



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 06:28 PM UTC

PDB ID : 8WIB / pdb_00008wib
EMDB ID : EMD-37562
Title : Cryo- EM structure of Mycobacterium smegmatis 70S ribosome, E- tRNA and RafH.
Authors : Kumar, N.; Sharma, S.; Kaushal, P.S.
Deposited on : 2023-09-24
Resolution : 3.50 Å(reported)
Based on initial model : 8WHX

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:

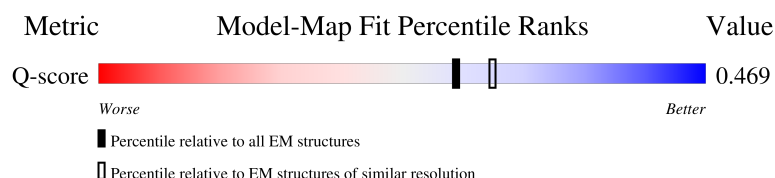
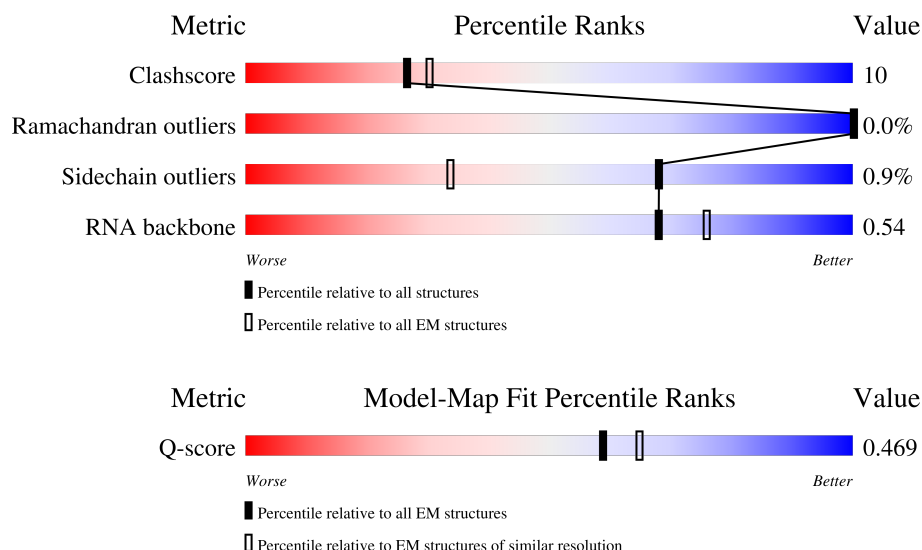
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 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	13950 (3.00 - 4.00)

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	E	278	
2	F	217	
3	G	215	

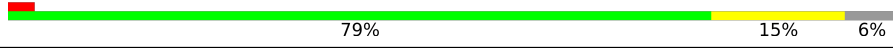
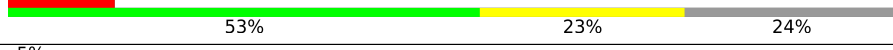
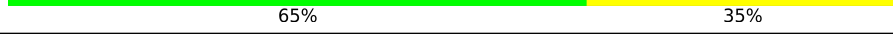
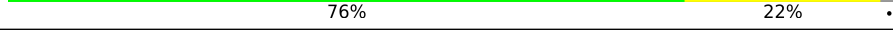
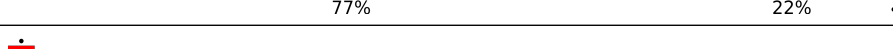
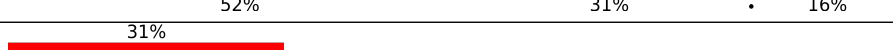
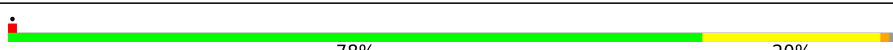
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Mol	Chain	Length	Quality of chain
4	H	187	
5	I	179	
6	J	151	
7	M	147	
8	N	122	
9	O	147	
10	Q	199	
11	R	127	
12	S	113	
13	T	129	
14	U	103	
15	V	153	
16	W	100	
17	X	105	
18	Z	88	
19	1	64	
20	2	77	
21	3	61	
22	5	57	
23	6	55	
24	7	47	
25	8	64	
26	4	75	
27	A	3119	
28	B	118	

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Mol	Chain	Length	Quality of chain
29	C	76	
30	a	1528	
31	v	33	
32	d	275	
33	e	201	
34	f	214	
35	g	96	
36	h	156	
37	i	132	
38	j	150	
39	k	101	
40	l	138	
41	m	124	
42	n	124	
43	o	101	
44	p	89	
45	q	156	
46	r	98	
47	s	84	
48	t	93	
49	u	86	
50	w	264	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 142247 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	E	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	209	Total	C	N	O	S	0	0
			1563	969	305	285	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	G	208	Total	C	N	O	S	0	0
			1562	965	294	301	2		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	H	180	Total	C	N	O	S	0	0
			1428	897	267	258	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	165	Total	C	N	O	S	0	0
			1260	792	229	238	1		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	41	Total	C	N	O	S	0	0
			308	195	55	57	1		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	O	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	117	Total	C	N	O	S	0	0
			919	577	178	162	2		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	R	125	Total	C	N	O	0	0
			951	583	198	170		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	S	111	Total	C	N	O	0	0
			888	559	166	163		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	T	123	Total	C	N	O	0	0
			982	610	202	170		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	U	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	V	113	Total	C	N	O	0	0
			864	538	170	156		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	W	96	Total	C	N	O	0	0
			751	476	137	138		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	X	92	Total	C	N	O	S	0	0
			706	441	132	131	2		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Z	77	Total	C	N	O	0	0
			574	355	121	98		

- Molecule 19 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	1	62	Total	C	N	O	S	0	0
			465	280	102	79	4		

- Molecule 20 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	2	63	Total	C	N	O	S	0	0
			527	322	102	102	1		

- Molecule 21 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	3	58	Total	C	N	O	0	0
			470	290	94	86		

- Molecule 22 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	5	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 23 is a protein called 50S ribosomal protein L33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	6	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 24 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	7	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 25 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	8	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 26 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	4	59	Total	C	N	O	S	0	0
			458	284	84	85	5		

- Molecule 27 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	A	3022	Total	C	N	O	P	0	0
			64906	28929	11938	21017	3022		

- Molecule 28 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B	117	Total	C	N	O	P	0	0
			2502	1117	465	803	117		

- Molecule 29 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	C	76	Total	C	N	O	P	0	0
			1622	723	294	529	76		

- Molecule 30 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	1515	Total	C	N	O	P	0	0
			32521	14485	5944	10577	1515		

- Molecule 31 is a protein called 30S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	v	31	Total	C	N	O	S	0	0
			271	166	69	35	1		

- Molecule 32 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	208	Total	C	N	O	S	0	0
			1660	1036	322	298	4		

- Molecule 33 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	200	Total	C	N	O	S	0	0
			1641	1028	316	295	2		

- Molecule 34 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	166	Total	C	N	O	S	0	0
			1208	761	228	215	4		

- Molecule 35 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	96	Total	C	N	O	S	0	0
			771	486	138	145	2		

- Molecule 36 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	153	Total	C	N	O	S	0	0
			1207	751	235	219	2		

- Molecule 37 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	131	Total	C	N	O	S	0	0
			1010	633	189	187	1		

- Molecule 38 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	126	Total	C	N	O		0	0
			994	630	194	170			

- Molecule 39 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	98	Total	C	N	O	S	0	0
			784	493	145	143	3		

- Molecule 40 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	115	Total	C	N	O	S	0	0
			855	528	170	156	1		

- Molecule 41 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	122	Total	C	N	O	S	0	0
			958	594	197	165	2		

- Molecule 42 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	116	Total	C	N	O	S	0	0
			935	572	191	169	3		

- Molecule 43 is a protein called 30S ribosomal protein S14A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	100	Total	C	N	O	S	0	0
			819	497	183	138	1		

- Molecule 44 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	p	88	Total	C	N	O		0	0
			720	449	147	124			

- Molecule 45 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	q	113	Total	C	N	O		0	0
			891	570	162	159			

- Molecule 46 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	r	94	Total	C	N	O	S	0	0
			748	469	142	135	2		

- Molecule 47 is a protein called 30S ribosomal protein S18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	s	65	Total	C	N	O	S	0	0
			513	318	102	90	3		

- Molecule 48 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	t	82	Total	C	N	O	S	0	0
			662	425	124	112	1		

- Molecule 49 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	u	85	Total	C	N	O	0	0
			660	402	139	119		

- Molecule 50 is a protein called Ribosome hibernation promotion factor RafH.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	126	Total	C	N	O	S	0	0
			1004	609	214	180	1		

There are 6 discrepancies between the modelled and reference sequences:

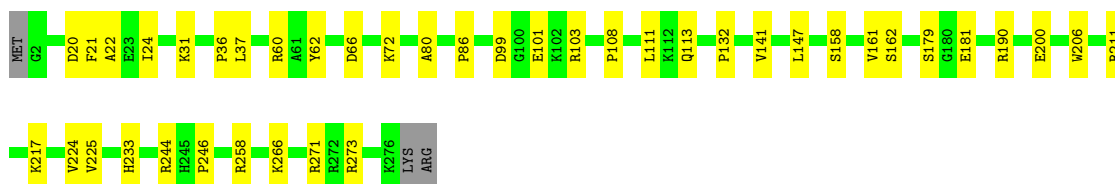
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w	260	HIS	-	expression tag	UNP A0QZ86
w	261	HIS	-	expression tag	UNP A0QZ86
w	262	HIS	-	expression tag	UNP A0QZ86
w	263	HIS	-	expression tag	UNP A0QZ86
w	264	HIS	-	expression tag	UNP A0QZ86

3 Residue-property plots [i](#)

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.

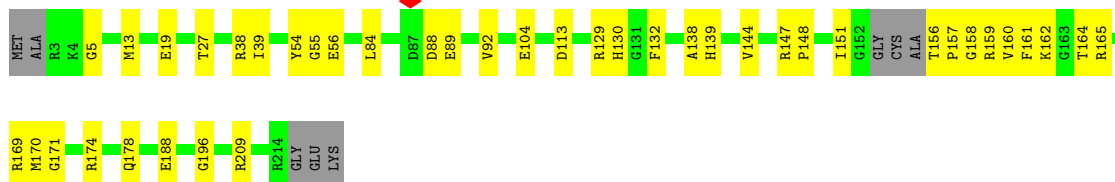
• Molecule 1: 50S ribosomal protein L2

Chain E: 



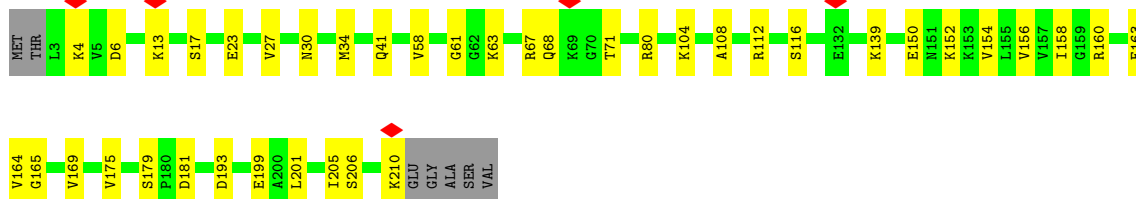
• Molecule 2: 50S ribosomal protein L3

Chain F: 



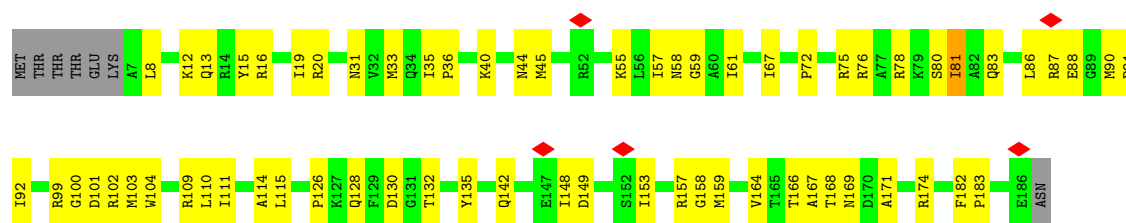
• Molecule 3: 50S ribosomal protein L4

Chain G: 

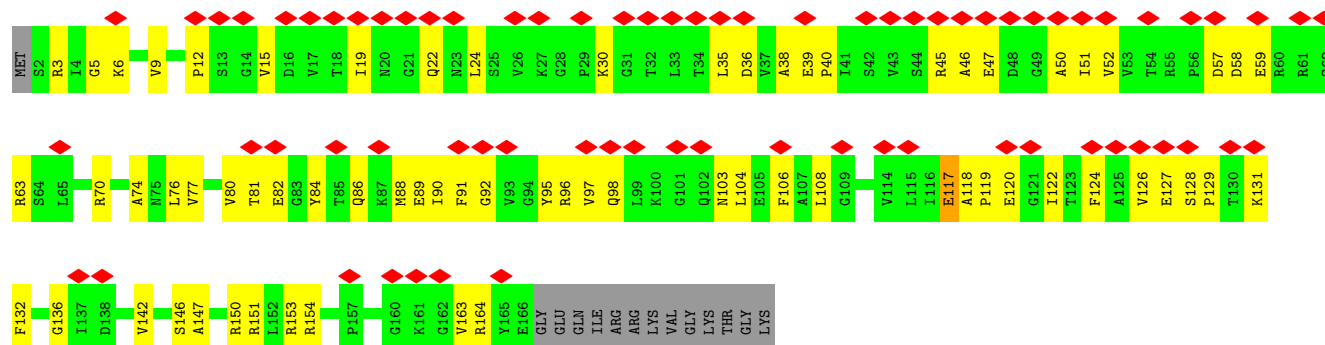
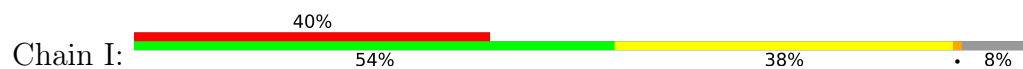


