
1	A	1992	C
1	A	1994	A
1	A	1995	A
1	A	2000	C
1	A	2001	C
1	A	2002	G
1	A	2015	G
1	A	2021	U
1	A	2022	G
1	A	2029	A
1	A	2031	A

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Mol	Chain	Res	Type
1	A	2036	C
1	A	2037	U
1	A	2038	U
1	A	2039	A
1	A	2060	A
1	A	2065	A
1	A	2066	C
1	A	2067	C
1	A	2069	U
1	A	2074	A
1	A	2079	C
1	A	2083	U
1	A	2085	A
1	A	2093	U
1	A	2097	A
1	A	2098	G
1	A	2099	U
1	A	2105	G
1	A	2113	G
1	A	2125	C
1	A	2126	U
1	A	2134	A
1	A	2135	A
1	A	2142	A
1	A	2147	G
1	A	2154	A
1	A	2160	A
1	A	2163	A
1	A	2165	C
1	A	2166	C
1	A	2169	A
1	A	2171	U
1	A	2172	A
1	A	2173	G
1	A	2174	G
1	A	2180	A
1	A	2181	A
1	A	2183	C
1	A	2187	C
1	A	2190	C
1	A	2192	A
1	A	2198	A

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Mol	Chain	Res	Type
1	A	2200	A
1	A	2204	U
1	A	2210	C
1	A	2211	U
1	A	2217	C
1	A	2218	C
1	A	2219	C
1	A	2220	A
1	A	2222	U
1	A	2224	C
1	A	2227	A
1	A	2228	A
1	A	2229	A
1	A	2230	A
1	A	2237	A
1	A	2239	A
1	A	2241	A
1	A	2242	U
1	A	2244	U
1	A	2245	A
1	A	2246	A
1	A	2250	A
1	A	2252	C
1	A	2260	A
1	A	2262	C
1	A	2263	C
1	A	2284	C
1	A	2285	U
1	A	2297	A
1	A	2299	U
1	A	2300	G
1	A	2315	A
1	A	2322	C
1	A	2324	U
1	A	2332	C
1	A	2345	G
1	A	2350	A
1	A	2351	U
1	A	2356	A
1	A	2357	C
1	A	2360	U
1	A	2361	G

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Mol	Chain	Res	Type
1	A	2362	A
1	A	2364	C
1	A	2365	U
1	A	2371	U
1	A	2372	U
1	A	2381	A
1	A	2390	A
1	A	2393	C
1	A	2404	U
1	A	2407	U
1	A	2414	C
1	A	2415	C
1	A	2416	U
1	A	2434	A
1	A	2443	C
1	A	2444	A
1	A	2446	A
1	A	2447	A
1	A	2451	A
1	A	2452	A
1	A	2458	A
1	A	2478	G
1	A	2493	C
1	A	2507	A
1	A	2508	C
1	A	2511	C
1	A	2520	C
1	A	2521	A
1	A	2522	U
1	A	2523	C
1	A	2524	A
1	A	2527	A
1	A	2530	A
1	A	2531	U
1	A	2532	U
1	A	2540	C
1	A	2546	G
1	A	2557	C
1	A	2558	A
1	A	2559	U
1	A	2560	G
1	A	2570	C

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Mol	Chain	Res	Type
1	A	2575	U
1	A	2592	G
1	A	2593	G
1	A	2594	U
1	A	2599	U
1	A	2601	A
1	A	2603	C
1	A	2607	U
1	A	2618	U
1	A	2626	U
1	A	2627	G
1	A	2629	A
1	A	2630	U
1	A	2632	A
1	A	2633	A
1	A	2634	U
1	A	2635	G
1	A	2645	G
1	A	2654	U
1	A	2656	U
1	A	2660	U
1	A	2683	C
1	A	2684	C
1	A	2686	G
1	A	2694	A
1	A	2696	A
1	A	2706	A
1	A	2709	A
1	A	2715	A
1	A	2718	C
1	A	2723	A
1	A	2724	G
1	A	2725	A
1	A	2732	G
1	A	2739	U
1	A	2740	A
1	A	2745	A
1	A	2747	U
1	A	2750	U
1	A	2755	A
1	A	2756	C
1	A	2757	A

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Mol	Chain	Res	Type
1	A	2758	G
1	A	2760	A
1	A	2791	A
1	A	2792	A
1	A	2803	A
1	A	2804	A
1	A	2810	G
1	A	2814	G
1	A	2831	G
1	A	2832	A
1	A	2833	A
1	A	2844	G
1	A	2847	C
1	A	2854	U
1	A	2864	U
1	A	2865	C
1	A	2881	C
1	A	2893	A
1	A	2906	C
1	A	2910	A
1	A	2912	C
1	A	2913	A
1	A	2916	G
1	A	2917	G
1	A	2918	A
1	A	2922	A
1	A	2926	A
1	A	2928	C
1	A	2935	A
1	A	2955	U
1	A	2956	A
1	A	2962	C
1	A	2963	A
1	A	2985	C
1	A	2990	A
1	A	2991	U
1	A	2992	G
1	A	2994	U
1	A	3000	A
1	A	3005	A
1	A	3007	C
1	A	3016	G

