



## wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 03:38 AM UTC

PDB ID : 9Y4H / pdb\_00009y4h  
EMDB ID : EMD-72483  
Title : Structure of guinea pig ribosome with P/E-tRNA and mRNA  
Authors : Gutierrez-Vargas, C.; De, S.; Maji, S.; Liu, Z.; Nieb, M.; Seluanov, A.; Gorbunova, V.; Frank, J.  
Deposited on : 2025-09-03  
Resolution : 4.70 Å(reported)  
Based on initial model : 4V6X

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

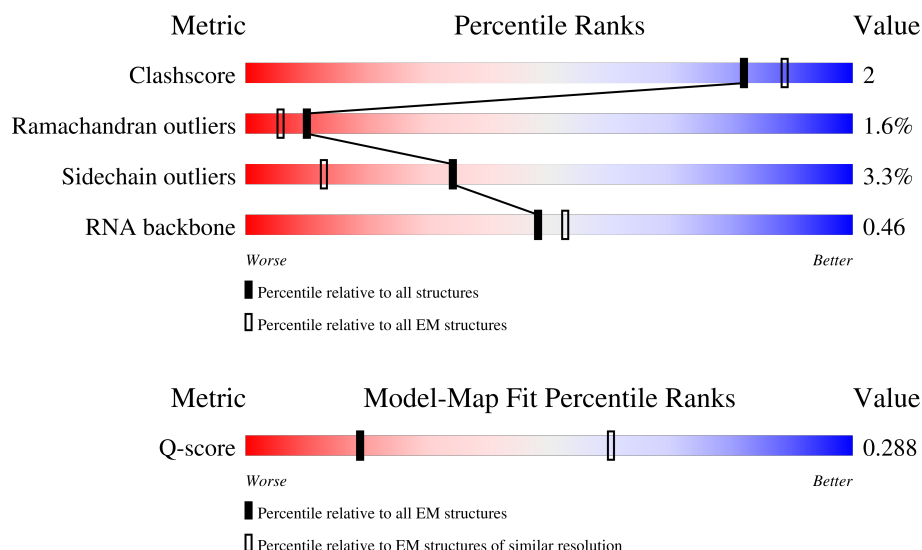
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.70 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.









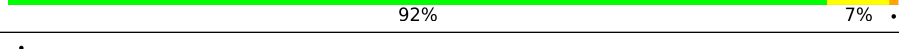
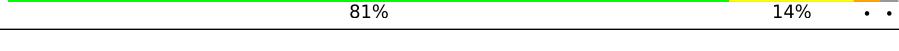
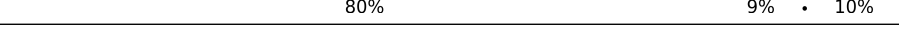
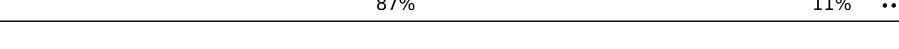
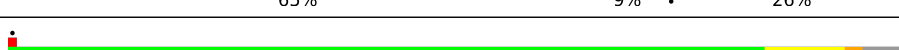

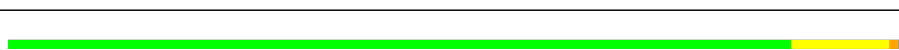

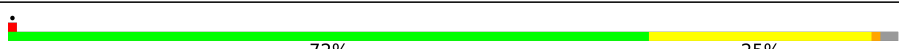



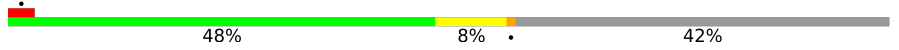

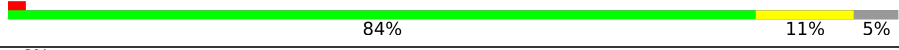
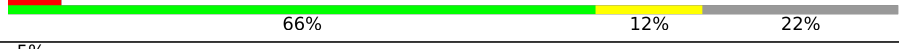



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	1989 ( 4.20 - 5.20 )

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  $\geq 3$ , 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	AO	151	<div> <div>70%</div> <div>12%</div> <div>•</div> <div>17%</div> </div>
2	AX	143	<div> <div>83%</div> <div>15%</div> <div>••</div> </div>
3	AN	151	<div> <div>91%</div> <div>8%</div> <div>••</div> </div>



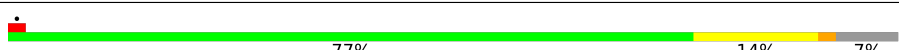
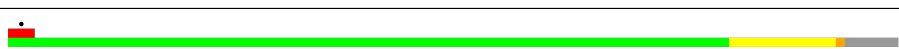

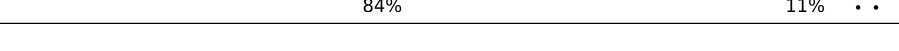
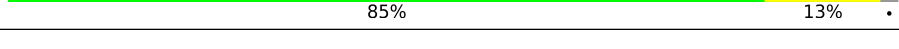



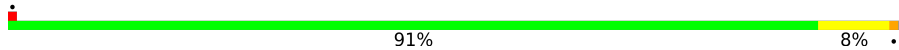

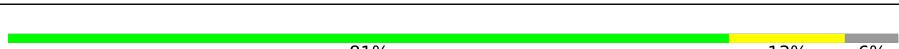


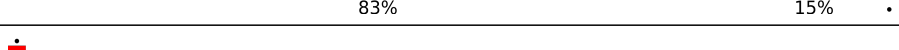


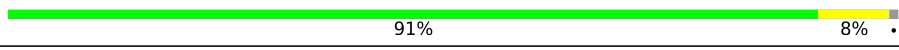





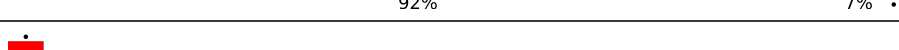
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Mol	Chain	Length	Quality of chain
4	AL	158	
5	AB	264	
6	AA	295	
7	AV	83	
8	AY	133	
9	Aa	115	
10	Ab	84	
11	Ae	59	
12	AJ	194	
13	AE	263	
14	AC	293	
15	AG	249	
16	AH	194	
17	AW	130	
18	AI	208	
19	B2	1803	
20	CW	157	
21	Ag	317	
22	AU	119	
23	AK	165	
24	AS	152	
25	Ad	56	
26	AR	135	
27	AP	145	
28	AT	145	


























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Mol	Chain	Length	Quality of chain
29	AZ	125	
30	Ac	69	
31	AD	243	
32	AF	204	
33	AQ	146	
34	CO	203	
35	CL	211	
36	CV	140	
37	CM	215	
38	Ca	148	
39	CN	204	
40	CI	214	
41	CD	297	
42	CQ	188	
43	CA	257	
44	CS	176	
45	CT	160	
46	CP	184	
47	CU	128	
48	CX	156	
49	CY	145	
50	CZ	136	
51	Cr	137	
52	Ch	123	
53	Cb	159	

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Mol	Chain	Length	Quality of chain
54	CB	403	
55	CF	248	
56	Cc	115	
57	Cd	125	
58	Ce	135	
59	Cf	110	
60	Cg	117	
61	Ci	105	
62	Cj	97	
63	Ck	70	
64	Cl	51	
65	CC	427	
66	Cm	52	
67	Cn	25	
68	Cp	92	
69	Co	106	
70	CJ	178	
71	CH	192	
72	CE	288	
73	CG	266	
74	A5	4010	
75	A7	121	
76	A8	157	
77	Cw	77	
78	Dd	7	

## 2 Entry composition [i](#)

There are 79 unique types of molecules in this entry. The entry contains 371528 atoms, of which 156643 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 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	AO	126	Total	C	H	N	O	S	0	0
			1921	580	973	188	174	6		

- Molecule 2 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AX	140	Total	C	H	N	O	S	0	0
			2257	691	1163	218	182	3		

- Molecule 3 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	AN	150	Total	C	H	N	O	S	0	0
			2502	773	1294	229	205	1		

- Molecule 4 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AL	147	Total	C	H	N	O	S	0	0
			2495	777	1279	226	207	6		

- Molecule 5 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	AB	215	Total	C	H	N	O	S	0	0
			3567	1110	1820	313	310	14		

- Molecule 6 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	AA	206	Total	C	H	N	O	S	0	0
			3250	1035	1626	287	294	8		

- Molecule 7 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	AV	81	Total	C	H	N	O	S	0	0
			1232	379	615	115	119	4		

- Molecule 8 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	AY	126	Total	C	H	N	O	S	0	0
			2111	646	1088	200	172	5		

- Molecule 9 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	Aa	98	Total	C	H	N	O	S	0	0
			1613	486	832	161	129	5		

- Molecule 10 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	Ab	84	Total	C	H	N	O	S	0	0
			1339	413	680	122	116	8		

- Molecule 11 is a protein called FAU ubiquitin like and ribosomal protein S30 fusion.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	Ae	58	Total	C	H	N	O	S	0	0
			972	287	511	101	72	1		

- Molecule 12 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	AJ	174	Total	C	H	N	O	S	0	0
			3025	931	1566	291	235	2		

- Molecule 13 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	AE	261	Total	C	H	N	O	S	0	0
			4254	1324	2181	385	355	9		

- Molecule 14 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	AC	218	Total	C	H	N	O	S	0	0
			3469	1096	1777	290	296	10		

- Molecule 15 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	AG	237	Total	C	H	N	O	S	0	0
			4008	1200	2085	387	329	7		

- Molecule 16 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	AH	179	Total	C	H	N	O	S	0	0
			2983	924	1534	266	258	1		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	AW	129	Total	C	H	N	O	S	0	0
			2113	659	1079	193	176	6		

- Molecule 18 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	AI	200	Total	C	H	N	O	S	0	0
			3364	1031	1720	324	284	5		

- Molecule 19 is a RNA chain called 18S rRNA (1803-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
19	B2	1773	Total	C	H	N	O	P	0	0
			56567	16783	18948	6729	12335	1772		

- Molecule 20 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	CW	118	Total	C	H	N	O	S	0	0
			1988	604	1023	199	158	4		

- Molecule 21 is a protein called Small ribosomal subunit protein RACK1.