• Molecule 4: 50S ribosomal protein L5

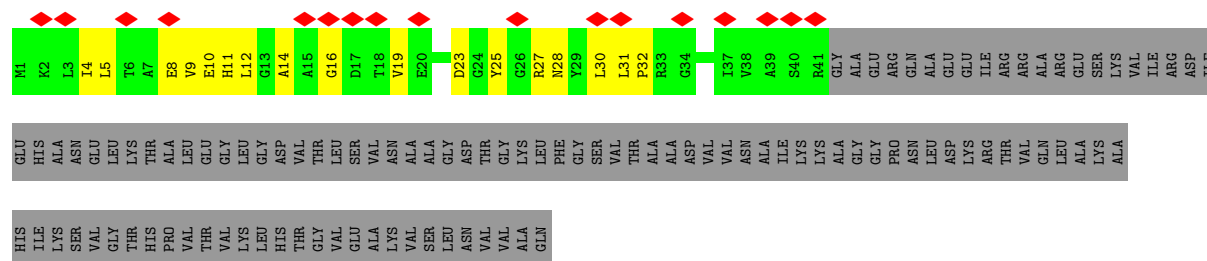
Chain H: 



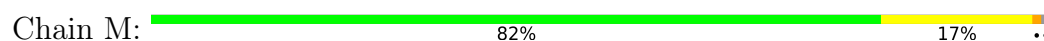
• Molecule 5: 50S ribosomal protein L6



• Molecule 6: 50S ribosomal protein L9



• Molecule 7: 50S ribosomal protein L13



• Molecule 8: 50S ribosomal protein L14



• Molecule 9: 50S ribosomal protein L15

MET	SER	V3
V22		
G23		
R24		
K29		
G30		
K31		
T32		
A33		
G34		
R36		
M55		
P56		
M59		
K63		
V80		
I83		
Q89		
E97		
L98		
L103		
G114		
T125		
I137		
T145		
E146		
I147		

- Chain Q:  50% 9% 41%

ALA	ASP	GLU	LYS	ALA	ASP	LYS	GLU	ALA	GLU	LYS	Q17	L20	VAL	GLU	GLU	THR	THR	GLU	ALA	P46	ALA	ALA	H54	GLU	GLU	SER	THR	GLU	ALA	ALA	ALA	GLU	GLU	THR	THR	VAL	GLU	VAL	Y87	Y116	THR	THR	THR	ALA	ALA	ALA	THR	VAL	THR	THR	ASP	GLU	GLU	ALA	ALA	ASN	ARG	ALA	ALA	ARG	ALA	ALA	SER	GLN	LYS	LYS	ALA	ALA	ASP	THR	LYS	GLU
MET	P2	P8	P8	L10	S14	Q17	L20	R33	R42	R45	P46	H54	R63	N67	I70	R71	D72	E82	Y87	Y116	R117	E118	LYS	THR	VAL	THR	THR	ASP	GLU	GLU	ALA	ALA	ASN	ARG	ALA	ALA	ARG	ALA	ALA	SER	GLN	LYS	LYS	ALA	ALA	ASP	THR	LYS	GLU																							

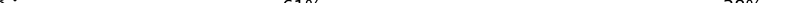
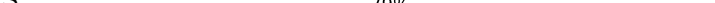
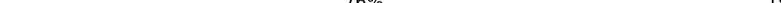
- Chain R:  5% 61% 38%

Diagram illustrating the human genome, showing 22 pairs of autosomes and the sex chromosomes (X and Y). The chromosomes are arranged in two rows, with the autosomes numbered 1 through 22. The sex chromosomes are labeled X and Y. The diagram shows the relative sizes and positions of the chromosomes within the genome.

- Chain S:  79% 19%

MET	N2	L12	R13	D14	D15	F19	G34	S35	K36	E37	R38	R48	R49	Q50	G51	G52	E56	R61	E70	I80	D81	H82	R83	D84	A84	K94	K95	I96	Y97	K105	K112	R112	K113	R114	R115	R116	R117	R118	R119	R120	R121	R122	R123	R124	R125	R126	R127	R128	R129	R130	R131	R132	R133	R134	R135	R136	R137	R138	R139	R140	R141	R142	R143	R144	R145	R146	R147	R148	R149	R150	R151	R152	R153	R154	R155	R156	R157	R158	R159	R160	R161	R162	R163	R164	R165	R166	R167	R168	R169	R170	R171	R172	R173	R174	R175	R176	R177	R178	R179	R180	R181	R182	R183	R184	R185	R186	R187	R188	R189	R190	R191	R192	R193	R194	R195	R196	R197	R198	R199	R200	R201	R202	R203	R204	R205	R206	R207	R208	R209	R210	R211	R212	R213	R214	R215	R216	R217	R218	R219	R220	R221	R222	R223	R224	R225	R226	R227	R228	R229	R230	R231	R232	R233	R234	R235	R236	R237	R238	R239	R240	R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300	R301	R302	R303	R304	R305	R306	R307	R308	R309	R310	R311	R312	R313	R314	R315	R316	R317	R318	R319	R320	R321	R322	R323	R324	R325	R326	R327	R328	R329	R330	R331	R332	R333	R334	R335	R336	R337	R338	R339	R340	R341	R342	R343	R344	R345	R346	R347	R348	R349	R350	R351	R352	R353	R354	R355	R356	R357	R358	R359	R360	R361	R362	R363	R364	R365	R366	R367	R368	R369	R370	R371	R372	R373	R374	R375	R376	R377	R378	R379	R380	R381	R382	R383	R384	R385	R386	R387	R388	R389	R390	R391	R392	R393	R394	R395	R396	R397	R398	R399	R400	R401	R402	R403	R404	R405	R406	R407	R408	R409	R410	R411	R412	R413	R414	R415	R416	R417	R418	R419	R420	R421	R422	R423	R424	R425	R426	R427	R428	R429	R430	R431	R432	R433	R434	R435	R436	R437	R438	R439	R440	R441	R442	R443	R444	R445	R446	R447	R448	R449	R450	R451	R452	R453	R454	R455	R456	R457	R458	R459	R460	R461	R462	R463	R464	R465	R466	R467	R468	R469	R470	R471	R472	R473	R474	R475	R476	R477	R478	R479	R480	R481	R482	R483	R484	R485	R486	R487	R488	R489	R490	R491	R492	R493	R494	R495	R496	R497	R498	R499	R500	R501	R502	R503	R504	R505	R506	R507	R508	R509	R510	R511	R512	R513	R514	R515	R516	R517	R518	R519	R520	R521	R522	R523	R524	R525	R526	R527	R528	R529	R530	R531	R532	R533	R534	R535	R536	R537	R538	R539	R540	R541	R542	R543	R544	R545	R546	R547	R548	R549	R550	R551	R552	R553	R554	R555	R556	R557	R558	R559	R560	R561	R562	R563	R564	R565	R566	R567	R568	R569	R570	R571	R572	R573	R574	R575	R576	R577	R578	R579	R580	R581	R582	R583	R584	R585	R586	R587	R588	R589	R590	R591	R592	R593	R594
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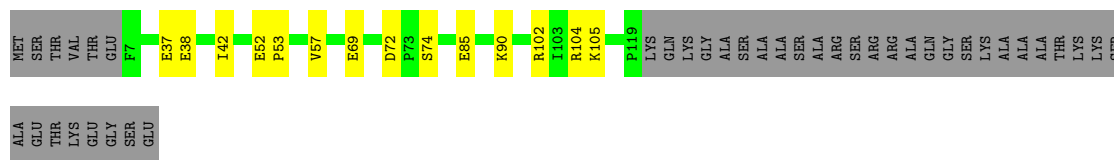
- Chain T:  76% 19% 5%

MET	A2	K12	T16	R25	G26	R30	R33	K36	E37	D49	K59	R64	A68	N72	D73	N77	R78	L83	V88	E89	L95	A96	E97	S101	L109	R114	E119	F124	SER	GLY	GLU	ALA	ALA	ALA
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- Chain U: 86% 11%

- Molecule 15: 50S ribosomal protein L22

Chain V:  65% 9% 26%



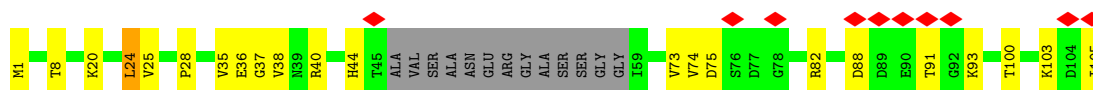
- Molecule 16: 50S ribosomal protein L23

Chain W:  84% 12%



- Molecule 17: 50S ribosomal protein L24

Chain X:  10% 67% 20% 12%



- Molecule 18: 50S ribosomal protein L27

Chain Z:  73% 15% 13%



- Molecule 19: 50S ribosomal protein L28

Chain 1:  59% 34%



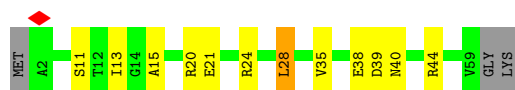
- Molecule 20: 50S ribosomal protein L29

Chain 2:  60% 22% 18%

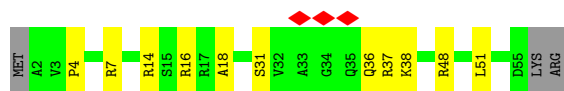
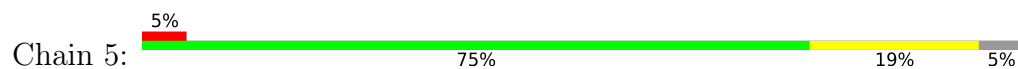


- Molecule 21: 50S ribosomal protein L30

Chain 3:  75% 18% 5%



- Molecule 22: 50S ribosomal protein L32



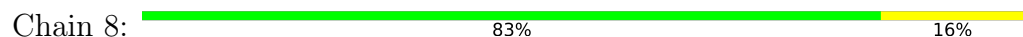
- Molecule 23: 50S ribosomal protein L33A



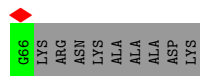
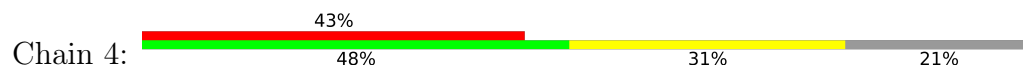
- Molecule 24: 50S ribosomal protein L34



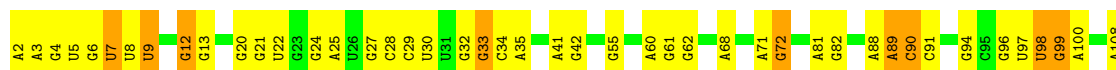
- Molecule 25: 50S ribosomal protein L35