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Mol	Chain	Res	Type
1	A	3022	G
1	A	3041	U
1	A	3042	U
1	A	3049	U
1	A	3053	A
1	A	3054	G
1	A	3059	A
1	A	3063	G
1	A	3070	G
1	A	3072	U
1	A	3093	C
1	A	3097	U
1	A	3098	U
1	A	3100	U
1	A	3102	U
1	A	3109	U
1	A	3113	A
1	A	3114	U
1	A	3123	G
1	A	3124	U
1	A	3129	A
1	A	3141	A
1	A	3150	U
1	A	3155	C
1	A	3157	C
1	A	3158	A
1	A	3162	C
1	A	3168	C
1	A	3169	C
1	A	3172	C
1	A	3180	A
1	A	3189	C
1	A	3190	A
1	A	3192	C
1	A	3196	G
1	A	3197	U
1	A	3200	U
1	A	3201	A
1	A	3204	C
1	A	3205	C
1	A	3207	A
1	A	3208	C

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Mol	Chain	Res	Type
1	A	3210	C
1	A	3211	C
1	A	3212	C
1	A	3217	A
1	A	3218	A
1	A	3220	A
1	A	3228	U
2	B	1607	U
2	B	1608	G
2	B	1609	U
2	B	1611	G
2	B	1613	U
2	B	1614	U
2	B	1615	A
2	B	1625	A
2	B	1644	G
2	B	1645	A
2	B	1651	A
2	B	1659	U
2	B	1669	G

All (29) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	1703	C
1	A	1709	G
1	A	1713	A
1	A	1805	A
1	A	1806	U
1	A	1807	U
1	A	1808	A
1	A	1809	U
1	A	1823	A
1	A	1871	A
1	A	1994	A
1	A	2165	C
1	A	2172	A
1	A	2186	C
1	A	2245	A
1	A	2361	G
1	A	2457	A
1	A	2507	A

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Mol	Chain	Res	Type
1	A	2530	A
1	A	2559	U
1	A	2628	U
1	A	2653	C
1	A	2905	A
1	A	2989	G
1	A	3041	U
1	A	3092	U
1	A	3123	G
1	A	3196	G
2	B	1607	U

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 monosaccharides 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	27,34,34	1.85	6 (22%)	34,54,54	2.37	8 (23%)

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	-	5/15/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	w	801	GCP	PG-O1G	5.44	1.61	1.50
59	w	801	GCP	C5-C6	4.43	1.49	1.41
59	w	801	GCP	PG-O3G	3.02	1.61	1.54
59	w	801	GCP	PG-O2G	-2.50	1.49	1.54
59	w	801	GCP	C5-C4	2.47	1.47	1.40
59	w	801	GCP	PB-O2B	2.36	1.61	1.56

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	w	801	GCP	PB-O3A-PA	-6.12	113.17	132.56
59	w	801	GCP	C4-C5-C6	-5.86	115.20	120.80
59	w	801	GCP	C2-N3-C4	4.79	120.82	115.36
59	w	801	GCP	C2-N1-C6	4.62	123.27	115.93
59	w	801	GCP	N3-C2-N1	-4.03	121.85	127.22
59	w	801	GCP	C5-C6-N1	-3.92	118.07	123.43
59	w	801	GCP	C1'-N9-C4	-3.92	119.76	126.64
59	w	801	GCP	C4-C5-N7	-2.44	106.86	109.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

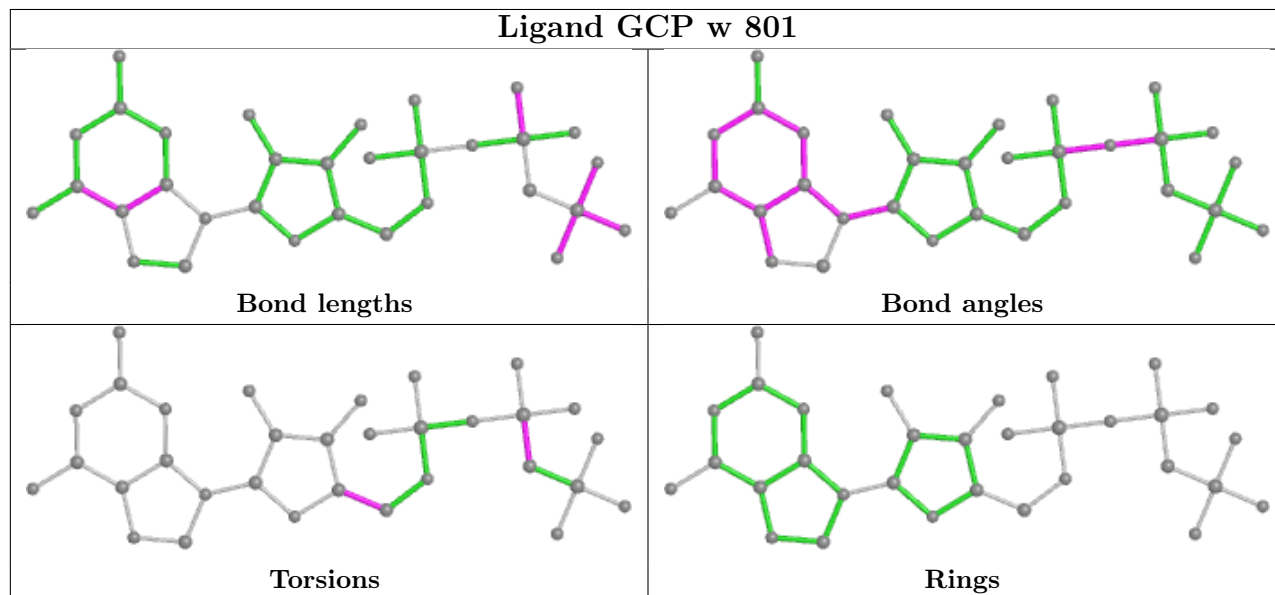
Mol	Chain	Res	Type	Atoms
59	w	801	GCP	PG-C3B-PB-O1B
59	w	801	GCP	PG-C3B-PB-O3A
59	w	801	GCP	O4'-C4'-C5'-O5'
59	w	801	GCP	C3'-C4'-C5'-O5'
59	w	801	GCP	PG-C3B-PB-O2B