Mol	Chain	Residues	Atoms						AltConf	Trace
21	Ag	299	Total	C	H	N	O	S	0	0
			4623	1474	2289	408	440	12		

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	AU	103	Total	C	H	N	O	S	0	0
			1699	511	882	155	147	4		

- Molecule 23 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	AK	95	Total	C	H	N	O	S	0	0
			1621	524	822	139	130	6		

- Molecule 24 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	AS	137	Total	C	H	N	O	S	0	0
			2327	714	1188	231	193	1		

- Molecule 25 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Ad	53	Total	C	H	N	O	S	0	0
			887	278	442	90	72	5		

- Molecule 26 is a protein called Small ribosomal subunit protein eS17.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	AR	105	Total	C	H	N	O	S	0	0
			1768	538	910	164	151	5		

- Molecule 27 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	AP	124	Total	C	H	N	O	S	0	0
			2136	659	1099	198	173	7		

- Molecule 28 is a protein called Small ribosomal subunit protein eS19.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	AT	141	Total	C	H	N	O	S	0	0
			2236	690	1135	212	196	3		

- Molecule 29 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	AZ	74	Total	C	H	N	O	S	0	0
			1243	380	649	110	103	1		

- Molecule 30 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	Ac	64	Total	C	H	N	O	S	0	0
			1041	308	535	102	94	2		

- Molecule 31 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	AD	227	Total	C	H	N	O	S	0	0
			3622	1125	1857	317	315	8		

- Molecule 32 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	AF	191	Total	C	H	N	O	S	0	0
			3067	943	1558	286	273	7		

- Molecule 33 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	AQ	141	Total	C	H	N	O	S	0	0
			2316	715	1192	212	194	3		

- Molecule 34 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	CO	199	Total	C	H	N	O	S	0	0
			3410	1053	1776	319	257	5		

- Molecule 35 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	CL	204	Total	C	H	N	O	S	0	0
			3406	1032	1757	343	270	4		

- Molecule 36 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	CV	129	Total	C	H	N	O	S	0	0
			1999	613	1030	182	169	5		

- Molecule 37 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	CM	139	Total	C	H	N	O	S	0	0
			2348	730	1209	218	183	8		

- Molecule 38 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	Ca	147	Total	C	H	N	O	S	0	0
			2372	736	1210	237	186	3		

- Molecule 39 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	CN	203	Total	C	H	N	O	S	0	0
			3448	1072	1747	359	266	4		

- Molecule 40 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	CI	202	Total	C	H	N	O	S	0	0
			3300	1037	1666	314	269	14		

- Molecule 41 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	CD	289	Total	C	H	N	O	S	0	0
			4723	1483	2370	429	427	14		

- Molecule 42 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	CQ	187	Total	C	H	N	O	S	0	0
			3142	944	1629	314	250	5		

- Molecule 43 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	CA	255	Total	C	H	N	O	S	0	0
			4008	1225	2051	399	327	6		

- Molecule 44 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	CS	175	Total	C	H	N	O	S	0	0
			2938	925	1485	283	235	10		

- Molecule 45 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	CT	159	Total	C	H	N	O	S	0	0
			2661	823	1363	252	217	6		

- Molecule 46 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	CP	152	Total	C	H	N	O	S	0	0
			2493	771	1260	240	213	9		

- Molecule 47 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	CU	102	Total	C	H	N	O	S	0	0
			1698	535	863	147	151	2		

- Molecule 48 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	CX	121	Total	C	H	N	O	S	0	0
			2072	636	1078	187	170	1		

- Molecule 49 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	CY	133	Total	C	H	N	O	S	0	0
			2300	695	1193	225	185	2		

- Molecule 50 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	CZ	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 51 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	Cr	134	Total	C	H	N	O	S	0	0
			2247	670	1164	227	180	6		

- Molecule 52 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	Ch	123	Total	C	H	N	O	S	0	0
			2183	646	1160	206	169	2		

- Molecule 53 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	Cb	68	Total	C	H	N	O	S	0	0
			1149	344	590	122	90	3		

- Molecule 54 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	CB	394	Total	C	H	N	O	S	0	0
			6484	2024	3306	596	544	14		

- Molecule 55 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms						AltConf	Trace
55	CF	229	Total	C	H	N	O	S	0	0
			3956	1226	2046	370	305	9		

- Molecule 56 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
56	Cc	100	Total	C	H	N	O	S	0	0
			1588	492	812	136	141	7		

- Molecule 57 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
57	Cd	113	Total	C	H	N	O	S	0	0
			1910	586	979	181	162	2		

- Molecule 58 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
58	Ce	129	Total	C	H	N	O	S	0	0
			2219	672	1158	217	166	6		

- Molecule 59 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
59	Cf	109	Total	C	H	N	O	S	0	0
			1786	555	910	174	144	3		

- Molecule 60 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
60	Cg	114	Total	C	H	N	O	S	0	0
			1905	566	999	187	147	6		

- Molecule 61 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
61	Ci	103	Total	C	H	N	O	S	0	0
			1765	526	925	178	130	6		

- Molecule 62 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
62	Cj	87	Total	C	H	N	O	S	0	0
			1470	440	754	159	112	5		

- Molecule 63 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
63	Ck	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

- Molecule 64 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
64	Cl	48	Total	C	H	N	O	S	0	0
			900	273	469	96	61	1		

- Molecule 65 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
65	CC	360	Total	C	H	N	O	S	0	0
			5900	1805	3033	573	476	13		

- Molecule 66 is a protein called Ubiquitin-ribosomal protein eL40 fusion protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
66	Cm	51	Total	C	H	N	O	S	0	0
			875	260	456	88	65	6		

- Molecule 67 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
67	Cn	25	Total	C	H	N	O	S	0	0
			529	145	289	64	28	3		

- Molecule 68 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
68	Cp	90	Total	C	H	N	O	S	0	0
			1458	442	755	135	119	7		

- Molecule 69 is a protein called Ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
69	Co	101	Total	C	H	N	O	S	0	0
			1720	517	893	170	134	6		

- Molecule 70 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
70	CJ	168	Total	C	H	N	O	S	0	0
			2732	853	1383	251	239	6		

- Molecule 71 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
71	CH	191	Total	C	H	N	O	S	0	0
			3129	960	1603	285	275	6		

- Molecule 72 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
72	CE	252	Total	C	H	N	O	S	0	0
			4253	1307	2217	387	338	4		

- Molecule 73 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
73	CG	246	Total	C	H	N	O	S	0	0
			4093	1256	2120	379	334	4		

- Molecule 74 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
74	A5	3875	Total	C	H	N	O	P	0	0
			122271	36174	40870	14718	26635	3874		

- Molecule 75 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
75	A7	121	Total	C	H	N	O	P	0	0
			3884	1150	1306	458	850	120		

- Molecule 76 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
76	A8	156	Total	C	H	N	O	P	0	0
			4996	1480	1682	585	1094	155		

- Molecule 77 is a RNA chain called tRNA.



Mol	Chain	Residues	Atoms						AltConf	Trace
77	Cw	77	Total	C	H	N	O	P	0	0
			2481	732	837	298	537	77		

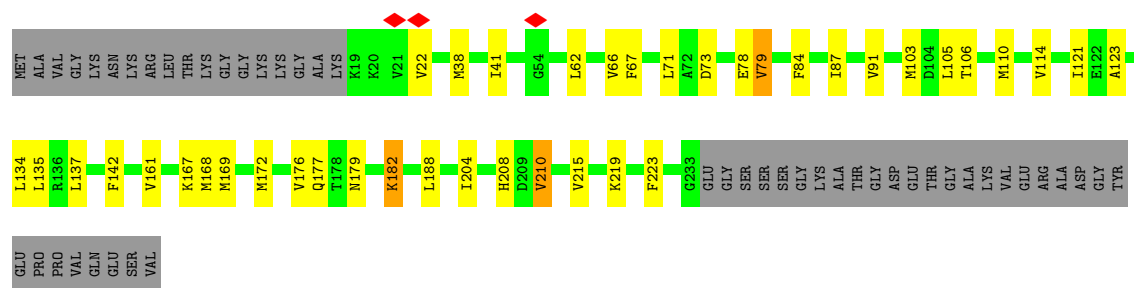
- Molecule 78 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
78	Dd	7	Total	C	H	N	O	P	0	0
			209	63	69	14	56	7		

- Molecule 79 is water.

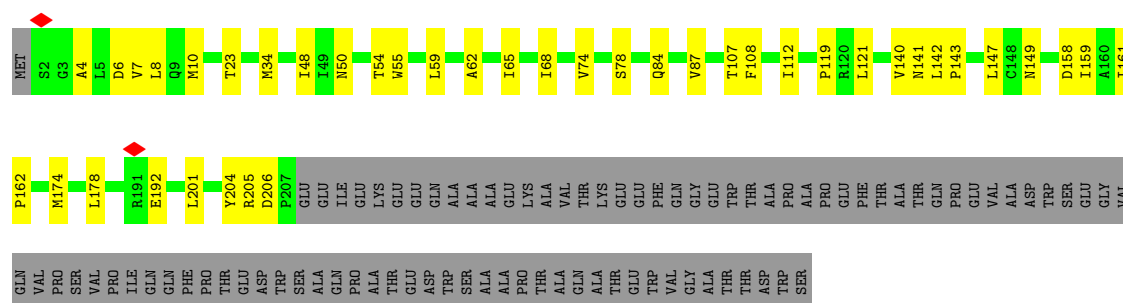
Mol	Chain	Residues	Atoms		AltConf
79	B2	2	Total	O	0
			2	2	
79	Cw	4	Total	O	0
			4	4	
79	Dd	1	Total	O	0
			1	1	