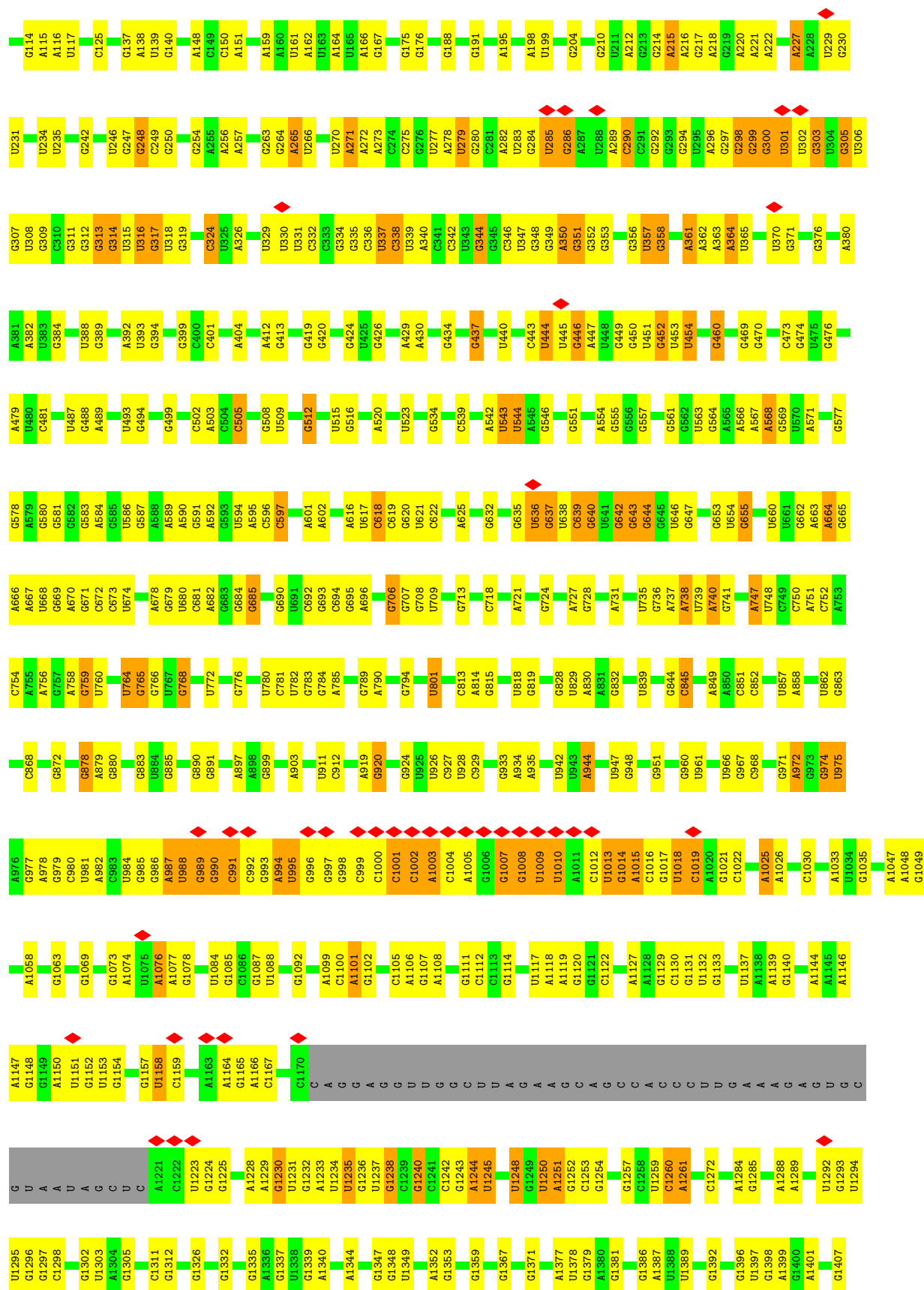


- Molecule 26: 50S ribosomal protein L31

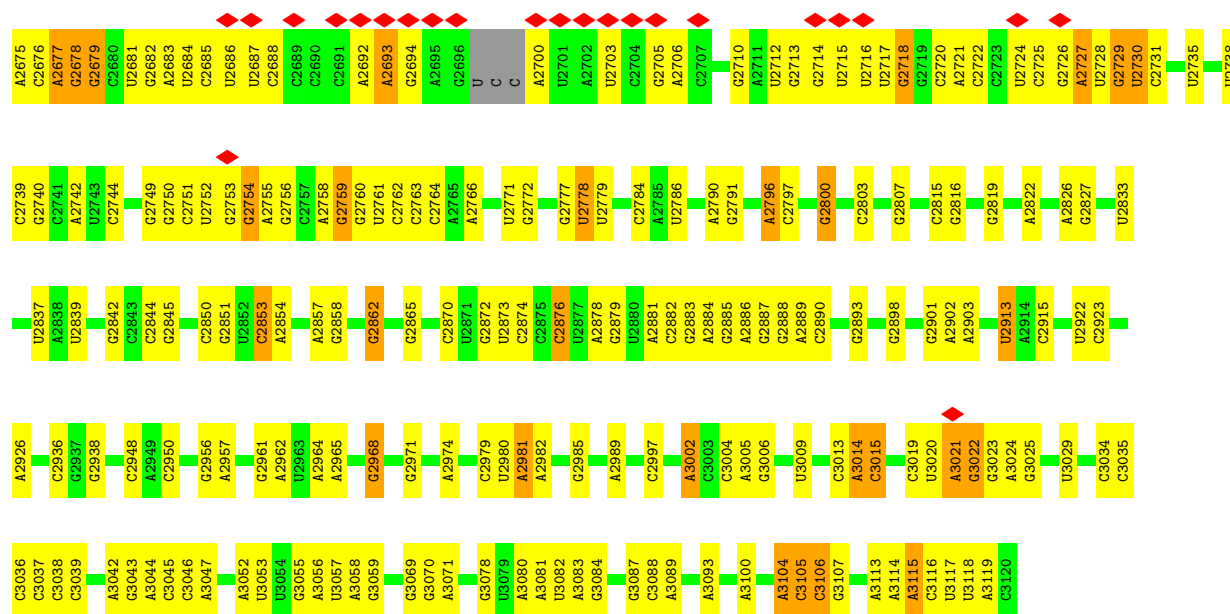


- Molecule 27: 23S rRNA



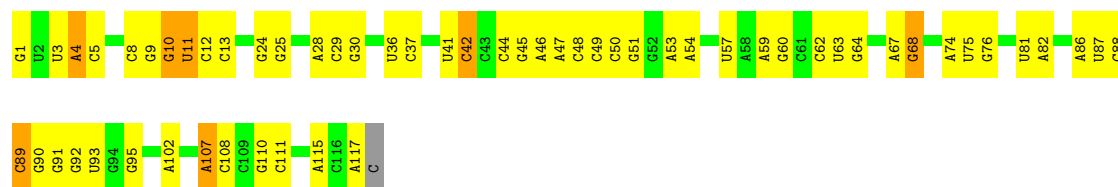


A2582	C2507	U2409	C2262	C2148	A2029	G1892	C1734	U1646	A1518	C1408
C2583	A2510	A2410	G2263	A2152	A2030	G1895	A1737	G1647	G1522	A1415
A2584	U2411	U2264	U2265	G2153	C2033	A1896	G1738	C1648	U1523	A1416
A2593	G2413	A2266	C2267	G2154	U2033	A1897	A1739	G1650	G1524	
G2599	C2417	U2353	G2280	A2160	C2043	G1900	G1754	A1652	G1528	G1424
A2600	U2418	U2355	A2276	A2161	A2046	C1901	A1756	G1653	U1529	G1426
A2601	C2419	G2276	G2277	A2162	A2046	G1922	G1757	G1654	G1530	
A2602	U2420	C2279	C2279	U2163	G2056	G1917	U1757	A1655	C1531	U1430
G2603	A2421	G2280	G2280	U2170	U2061	G1921	G1758	G1656	G1532	C1431
U2604	A2422	G2281	G2281	C2171	G2062	G1922	A1759	G1657	U1533	
C2605	U2425	A2284	A2284	A2176	G2062	G1923	U1767	G1658	C1534	C1435
G2606	G2426	A2285	A2285	U2176	G2063	G1923	G1786	U1659	C1535	C1436
G2607	G2427	A2286	A2286	U2179	A2065	G1927	A1787	A1660	A1536	A1437
G2608	C2431	C2287	C2287	U2188	A2070	G1933	G1788	G1670	U1537	G1438
A2609	A2434	C2288	C2288	G2188	A2071	G1937	A1789	A1673	A1538	U1444
G2613	U2435	C2289	C2289	C2191	G2074	U1937	A1790	G1674	G1541	C1448
U2614	A2436	A2294	A2294	C2191	G2075	G1938	A1791	A1676	A1542	C1449
G2615	U2443	C2295	C2295	A2194	G2075	U1939	A1792	G1677	A1543	
A2616	C2444	C2299	C2299	U2195	A2084	U1946	U1798	U1678	U1544	G1452
U2617	G2447	G2311	G2311	G2196	C2085	U1947	A1803	A1680	C1545	U1455
C2618	G2448	G2316	G2316	C2212	U2086	U1948	G1804	U1681	A1546	G1456
C2622	A2449	G2317	G2317	A2212	C2087	A1949	G1805	G1682	C1547	C1465
A2623	U2451	G2318	G2318	U2215	C2088	G1950	A1806	G1684	G1548	C1466
U2626	A2436	U2319	U2319	G2216	C2089	G1950	C1807	G1685	G1549	U1467
C2627	U2457	G2320	G2320	U2217	U2090	A1985	G1815	A1690	G1550	A1468
A2630	G2458	U2321	U2321	A2221	U2091	C1973	A1826	A1691	U1551	A1469
U2631	G2462	G2322	G2322	C2224	U2092	A1974	G1826	G1703	A1552	G1470
G2632	U2463	G2323	G2323	U2224	G2093	A1975	C1830	U1704	U1553	C1472
U2633	A2464	A2324	A2324	G2236	G2094	U1981	G1840	A1706	A1555	G1476
A2634	G2465	U2325	U2325	A2237	G2095	A1990	U1854	G1707	C1557	C1477
U2635	U2466	C2326	C2326	U2238	G2096	G1991	A1855	G1710	C1558	A1480
G2636	U2467	C2327	C2327	A2239	G2097	U1992	G1865	A1711	A1559	C1485
A2637	U2468	G2328	G2328	U2240	U2098	U1996	A1866	G1714	U1560	G1486
U2638	U2469	U2329	U2329	C2244	G2099	U1996	G1866	A1715	C1561	U1487
C2639	A2470	U2330	U2330	C2245	A2106	U1996	U1870	G1720	A1493	U1494
G2640	U2471	U2331	U2331	G2246	G2107	A2001	G1871	G1724	A1499	A1500
U2641	C2472	U2332	U2332	C2247	A2108	A2002	G1872	G1725	C1501	G1502
A2642	U2473	G2333	G2333	A2248	A2109	A2004	A1876	C1726	C1502	
U2643	G2474	U2334	U2334	C2249	A2113	C2005	U1877	U1630	G1507	G1508
C2644	U2482	U2335	U2335	G2250	A2114	C2006	U1877	A1631	U1509	U1510
U2645	C2488	U2336	U2336	G2251	G2130	C2007	G1885	U1732	A1511	
A2646	U2489	U2337	U2337	A2252	A2137	G2016	G1888	A1733	C1634	
U2647	A2490	U2338	U2338	A2253	A2137	C2017	G1839	A1640	C1639	
G2648	U2491	A2339	A2339	A2254	U2141	G2018	U1641	U1642	A1640	
A2649	C2492	C2340	C2340	A2255	A2142	C2019	U1642	G1645	U1642	
U2650	U2493	G2341	G2341	A2256	A2143	A2020	C1733		C	
C2651	U2494	U2342	U2342	A2257	A2144	A2020			A	
A2652	G2495	G2343	G2343	A2258	U2147	A2026			A	
U2653	U2503	U2344	U2344	U2259					A	
G2654	G2504	G2345	G2345	U2261					A	
A2655		G2346	G2346						A	
U2656		G2347	G2347						A	
G2657		G2348	G2348						A	
A2658									A	
U2659									A	
C2660									A	
G2661									A	
U2662									A	
A2663									A	
U2664									A	
G2665									A	
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U2667									A	
G2671									A	
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U2673									A	
A2674									A	