There are no ring outliers.

No monomer is involved in short contacts.

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
34	N	1

All 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

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	u	615:UNK	C	700:UNK	N	15.49
1	w	455:LEU	C	478:LEU	N	11.53
1	A	2580:U	O3'	2581:A	P	3.69
1	N	230:LEU	C	231:SER	N	1.19

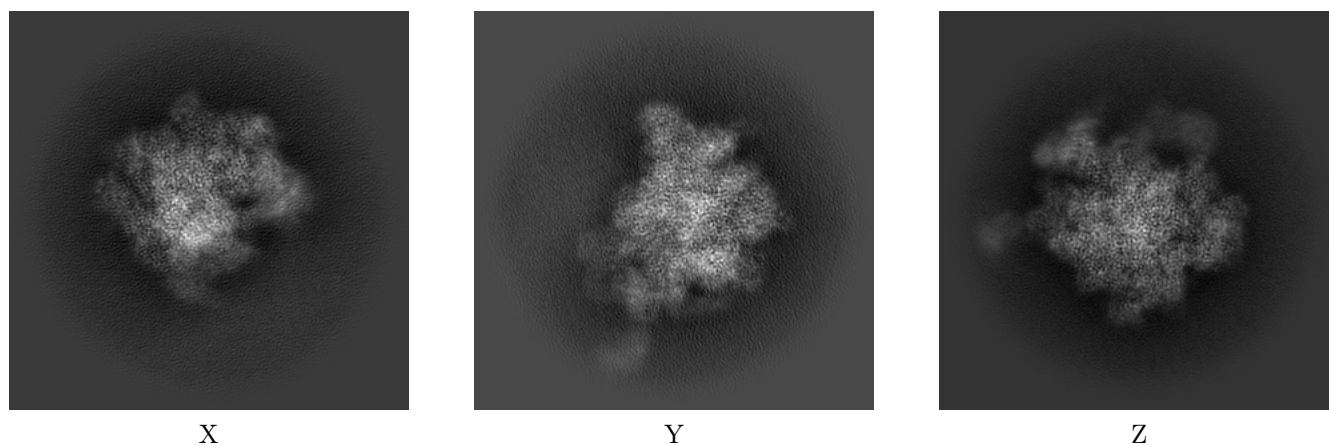
6 Map visualisation [i](#)

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](#)

