



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:38 PM UTC

PDB ID : 5XY3 / pdb_00005xy3
EMDB ID : EMD-6784
Title : Large subunit of Trichomonas vaginalis ribosome
Authors : Li, Z.; Guo, Q.; Zheng, L.; Ji, Y.; Xie, Y.; Lai, D.; Lun, Z.; Suo, X.; Gao, N.
Deposited on : 2017-07-06
Resolution : 3.20 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:

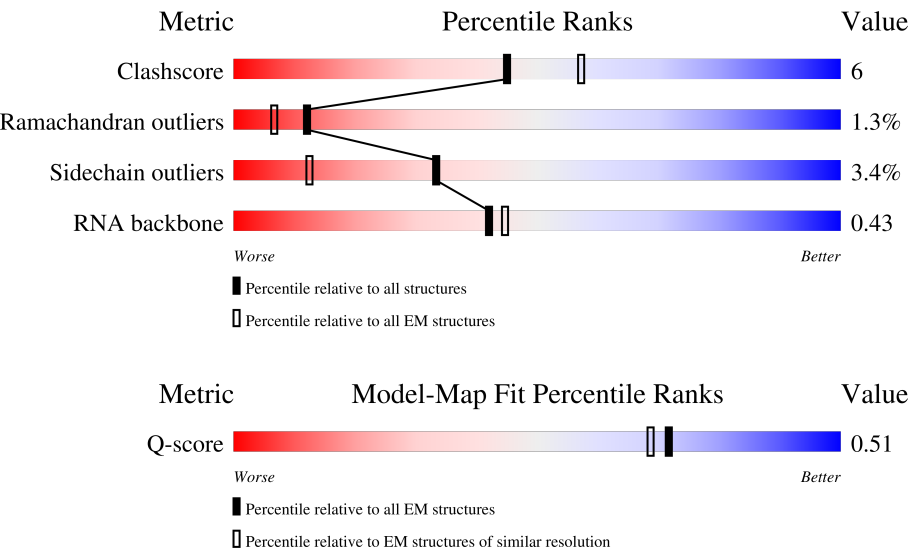
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	1	2765	
2	3	118	
3	4	162	

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Mol	Chain	Length	Quality of chain
4	A	251	
5	B	415	
6	C	370	
7	D	308	
8	E	151	
9	F	239	
10	G	244	
11	H	197	
12	I	209	
13	J	169	
14	L	189	
15	M	128	
16	N	204	
17	O	200	
18	P	164	
19	Q	186	
20	R	178	
21	S	176	
22	T	159	
23	U	106	
24	V	140	
25	W	113	
26	X	140	
27	Y	138	
28	Z	139	

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Mol	Chain	Length	Quality of chain
29	a	151	
30	b	58	
31	c	112	
32	d	110	
33	e	132	
34	f	102	
35	g	116	
36	h	124	
37	i	91	
38	j	81	
39	k	74	
40	l	51	
41	m	132	
42	o	104	
43	p	92	

2 Entry composition

There are 43 unique types of molecules in this entry. The entry contains 107145 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2544	Total	C	N	O	P	0	0
			54325	24285	9748	17748	2544		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	117	Total	C	N	O	P	0	0
			2493	1112	449	815	117		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	154	Total	C	N	O	P	0	0
			3289	1472	595	1068	154		

- Molecule 4 is a protein called Ribosomal protein L8, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	237	Total	C	N	O	S	0	0
			1785	1105	365	306	9		

- Molecule 5 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	400	Total	C	N	O	S	0	0
			3175	2002	608	554	11		

- Molecule 6 is a protein called Ribosomal protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	362	Total	C	N	O	S	0	0
			2772	1751	513	501	7		

- Molecule 7 is a protein called Ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	272	Total	C	N	O	S	0	0
			2167	1384	394	384	5		

- Molecule 8 is a protein called 60S ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	135	Total	C	N	O	S	0	0
			1014	651	180	181	2		

- Molecule 9 is a protein called Ribosomal protein L30p/L7e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	231	Total	C	N	O	S	0	0
			1832	1174	330	324	4		

- Molecule 10 is a protein called Ribosomal protein L7Ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	174	Total	C	N	O	S	0	0
			1384	892	245	239	8		

- Molecule 11 is a protein called Ribosomal protein L6, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	192	Total	C	N	O	S	0	0
			1556	994	274	281	7		

- Molecule 12 is a protein called Ribosomal protein, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	195	Total	C	N	O	S	0	0
			1569	989	304	264	12		

- Molecule 13 is a protein called 60S ribosomal protein L11, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	164	Total	C	N	O	S	0	0
			1320	827	258	230	5		

- Molecule 14 is a protein called Ribosomal protein L13e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	185	Total	C	N	O	S	0	0
			1498	947	296	252	3		

- Molecule 15 is a protein called Ribosomal protein L14, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	124	Total	C	N	O	S	0	0
			1004	650	176	177	1		

- Molecule 16 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	N	202	Total	C	N	O	S	0	0
			1696	1076	343	271	6		

- Molecule 17 is a protein called Ribosomal protein L13, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	196	Total	C	N	O	S	0	0
			1559	988	295	271	5		

- Molecule 18 is a protein called Ribosomal protein L22, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	155	Total	C	N	O	S	0	0
			1230	781	231	211	7		

- Molecule 19 is a protein called 60S ribosomal protein L18, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	185	Total	C	N	O	S	0	0
			1465	907	295	255	8		

- Molecule 20 is a protein called 60S ribosomal protein L19-3, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	162	Total	C	N	O	S	0	0
			1299	805	277	213	4		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	175	Total	C	N	O	S	0	0
			1384	882	252	247	3		

- Molecule 22 is a protein called Ribosomal protein L21e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	158	Total	C	N	O	S	0	0
			1255	797	249	207	2		

- Molecule 23 is a protein called 60S ribosomal protein L22-1, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	97	Total	C	N	O	S	0	0
			794	511	140	141	2		

- Molecule 24 is a protein called 60S ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	134	Total	C	N	O	S	0	0
			986	622	185	172	7		

- Molecule 25 is a protein called Ribosomal protein L24e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	59	Total	C	N	O	S	0	0
			513	323	108	79	3		

- Molecule 26 is a protein called Ribosomal protein L23, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	101	Total	C	N	O	S	0	0
			803	518	141	141	3		

- Molecule 27 is a protein called Ribosomal protein L24, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1068	671	204	188	5		

- Molecule 28 is a protein called Ribosomal protein L27e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1042	682	184	172	4		

- Molecule 29 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	149	Total	C	N	O	S	0	0
			1179	749	229	196	5		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	50	Total	C	N	O	S	0	0
			415	256	92	65	2		

- Molecule 31 is a protein called 60S ribosomal protein L30, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	96	Total	C	N	O	S	0	0
			727	462	121	140	4		

- Molecule 32 is a protein called Ribosomal protein L31e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	99	Total	C	N	O	S	0	0
			783	497	149	134	3		

- Molecule 33 is a protein called Ribosomal protein L32, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	123	Total	C	N	O	S	0	0
			1003	633	198	169	3		

- Molecule 34 is a protein called Ribosomal protein L35Ae, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	97	Total	C	N	O	S	0	0
			781	511	137	131	2		

- Molecule 35 is a protein called Ribosomal protein L34e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	115	Total	C	N	O	S	0	0
			921	565	191	158	7		

- Molecule 36 is a protein called Ribosomal protein L29, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			984	623	190	169	2		

- Molecule 37 is a protein called Ribosomal protein L36e, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	73	Total	C	N	O	S	0	0
			616	385	128	101	2		

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	77	Total	C	N	O	S	0	0
			616	380	128	101	7		

- Molecule 39 is a protein called Ribosomal protein L38e, putative.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	k	68	Total	C	N	O	0	0
			547	358	90	99		

- Molecule 40 is a protein called 60S ribosomal protein L39, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			428	267	97	59	5		

- Molecule 41 is a protein called Ubiquitin, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			417	254	89	69	5		

- Molecule 42 is a protein called 60S ribosomal protein L44, putative.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	93	Total	C	N	O	S	0	0
			773	486	158	121	8		

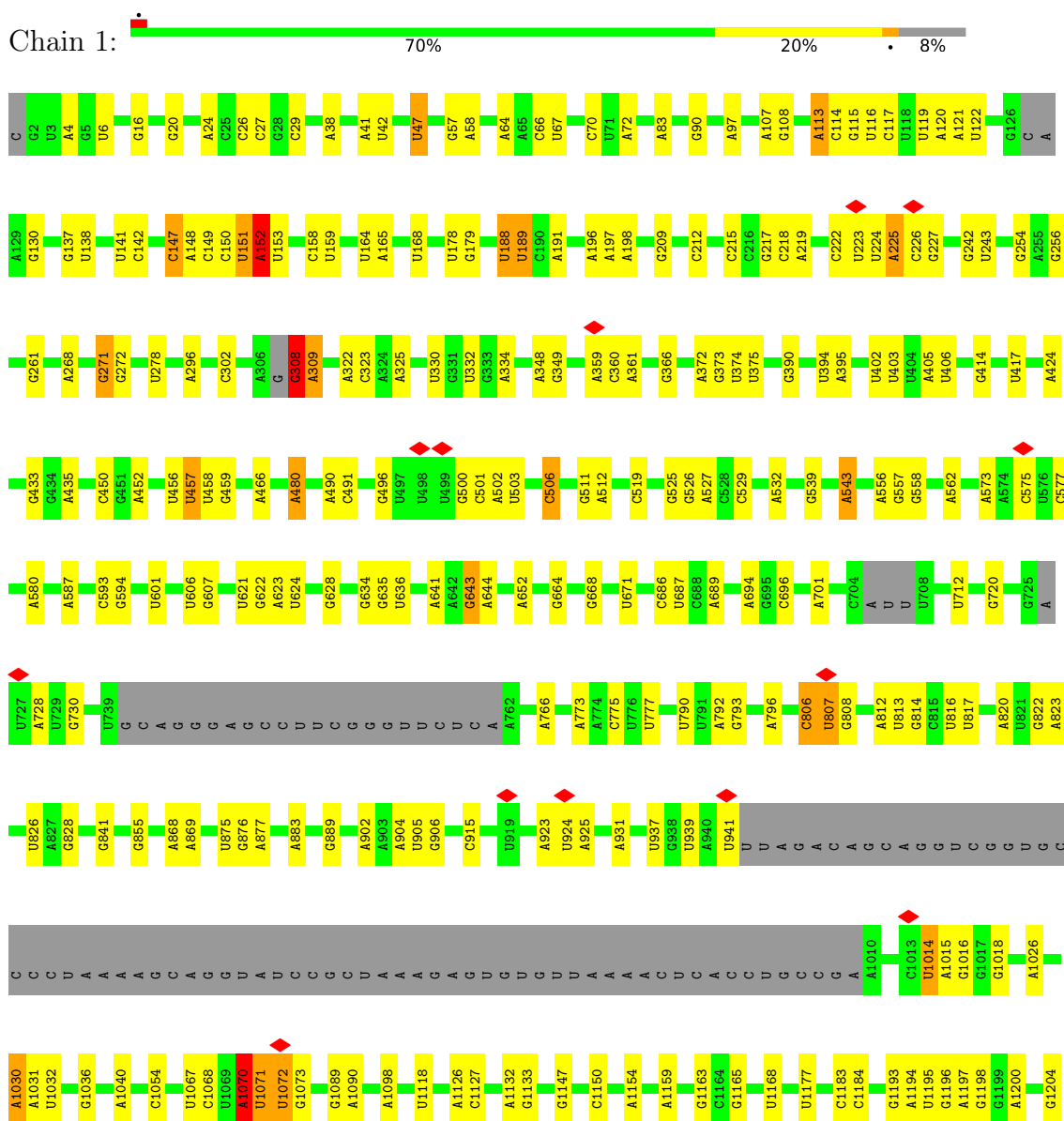
- Molecule 43 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	89	Total	C	N	O	S	0	0
			678	426	133	114	5		

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.