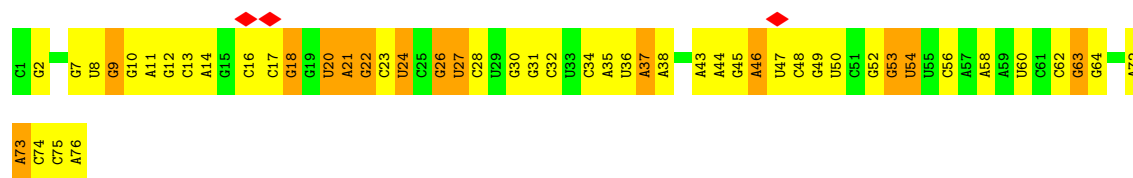
• Molecule 28: 5S rRNA

Chain B: 50% 43% 6%



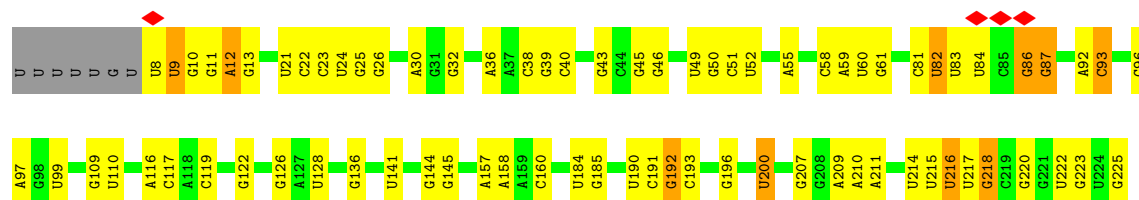
• Molecule 29: E-tRNA

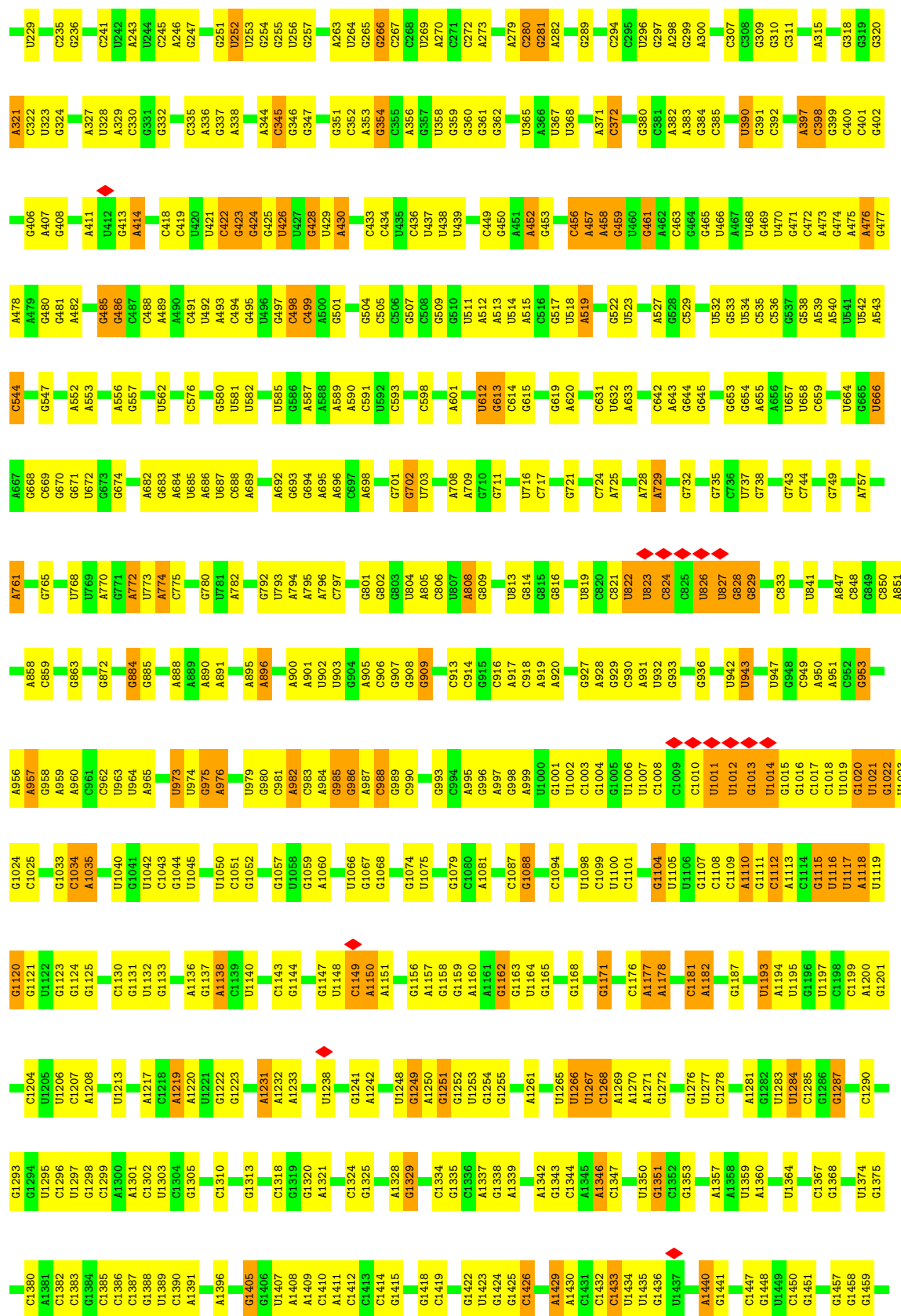
Chain C: 34% 47% 18%

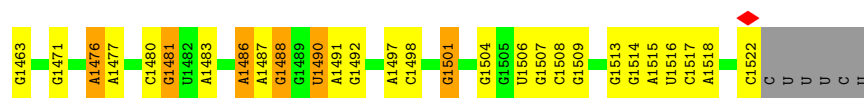


• Molecule 30: 16S rRNA

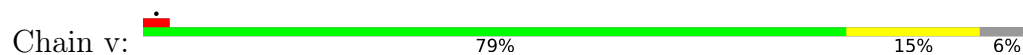
Chain a: 53% 39% 8%



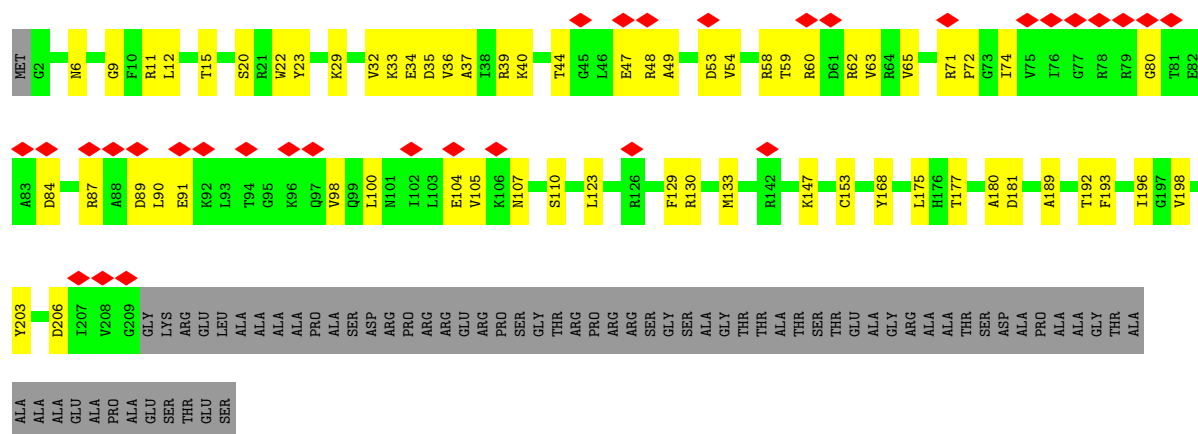




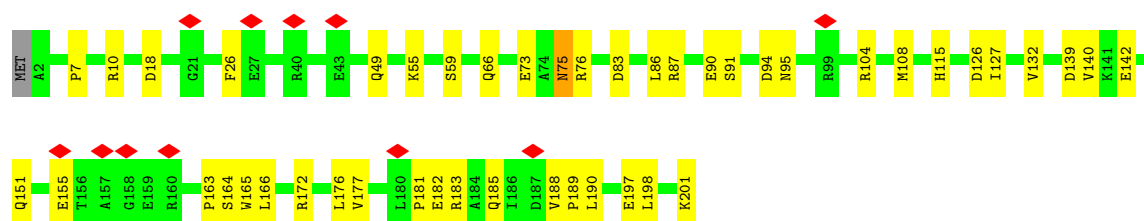
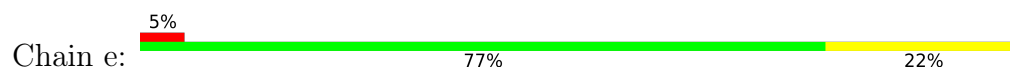
- Molecule 31: 30S ribosomal protein S22



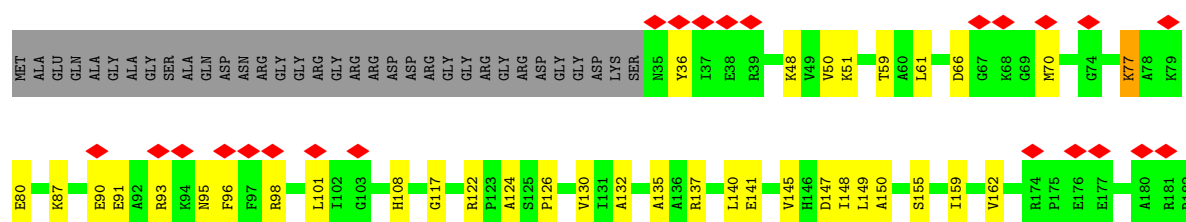
- Molecule 32: 30S ribosomal protein S3



- Molecule 33: 30S ribosomal protein S4

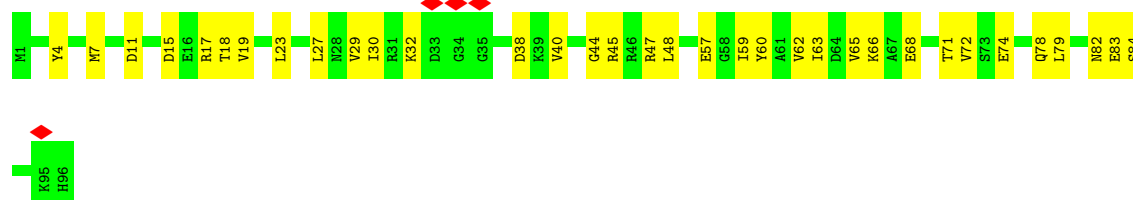


- Molecule 34: 30S ribosomal protein S5

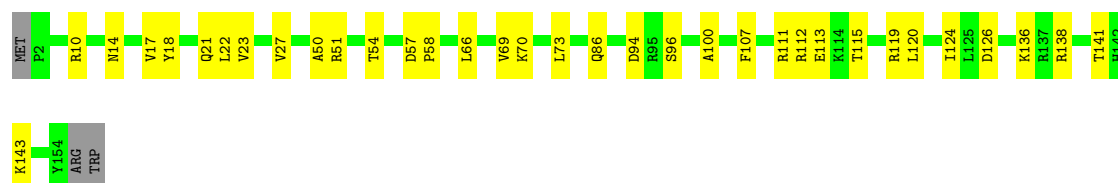
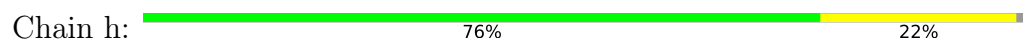




- Molecule 35: 30S ribosomal protein S6



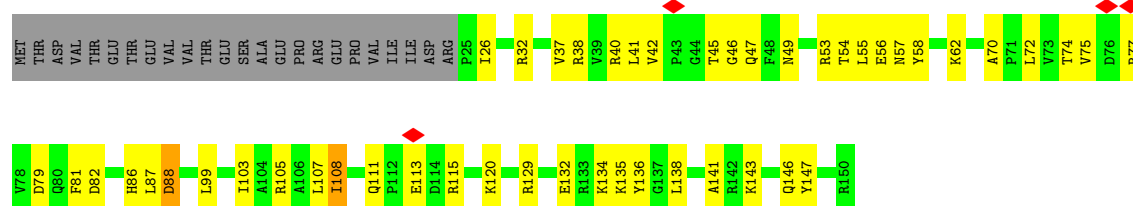
- Molecule 36: 30S ribosomal protein S7



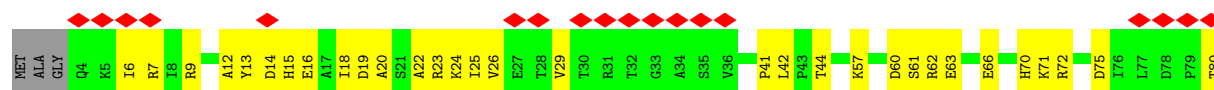
- Molecule 37: 30S ribosomal protein S8

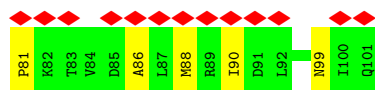


- Molecule 38: 30S ribosomal protein S9



- Molecule 39: 30S ribosomal protein S10





- Molecule 40: 30S ribosomal protein S11

Chain l: 57% 25% 17%



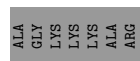
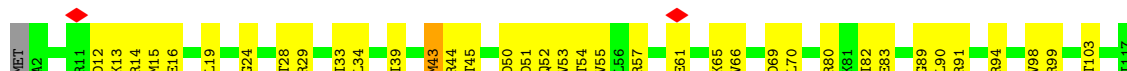
- Molecule 41: 30S ribosomal protein S12

Chain m: 78% 20%



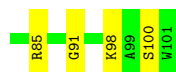
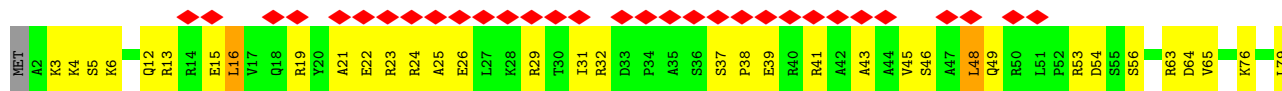
- Molecule 42: 30S ribosomal protein S13

Chain n: 64% 29% 6%



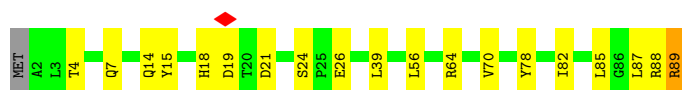
- Molecule 43: 30S ribosomal protein S14A

Chain o: 31% 60% 37% 2%

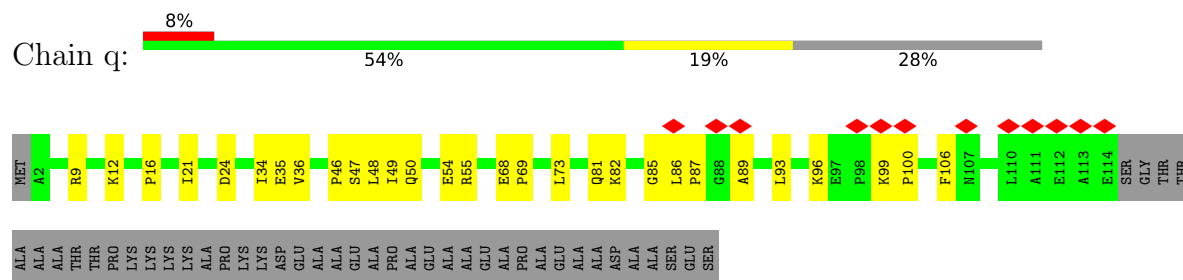


- Molecule 44: 30S ribosomal protein S15

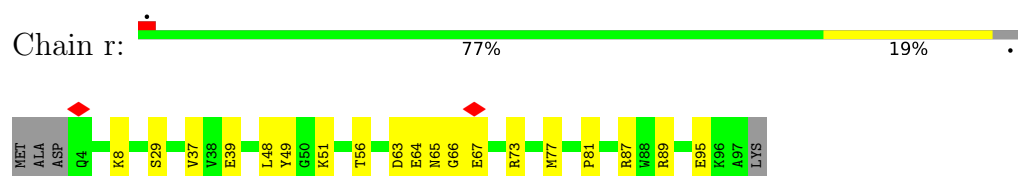
Chain p: 78% 20% 2%



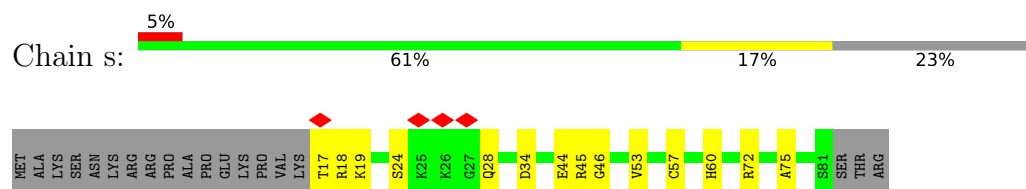
- Molecule 45: 30S ribosomal protein S16



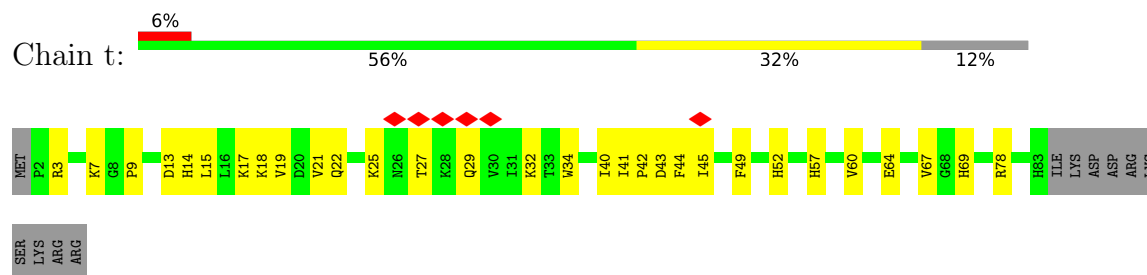
- Molecule 46: 30S ribosomal protein S17



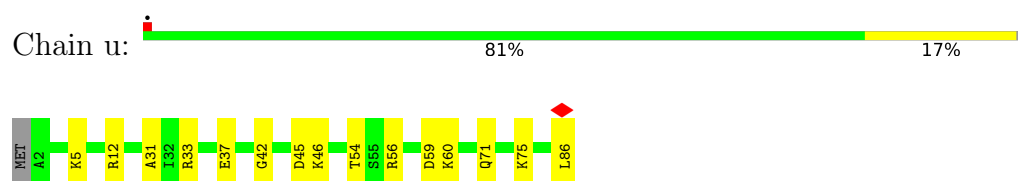
- Molecule 47: 30S ribosomal protein S18B