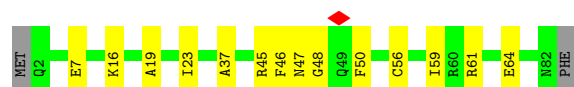
- Molecule 6: 40S ribosomal protein SA

Chain AA: 56% 14% 30%



- Molecule 7: 40S ribosomal protein S21

Chain AV: 81% 17% 2%



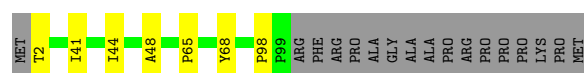
- Molecule 8: 40S ribosomal protein S24

Chain AY: 81% 13% 5%



- Molecule 9: 40S ribosomal protein S26

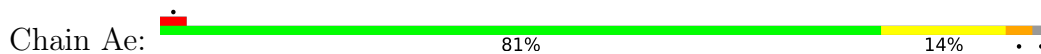
Chain Aa: 79% 6% 15%



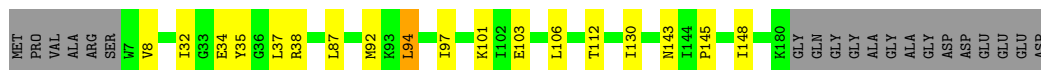
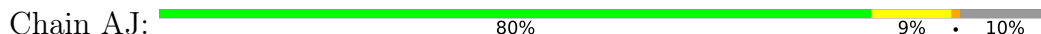
- Molecule 10: 40S ribosomal protein S27

Chain Ab: 92% 7% 1%

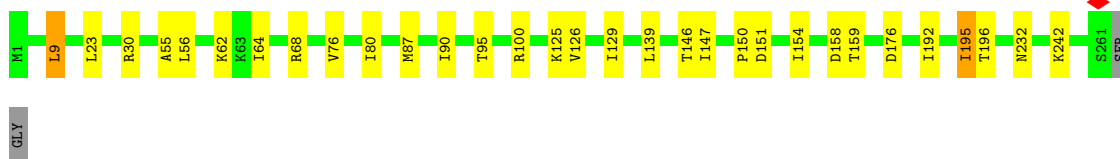
- Molecule 11: FAU ubiquitin like and ribosomal protein S30 fusion



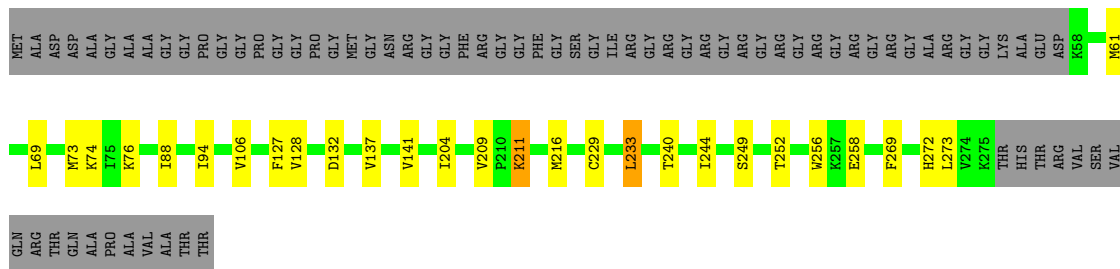
- Molecule 12: Small ribosomal subunit protein uS4



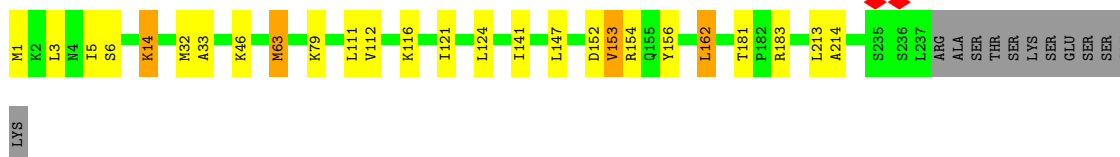
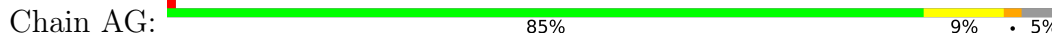
- Molecule 13: 40S ribosomal protein S4, X isoform



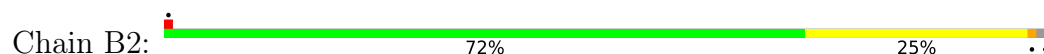
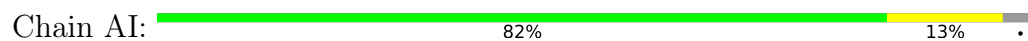
- Molecule 14: 40S ribosomal protein S2



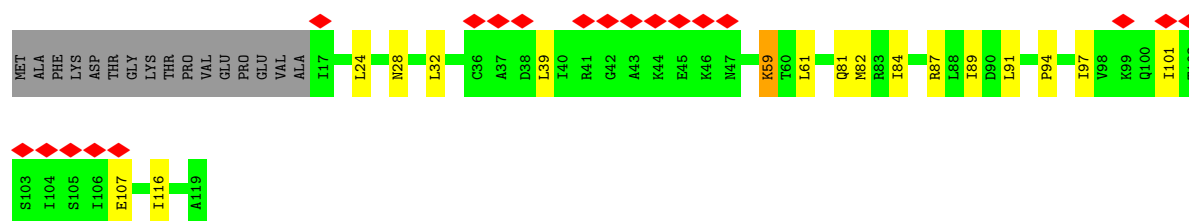
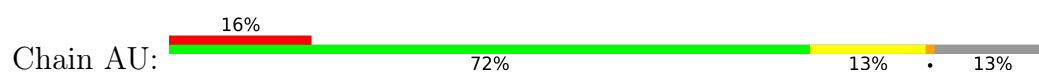
- Molecule 15: 40S ribosomal protein S6



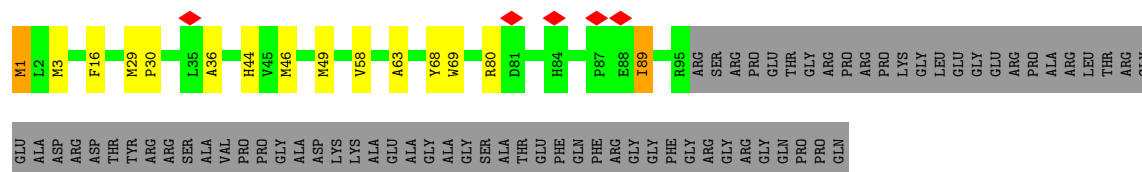
- Chain AH:  78% 13% 8%



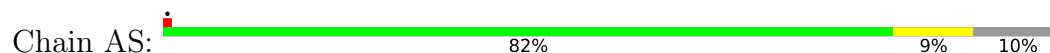




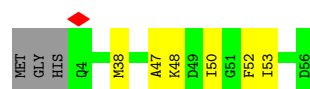
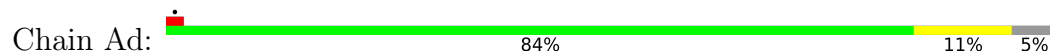
- Molecule 23: 40S ribosomal protein S10



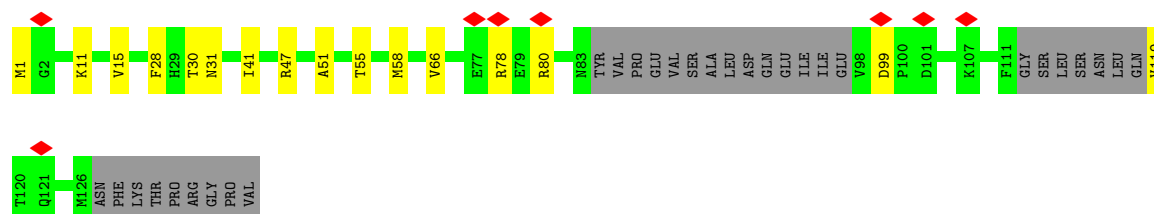
- Molecule 24: Small ribosomal subunit protein uS13



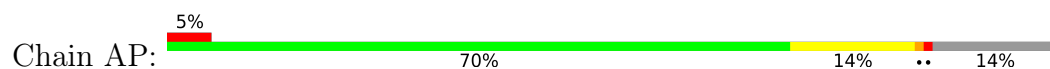
- Molecule 25: Small ribosomal subunit protein uS14

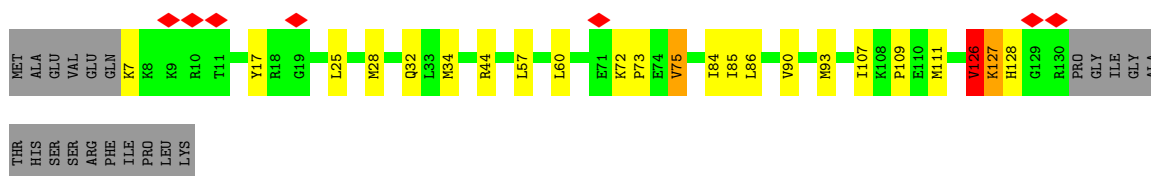


- Molecule 26: Small ribosomal subunit protein eS17



- Molecule 27: 40S ribosomal protein S15





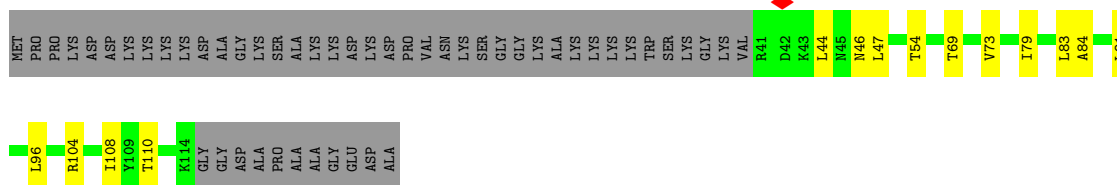
- Molecule 28: Small ribosomal subunit protein eS19

Chain AT: 82% 14% ..