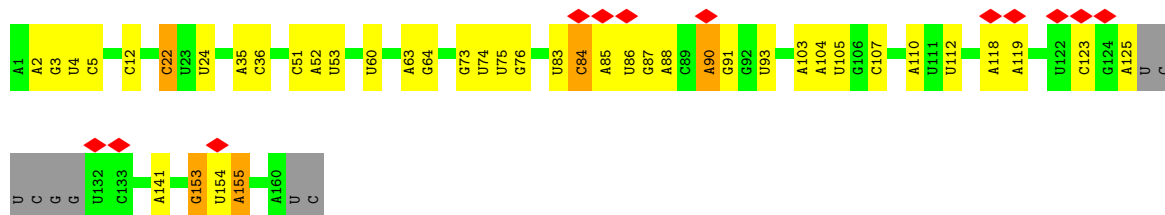
• Molecule 1: 25S ribosomal RNA



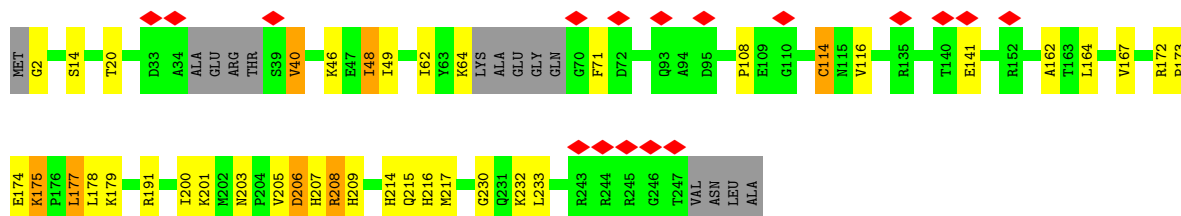
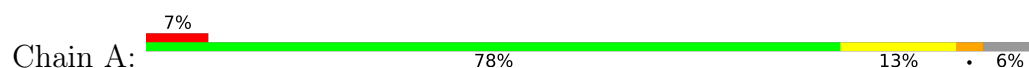




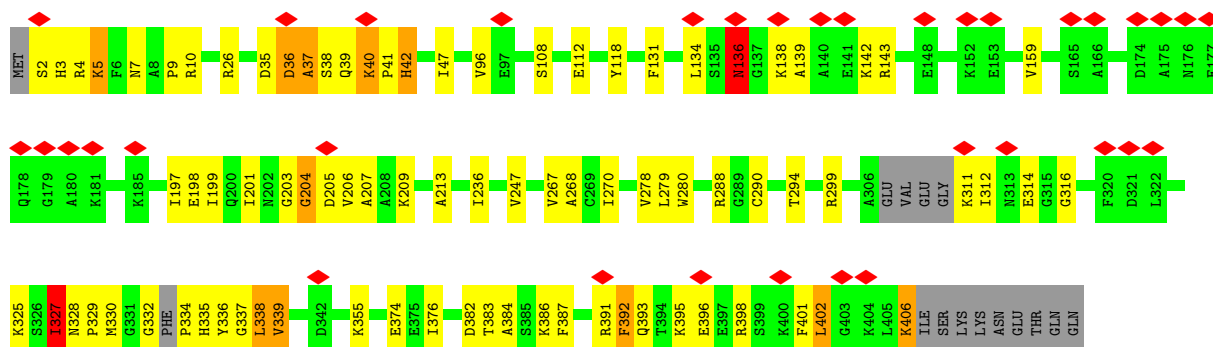
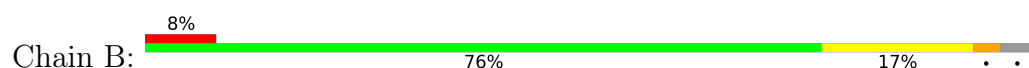
- Molecule 3: 5.8S ribosomal RNA



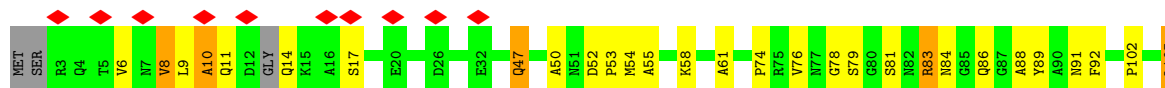
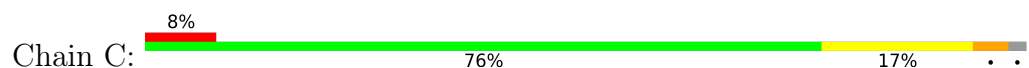
- Molecule 4: Ribosomal protein L8, putative

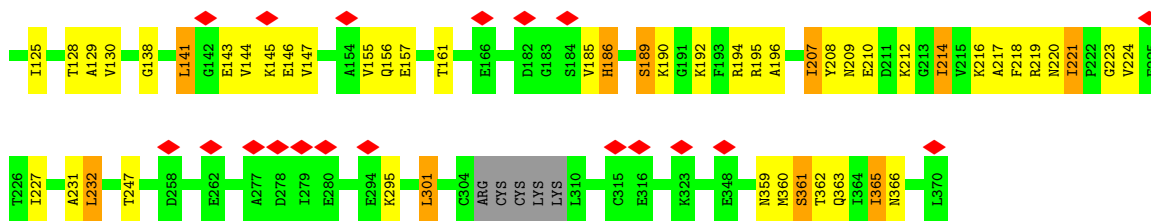


- Molecule 5: Uncharacterized protein

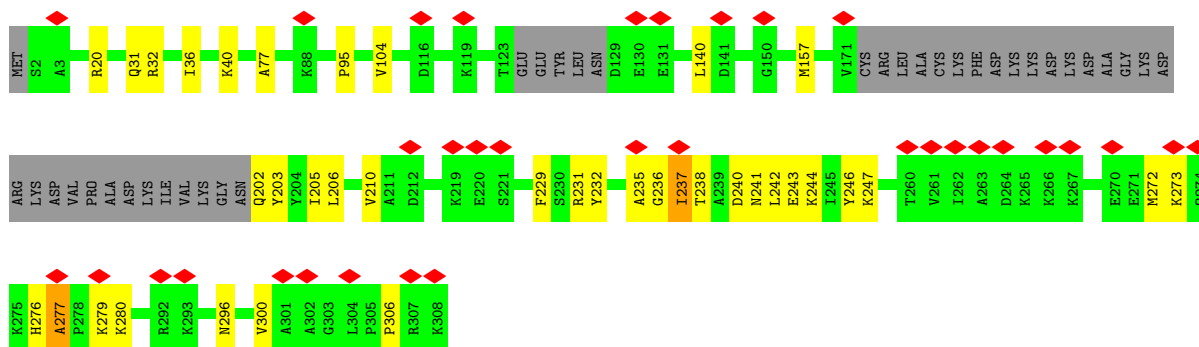
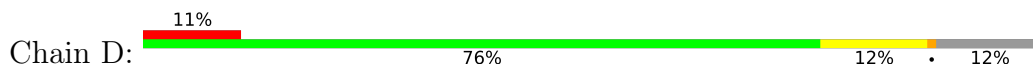


- Molecule 6: Ribosomal protein, putative

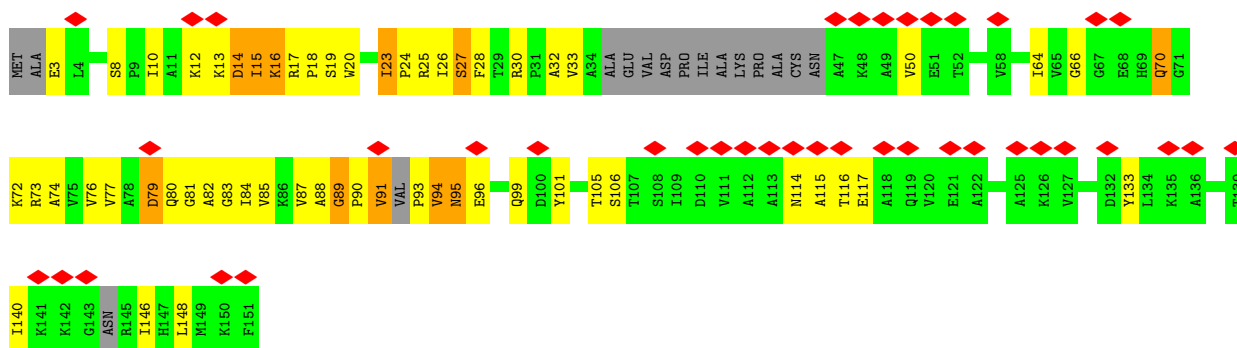




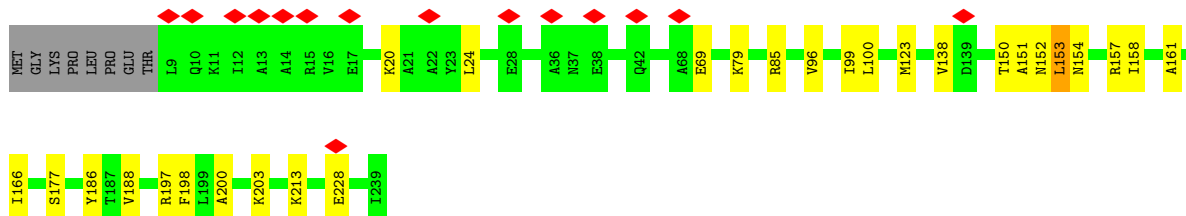
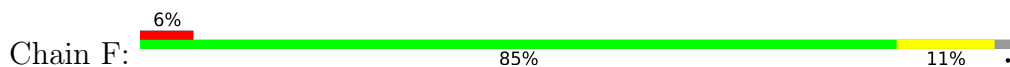
• Molecule 7: Ribosomal protein L5



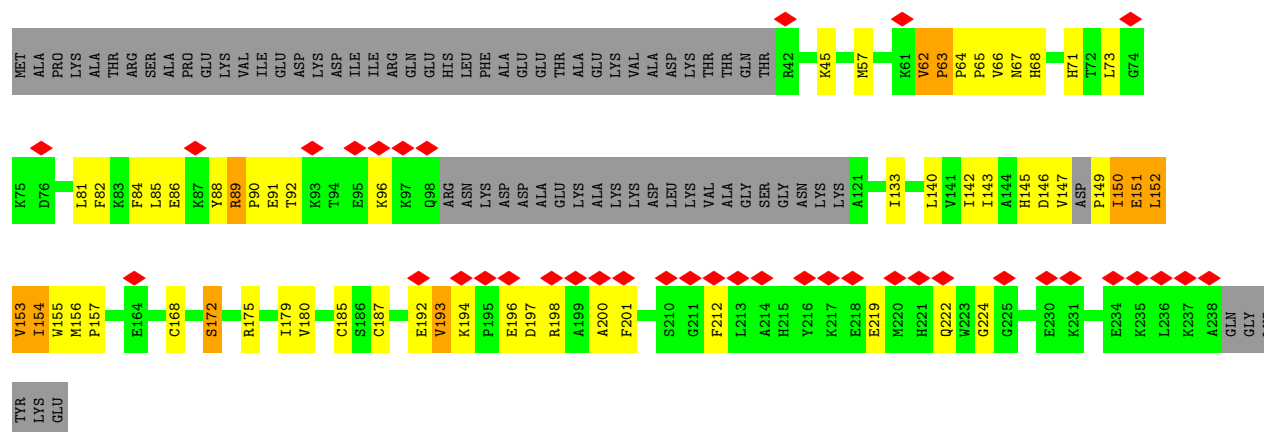
• Molecule 8: 60S ribosomal protein L6, putative