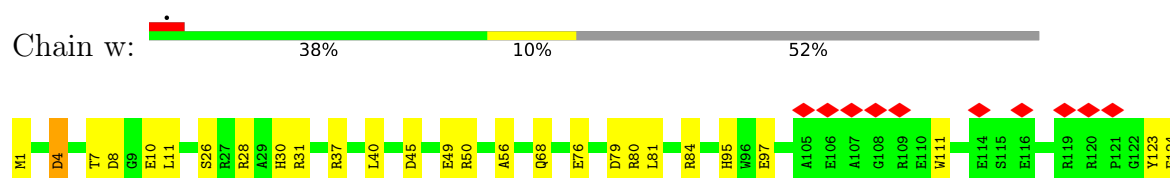
- Molecule 48: 30S ribosomal protein S19



- Molecule 49: 30S ribosomal protein S20



- Molecule 50: Ribosome hibernation promotion factor RafH



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	44299	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	NONE; CTF correction in Relion3.1.4	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.34	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.221	Depositor
Minimum map value	-0.033	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.045	Depositor
Map size ($\text{\AA}$)	406.6, 406.6, 406.6	wwPDB
Map dimensions	380, 380, 380	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.07, 1.07, 1.07	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	E	0.32	0/2153	0.34	0/2895
2	F	0.32	0/1584	0.46	1/2130 (0.0%)
3	G	0.33	0/1585	0.47	0/2143
4	H	0.23	0/1450	0.40	0/1951
5	I	0.18	0/1281	0.45	0/1733
6	J	0.31	0/311	0.49	0/419
7	M	0.31	0/1157	0.35	0/1567
8	N	0.30	0/946	0.37	0/1268
9	O	0.29	0/1091	0.39	0/1457
10	Q	0.31	0/936	0.42	0/1256
11	R	0.27	0/961	0.53	0/1291
12	S	0.30	0/902	0.44	0/1212
13	T	0.33	0/994	0.38	0/1333
14	U	0.31	0/764	0.36	0/1030
15	V	0.30	0/878	0.38	0/1192
16	W	0.31	0/761	0.37	0/1023
17	X	0.27	0/712	0.45	0/952
18	Z	0.30	0/583	0.34	0/782
19	1	0.32	0/473	0.52	0/634
20	2	0.28	0/530	0.48	0/708
21	3	0.36	0/473	0.43	0/635
22	5	0.23	0/427	0.32	0/572
23	6	0.38	0/405	0.84	1/542 (0.2%)
24	7	0.35	0/380	0.38	0/500
25	8	0.26	0/507	0.31	0/672
26	4	0.22	0/467	0.45	0/626
27	A	0.31	0/72677	0.32	0/113395
28	B	0.28	0/2799	0.33	0/4362
29	C	0.16	0/1812	0.35	0/2821
30	a	0.18	0/36400	0.27	0/56798
31	v	0.12	0/271	0.26	0/348
32	d	0.16	0/1684	0.36	0/2261
33	e	0.16	0/1672	0.32	0/2251
34	f	0.16	0/1224	0.33	0/1653

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	g	0.20	0/782	0.42	0/1059
36	h	0.18	0/1225	0.40	0/1653
37	i	0.19	0/1025	0.32	0/1385
38	j	0.20	0/1012	0.44	0/1362
39	k	0.21	0/798	0.48	0/1081
40	l	0.17	0/873	0.36	0/1180
41	m	0.19	0/969	0.34	0/1294
42	n	0.20	0/942	0.50	0/1260
43	o	0.26	0/830	0.45	0/1106
44	p	0.24	0/729	0.51	0/977
45	q	0.19	0/908	0.38	0/1226
46	r	0.18	0/759	0.39	0/1016
47	s	0.20	0/518	0.41	0/693
48	t	0.21	0/680	0.45	0/915
49	u	0.20	0/663	0.39	0/882
50	w	0.18	0/1023	0.36	0/1381
All	All	0.27	0/154986	0.33	2/232882 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	6	50	PRO	CA-N-CD	-9.62	98.53	112.00
2	F	151	ILE	N-CA-C	-6.84	106.83	113.53

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2110	0	2165	32	0
2	F	1563	0	1608	31	0
3	G	1562	0	1600	32	0
4	H	1428	0	1457	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	1260	0	1300	59	0
6	J	308	0	323	12	0
7	M	1130	0	1167	21	0
8	N	938	0	1000	11	0
9	O	1078	0	1151	14	0
10	Q	919	0	959	13	0
11	R	951	0	986	43	0
12	S	888	0	913	18	0
13	T	982	0	1033	20	0
14	U	754	0	802	9	0
15	V	864	0	903	11	0
16	W	751	0	797	9	0
17	X	706	0	757	16	0
18	Z	574	0	591	10	0
19	1	465	0	479	21	0
20	2	527	0	538	11	0
21	3	470	0	497	11	0
22	5	423	0	463	11	0
23	6	397	0	407	18	0
24	7	377	0	411	12	0
25	8	502	0	541	7	0
26	4	458	0	447	36	0
27	A	64906	0	32655	926	0
28	B	2502	0	1274	42	0
29	C	1622	0	825	48	0
30	a	32521	0	16365	492	0
31	v	271	0	329	5	0
32	d	1660	0	1707	44	0
33	e	1641	0	1668	34	0
34	f	1208	0	1276	34	0
35	g	771	0	797	38	0
36	h	1207	0	1259	26	0
37	i	1010	0	1046	24	0
38	j	994	0	1050	43	0
39	k	784	0	816	41	0
40	l	855	0	863	26	0
41	m	958	0	1045	21	0
42	n	935	0	985	41	0
43	o	819	0	866	39	0
44	p	720	0	760	15	0
45	q	891	0	935	20	0
46	r	748	0	795	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	s	513	0	540	11	0
48	t	662	0	677	27	0
49	u	660	0	712	10	0
50	w	1004	0	991	34	0
All	All	142247	0	93531	2300	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 10.

The worst 5 of 2300 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)
29:C:34:C:O2	50:w:31:ARG:NE	1.61	1.34
27:A:1611:A:H2	35:g:17:ARG:NH2	1.29	1.30
29:C:34:C:O2	50:w:31:ARG:CZ	1.94	1.15
29:C:34:C:O2	50:w:31:ARG:NH2	1.80	1.13
27:A:1611:A:C2	35:g:17:ARG:NH2	2.17	1.12

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	273/278 (98%)	267 (98%)	6 (2%)	0	100	100
2	F	205/217 (94%)	200 (98%)	5 (2%)	0	100	100
3	G	206/215 (96%)	199 (97%)	7 (3%)	0	100	100
4	H	178/187 (95%)	173 (97%)	5 (3%)	0	100	100
5	I	163/179 (91%)	159 (98%)	4 (2%)	0	100	100
6	J	39/151 (26%)	37 (95%)	2 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	M	144/147 (98%)	143 (99%)	1 (1%)	0	100	100
8	N	120/122 (98%)	117 (98%)	3 (2%)	0	100	100
9	O	143/147 (97%)	133 (93%)	10 (7%)	0	100	100
10	Q	115/199 (58%)	112 (97%)	3 (3%)	0	100	100
11	R	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
12	S	109/113 (96%)	103 (94%)	6 (6%)	0	100	100
13	T	121/129 (94%)	120 (99%)	1 (1%)	0	100	100
14	U	98/103 (95%)	96 (98%)	2 (2%)	0	100	100
15	V	111/153 (72%)	109 (98%)	2 (2%)	0	100	100
16	W	94/100 (94%)	93 (99%)	1 (1%)	0	100	100
17	X	88/105 (84%)	86 (98%)	2 (2%)	0	100	100
18	Z	75/88 (85%)	71 (95%)	4 (5%)	0	100	100
19	1	60/64 (94%)	56 (93%)	4 (7%)	0	100	100
20	2	61/77 (79%)	59 (97%)	2 (3%)	0	100	100
21	3	56/61 (92%)	54 (96%)	2 (4%)	0	100	100
22	5	52/57 (91%)	52 (100%)	0	0	100	100
23	6	46/55 (84%)	43 (94%)	3 (6%)	0	100	100
24	7	44/47 (94%)	44 (100%)	0	0	100	100
25	8	61/64 (95%)	60 (98%)	1 (2%)	0	100	100
26	4	55/75 (73%)	54 (98%)	1 (2%)	0	100	100
31	v	29/33 (88%)	29 (100%)	0	0	100	100
32	d	206/275 (75%)	197 (96%)	9 (4%)	0	100	100
33	e	198/201 (98%)	192 (97%)	6 (3%)	0	100	100
34	f	164/214 (77%)	159 (97%)	5 (3%)	0	100	100
35	g	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
36	h	151/156 (97%)	148 (98%)	3 (2%)	0	100	100
37	i	129/132 (98%)	126 (98%)	3 (2%)	0	100	100
38	j	124/150 (83%)	115 (93%)	9 (7%)	0	100	100
39	k	96/101 (95%)	91 (95%)	4 (4%)	1 (1%)	12	44
40	l	113/138 (82%)	109 (96%)	4 (4%)	0	100	100
41	m	120/124 (97%)	113 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	n	114/124 (92%)	110 (96%)	4 (4%)	0	100	100
43	o	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
44	p	86/89 (97%)	86 (100%)	0	0	100	100
45	q	111/156 (71%)	105 (95%)	6 (5%)	0	100	100
46	r	92/98 (94%)	87 (95%)	5 (5%)	0	100	100
47	s	63/84 (75%)	62 (98%)	1 (2%)	0	100	100
48	t	80/93 (86%)	76 (95%)	4 (5%)	0	100	100
49	u	83/86 (96%)	83 (100%)	0	0	100	100
50	w	124/264 (47%)	119 (96%)	5 (4%)	0	100	100
All	All	5115/5975 (86%)	4956 (97%)	158 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
39	k	57	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	215/218 (99%)	215 (100%)	0	100	100
2	F	159/163 (98%)	155 (98%)	4 (2%)	42	63
3	G	168/173 (97%)	168 (100%)	0	100	100
4	H	149/156 (96%)	147 (99%)	2 (1%)	61	72
5	I	139/150 (93%)	137 (99%)	2 (1%)	59	71
6	J	31/116 (27%)	31 (100%)	0	100	100
7	M	119/120 (99%)	117 (98%)	2 (2%)	53	70
8	N	100/100 (100%)	99 (99%)	1 (1%)	68	75
9	O	112/114 (98%)	111 (99%)	1 (1%)	70	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	Q	96/158 (61%)	95 (99%)	1 (1%)	68	75
11	R	93/94 (99%)	93 (100%)	0	100	100
12	S	98/100 (98%)	98 (100%)	0	100	100
13	T	96/99 (97%)	95 (99%)	1 (1%)	68	75
14	U	81/83 (98%)	81 (100%)	0	100	100
15	V	89/117 (76%)	89 (100%)	0	100	100
16	W	83/85 (98%)	83 (100%)	0	100	100
17	X	79/86 (92%)	77 (98%)	2 (2%)	42	63
18	Z	56/63 (89%)	56 (100%)	0	100	100
19	1	50/51 (98%)	47 (94%)	3 (6%)	17	44
20	2	58/66 (88%)	58 (100%)	0	100	100
21	3	52/54 (96%)	51 (98%)	1 (2%)	50	68
22	5	43/46 (94%)	42 (98%)	1 (2%)	44	64
23	6	46/52 (88%)	46 (100%)	0	100	100
24	7	35/36 (97%)	35 (100%)	0	100	100
25	8	53/54 (98%)	53 (100%)	0	100	100
26	4	51/63 (81%)	51 (100%)	0	100	100
31	v	29/31 (94%)	29 (100%)	0	100	100
32	d	170/212 (80%)	169 (99%)	1 (1%)	78	79
33	e	175/176 (99%)	174 (99%)	1 (1%)	78	79
34	f	121/147 (82%)	120 (99%)	1 (1%)	73	77
35	g	85/85 (100%)	85 (100%)	0	100	100
36	h	129/132 (98%)	128 (99%)	1 (1%)	73	77
37	i	107/108 (99%)	107 (100%)	0	100	100
38	j	102/125 (82%)	100 (98%)	2 (2%)	48	67
39	k	89/90 (99%)	88 (99%)	1 (1%)	65	74
40	l	89/105 (85%)	87 (98%)	2 (2%)	45	65
41	m	103/105 (98%)	103 (100%)	0	100	100
42	n	99/104 (95%)	98 (99%)	1 (1%)	68	75
43	o	85/86 (99%)	83 (98%)	2 (2%)	43	64
44	p	76/77 (99%)	74 (97%)	2 (3%)	40	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	q	92/118 (78%)	92 (100%)	0	100	100
46	r	80/83 (96%)	80 (100%)	0	100	100
47	s	55/72 (76%)	54 (98%)	1 (2%)	51	69
48	t	73/84 (87%)	73 (100%)	0	100	100
49	u	69/70 (99%)	69 (100%)	0	100	100
50	w	98/215 (46%)	97 (99%)	1 (1%)	68	75
All	All	4277/4842 (88%)	4240 (99%)	37 (1%)	68	76

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	l	35	THR
47	s	24	SER
40	l	128	ASN
43	o	48	LEU
10	Q	54	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
40	l	84	GLN
48	t	14	HIS
49	u	3	ASN
11	R	53	ASN
10	Q	62	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
27	A	3018/3119 (96%)	552 (18%)	16 (0%)
28	B	116/118 (98%)	17 (14%)	1 (0%)
29	C	75/76 (98%)	29 (38%)	3 (4%)
30	a	1514/1528 (99%)	265 (17%)	0
All	All	4723/4841 (97%)	863 (18%)	20 (0%)

5 of 863 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
27	A	7	U
27	A	9	U
27	A	12	G
27	A	20	G
27	A	29	C

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
27	A	2381	A
29	C	17	C
29	C	53	G
29	C	20	U
27	A	643	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 [i](#)

There are no chain breaks in this entry.