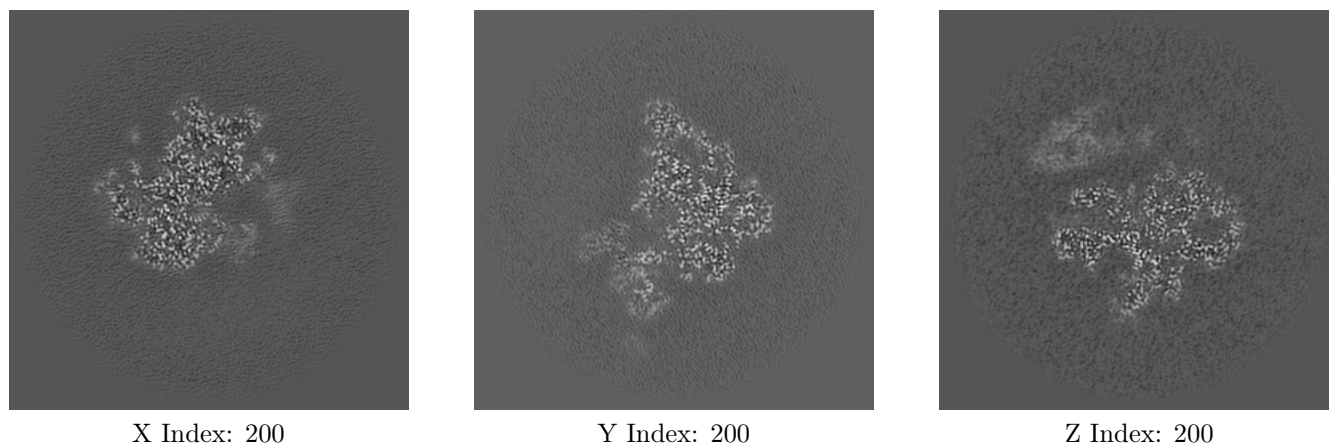
6.1.1 Primary map



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

6.2 Central slices [i](#)

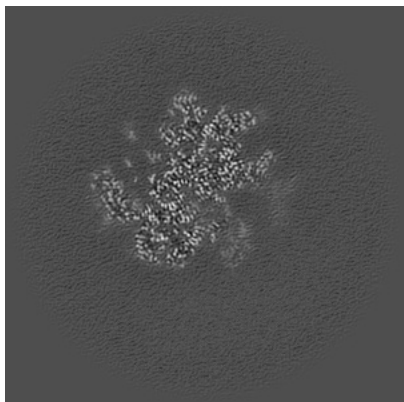
6.2.1 Primary map



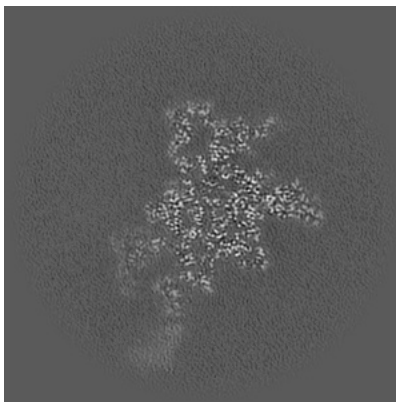
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

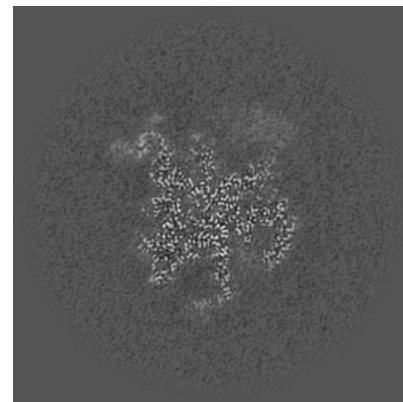
6.3.1 Primary map



X Index: 195



Y Index: 179

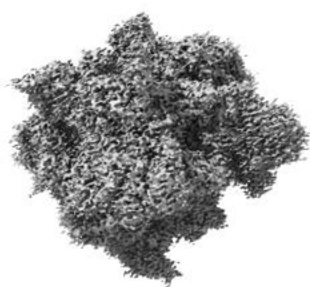


Z Index: 232

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

6.4 Orthogonal surface views [i](#)

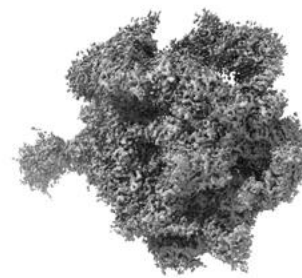
6.4.1 Primary map



X



Y



Z

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.