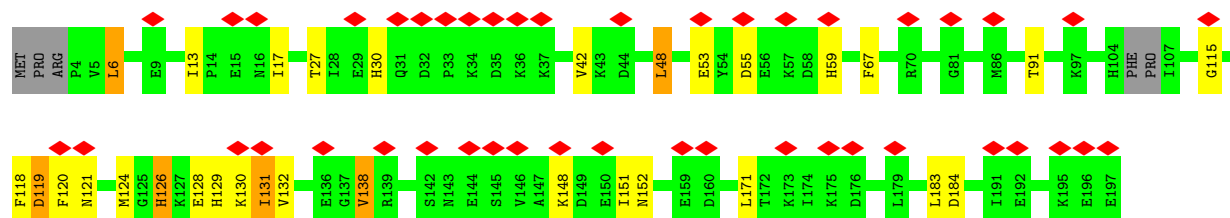
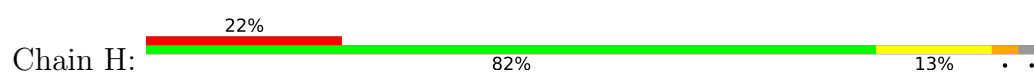
• Molecule 9: Ribosomal protein L30p/L7e, putative



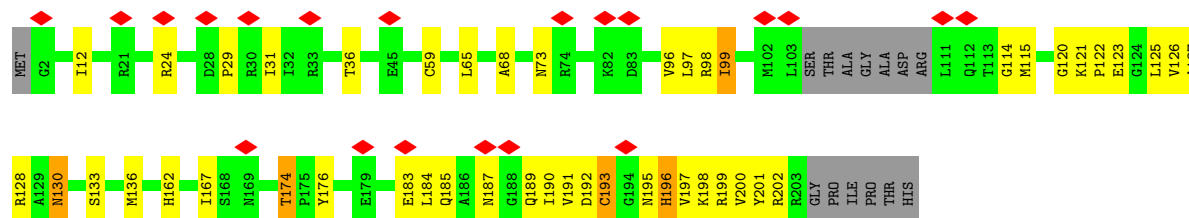
• Molecule 10: Ribosomal protein L7Ae, putative



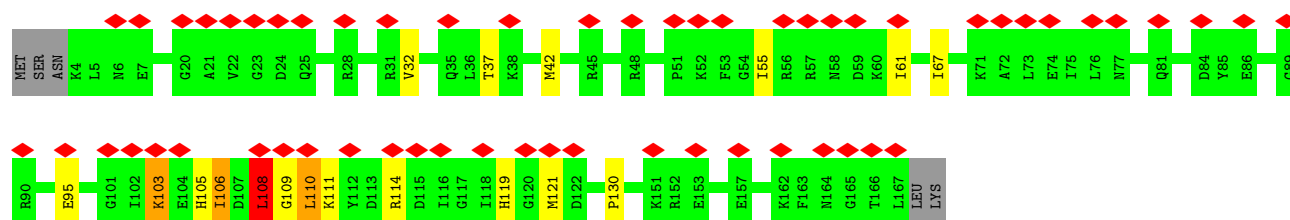
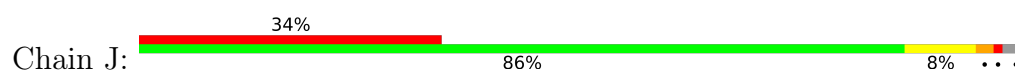
- Molecule 11: Ribosomal protein L6, putative



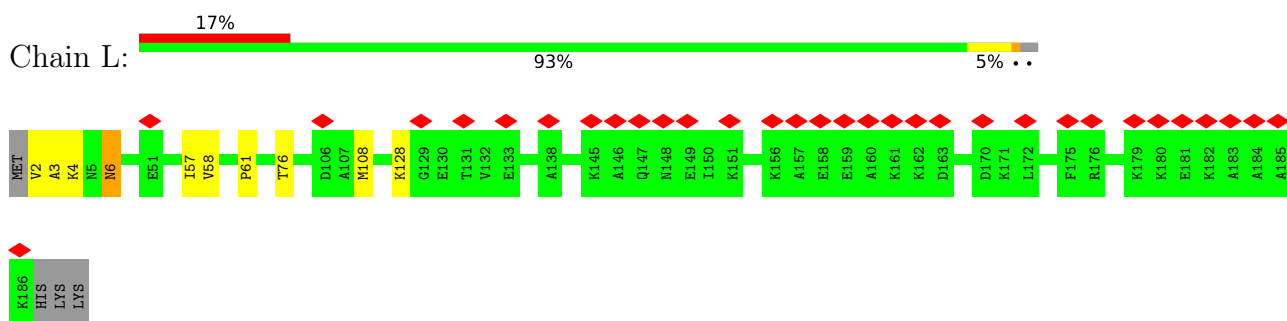
- Molecule 12: Ribosomal protein, putative



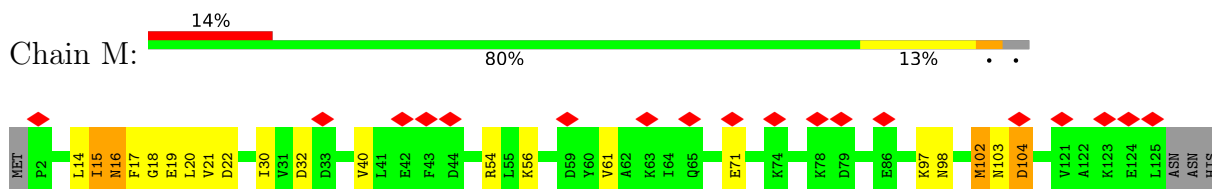
- Molecule 13: 60S ribosomal protein L11, putative



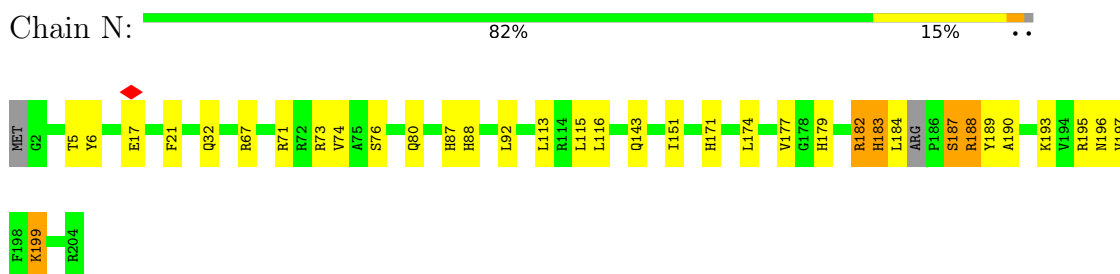
- Molecule 14: Ribosomal protein L13e, putative



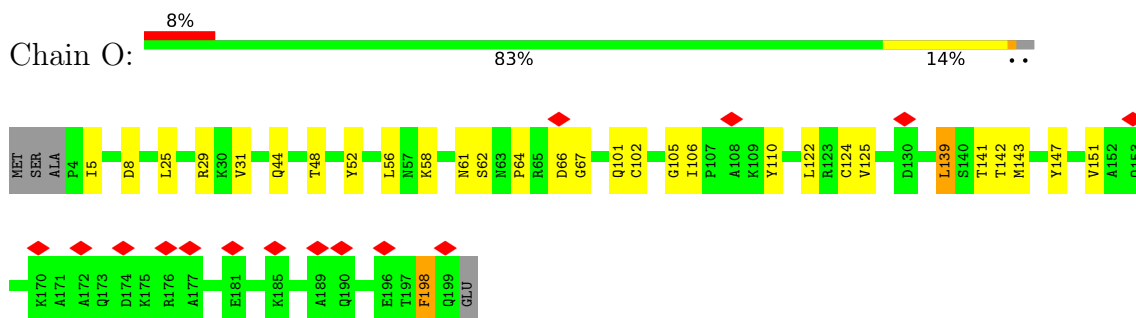
- Molecule 15: Ribosomal protein L14, putative



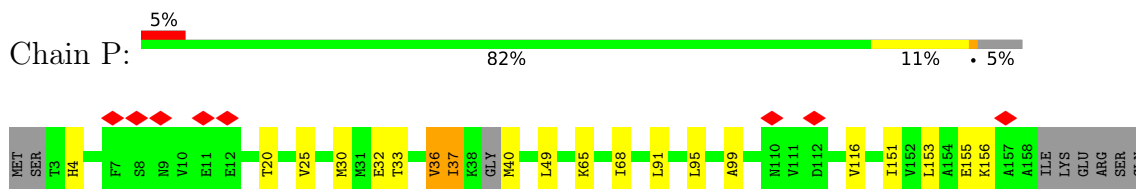
- Molecule 16: Ribosomal protein L15



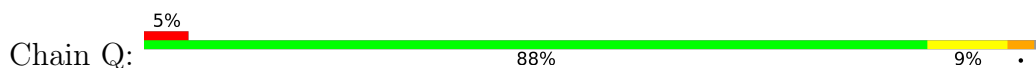
- Molecule 17: Ribosomal protein L13, putative



- Molecule 18: Ribosomal protein L22, putative

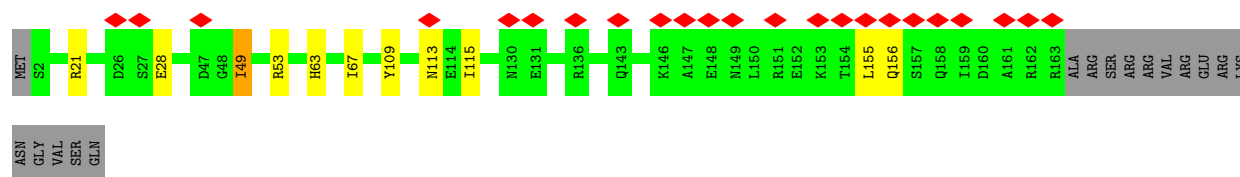
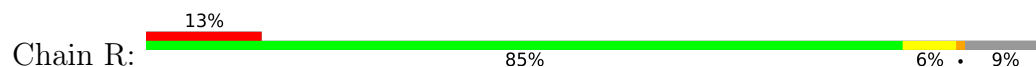