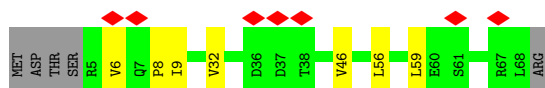
- Molecule 29: 40S ribosomal protein S25

Chain AZ: 48% 11% 41%



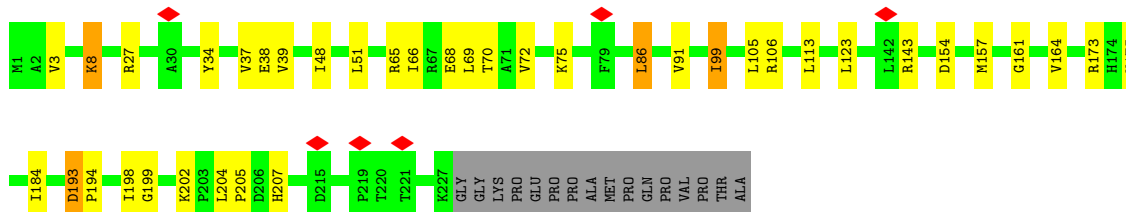
- Molecule 30: 40S ribosomal protein S28

Chain Ac: 10% 83% 10% 7%



- Molecule 31: 40S ribosomal protein S3

Chain AD: 77% 14% 7%

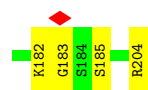


- Molecule 32: Small ribosomal subunit protein uS7

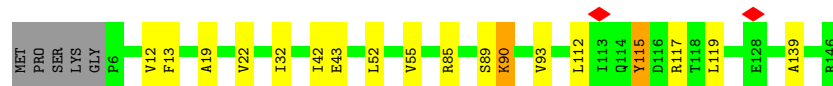
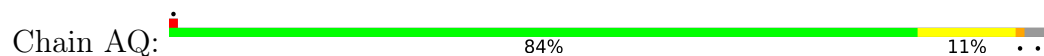
Chain AF: 81% 12% 6%



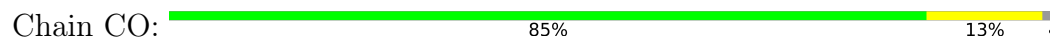




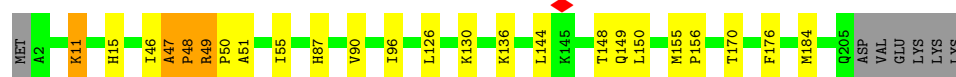
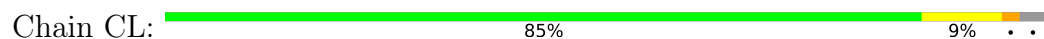
- Molecule 33: Small ribosomal subunit protein uS9



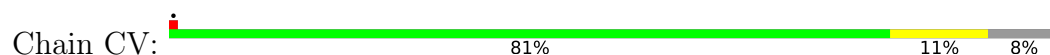
- Molecule 34: 60S ribosomal protein L13a



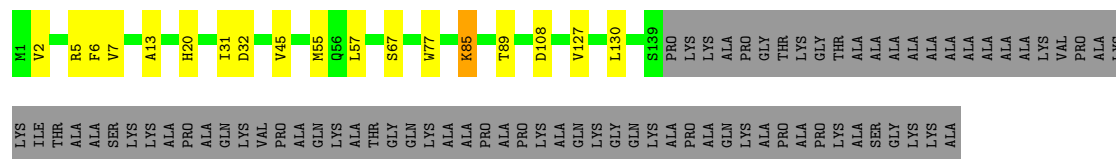
- Molecule 35: 60S ribosomal protein L13



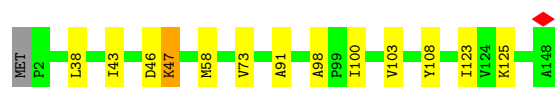
- Molecule 36: Large ribosomal subunit protein uL14



- Molecule 37: 60S ribosomal protein L14

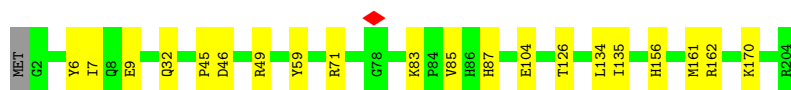


- Molecule 38: 60S ribosomal protein L27a




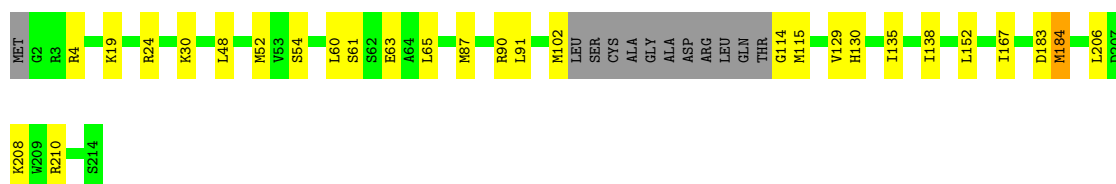
- Molecule 39: Ribosomal protein L15

Chain CN:  90% 10%



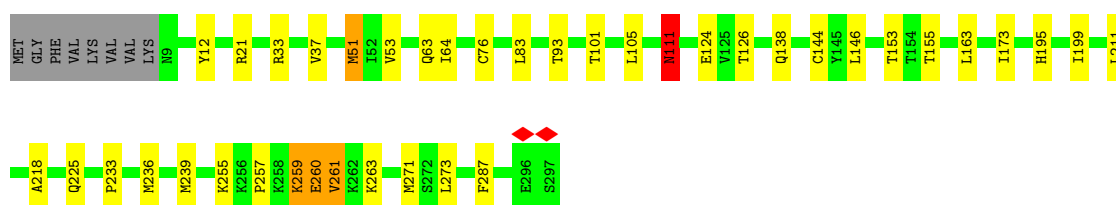
- Molecule 40: 60S ribosomal protein L10-like

Chain CI:  81% 13% 6%




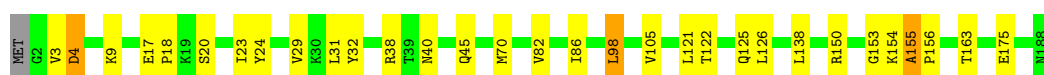
- Molecule 41: 60S ribosomal protein L5

Chain CD:  84% 12% ..



- Molecule 42: 60S ribosomal protein L18

Chain CQ:  83% 15% ..




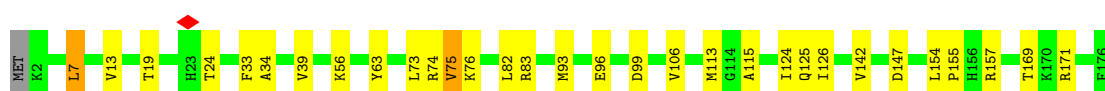
- Molecule 43: Large ribosomal subunit protein uL2

Chain CA:  89% 10% .



- Molecule 44: 60S ribosomal protein L18a

Chain CS:  82% 16% ..



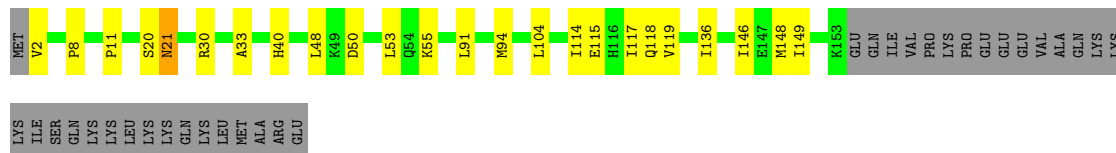
- Molecule 45: Large ribosomal subunit protein eL21

Chain CT:  91% 8%



- Molecule 46: 60S ribosomal protein L17

Chain CP:  70% 12% 17%



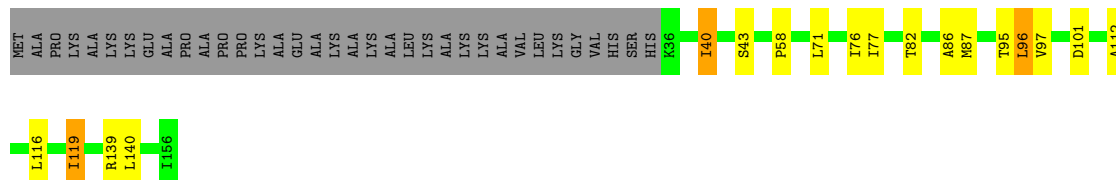
- Molecule 47: 60S ribosomal protein L22

Chain CU:  69% 11% 20%




- Molecule 48: 60S ribosomal protein L23a

Chain CX:  66% 10% 22%



- Molecule 49: Large ribosomal subunit protein uL24

Chain CY:  85% 6% 8%

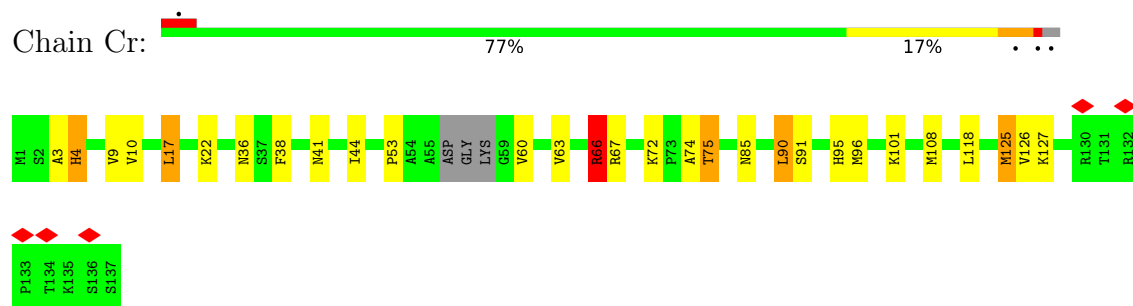


- Molecule 50: 60S ribosomal protein L27

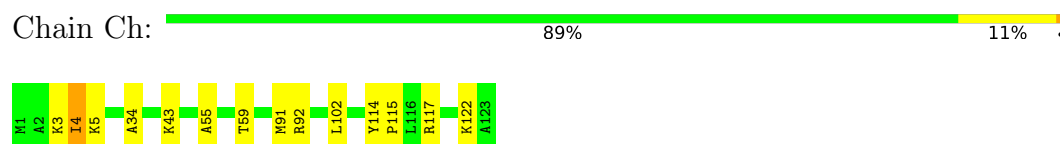
Chain CZ:  92% 7%



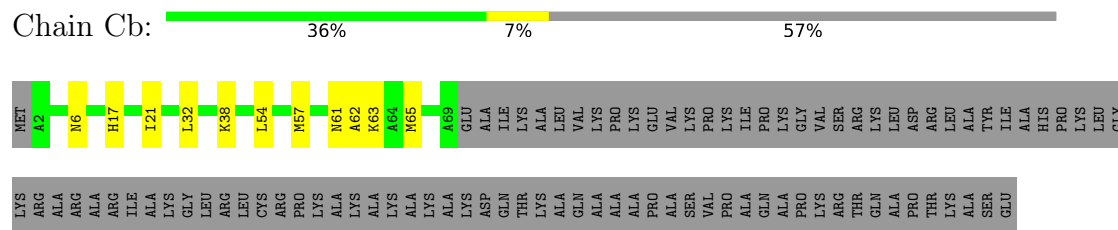
- Molecule 51: Large ribosomal subunit protein eL28