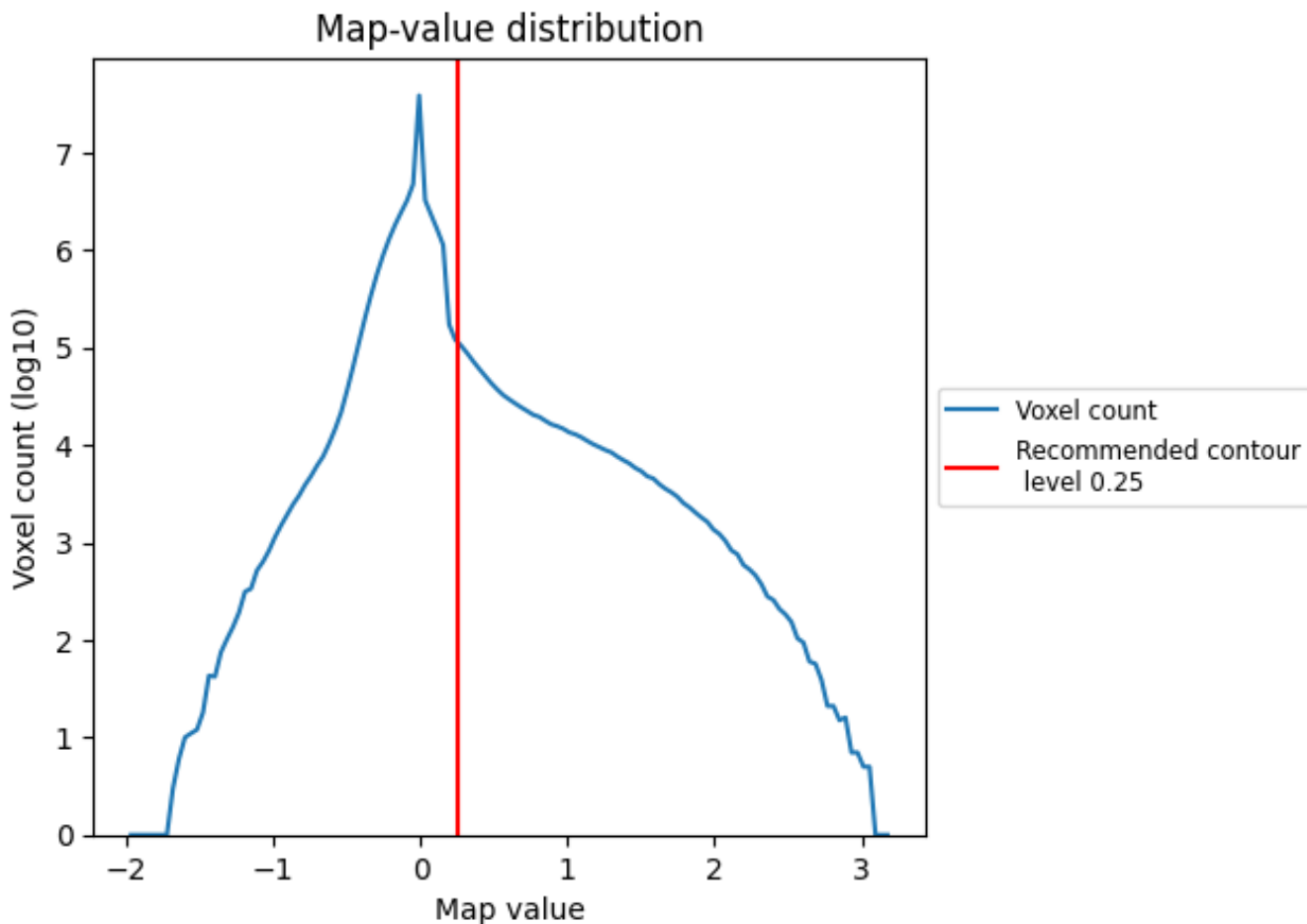
6.5 Mask visualisation

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

7 Map analysis [i](#)

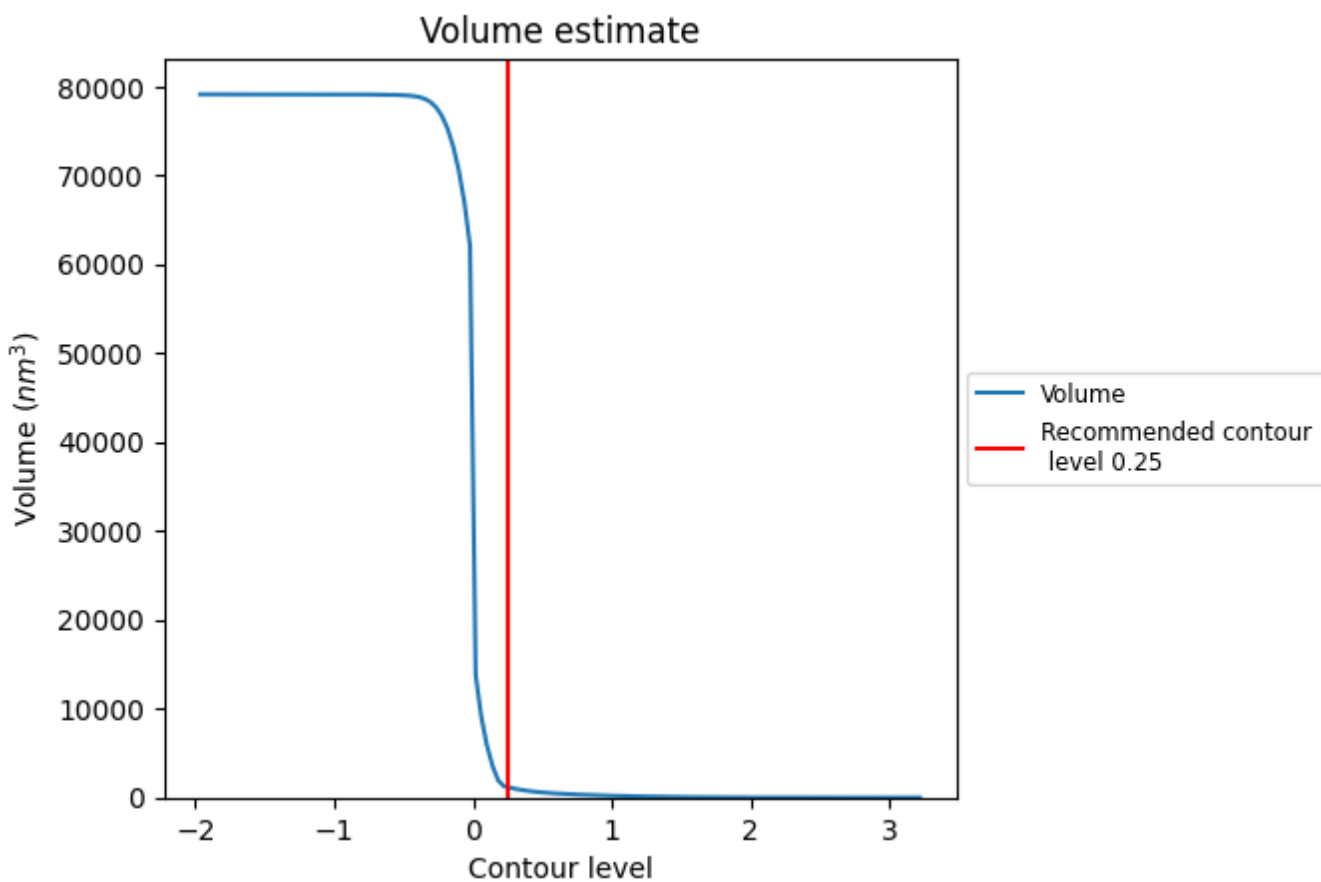
This section contains the results of statistical analysis of the map.