- Molecule 19: 60S ribosomal protein L18, putative

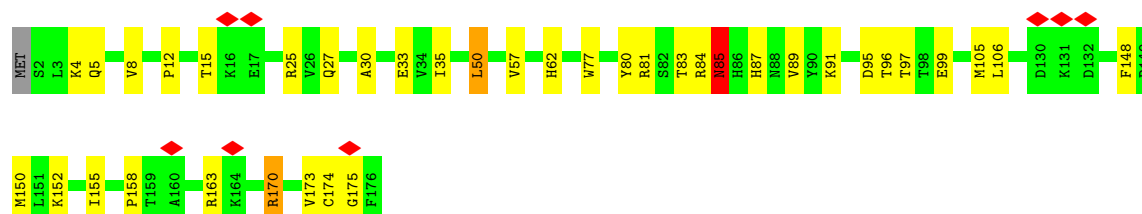
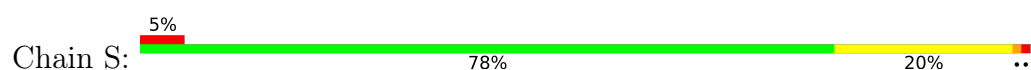




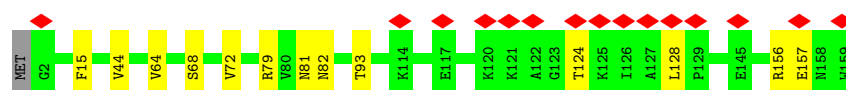
- Molecule 20: 60S ribosomal protein L19-3, putative



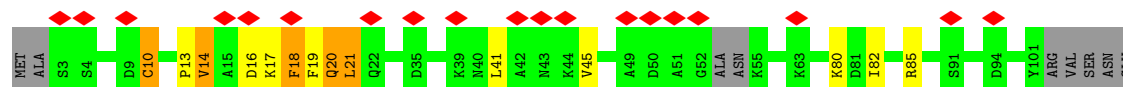
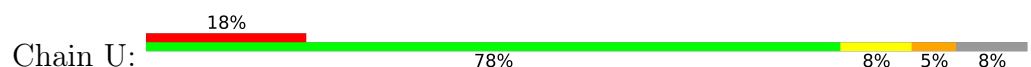
- Molecule 21: 60S ribosomal protein L18a



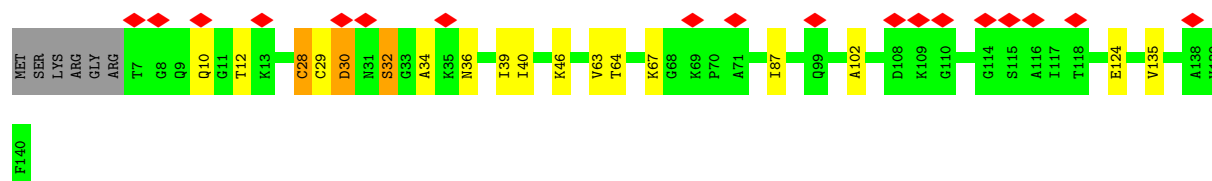
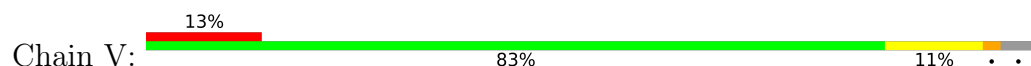
- Molecule 22: Ribosomal protein L21e, putative



- Molecule 23: 60S ribosomal protein L22-1, putative

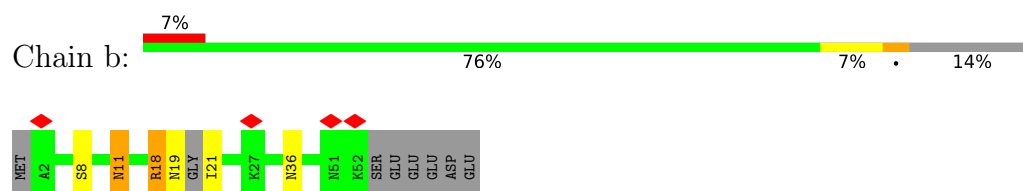


- Molecule 24: 60S ribosomal protein L23, putative

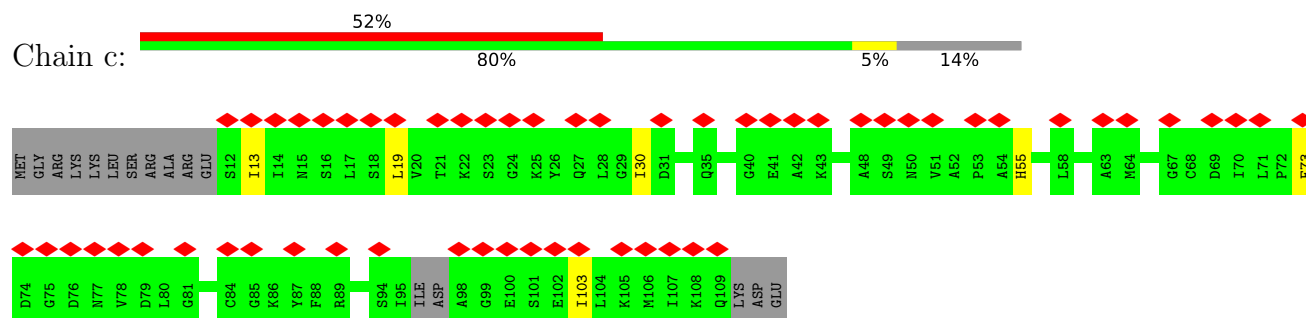


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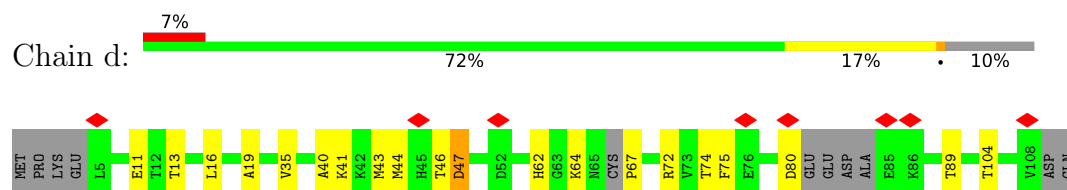
- Molecule 30: 60S ribosomal protein L29



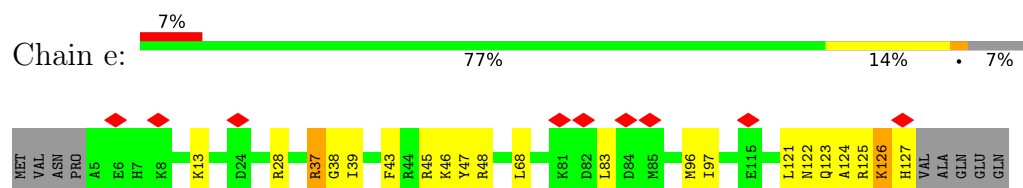
- Molecule 31: 60S ribosomal protein L30, putative



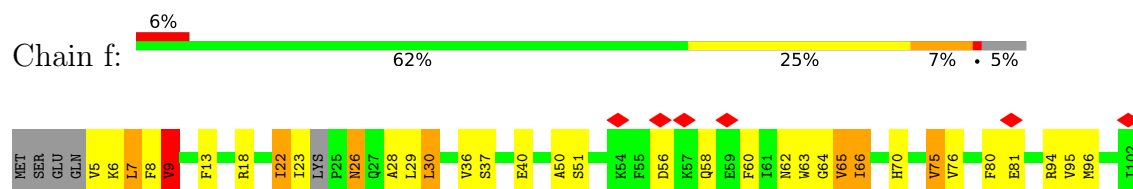
- Molecule 32: Ribosomal protein L31e, putative



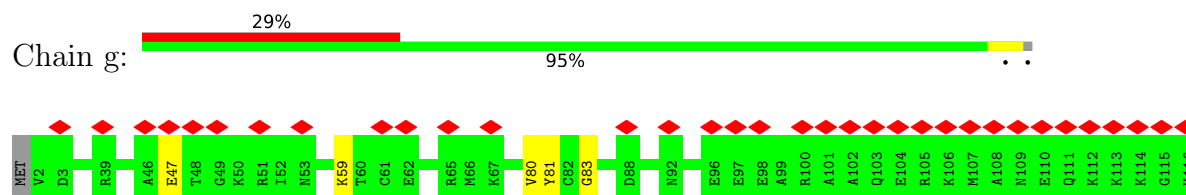
- Molecule 33: Ribosomal protein L32, putative



- Molecule 34: Ribosomal protein L35Ae, putative



- Molecule 35: Ribosomal protein L34e, putative



- Molecule 36: Ribosomal protein L29, putative

Chain h:

Chain i:

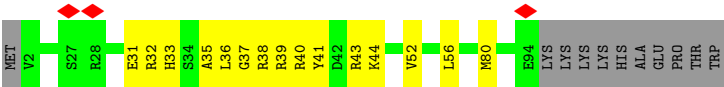
Chain j:

Chain k:

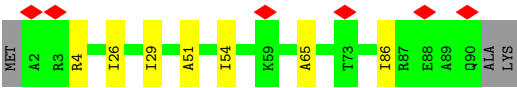
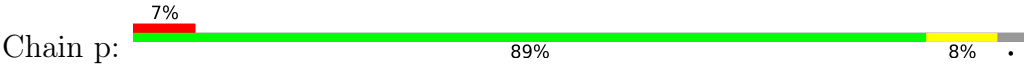
Chain 1:

Chain m:

Chain o:



• Molecule 43: Uncharacterized protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57162	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 ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.399	Depositor
Minimum map value	-0.231	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.044	Depositor
Map size (Å)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.36	0/60789	0.67	35/94723 (0.0%)
2	3	0.38	0/2785	0.68	2/4339 (0.0%)
3	4	0.36	0/3681	0.66	1/5732 (0.0%)
4	A	0.55	0/1822	0.81	4/2450 (0.2%)
5	B	0.52	0/3237	0.81	9/4340 (0.2%)
6	C	0.58	0/2819	0.93	13/3816 (0.3%)
7	D	0.53	0/2201	0.84	7/2950 (0.2%)
8	E	0.59	0/1028	1.02	8/1388 (0.6%)
9	F	0.54	0/1864	0.82	2/2507 (0.1%)
10	G	0.64	0/1409	1.00	9/1892 (0.5%)
11	H	0.50	0/1589	0.74	1/2136 (0.0%)
12	I	0.53	0/1603	0.83	3/2151 (0.1%)
13	J	0.51	0/1341	0.78	2/1797 (0.1%)
14	L	0.51	0/1525	0.76	0/2042
15	M	0.50	0/1020	0.85	2/1371 (0.1%)
16	N	0.53	0/1739	0.83	4/2332 (0.2%)
17	O	0.57	0/1591	0.85	3/2141 (0.1%)
18	P	0.49	0/1260	0.76	2/1701 (0.1%)
19	Q	0.54	0/1488	0.82	4/1996 (0.2%)
20	R	0.53	0/1314	0.84	2/1754 (0.1%)
21	S	0.55	0/1416	0.80	3/1922 (0.2%)
22	T	0.51	0/1288	0.69	0/1743
23	U	0.54	0/809	0.86	3/1085 (0.3%)
24	V	0.52	0/1000	0.71	1/1346 (0.1%)
25	W	0.51	0/530	0.68	0/705
26	X	0.51	0/819	0.71	0/1106
27	Y	0.53	0/1082	0.78	1/1447 (0.1%)
28	Z	0.52	0/1061	0.76	0/1428
29	a	0.53	0/1209	0.77	1/1619 (0.1%)
30	b	0.51	0/423	0.79	1/559 (0.2%)
31	c	0.55	0/735	0.76	0/987
32	d	0.57	0/794	0.81	2/1065 (0.2%)
33	e	0.51	0/1027	0.79	2/1381 (0.1%)
34	f	0.56	0/799	0.86	3/1075 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.51	0/933	0.75	0/1243
36	h	0.55	0/993	0.80	0/1316
37	i	0.51	0/627	0.82	0/835
38	j	0.61	0/631	0.98	5/839 (0.6%)
39	k	0.52	0/557	0.84	2/752 (0.3%)
40	l	0.51	0/436	0.83	0/580
41	m	0.53	0/422	0.89	1/558 (0.2%)
42	o	0.48	0/788	0.67	1/1038 (0.1%)
43	p	0.52	0/688	0.74	0/919
All	All	0.44	0/115172	0.73	139/169106 (0.1%)

There are no bond length outliers.