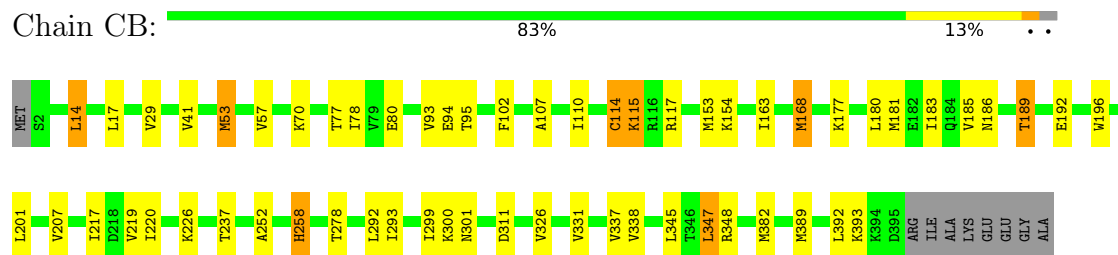
- Molecule 52: 60S ribosomal protein L35



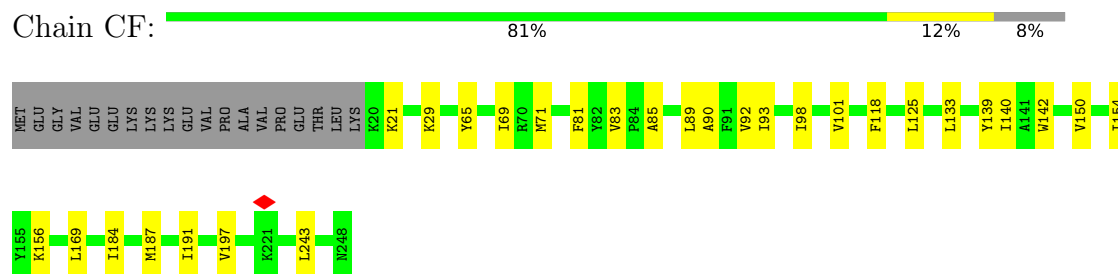
- Molecule 53: 60S ribosomal protein L29



- Molecule 54: 60S ribosomal protein L3



- Molecule 55: 60S ribosomal protein L7



- Molecule 56: Large ribosomal subunit protein eL30





- Molecule 57: Large ribosomal subunit protein eL31

Chain Cd: 84% 6% 10%



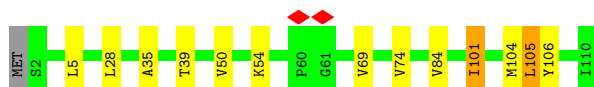
- Molecule 58: Ribosomal protein L32

Chain Ce: 79% 16% 5%



- Molecule 59: 60S ribosomal protein L35a

Chain Cf: 87% 10% 3%



- Molecule 60: Large ribosomal subunit protein eL34

Chain Cg: 89% 8% 3%



- Molecule 61: 60S ribosomal protein L36

Chain Ci: 87% 11% 2%




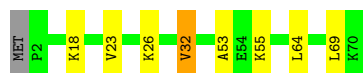
- Molecule 62: Ribosomal protein L37

Chain Cj: 71% 19% 10%




- Molecule 63: Large ribosomal subunit protein eL38

Chain Ck:  87% 10% ..



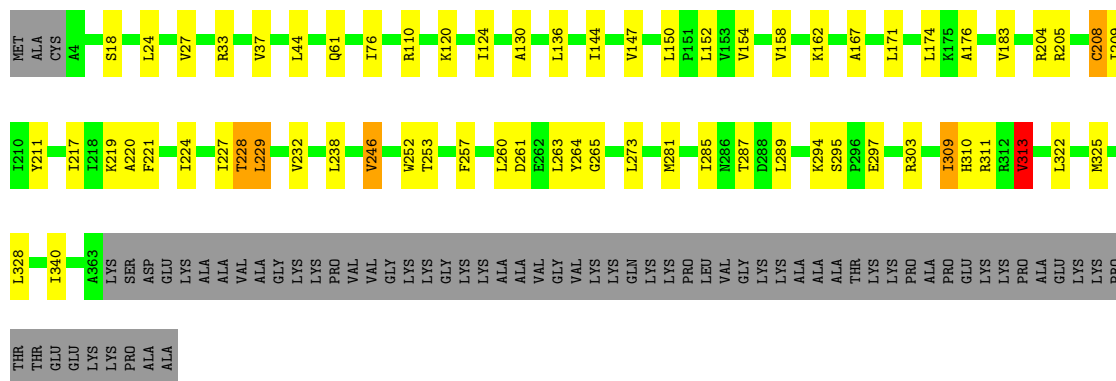
- Molecule 64: 60S ribosomal protein L39

Chain Cl:  82% 10% • 6%




- Molecule 65: 60S ribosomal protein L4

Chain CC:  69% 14% • 16%



- Molecule 66: Ubiquitin-ribosomal protein eL40 fusion protein

Chain Cm:  75% 23% •




- Molecule 67: 60S ribosomal protein L41

Chain Cn:  96% •




- Molecule 68: Large ribosomal subunit protein eL43

Chain Cp:  85% 12% ..




- Molecule 69: Ribosomal protein L36a

Chain Co:  81% 13% • 5%



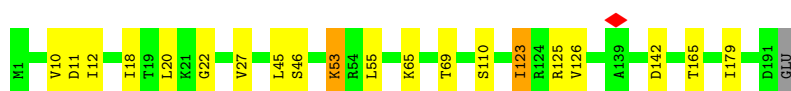
- Molecule 70: Large ribosomal subunit protein uL5