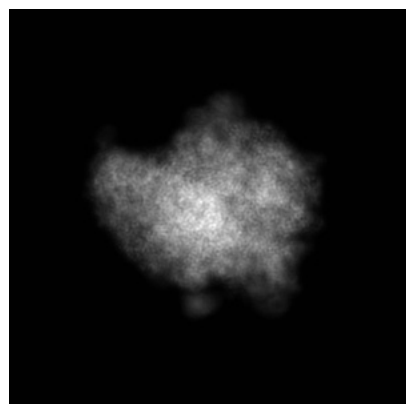
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37562. These allow visual inspection of the internal detail of the map and identification of artifacts.

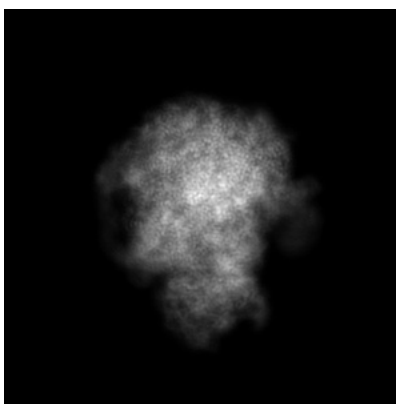
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

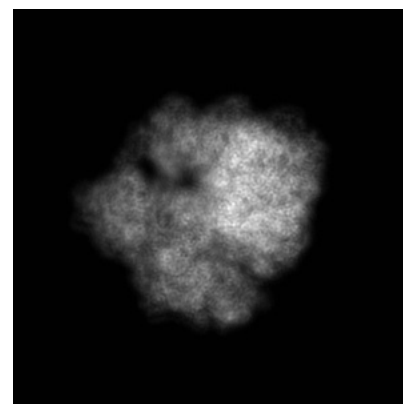
6.1.1 Primary map



X

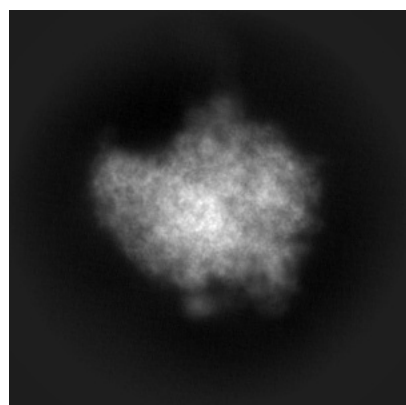


Y

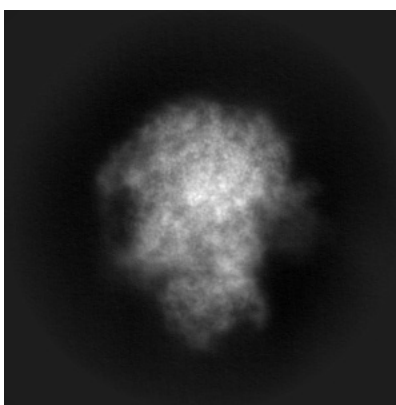


Z

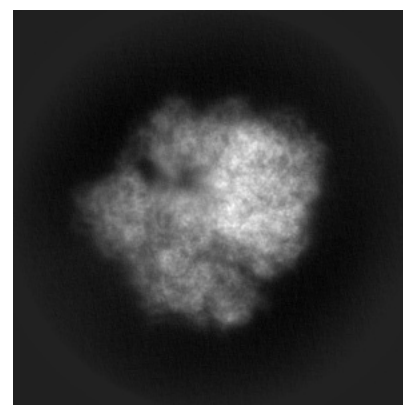
6.1.2 Raw map



X



Y

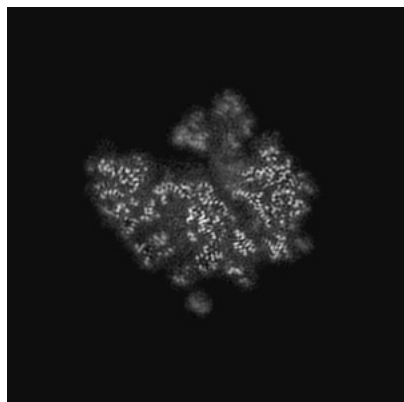


Z

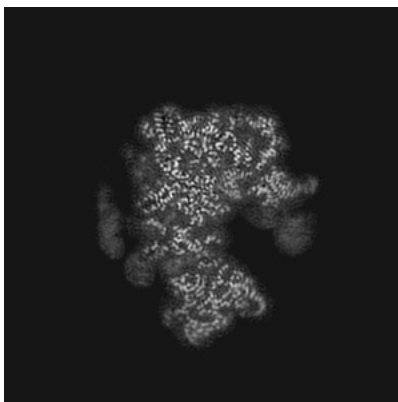
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

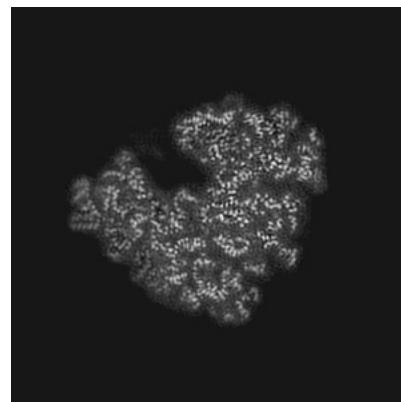
6.2.1 Primary map



X Index: 190

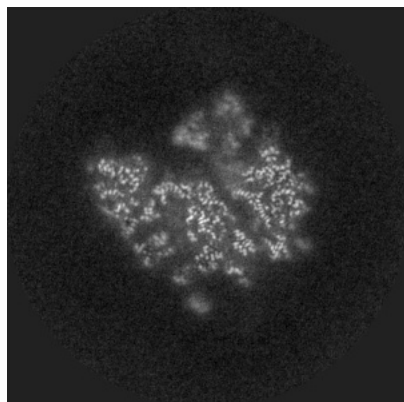


Y Index: 190

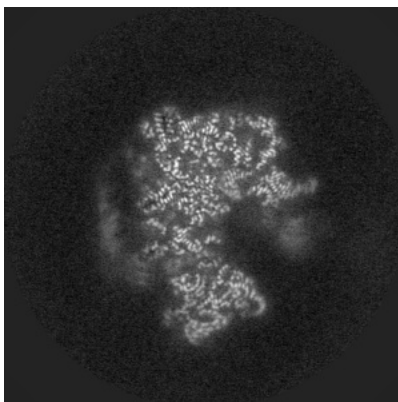


Z Index: 190

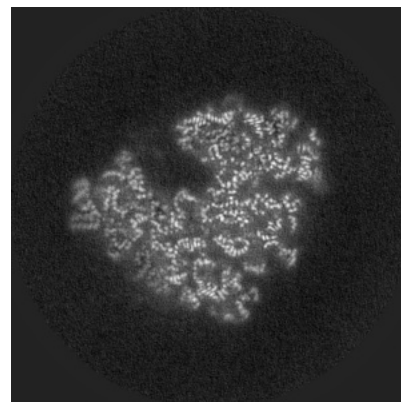
6.2.2 Raw map



X Index: 190



Y Index: 190

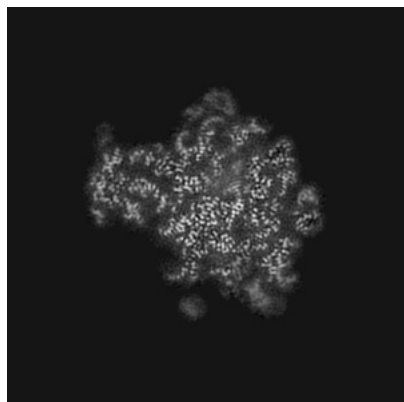


Z Index: 190

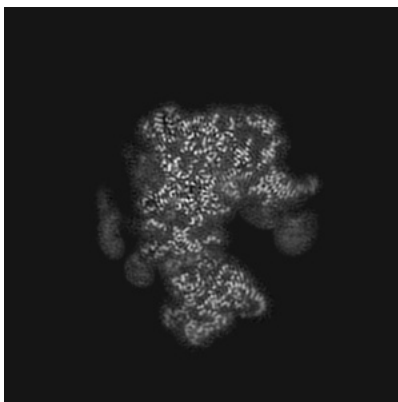
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

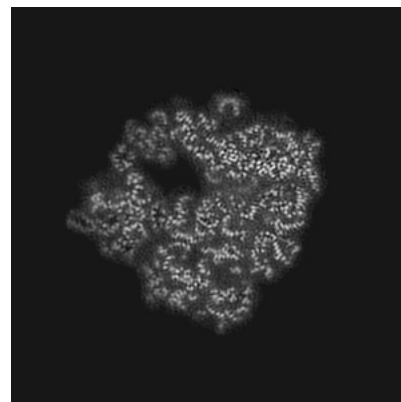
6.3.1 Primary map



X Index: 213

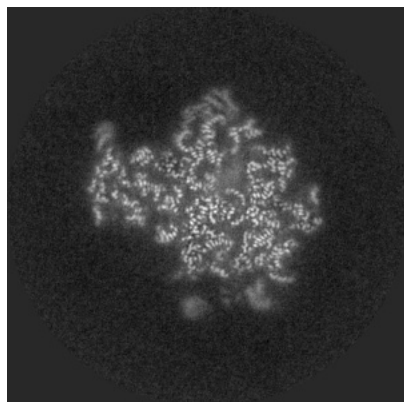


Y Index: 191

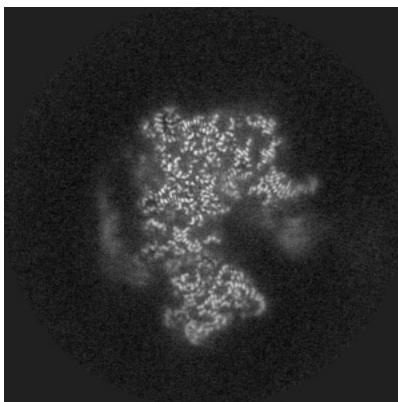


Z Index: 200

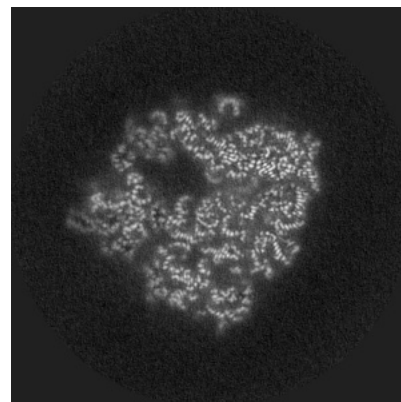
6.3.2 Raw map



X Index: 209



Y Index: 191

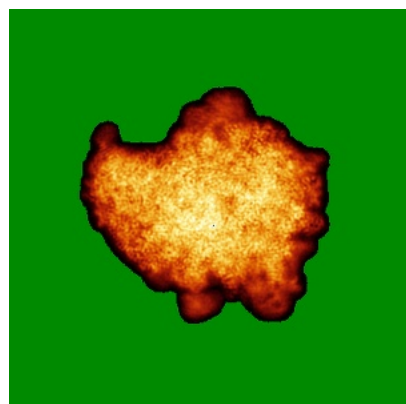


Z Index: 200

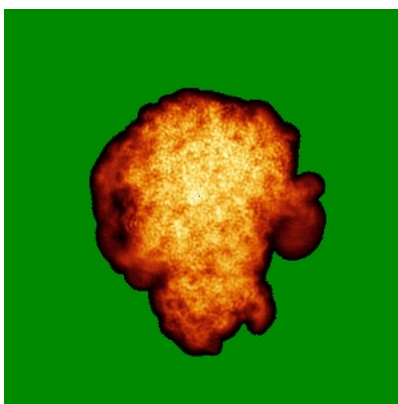
The images above show the largest variance slices of the map in three orthogonal directions.

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

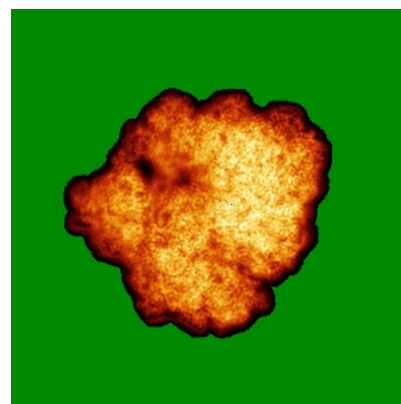
6.4.1 Primary map



X

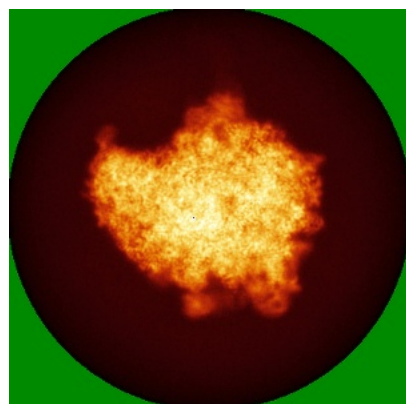


Y

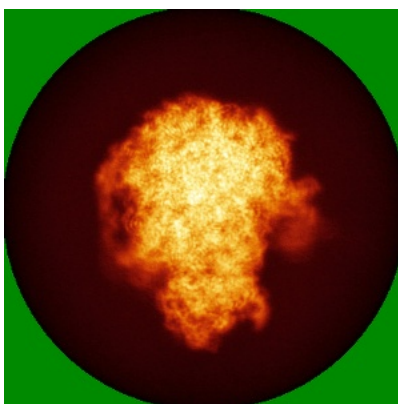


Z

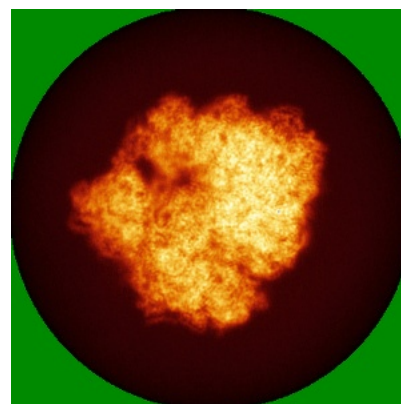
6.4.2 Raw map



X



Y

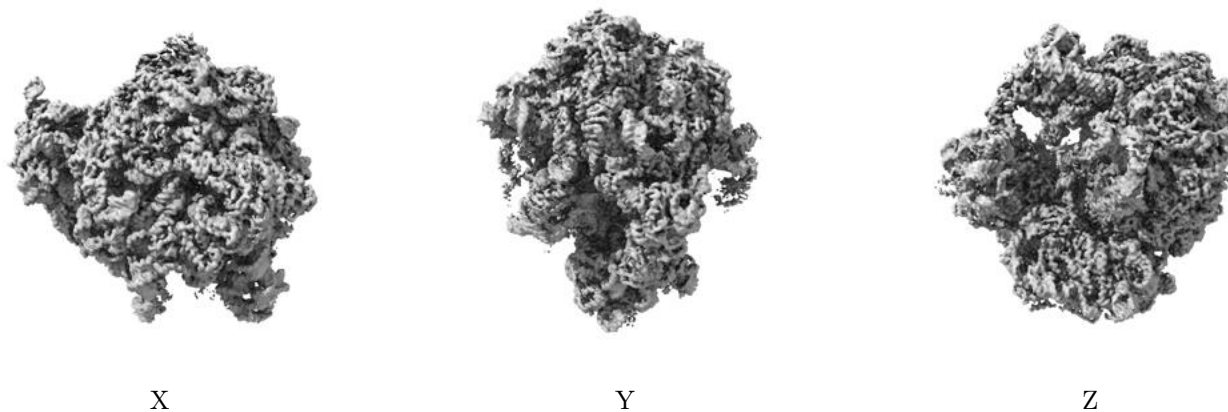


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.045. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