The worst 5 of 139 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	J	108	LEU	N-CA-C	10.29	122.08	111.07
5	B	338	LEU	N-CA-C	9.14	121.24	111.28
8	E	20	TRP	N-CA-C	9.09	121.27	111.36
1	1	1348	U	C4'-C3'-O3'	9.03	122.95	109.40
9	F	158	ILE	N-CA-C	8.56	116.98	109.02

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	54325	0	27334	137	0
2	3	2493	0	1268	6	0
3	4	3289	0	1657	12	0
4	A	1785	0	1814	46	0
5	B	3175	0	3279	128	0
6	C	2772	0	2885	101	0
7	D	2167	0	2281	54	0
8	E	1014	0	1076	99	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	F	1832	0	1902	26	0
10	G	1384	0	1464	110	0
11	H	1556	0	1555	33	0
12	I	1569	0	1606	78	0
13	J	1320	0	1360	23	0
14	L	1498	0	1574	12	0
15	M	1004	0	1049	27	0
16	N	1696	0	1738	33	0
17	O	1559	0	1598	29	0
18	P	1230	0	1245	14	0
19	Q	1465	0	1513	19	0
20	R	1299	0	1353	3	0
21	S	1384	0	1419	35	0
22	T	1255	0	1294	16	0
23	U	794	0	806	27	0
24	V	986	0	1047	8	0
25	W	513	0	496	13	0
26	X	803	0	853	0	0
27	Y	1068	0	1137	35	0
28	Z	1042	0	1071	15	0
29	a	1179	0	1197	33	0
30	b	415	0	420	14	0
31	c	727	0	748	2	0
32	d	783	0	834	13	0
33	e	1003	0	1032	26	0
34	f	781	0	815	47	0
35	g	921	0	963	1	0
36	h	984	0	1085	2	0
37	i	616	0	640	2	0
38	j	616	0	606	22	0
39	k	547	0	590	15	0
40	l	428	0	471	16	0
41	m	417	0	444	15	0
42	o	773	0	820	18	0
43	p	678	0	727	5	0
All	All	107145	0	79066	1170	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 6.

The worst 5 of 1170 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)
4:A:64:LYS:HB2	4:A:71:PHE:CD1	1.22	1.67
23:U:17:LYS:HE3	23:U:85:ARG:CD	1.42	1.45
21:S:5:GLN:NE2	21:S:27:GLN:HE21	1.14	1.37
23:U:17:LYS:CE	23:U:85:ARG:HD3	1.53	1.37
28:Z:102:ALA:HB1	28:Z:110:LYS:CG	1.57	1.35

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	
4	A	231/251 (92%)	210 (91%)	18 (8%)	3 (1%)	9	40
5	B	394/415 (95%)	357 (91%)	32 (8%)	5 (1%)	9	40
6	C	356/370 (96%)	329 (92%)	16 (4%)	11 (3%)	3	22
7	D	266/308 (86%)	238 (90%)	26 (10%)	2 (1%)	16	50
8	E	127/151 (84%)	113 (89%)	8 (6%)	6 (5%)	2	14
9	F	229/239 (96%)	215 (94%)	11 (5%)	3 (1%)	9	40
10	G	168/244 (69%)	151 (90%)	14 (8%)	3 (2%)	6	34
11	H	188/197 (95%)	175 (93%)	8 (4%)	5 (3%)	4	25
12	I	191/209 (91%)	175 (92%)	15 (8%)	1 (0%)	24	59
13	J	162/169 (96%)	155 (96%)	5 (3%)	2 (1%)	10	42
14	L	183/189 (97%)	167 (91%)	14 (8%)	2 (1%)	11	43
15	M	122/128 (95%)	118 (97%)	3 (2%)	1 (1%)	16	50
16	N	198/204 (97%)	189 (96%)	9 (4%)	0	100	100
17	O	194/200 (97%)	188 (97%)	3 (2%)	3 (2%)	8	37
18	P	151/164 (92%)	138 (91%)	12 (8%)	1 (1%)	18	52
19	Q	183/186 (98%)	168 (92%)	14 (8%)	1 (0%)	24	59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	R	160/178 (90%)	150 (94%)	9 (6%)	1 (1%)	21	56
21	S	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
22	T	156/159 (98%)	145 (93%)	10 (6%)	1 (1%)	21	56
23	U	93/106 (88%)	83 (89%)	9 (10%)	1 (1%)	11	43
24	V	132/140 (94%)	124 (94%)	7 (5%)	1 (1%)	16	50
25	W	57/113 (50%)	54 (95%)	2 (4%)	1 (2%)	6	34
26	X	99/140 (71%)	92 (93%)	7 (7%)	0	100	100
27	Y	132/138 (96%)	124 (94%)	7 (5%)	1 (1%)	16	50
28	Z	129/139 (93%)	117 (91%)	8 (6%)	4 (3%)	3	22
29	a	147/151 (97%)	135 (92%)	8 (5%)	4 (3%)	4	25
30	b	46/58 (79%)	44 (96%)	2 (4%)	0	100	100
31	c	92/112 (82%)	86 (94%)	5 (5%)	1 (1%)	11	43
32	d	93/110 (84%)	91 (98%)	2 (2%)	0	100	100
33	e	121/132 (92%)	113 (93%)	5 (4%)	3 (2%)	4	27
34	f	93/102 (91%)	83 (89%)	8 (9%)	2 (2%)	5	29
35	g	113/116 (97%)	105 (93%)	6 (5%)	2 (2%)	6	34
36	h	120/124 (97%)	112 (93%)	7 (6%)	1 (1%)	16	50
37	i	71/91 (78%)	64 (90%)	7 (10%)	0	100	100
38	j	73/81 (90%)	69 (94%)	4 (6%)	0	100	100
39	k	66/74 (89%)	64 (97%)	2 (3%)	0	100	100
40	l	48/51 (94%)	43 (90%)	5 (10%)	0	100	100
41	m	50/132 (38%)	46 (92%)	3 (6%)	1 (2%)	6	31
42	o	91/104 (88%)	87 (96%)	4 (4%)	0	100	100
43	p	87/92 (95%)	82 (94%)	5 (6%)	0	100	100
All	All	5785/6443 (90%)	5365 (93%)	347 (6%)	73 (1%)	12	40

5 of 73 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	42	HIS
7	D	306	PRO
8	E	15	ILE
8	E	94	VAL
10	G	193	VAL

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	
4	A	181/191 (95%)	170 (94%)	11 (6%)	17	49
5	B	333/347 (96%)	318 (96%)	15 (4%)	24	58
6	C	294/301 (98%)	284 (97%)	10 (3%)	32	64
7	D	225/256 (88%)	224 (100%)	1 (0%)	84	86
8	E	106/118 (90%)	99 (93%)	7 (7%)	15	47
9	F	185/192 (96%)	182 (98%)	3 (2%)	55	75
10	G	151/209 (72%)	145 (96%)	6 (4%)	28	61
11	H	171/179 (96%)	163 (95%)	8 (5%)	23	57
12	I	167/177 (94%)	163 (98%)	4 (2%)	43	70
13	J	139/144 (96%)	134 (96%)	5 (4%)	31	63
14	L	150/155 (97%)	147 (98%)	3 (2%)	48	72
15	M	103/107 (96%)	98 (95%)	5 (5%)	22	55
16	N	175/177 (99%)	161 (92%)	14 (8%)	11	40
17	O	160/163 (98%)	153 (96%)	7 (4%)	25	59
18	P	127/135 (94%)	125 (98%)	2 (2%)	55	75
19	Q	151/153 (99%)	148 (98%)	3 (2%)	48	72
20	R	130/156 (83%)	127 (98%)	3 (2%)	44	70
21	S	149/151 (99%)	140 (94%)	9 (6%)	17	50
22	T	131/132 (99%)	129 (98%)	2 (2%)	57	76
23	U	85/92 (92%)	83 (98%)	2 (2%)	43	70
24	V	103/108 (95%)	96 (93%)	7 (7%)	14	46
25	W	51/94 (54%)	51 (100%)	0	100	100
26	X	89/117 (76%)	88 (99%)	1 (1%)	65	79
27	Y	118/122 (97%)	114 (97%)	4 (3%)	32	64
28	Z	102/119 (86%)	101 (99%)	1 (1%)	68	80
29	a	120/122 (98%)	116 (97%)	4 (3%)	33	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	b	42/49 (86%)	40 (95%)	2 (5%)	23	56
31	c	81/95 (85%)	80 (99%)	1 (1%)	63	79
32	d	84/94 (89%)	80 (95%)	4 (5%)	23	56
33	e	108/116 (93%)	105 (97%)	3 (3%)	38	68
34	f	85/90 (94%)	78 (92%)	7 (8%)	10	39
35	g	97/98 (99%)	96 (99%)	1 (1%)	68	80
36	h	103/105 (98%)	101 (98%)	2 (2%)	50	73
37	i	65/82 (79%)	64 (98%)	1 (2%)	57	76
38	j	62/66 (94%)	57 (92%)	5 (8%)	11	39
39	k	63/68 (93%)	62 (98%)	1 (2%)	55	75
40	l	46/47 (98%)	45 (98%)	1 (2%)	45	71
41	m	45/116 (39%)	43 (96%)	2 (4%)	25	59
42	o	84/94 (89%)	82 (98%)	2 (2%)	43	70
43	p	67/69 (97%)	66 (98%)	1 (2%)	57	76
All	All	4928/5406 (91%)	4758 (97%)	170 (3%)	33	64

5 of 170 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	S	174	CYS
32	d	104	THR
23	U	21	LEU
27	Y	96	SER
34	f	65	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 112 such sidechains are listed below:

Mol	Chain	Res	Type
15	M	67	ASN
42	o	33	HIS
21	S	5	GLN
39	k	32	ASN
35	g	103	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2532/2765 (91%)	534 (21%)	97 (3%)
2	3	116/118 (98%)	26 (22%)	3 (2%)
3	4	152/162 (93%)	40 (26%)	6 (3%)
All	All	2800/3045 (91%)	600 (21%)	106 (3%)

5 of 600 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	4	A
1	1	6	U
1	1	16	G
1	1	20	G
1	1	24	A

5 of 106 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1687	G
1	1	2131	G
2	3	112	U
1	1	1787	C
1	1	1958	G

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

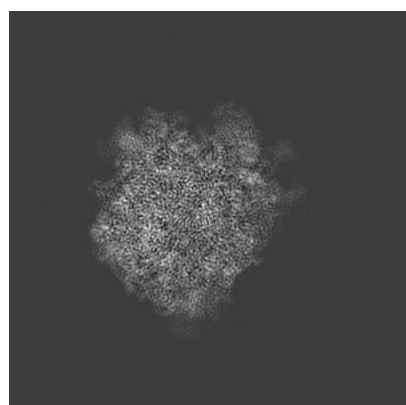
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6784. These allow visual inspection of the internal detail of the map and identification of artifacts.