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.

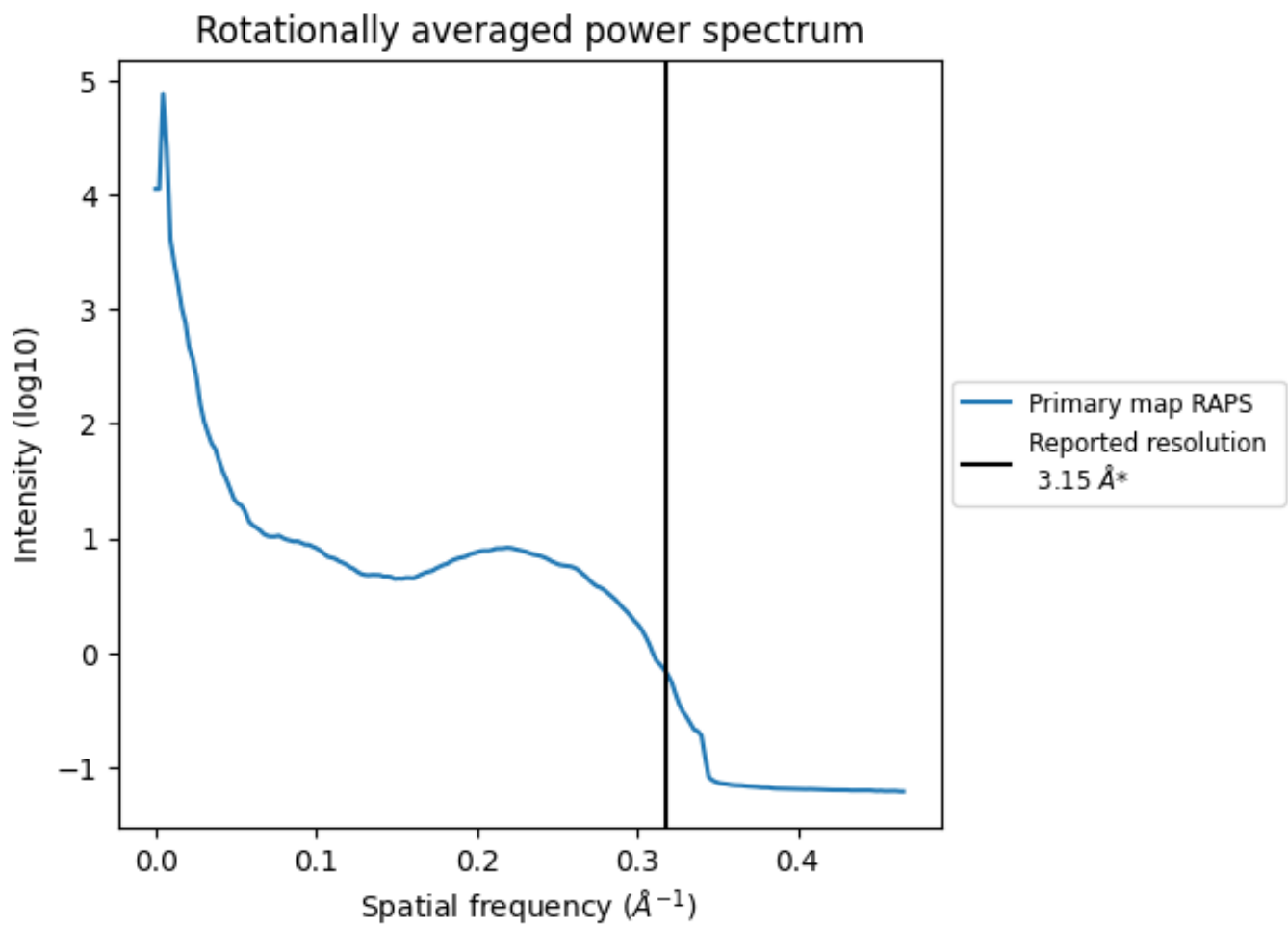
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1170 nm³; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.317 Å⁻¹

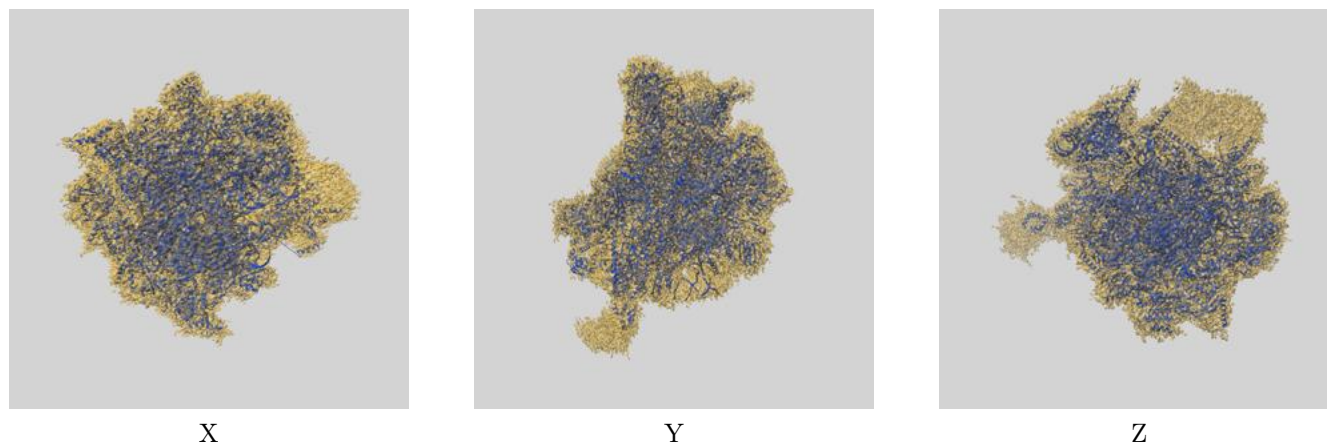
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