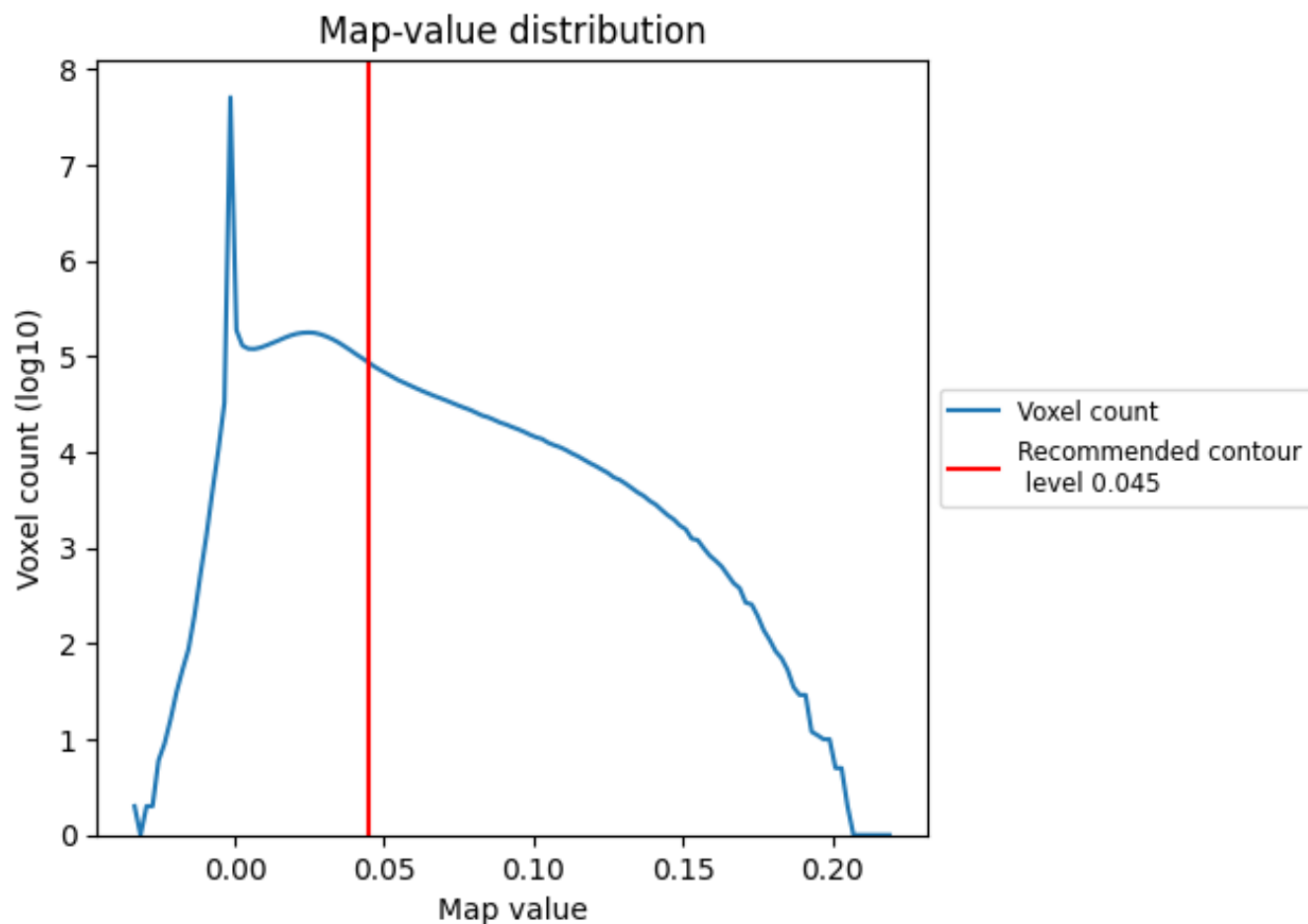
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

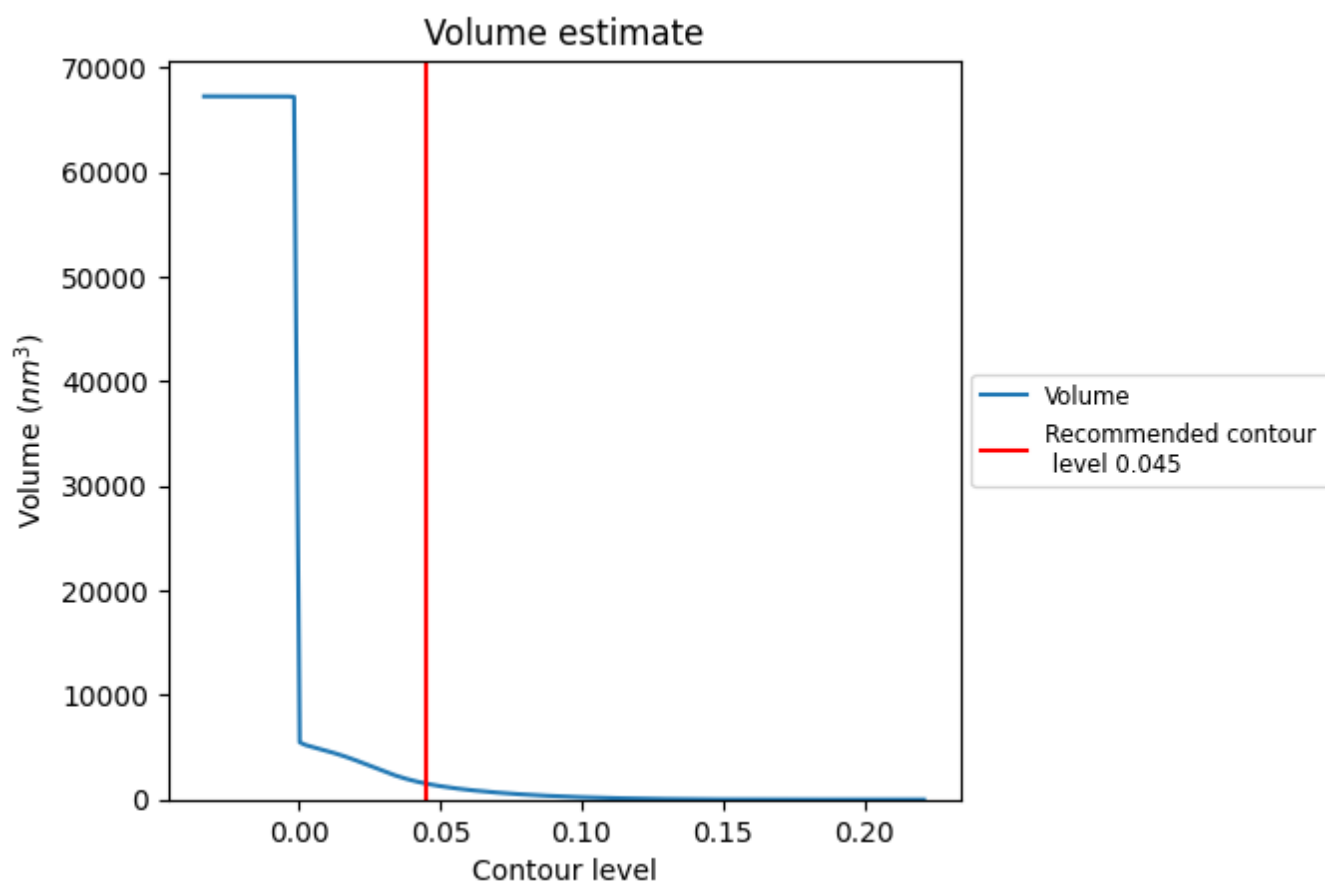
This section contains the results of statistical analysis of the map.

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.

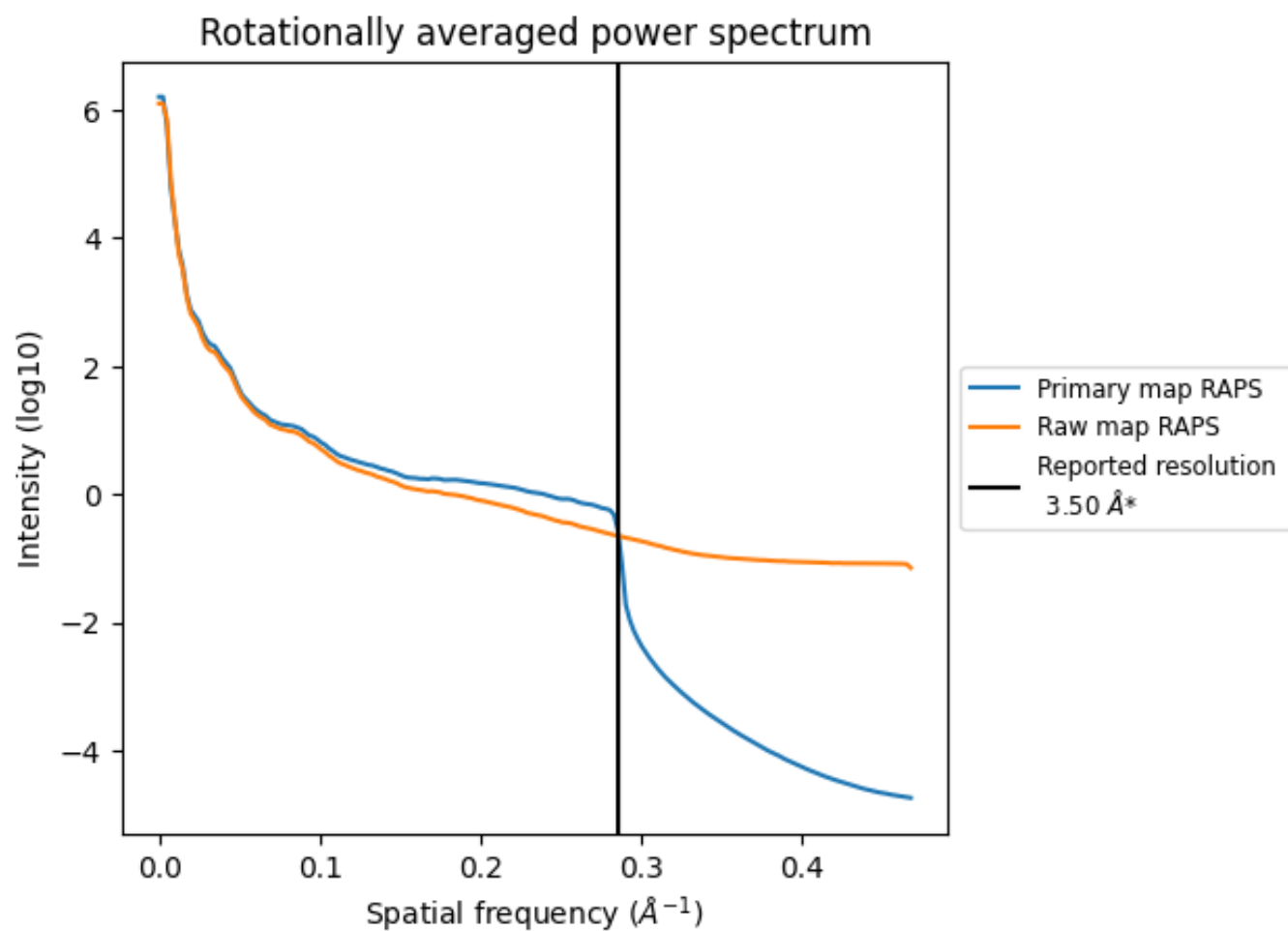
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1530 nm³; this corresponds to an approximate mass of 1382 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 ⓘ