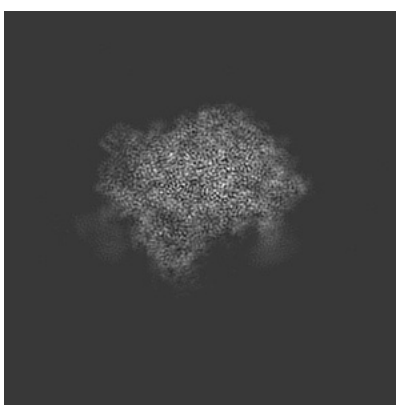
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

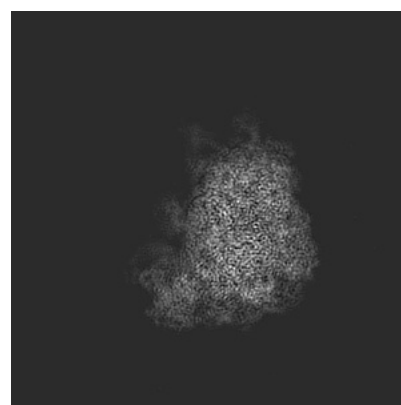
6.1.1 Primary map



X



Y

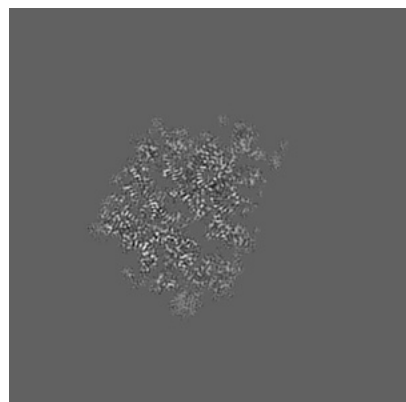


Z

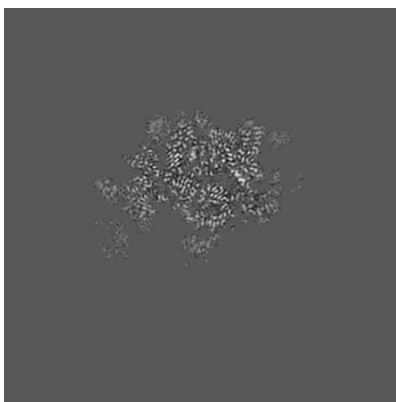
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

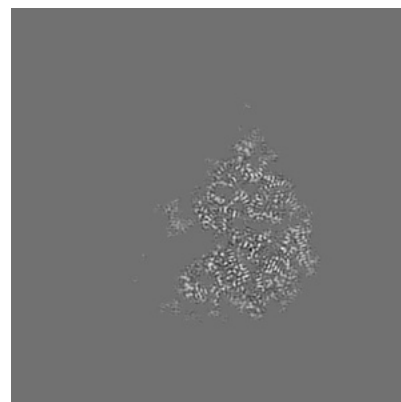
6.2.1 Primary map



X Index: 160



Y Index: 160

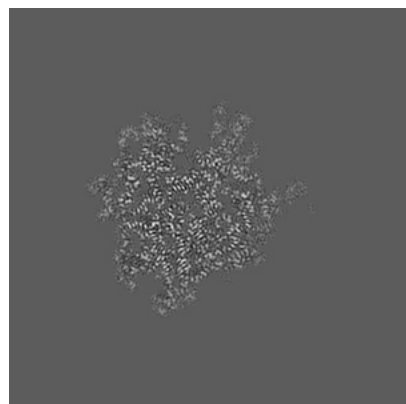


Z Index: 160

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

6.3 Largest variance slices [i](#)

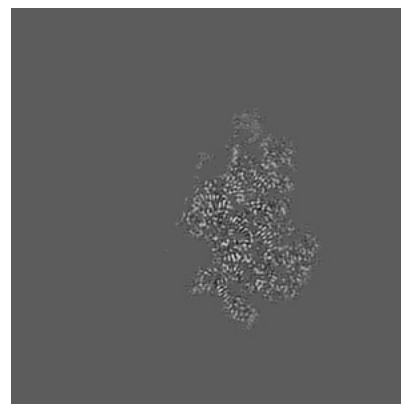
6.3.1 Primary map



X Index: 189



Y Index: 120

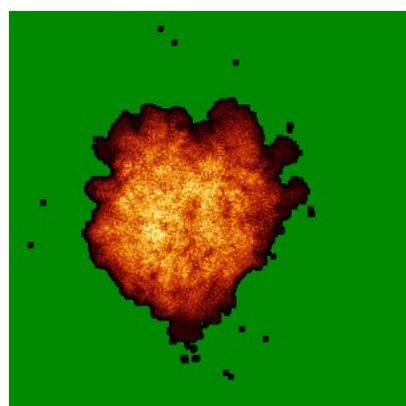


Z Index: 174

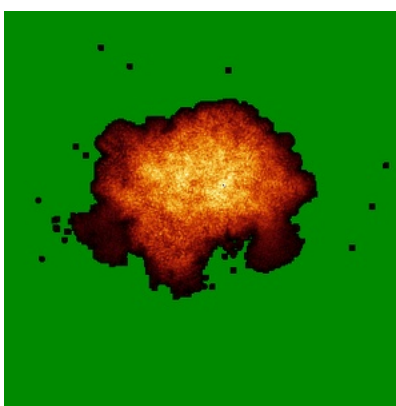
The images above show the largest variance slices of the map in three orthogonal directions.

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

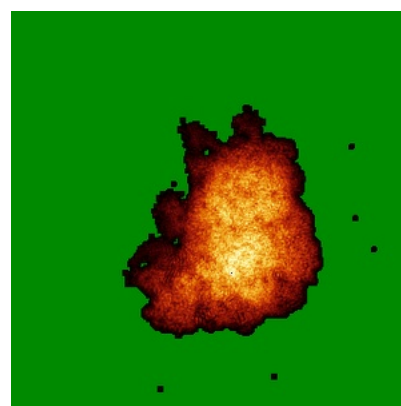
6.4.1 Primary map



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 0.044. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

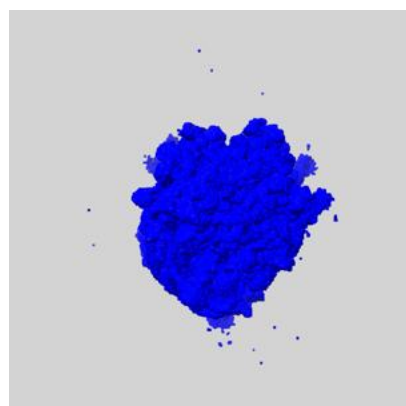
6.6 Mask visualisation [i](#)

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

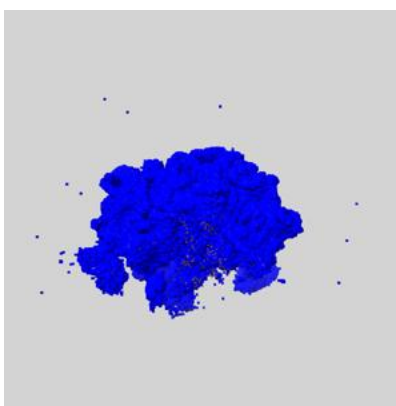
A mask typically either:

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

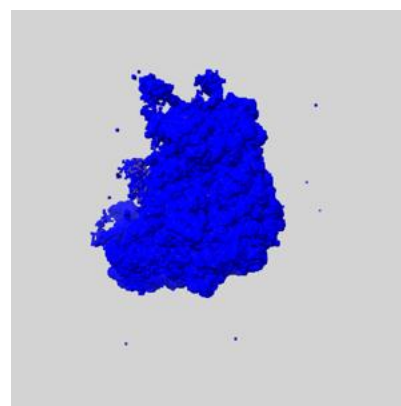
6.6.1 emd_6784_msk_1.map [i](#)