Chain CJ:  80% 13% • 6%



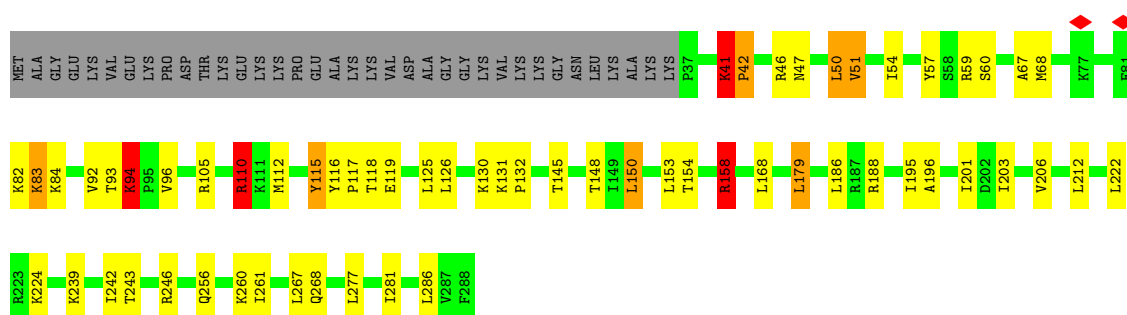
- Molecule 71: 60S ribosomal protein L9

Chain CH:  89% 9% ••




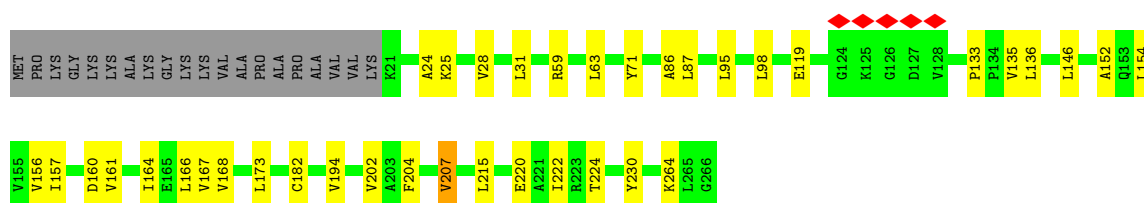
- Molecule 72: 60S ribosomal protein L6

Chain CE:  66% 18% •• 12%




- Molecule 73: 60S ribosomal protein L7a

Chain CG:  78% 14% 8%



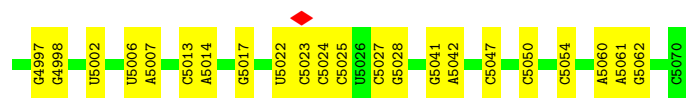
- Molecule 74: 28S ribosomal RNA

Chain A5:  72% 24% ••

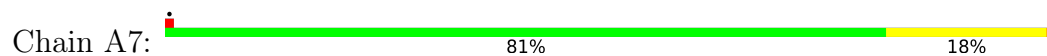
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G2001	G1854	A1742	G1592	A1420	U1297	A	C	C928	C668	C486	A305	G164	U13
G2003	G1855	U1428	U1596	U1429	C1301	G	G1046	A929	G669	G487	A306	G170	C14
U2004	G1869	C1436	G1597	C1437	U1302	U	G1051	C931	C678	G488	C309	U171	A15
U2008	A1874	U1440	C1612	U1441	A1303	U	G1052	A932	C678	C489	G310	C172	G19
A2009	C1881	U1445	G1613	U1446	C1304	C	C	C934	C685	C490	G315	U177	U20
A2010	U1756	U1446	C1614	U1447	C1308	U	C	A935	A686	G497	U316	G177	G21
C2016	U1757	U1447	G1624	U1448	U1317	C	C	U937	U687	G498	C322	U184	A25
G2024	G1758	U1448	G1625	U1449	C1318	U	C	U938	U688	G499	U333	U185	A39
A2025	U1759	U1449	G1626	U1450	A1322	U	C	C939	U689	G500	A334	G186	G40
A2026	G1761	U1450	A1630	U1451	U1326	G	U1063	U945	C690	G501	A336	U187	A44
G2046	G1764	U1451	A1631	U1452	C1344	C1232	C	U946	C696	C502	C340	A197	G48
A2047	A1765	U1452	A1632	U1453	U1344	G1233	C	C947	G697	C503	C350	U200	U49
U2048	G1769	U1453	A1633	U1454	C1344	C1233	C	G952	G704	G504	U357	U200	G55
C2051	U1776	U1454	A1634	U1455	A1354	G1242	U1102	G955	G708	G505	C361	C201	G58
G2052	C1777	U1455	A1635	U1456	U1355	G1243	C1110	A956	C712	G506	G373	A208	A59
G2056	C1778	U1456	A1636	U1457	C1357	G1244	U	G957	G720	C507	G379	U209	A64
A2069	U1781	U1457	A1637	U1458	G1358	C1245	C	G958	G727	C508	C387	C210	A65
C2083	A1787	U1458	A1638	U1459	G1359	A	C	A960	U728	C	C391	C215	A73
C2094	U1788	U1459	A1639	U1460	U1360	A	C	G961	G729	C	C406	C216	G74
G2095	C1789	U1460	A1640	U1461	G1361	G1245	C	G962	G730	C	A407	C217	G75
A2099	G1803	U1461	A1641	U1462	C1365	C1251	G	A963	G734	C	A408	C218	A76
G2099	A1804	U1462	A1642	U1463	G1366	G	C	G964	G735	C	A409	C219	G91
A2099	A1805	U1463	A1643	U1464	C1367	U1259	C	A965	G736	C	A410	C220	A108
G2099	G1806	U1464	A1644	U1465	A1368	G1260	C	G966	G737	C	G411	C221	G109
G2099	A1807	U1465	A1645	U1466	C1369	G1261	C	G967	G741	C	G412	C222	C112
G2099	G1808	U1466	A1646	U1467	G1370	G1262	C	G968	G744	C	G413	C223	C115
G2099	A1809	U1467	A1647	U1468	A1371	G1263	C	G969	G745	C	G414	C224	G116
G2099	G1810	U1468	A1648	U1469	A1372	G1264	C	G970	G746	C	G415	C225	C117
G2099	C1812	U1469	A1649	U1470	A1373	G1265	C	G971	G747	C	G423	A235	G118
G2099	G1813	U1470	A1650	U1471	G1377	G1266	C	G972	G748	C	G431	A243	G119
G2099	A1814	U1471	A1651	U1472	C1378	G1267	C	G973	G749	C	U432	A246	G125
G2099	G1815	U1472	A1652	U1473	G1379	G1268	C	C974	G750	C	A433	C265	C136
G2099	A1816	U1473	A1653	U1474	G1380	G1269	C	U982	G890	C	C449	C276	G142
G2099	G1817	U1474	A1654	U1475	U1381	G1270	C	C983	G891	C	G450	C277	G143
G2099	A1818	U1475	A1655	U1476	A1387	G1271	C	G984	G892	C	G451	C278	G144
G2099	G1819	U1476	A1656	U1477	G1394	G1272	C	C	G893	C	G452	G280	A149
G2099	A1820	U1477	A1657	U1478	A1397	G1273	C	C	G894	C	G453	G294	U150
G2099	G1821	U1478	A1658	U1479	A1398	G1274	C	C	U911	C	G454	G294	G294
G2099	A1822	U1479	A1659	U1480	G1399	G1275	C	C	G912	C	G455	G294	G294
G2099	G1823	U1480	A1660	U1481	C1407	G1276	C	C	A917	C	G456	G294	G294
G2099	A1824	U1481	A1661	U1482	G1408	G1277	C	C	G918	C	G457	G294	G294
G2099	G1825	U1482	A1662	U1483	U1409	G1278	C	C	G919	C	G458	G294	G294
G2099	A1826	U1483	A1663	U1484	C	G1279	C	C	G920	C	G459	G294	G294
G2099	G1827	U1484	A1664	U1485	U	G1280	C	C	G921	C	G460	G294	G294
G2099	A1828	U1485	A1665	U1486	C	G1281	C	C	G922	C	G461	G294	G294
G2099	G1829	U1486	A1666	U1487	A1399	G1282	C	C	G923	C	G462	G294	G294
G2099	A1830	U1487	A1667	U1488	G1399	G1283	C	C	G924	C	G463	G294	G294
G2099	G1831	U1488	A1668	U1489	C1407	G1284	C	C	G925	C	G464	G294	G294
G2099	A1832	U1489	A1669	U1490	G1408	G1285	C	C	G926	C	G465	G294	G294
G2099	G1833	U1490	A1670	U1491	U	G1286	C	C	G927	C	G466	G294	G294
G2099	A1834	U1491	A1671	U1492	C	G1287	C	C	G928	C	G467	G294	G294
G2099	G1835	U1492	A1672	U1493	C	G1288	C	C	G929	C	G468	G294	G294
G2099	A1836	U1493	A1673	U1494	C	G1289	C	C	G930	C	G469	G294	G294
G2099	G1837	U1494	A1674	U1495	C	G1290	C	C	G931	C	G470	G294	G294
G2099	A1838	U1495	A1675	U1496	C	G1291	C	C	G932	C	G471	G294	G294
G2099	G1839	U1496	A1676	U1497	C	G1292	C	C	G933	C	G472	G294	G294
G2099	A1840	U1497	A1677	U1498	C	G1293	C	C	G934	C	G473	G294	G294
G2099	G1841	U1498	A1678	U1499	C	G1294	C	C	G935	C	G474	G294	G294
G2099	A1842	U1499	A1679	U1500	C	G1295	C	C	G936	C	G475	G294	G294
G2099	G1843	U1500	A1680	U1501	C	G1296	C	C	G937	C	G476	G294	G294
G2099	A1844	U1501	A1681	U1502	C	G1297	C	C	G938	C	G477	G294	G294
G2099	G1845	U1502	A1682	U1503	C	G1298	C	C	G939	C	G478	G294	G294
G2099	A1846	U1503	A1683	U1504	C	G1299	C	C	G940	C	G479	G294	G294
G2099	G1847	U1504	A1684	U1505	C	G1300	C	C	G941	C	G480	G294	G294
G2099	A1848	U1505	A1685	U1506	C	G1301	C	C	G942	C	G481	G294	G294
G2099	G1849	U1506	A1686	U1507	C	G1302	C	C	G943	C	G482	G294	G294
G2099	A1850	U1507	A1687	U1508	C	G1303	C	C	G944	C	G483	G294	G294
G2099	G1851	U1508	A1688	U1509	C	G1304	C	C	G945	C	G484	G294	G294
G2099	A1852	U1509	A1689	U1510	C	G1305	C	C	G946	C	G485	G294	G294
G2099	G1853	U1510	A1690	U1511	C	G1306	C	C	G947	C	G486	G294	G294
G2099	A1854	U1511	A1691	U1512	C	G1307	C	C	G948	C	G487	G294	G294
G2099	G1855	U1512	A1692	U1513	C	G1308	C	C	G949	C	G488	G294	G294
G2099	A1856	U1513	A1693	U1514	C	G1309	C	C	G950	C	G489	G294	G294
G2099	G1857	U1514	A1694	U1515	C	G1310	C	C	G951	C	G490	G294	G294
G2099	A1858	U1515	A1695	U1516	C	G1311	C	C	G952	C	G491	G294	G294
G2099	G1859	U1516	A1696	U1517	C	G1312	C	C	G953	C	G492	G294	G294
G2099	A1860	U1517	A1697	U1518	C	G1313	C	C	G954	C	G493	G294	G294
G2099	G1861	U1518	A1698	U1519	C	G1314	C	C	G955	C	G494	G294	G294
G2099	A1862	U1519	A1699	U1520	C	G1315	C	C	G956	C	G495	G294	G294
G2099	G1863	U1520	A1700	U1521	C	G1316	C	C	G957	C	G496	G294	G294
G2099	A1864	U1521	A1701	U1522	C	G1317	C	C	G958	C	G497	G294	G294
G2099	G1865	U1522	A1702	U1523	C	G1318	C	C	G959	C	G498	G294	G294
G2099	A1866	U1523	A1703	U1524	C	G1319	C	C	G960	C	G499	G294	G294
G2099	G1867	U1524	A1704	U1525	C	G1320	C	C	G961	C	G500	G294	G294
G2099	A1868	U1525	A1705	U1526	C	G1321	C	C	G962	C	G501	G294	G294
G2099	G1869	U1526	A1706	U1527	C	G1322	C	C	G963	C	G502	G294	G294
G2099	A1870	U1527	A1707	U1528	C	G1323	C	C	G964	C	G503	G294	G294
G2099	G1871	U1528	A1708	U1529	C	G1324	C	C	G965	C	G504	G294	G294
G2099	A1872	U1529	A1709	U1530	C	G1325	C	C	G966	C	G505	G294	G294
G2099	G1873	U1530	A1710	U1531	C	G1326	C	C	G967	C	G506	G294	G294
G2099	A1874	U1531	A1711	U1532	C	G1327	C	C	G968	C	G507	G294	G294
G2099	G1875	U1532	A1712	U1533	C	G1328	C	C	G969	C	G508	G294	G294
G2099	A1876	U1533	A1713	U1534	C	G1329	C	C	G970	C	G509	G294	G294
G2099	G1877	U1534	A1714	U1535	C	G1330	C	C	G971	C	G510	G294	G294
G2099	A1878	U1535	A1715	U1536	C	G1331	C	C	G972	C	G511	G294	G294
G2099	G1879	U1536	A1716	U1537	C	G1332	C	C	G973	C	G512	G294	G294
G2099	A1880	U1537	A1717	U1538	C	G1333	C	C	G974	C	G513	G294	G294
G2099	G1881	U1538	A1718	U1539	C	G1334	C	C	G975	C	G514	G294	G294
G2099	A1882	U1539	A1719	U1540	C	G1335	C	C	G976	C	G515	G294	G294
G2099	G1883	U1540	A1720	U1541	C	G1336	C	C	G977	C	G516	G294	G294
G2099	A1884	U1541	A1721	U1542	C	G1337	C	C	G978	C	G517	G294	G294
G2099	G1885	U1542	A1722	U1543	C	G1338	C	C	G979	C	G518	G294	G294
G2099	A1886	U1543	A1723	U1544	C	G1339	C	C	G980	C	G519	G294	G294
G2099	G1887	U1544	A1724	U1545	C	G1340	C	C	G981	C	G520	G294	G294
G2099	A1												