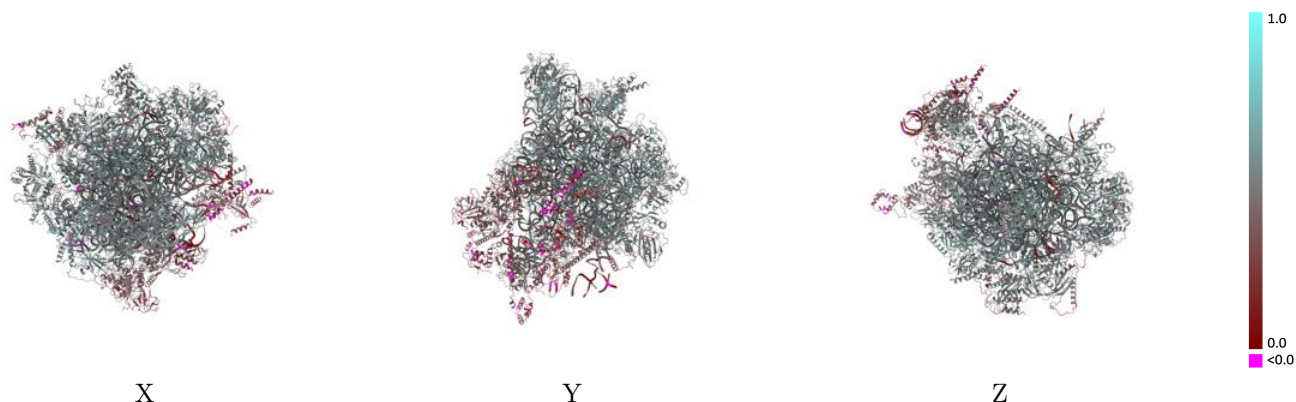
This section contains information regarding the fit between EMDB map EMD-23121 and PDB model 7L20. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



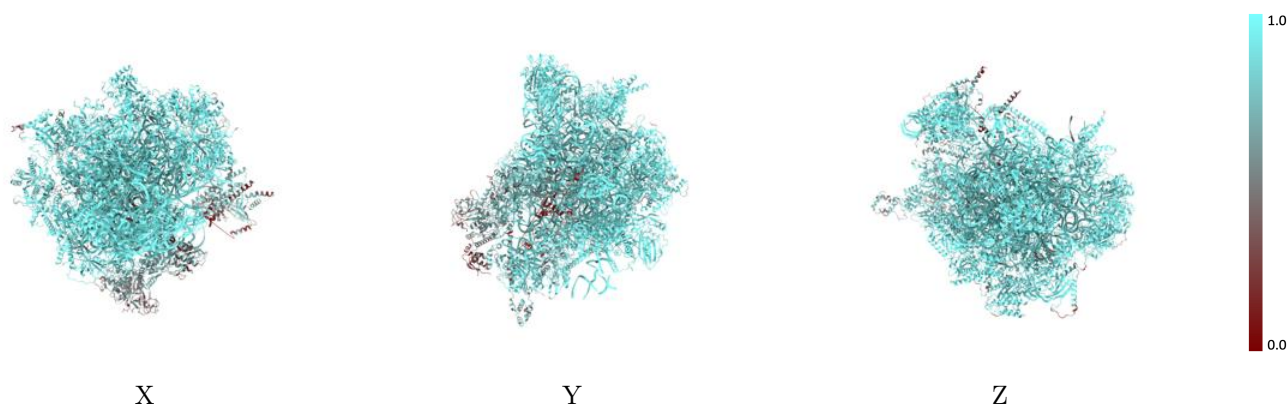
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