X



Y

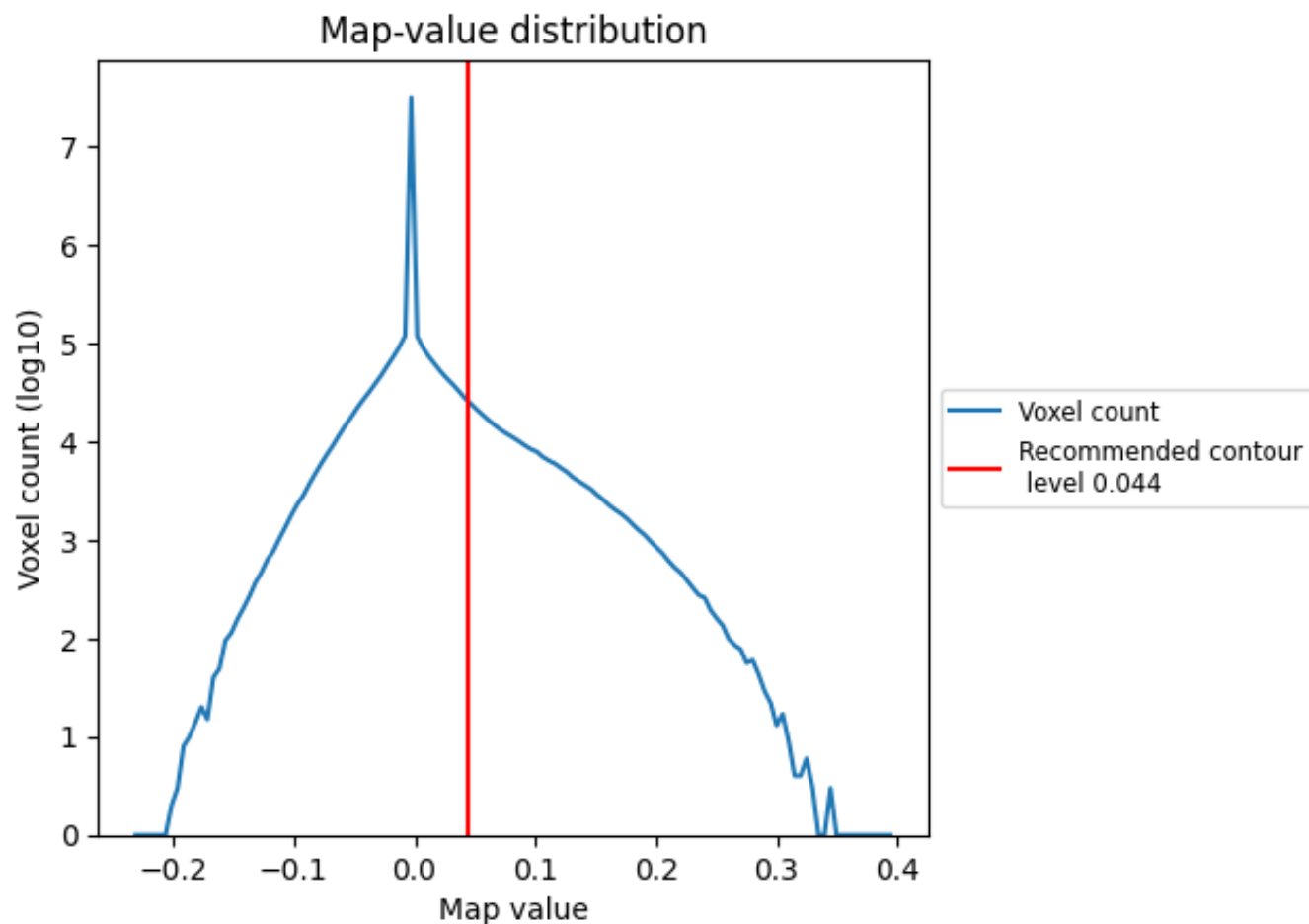


Z

7 Map analysis [i](#)

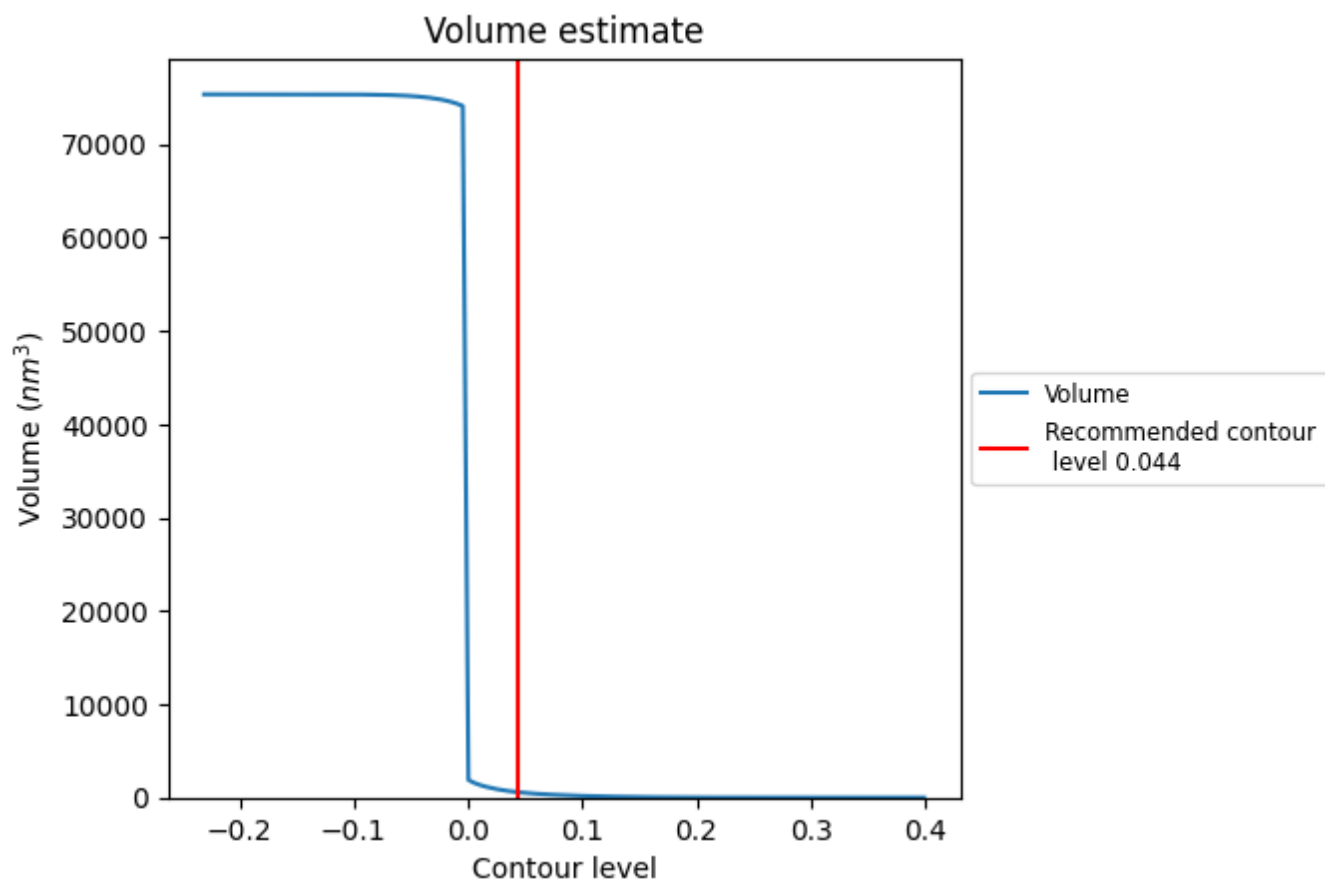
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

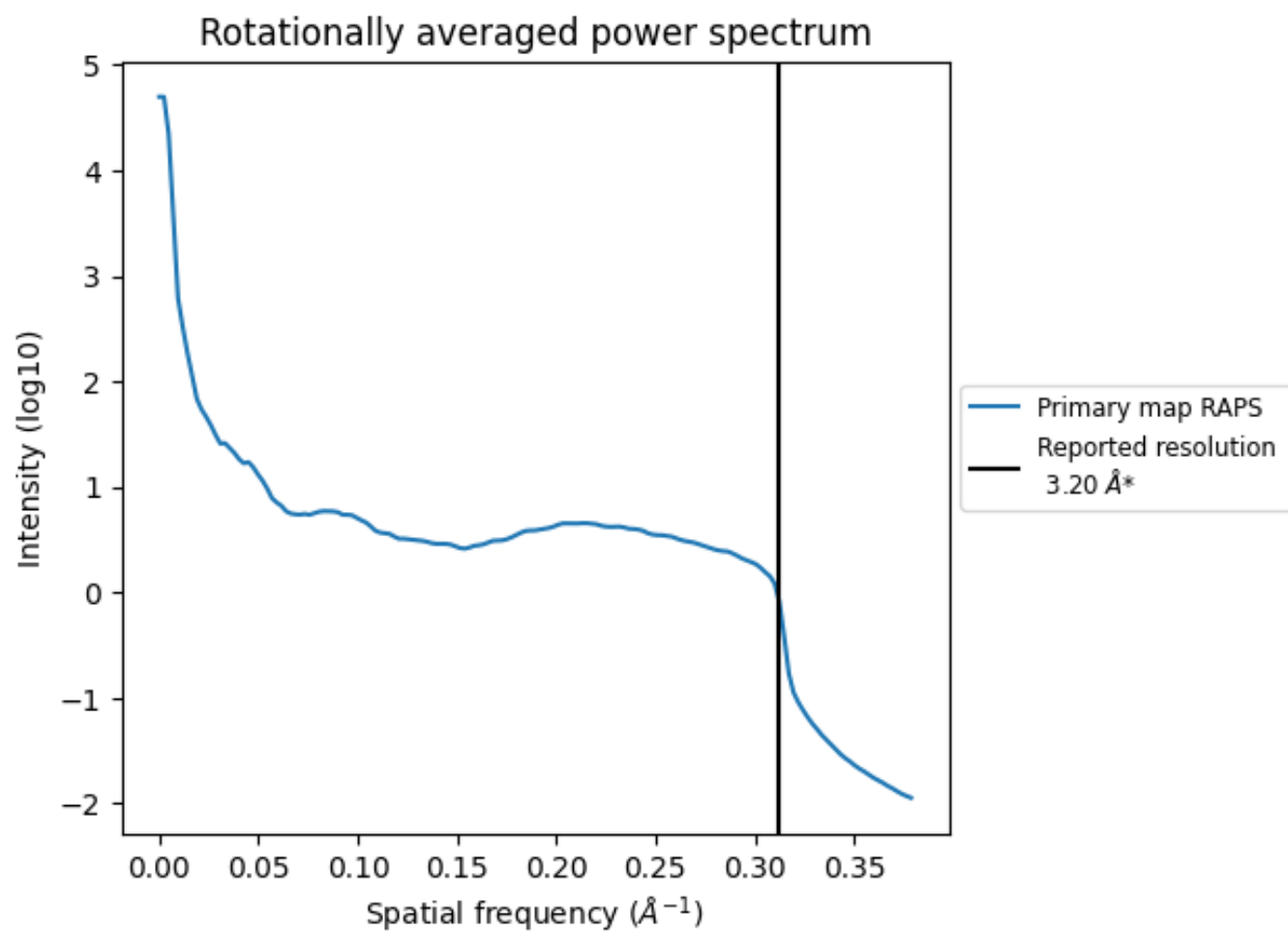
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 572 nm^3 ; this corresponds to an approximate mass of 517 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 ⓘ