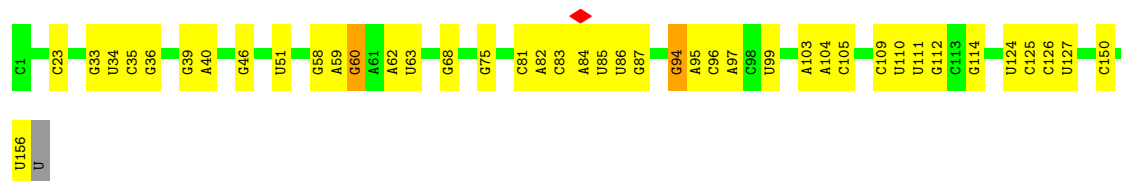
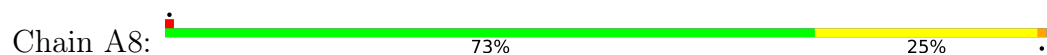




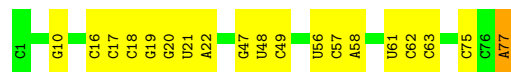
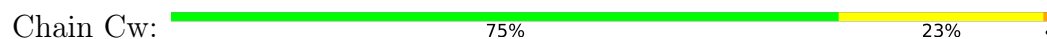
- Molecule 75: 5S ribosomal RNA



- Molecule 76: 5.8S ribosomal RNA



- Molecule 77: tRNA



- Molecule 78: mRNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	42298	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.028	Depositor
Minimum map value	-0.008	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	392.0, 392.0, 392.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.98, 0.98, 0.98	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	AO	0.25	0/960	0.62	0/1286
2	AX	0.26	0/1112	0.59	0/1485
3	AN	0.26	0/1232	0.61	0/1656
4	AL	0.21	0/1238	0.50	0/1652
5	AB	0.24	0/1774	0.57	0/2372
6	AA	0.30	0/1661	0.66	0/2259
7	AV	0.30	0/623	0.76	0/834
8	AY	0.25	0/1040	0.61	0/1382
9	Aa	0.21	0/794	0.48	0/1065
10	Ab	0.24	0/673	0.59	0/902
11	Ae	0.29	0/467	0.73	0/615
12	AJ	0.22	0/1483	0.50	0/1980
13	AE	0.23	0/2115	0.54	0/2846
14	AC	0.26	0/1728	0.61	0/2333
15	AG	0.23	0/1946	0.49	0/2590
16	AH	0.28	0/1471	0.65	0/1969
17	AW	0.26	0/1051	0.60	0/1406
18	AI	0.25	0/1672	0.61	0/2228
19	B2	0.15	0/42050	0.37	10/65520 (0.0%)
20	CW	0.26	0/979	0.60	0/1295
21	Ag	0.22	0/2389	0.49	0/3249
22	AU	0.26	0/827	0.58	0/1110
23	AK	0.35	0/823	0.76	2/1111 (0.2%)
24	AS	0.24	0/1157	0.58	0/1548
25	Ad	0.27	0/455	0.61	0/603
26	AR	0.27	0/866	0.60	1/1154 (0.1%)
27	AP	0.25	0/1056	0.58	0/1406
28	AT	0.23	0/1119	0.56	0/1499
29	AZ	0.25	0/600	0.56	0/805
30	Ac	0.22	0/508	0.55	0/680
31	AD	0.29	0/1793	0.57	0/2414
32	AF	0.22	0/1531	0.50	0/2059
33	AQ	0.26	0/1142	0.54	0/1528
34	CO	0.30	0/1666	0.64	0/2228

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	CL	0.32	1/1680 (0.1%)	0.65	0/2249
36	CV	0.26	0/983	0.61	0/1319
37	CM	0.24	0/1161	0.59	0/1552
38	Ca	0.23	0/1191	0.61	0/1591
39	CN	0.25	0/1746	0.52	0/2338
40	CI	0.32	0/1673	0.76	3/2233 (0.1%)
41	CD	0.29	0/2398	0.66	5/3210 (0.2%)
42	CQ	0.27	0/1537	0.64	0/2052
43	CA	0.25	0/1995	0.61	2/2674 (0.1%)
44	CS	0.28	0/1493	0.70	2/2003 (0.1%)
45	CT	0.25	0/1326	0.58	0/1770
46	CP	0.26	0/1259	0.56	0/1689
47	CU	0.23	0/849	0.57	0/1137
48	CX	0.28	0/1011	0.61	0/1356
49	CY	0.21	0/1124	0.49	0/1494
50	CZ	0.22	0/1130	0.50	0/1507
51	Cr	0.35	0/1098	0.89	1/1467 (0.1%)
52	Ch	0.25	0/1031	0.62	2/1361 (0.1%)
53	Cb	0.27	0/569	0.64	0/750
54	CB	0.25	0/3246	0.62	0/4345
55	CF	0.25	0/1945	0.58	0/2589
56	Cc	0.30	0/787	0.65	0/1057
57	Cd	0.24	0/946	0.60	0/1272
58	Ce	0.25	0/1079	0.60	0/1439
59	Cf	0.28	0/895	0.68	0/1198
60	Cg	0.29	0/916	0.64	1/1220 (0.1%)
61	Ci	0.26	0/851	0.61	0/1125
62	Cj	0.29	0/731	0.62	0/966
63	Ck	0.23	0/575	0.51	0/761
64	Cl	0.28	0/441	0.62	0/583
65	CC	0.28	0/2921	0.67	1/3924 (0.0%)
66	Cm	0.26	0/425	0.63	0/564
67	Cn	0.17	0/241	0.44	0/305
68	Cp	0.25	0/713	0.60	0/946
69	Co	0.30	0/840	0.69	0/1107
70	CJ	0.27	0/1372	0.58	0/1836
71	CH	0.23	0/1545	0.54	0/2077
72	CE	0.35	0/2076	0.81	6/2778 (0.2%)
73	CG	0.25	0/2006	0.55	0/2697
74	A5	0.15	0/90934	0.38	6/141664 (0.0%)
75	A7	0.14	0/2880	0.32	0/4489
76	A8	0.16	0/3701	0.38	0/5766
77	Cw	0.13	0/1836	0.28	0/2859

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	Dd	0.15	0/153	0.36	0/234
All	All	0.20	1/231310 (0.0%)	0.47	42/340622 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	AL	0	1
7	AV	0	2
11	Ae	0	1
12	AJ	0	1
20	CW	0	2
22	AU	0	1
23	AK	0	1
34	CO	0	1
40	CI	0	1
42	CQ	0	2
51	Cr	0	2
54	CB	0	2
59	Cf	0	1
62	Cj	0	2
70	CJ	0	2
72	CE	0	9
74	A5	1	0
All	All	1	31

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	CL	11	LYS	C-N	7.17	1.42	1.33

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	CI	114	GLY	CA-C-N	10.87	140.11	123.05
40	CI	114	GLY	C-N-CA	10.87	140.11	123.05
74	A5	2097	U	O4'-C1'-N1	8.32	120.69	108.20
74	A5	2097	U	N1-C1'-C2'	8.19	126.28	114.00
74	A5	4942	C	N1-C1'-C2'	7.84	125.77	114.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
74	A5	2126	G	C1'

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	AJ	38	ARG	Sidechain
4	AL	151	THR	Peptide
7	AV	48	GLY	Peptide
7	AV	61	ARG	Sidechain
11	Ae	46	VAL	Peptide

## 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	AO	948	973	976	14	0
2	AX	1094	1163	1164	13	0
3	AN	1208	1294	1294	7	0
4	AL	1216	1279	1280	6	0
5	AB	1747	1820	1829	24	0
6	AA	1624	1626	1632	21	0
7	AV	617	615	614	5	0
8	AY	1023	1088	1090	14	0
9	Aa	781	832	830	6	0
10	Ab	659	680	683	3	0
11	Ae	461	511	514	4	0
12	AJ	1459	1566	1575	8	0
13	AE	2073	2181	2181	18	0
14	AC	1692	1777	1783	15	0
15	AG	1923	2085	2089	16	0
16	AH	1449	1534	1537	15	0
17	AW	1034	1079	1080	6	0
18	AI	1644	1720	1718	11	0
19	B2	37619	18948	18979	47	0
20	CW	965	1023	1029	1	0
21	Ag	2334	2289	2288	16	0
22	AU	817	882	882	10	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	AK	799	822	823	9	0
24	AS	1139	1188	1191	8	0
25	Ad	445	442	442	7	0
26	AR	858	910	917	12	0
27	AP	1037	1099	1098	12	0
28	AT	1101	1135	1135	13	0
29	AZ	594	649	653	12	0
30	Ac	506	535	536	6	0
31	AD	1765	1857	1865	28	0
32	AF	1509	1558	1563	15	0
33	AQ	1124	1192	1193	8	0
34	CO	1634	1776	1779	17	0
35	CL	1649	1757	1760	15	0
36	CV	969	1030	1031	7	0
37	CM	1139	1209	1209	10	0
38	Ca	1162	1210	1213	8	0
39	CN	1701	1747	1749	17	0
40	CI	1634	1666	1671	13	0
41	CD	2353	2370	2372	23	0
42	CQ	1513	1629	1628	17	0
43	CA	1957	2051	2055	16	0
44	CS	1453	1485	1490	21	0
45	CT	1298	1363	1366	10	0
46	CP	1233	1260	1263	15	0
47	CU	835	863	865	10	0
48	CX	994	1078	1079	10	0
49	CY	1107	1193	1193	6	0
50	CZ	1107	1182	1182	9	0
51	Cr	1083	1164	1168	19	0
52	Ch	1023	1160	1160	9	0
53	Cb	559	590	590	9	0
54	CB	3178	3306	3314	31	0
55	CF	1910	2046	2048	18	0
56	Cc	776	812	812	12	0
57	Cd	931	979	980	6	0
58	Ce	1061	1158	1159	12	0
59	Cf	876	910	912	8	0
60	Cg	906	999	999	4	0
61	Ci	840	925	929	9	0
62	Cj	716	754	750	9	0
63	Ck	569	637	637	4	0
64	Cl	431	469	469	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
65	CC	2867	3033	3039	43	0
66	Cm	419	456	452	5	0
67	Cn	240	289	289	1	0
68	Cp	703	755	755	8	0
69	Co	827	893	892	6	0
70	CJ	1349	1383	1381	12	0
71	CH	1526	1603	1605	10	0
72	CE	2036	2217	2222	32	0
73	CG	1973	2120	2128	25	0
74	A5	81401	40870	40887	101	0
75	A7	2578	1306	1306	6	0
76	A8	3314	1682	1683	3	0
77	Cw	1644	837	837	1	0
78	Dd	140	69	71	0	0
79	B2	2	0	0	0	0
79	Cw	4	0	0	0	0
79	Dd	1	0	0	0	0
All	All	214885	156643	156842	891	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 2.