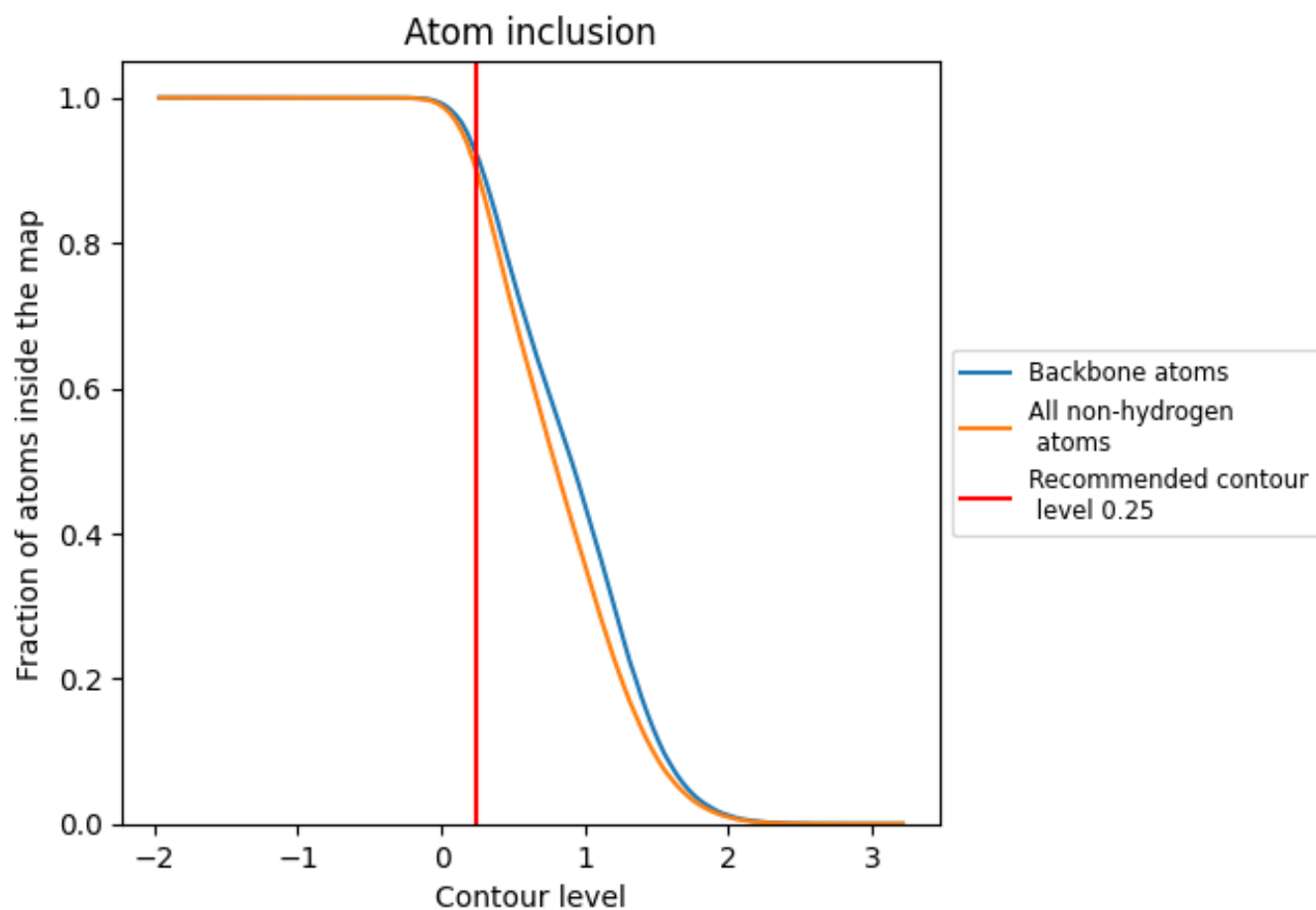
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.8979	 0.4720
0	 0.9449	 0.5340
1	 0.9333	 0.5240
2	 0.9611	 0.5740
3	 0.9549	 0.5720
4	 0.9725	 0.5740
5	 0.9531	 0.5150
6	 0.9348	 0.4680
7	 0.9255	 0.4850
8	 0.7821	 0.3180
9	 0.9507	 0.5210
A	 0.9315	 0.4740
B	 0.9370	 0.3360
D	 0.9578	 0.5400
E	 0.9528	 0.5470
F	 0.9545	 0.5400
H	 0.9282	 0.4970
I	 0.8805	 0.4210
J	 0.7825	 0.3140
K	 0.9639	 0.5510
L	 0.9516	 0.5370
M	 0.9579	 0.5410
N	 0.9431	 0.5450
O	 0.9500	 0.5410
P	 0.9520	 0.5080
Q	 0.9478	 0.5380
R	 0.9368	 0.5510
S	 0.9574	 0.5510
T	 0.9480	 0.5530
TA	 0.6076	 0.1640
TB	 0.6009	 0.1610
TC	 0.2585	 0.1400
U	 0.9177	 0.5120
V	 0.9122	 0.4810
W	 0.9378	 0.5500



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Chain	Atom inclusion	Q-score
X	 0.9377	 0.5250
Y	 0.9509	 0.5320
Z	 0.9510	 0.5530
a	 0.8706	 0.4760
b	 0.9561	 0.5480
c	 0.9279	 0.5070
d	 0.8631	 0.4480
e	 0.7420	 0.2390
f	 0.7581	 0.3490
g	 0.9335	 0.5230
h	 0.9186	 0.4730
i	 0.9497	 0.5560
j	 0.9107	 0.5070
k	 0.9156	 0.4430
l	 0.8679	 0.4000
m	 0.8499	 0.3360
o	 0.9396	 0.5430
p	 0.8531	 0.4360
q	 0.8353	 0.4010
r	 0.9547	 0.5280
s	 0.9370	 0.5180
u	 0.3169	 0.0710
w	 0.5883	 0.2990
z	 0.6478	 0.3260