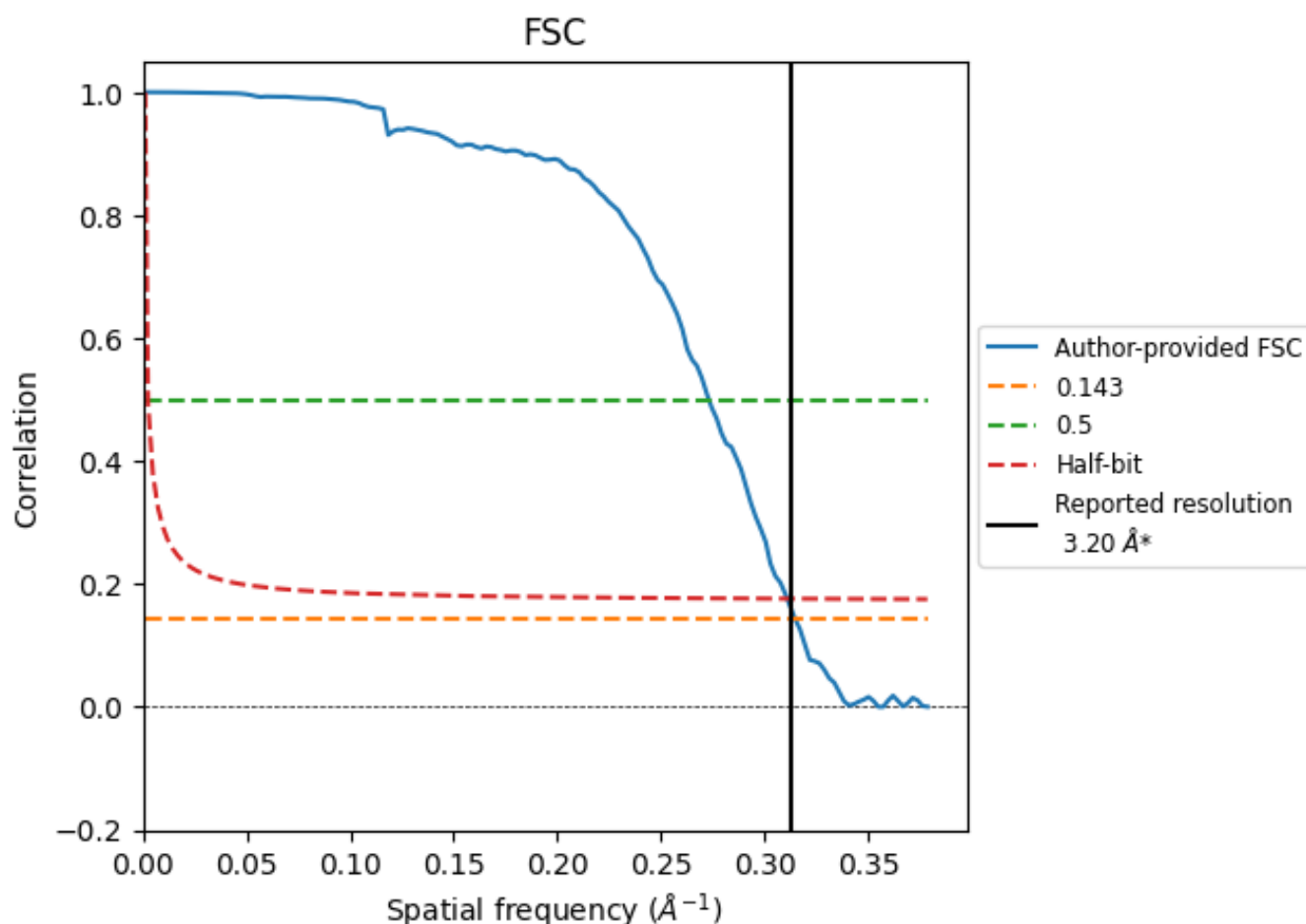


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

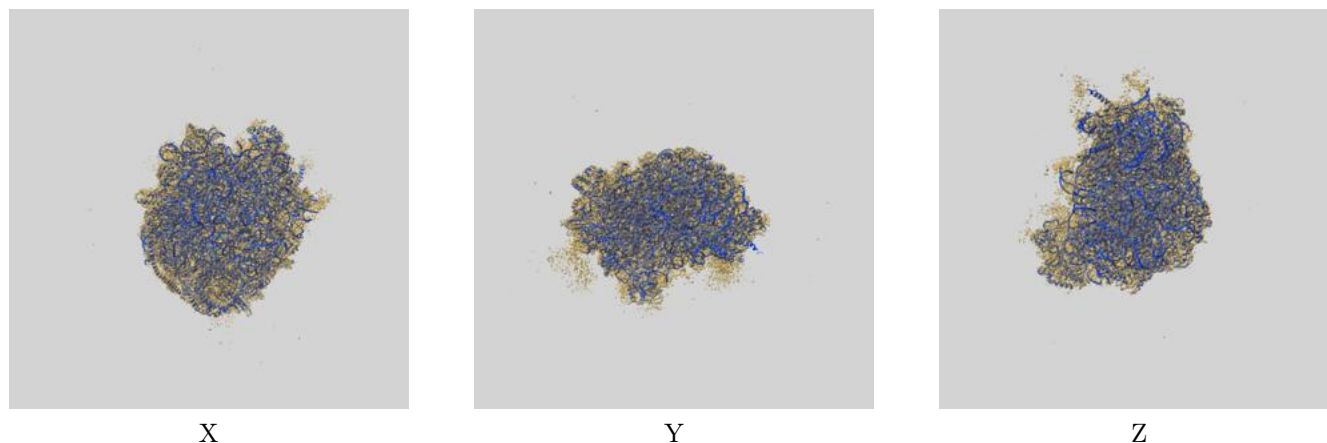
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.18	3.66	3.21
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

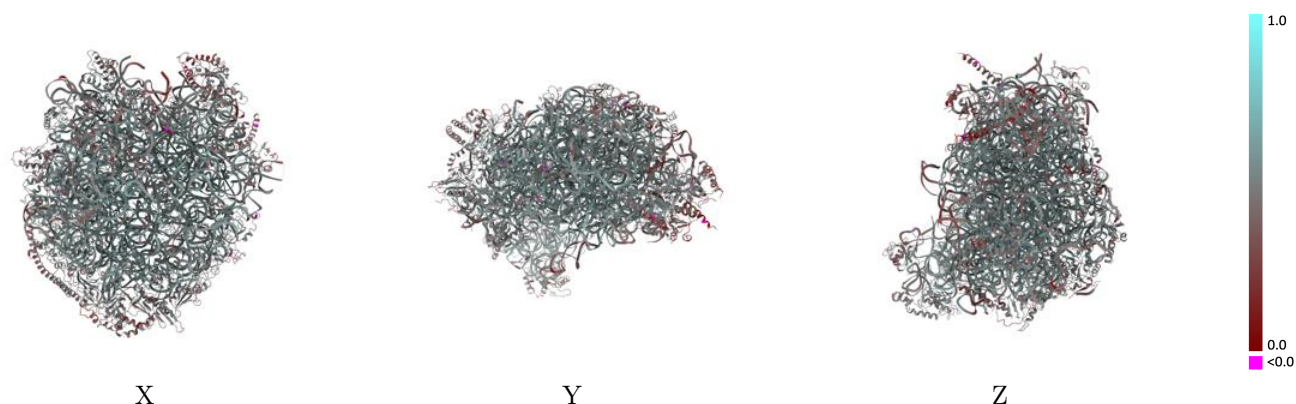
This section contains information regarding the fit between EMDB map EMD-6784 and PDB model 5XY3. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

9.1 Map-model overlay [i](#)



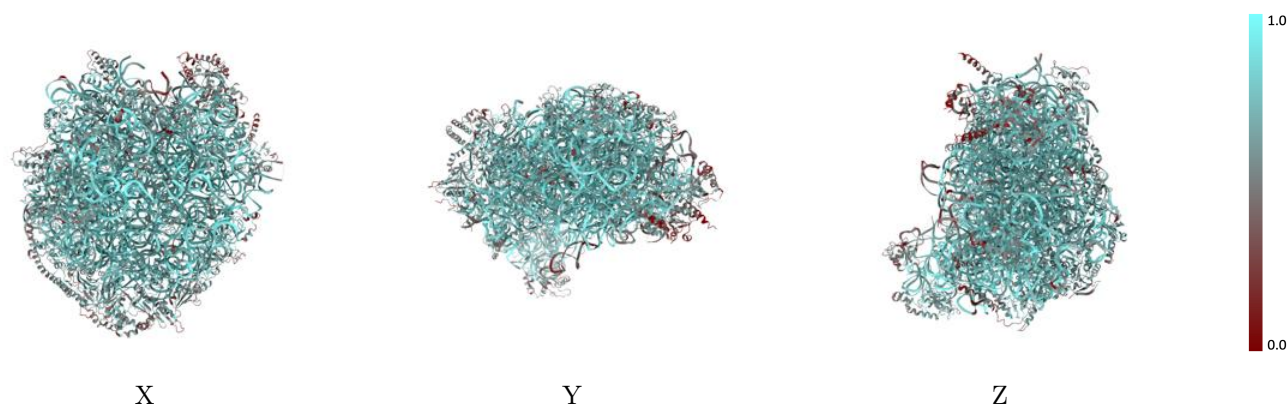
The images above show the 3D surface view of the map at the recommended contour level 0.044 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



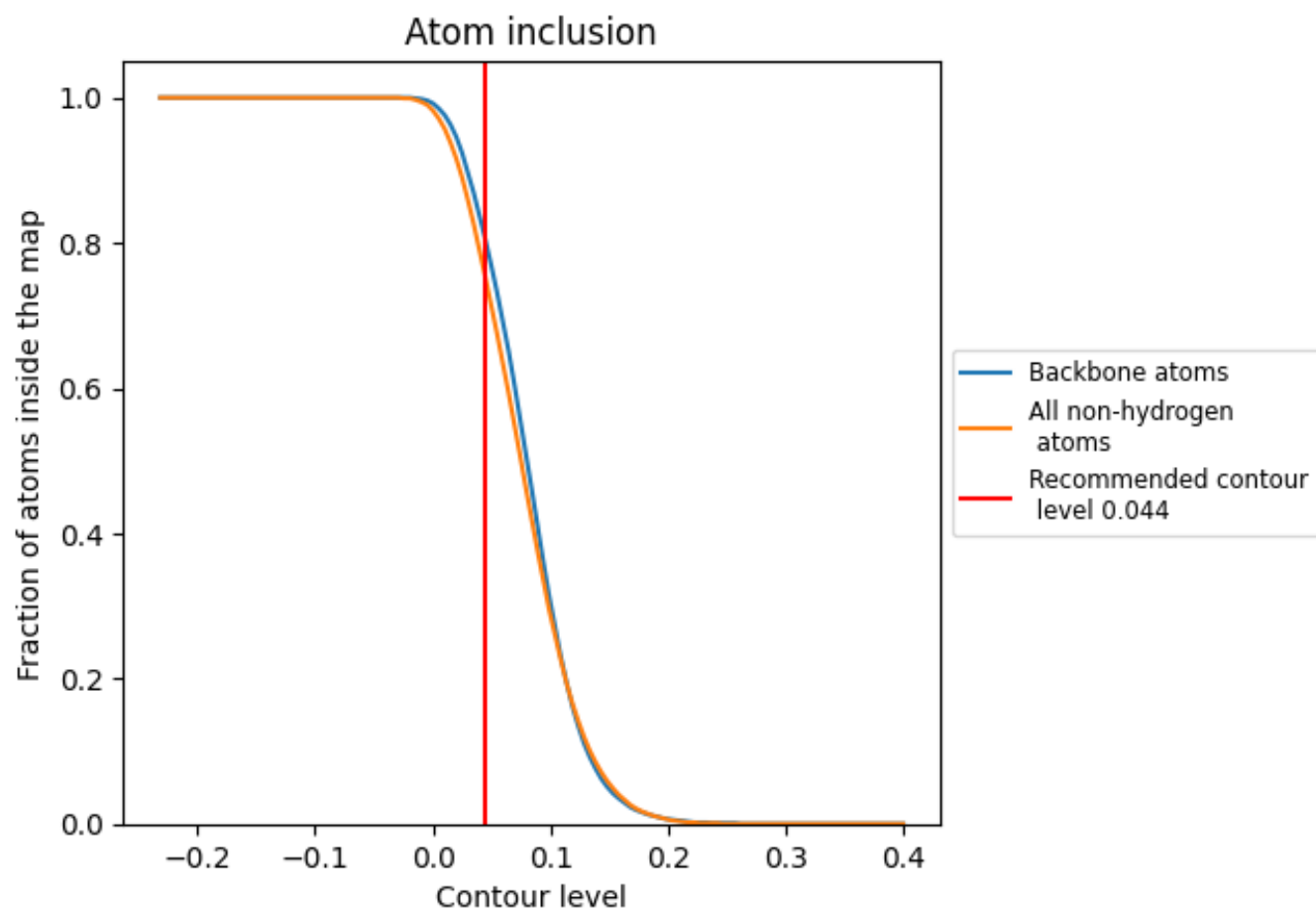
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.044).

9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 76% 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 (0.044) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7590	 0.5100
1	 0.8440	 0.5360
3	 0.8460	 0.5180
4	 0.7780	 0.5050
A	 0.7020	 0.5180
B	 0.6950	 0.5050
C	 0.6870	 0.4940
D	 0.6430	 0.4700
E	 0.5510	 0.4410
F	 0.7010	 0.4880
G	 0.5750	 0.4470
H	 0.5680	 0.4500
I	 0.6860	 0.5060
J	 0.4960	 0.4080
L	 0.6440	 0.4690
M	 0.6040	 0.4480
N	 0.7840	 0.5430
O	 0.6870	 0.4990
P	 0.7310	 0.5160
Q	 0.7240	 0.5130
R	 0.6510	 0.4680
S	 0.7070	 0.5060
T	 0.7110	 0.5000
U	 0.5720	 0.4450
V	 0.6490	 0.4880
W	 0.4270	 0.3950
X	 0.6530	 0.4860
Y	 0.6190	 0.4540
Z	 0.4440	 0.3740
a	 0.7400	 0.5220
b	 0.7270	 0.5050
c	 0.3700	 0.3400
d	 0.6800	 0.5040
e	 0.7010	 0.5090
f	 0.7130	 0.5210



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Chain	Atom inclusion	Q-score
g	 0.5440	 0.4090
h	 0.5860	 0.4390
i	 0.6110	 0.4600
j	 0.7870	 0.5490
k	 0.5590	 0.4370
l	 0.7100	 0.5130
m	 0.6140	 0.4650
o	 0.6820	 0.5070
p	 0.6450	 0.4780