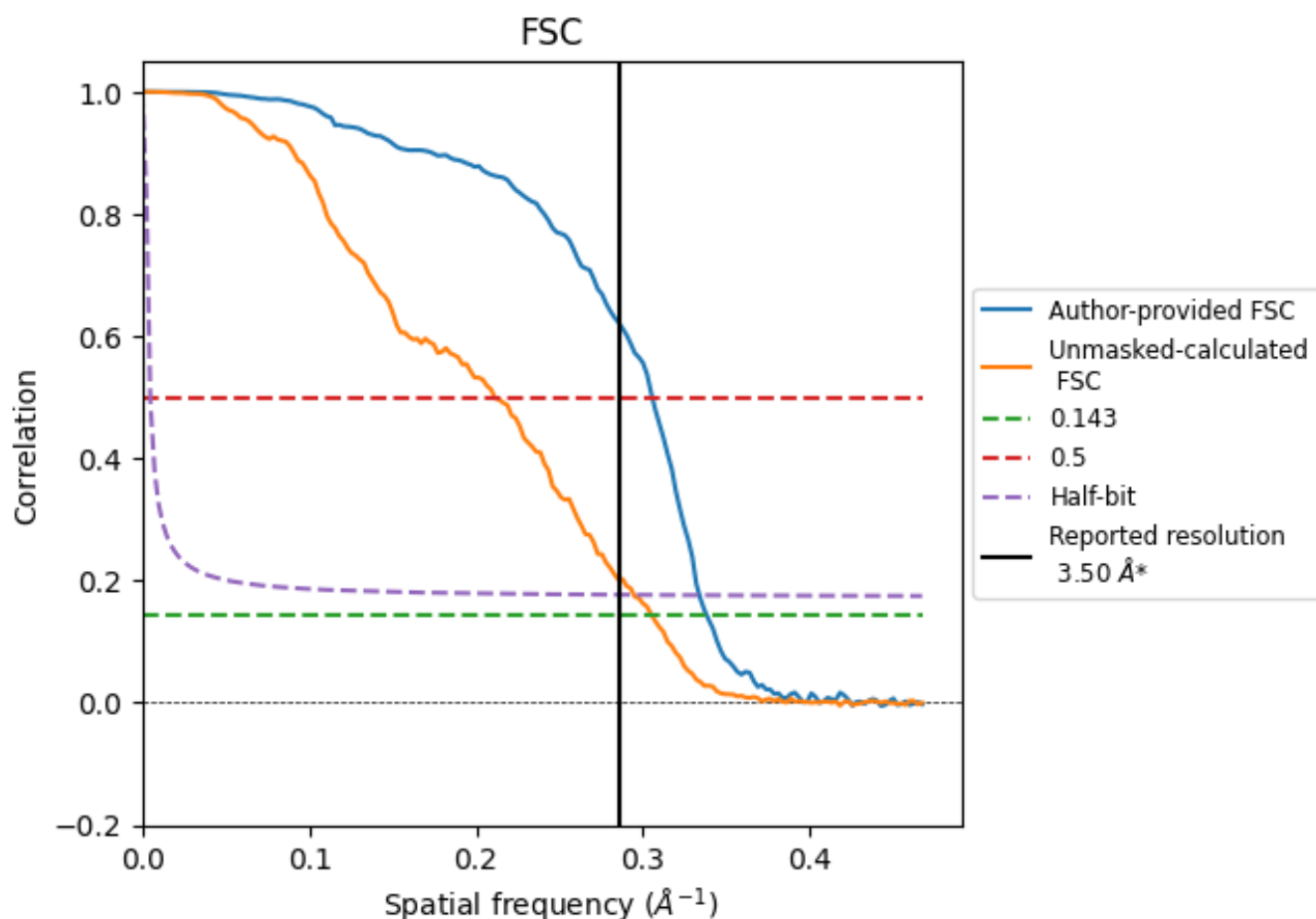


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

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 $0.286 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

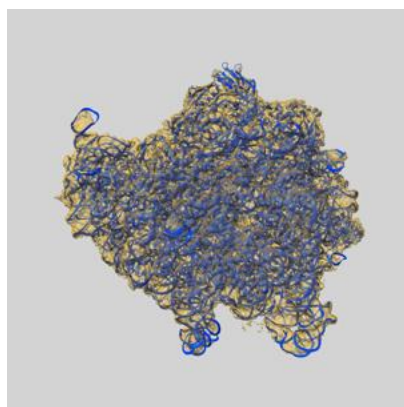
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	Other
Reported by author	-	-	-	3.50
Author-provided FSC curve	2.96	3.27	2.99	-
Unmasked-calculated*	3.28	4.73	3.39	-

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

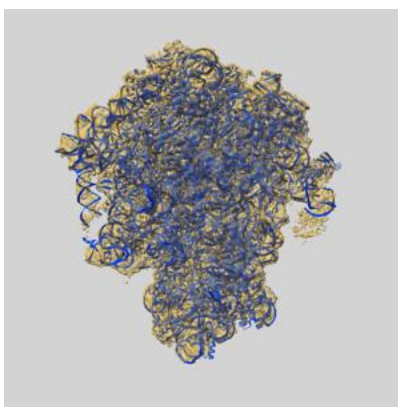
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37562 and PDB model 8WIB. Per-residue inclusion information can be found in section 3 on page 13.

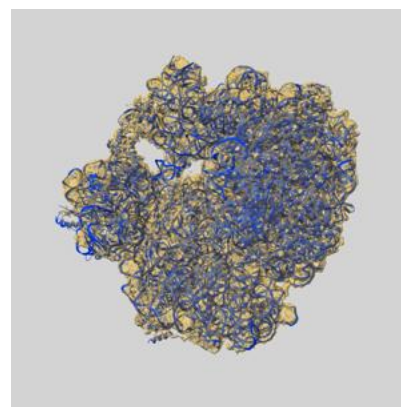
9.1 Map-model overlay [i](#)



X



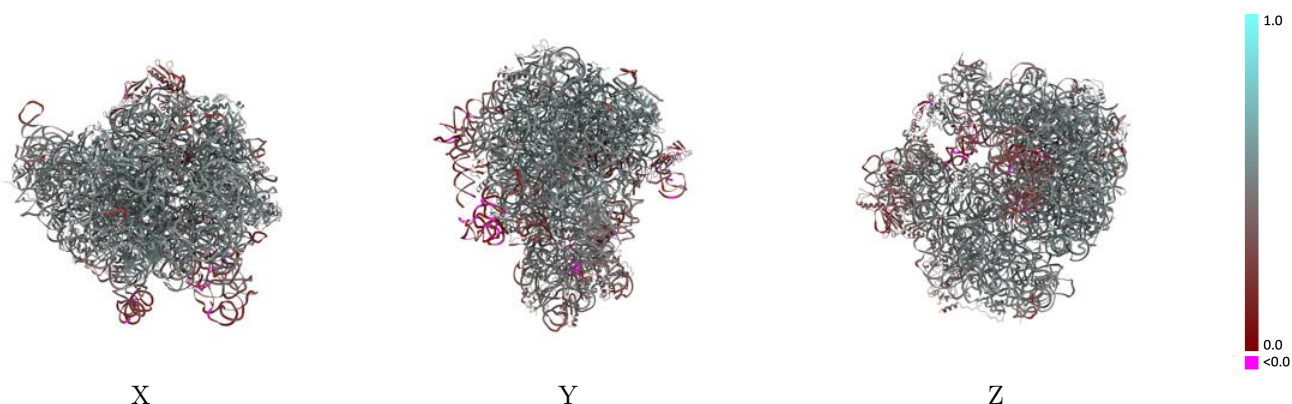
Y



Z

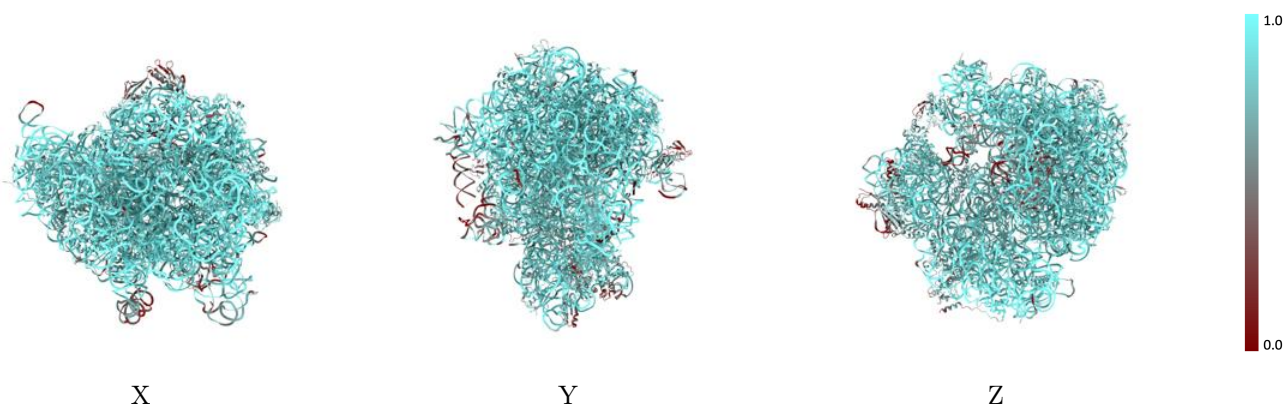
The images above show the 3D surface view of the map at the recommended contour level 0.045 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



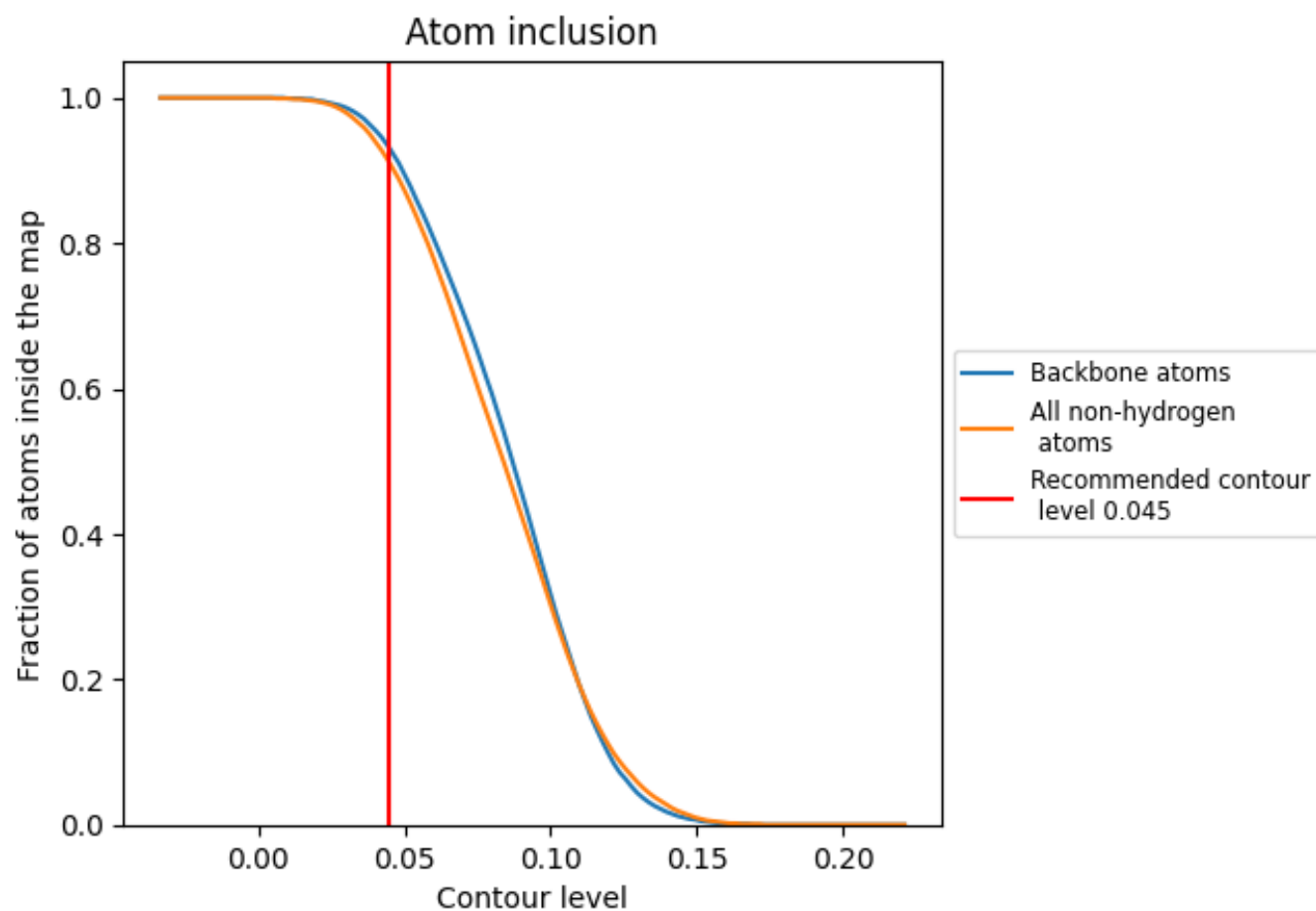
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.045).

9.4 Atom inclusion ⓘ



At the recommended contour level, 93% of all backbone atoms, 91% 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 (0.045) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9100	 0.4690
1	 0.9260	 0.4990
2	 0.8520	 0.4820
3	 0.8990	 0.5140
4	 0.3920	 0.1710
5	 0.8680	 0.5320
6	 0.8160	 0.4510
7	 0.9890	 0.5160
8	 0.9400	 0.5290
A	 0.9330	 0.4690
B	 0.9650	 0.4610
C	 0.8510	 0.2860
E	 0.9610	 0.5460
F	 0.9090	 0.5210
G	 0.8680	 0.5040
H	 0.8000	 0.4400
I	 0.4440	 0.2230
J	 0.5170	 0.2470
M	 0.9160	 0.5140
N	 0.9210	 0.5290
O	 0.8980	 0.5190
Q	 0.9590	 0.5400
R	 0.8390	 0.4630
S	 0.8910	 0.5100
T	 0.9470	 0.5350
U	 0.8850	 0.5460
V	 0.9500	 0.5420
W	 0.8920	 0.5230
X	 0.7780	 0.4700
Z	 0.9210	 0.5190
a	 0.9690	 0.4820
d	 0.6600	 0.3720
e	 0.7670	 0.4320
f	 0.5970	 0.4420
g	 0.8180	 0.4760



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Chain	Atom inclusion	Q-score
h	 0.8240	 0.4440
i	 0.8950	 0.5090
j	 0.8050	 0.4460
k	 0.5410	 0.3550
l	 0.8570	 0.4800
m	 0.8670	 0.4990
n	 0.8150	 0.4220
o	 0.5800	 0.3510
p	 0.8750	 0.4770
q	 0.8210	 0.4730
r	 0.8880	 0.5070
s	 0.8300	 0.4530
t	 0.7820	 0.4260
u	 0.8940	 0.4880
v	 0.9090	 0.4830
w	 0.8260	 0.4510