The worst 5 of 891 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)
74:A5:3653:A:N6	74:A5:3691:G:C2	2.17	1.13
19:B2:191:A:H62	19:B2:208:G:H21	1.12	0.98
74:A5:664:G:N2	74:A5:667:A:C2	2.37	0.92
74:A5:3653:A:N6	74:A5:3691:G:N3	2.16	0.92
70:CJ:24:ILE:HD11	74:A5:4251:A:H62	1.37	0.87

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	AO	124/151 (82%)	106 (86%)	15 (12%)	3 (2%)	4	27
2	AX	138/143 (96%)	121 (88%)	16 (12%)	1 (1%)	18	55
3	AN	148/151 (98%)	127 (86%)	19 (13%)	2 (1%)	9	39
4	AL	143/158 (90%)	123 (86%)	18 (13%)	2 (1%)	9	39
5	AB	213/264 (81%)	186 (87%)	23 (11%)	4 (2%)	6	32
6	AA	204/295 (69%)	177 (87%)	25 (12%)	2 (1%)	12	47
7	AV	79/83 (95%)	63 (80%)	13 (16%)	3 (4%)	2	19
8	AY	124/133 (93%)	108 (87%)	13 (10%)	3 (2%)	4	27
9	Aa	96/115 (84%)	80 (83%)	15 (16%)	1 (1%)	12	47
10	Ab	82/84 (98%)	71 (87%)	9 (11%)	2 (2%)	4	27
11	Ae	56/59 (95%)	46 (82%)	8 (14%)	2 (4%)	2	20
12	AJ	172/194 (89%)	161 (94%)	10 (6%)	1 (1%)	21	59
13	AE	259/263 (98%)	224 (86%)	30 (12%)	5 (2%)	6	32
14	AC	216/293 (74%)	199 (92%)	17 (8%)	0	100	100
15	AG	235/249 (94%)	217 (92%)	15 (6%)	3 (1%)	9	41
16	AH	177/194 (91%)	160 (90%)	13 (7%)	4 (2%)	5	28
17	AW	127/130 (98%)	111 (87%)	15 (12%)	1 (1%)	16	53
18	AI	196/208 (94%)	169 (86%)	20 (10%)	7 (4%)	2	20
20	CW	114/157 (73%)	98 (86%)	13 (11%)	3 (3%)	4	25
21	Ag	293/317 (92%)	253 (86%)	38 (13%)	2 (1%)	18	55
22	AU	101/119 (85%)	87 (86%)	13 (13%)	1 (1%)	12	47
23	AK	93/165 (56%)	67 (72%)	23 (25%)	3 (3%)	3	21
24	AS	135/152 (89%)	115 (85%)	18 (13%)	2 (2%)	8	38
25	Ad	51/56 (91%)	44 (86%)	7 (14%)	0	100	100
26	AR	99/135 (73%)	90 (91%)	9 (9%)	0	100	100
27	AP	122/145 (84%)	93 (76%)	26 (21%)	3 (2%)	4	26
28	AT	139/145 (96%)	126 (91%)	10 (7%)	3 (2%)	5	28
29	AZ	72/125 (58%)	57 (79%)	14 (19%)	1 (1%)	9	39
30	Ac	62/69 (90%)	53 (86%)	9 (14%)	0	100	100
31	AD	225/243 (93%)	185 (82%)	37 (16%)	3 (1%)	9	41

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
32	AF	189/204 (93%)	170 (90%)	19 (10%)	0	100	100
33	AQ	139/146 (95%)	120 (86%)	14 (10%)	5 (4%)	2	20
34	CO	197/203 (97%)	179 (91%)	15 (8%)	3 (2%)	8	38
35	CL	202/211 (96%)	169 (84%)	23 (11%)	10 (5%)	1	16
36	CV	127/140 (91%)	119 (94%)	7 (6%)	1 (1%)	16	53
37	CM	137/215 (64%)	121 (88%)	12 (9%)	4 (3%)	3	23
38	Ca	145/148 (98%)	120 (83%)	23 (16%)	2 (1%)	9	39
39	CN	201/204 (98%)	180 (90%)	21 (10%)	0	100	100
40	CI	198/214 (92%)	177 (89%)	21 (11%)	0	100	100
41	CD	287/297 (97%)	258 (90%)	24 (8%)	5 (2%)	7	35
42	CQ	185/188 (98%)	157 (85%)	25 (14%)	3 (2%)	7	37
43	CA	253/257 (98%)	231 (91%)	21 (8%)	1 (0%)	30	67
44	CS	173/176 (98%)	143 (83%)	27 (16%)	3 (2%)	7	35
45	CT	157/160 (98%)	143 (91%)	13 (8%)	1 (1%)	21	59
46	CP	150/184 (82%)	137 (91%)	11 (7%)	2 (1%)	9	41
47	CU	100/128 (78%)	86 (86%)	13 (13%)	1 (1%)	12	47
48	CX	119/156 (76%)	101 (85%)	15 (13%)	3 (2%)	4	26
49	CY	131/145 (90%)	118 (90%)	12 (9%)	1 (1%)	16	53
50	CZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
51	Cr	130/137 (95%)	102 (78%)	24 (18%)	4 (3%)	3	21
52	Ch	121/123 (98%)	107 (88%)	11 (9%)	3 (2%)	4	26
53	Cb	66/159 (42%)	59 (89%)	7 (11%)	0	100	100
54	CB	392/403 (97%)	355 (91%)	32 (8%)	5 (1%)	9	41
55	CF	227/248 (92%)	208 (92%)	17 (8%)	2 (1%)	14	49
56	Cc	98/115 (85%)	90 (92%)	7 (7%)	1 (1%)	12	47
57	Cd	111/125 (89%)	95 (86%)	15 (14%)	1 (1%)	14	49
58	Ce	127/135 (94%)	112 (88%)	14 (11%)	1 (1%)	16	53
59	Cf	107/110 (97%)	88 (82%)	19 (18%)	0	100	100
60	Cg	112/117 (96%)	95 (85%)	16 (14%)	1 (1%)	14	49
61	Ci	101/105 (96%)	91 (90%)	8 (8%)	2 (2%)	6	31
62	Cj	85/97 (88%)	73 (86%)	11 (13%)	1 (1%)	10	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
63	Ck	67/70 (96%)	61 (91%)	5 (8%)	1 (2%)	8	38
64	Cl	46/51 (90%)	43 (94%)	3 (6%)	0	100	100
65	CC	358/427 (84%)	298 (83%)	53 (15%)	7 (2%)	6	31
66	Cm	49/52 (94%)	45 (92%)	3 (6%)	1 (2%)	6	31
67	Cn	23/25 (92%)	23 (100%)	0	0	100	100
68	Cp	88/92 (96%)	79 (90%)	9 (10%)	0	100	100
69	Co	99/106 (93%)	81 (82%)	13 (13%)	5 (5%)	1	15
70	CJ	166/178 (93%)	154 (93%)	9 (5%)	3 (2%)	6	33
71	CH	189/192 (98%)	173 (92%)	15 (8%)	1 (0%)	24	63
72	CE	250/288 (87%)	188 (75%)	49 (20%)	13 (5%)	1	15
73	CG	244/266 (92%)	211 (86%)	30 (12%)	3 (1%)	10	43
All	All	10774/12128 (89%)	9398 (87%)	1209 (11%)	167 (2%)	10	37

5 of 167 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AN	138	ASN
7	AV	50	PHE
9	Aa	98	PRO
11	Ae	45	VAL
11	Ae	47	PRO

### 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	AO	99/119 (83%)	92 (93%)	7 (7%)	13	36
2	AX	113/115 (98%)	107 (95%)	6 (5%)	20	42
3	AN	130/131 (99%)	128 (98%)	2 (2%)	57	71
4	AL	134/142 (94%)	130 (97%)	4 (3%)	36	57
5	AB	196/231 (85%)	191 (97%)	5 (3%)	40	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	AA	172/243 (71%)	162 (94%)	10 (6%)	18	40
7	AV	65/67 (97%)	62 (95%)	3 (5%)	24	46
8	AY	108/115 (94%)	106 (98%)	2 (2%)	50	66
9	Aa	85/98 (87%)	85 (100%)	0	100	100
10	Ab	76/76 (100%)	75 (99%)	1 (1%)	61	72
11	Ae	47/48 (98%)	44 (94%)	3 (6%)	16	38
12	AJ	156/168 (93%)	151 (97%)	5 (3%)	34	56
13	AE	224/225 (100%)	222 (99%)	2 (1%)	70	77
14	AC	184/225 (82%)	172 (94%)	12 (6%)	15	38
15	AG	207/218 (95%)	200 (97%)	7 (3%)	32	55
16	AH	161/174 (92%)	153 (95%)	8 (5%)	22	43
17	AW	112/113 (99%)	107 (96%)	5 (4%)	24	47
18	AI	174/180 (97%)	166 (95%)	8 (5%)	24	46
20	CW	97/126 (77%)	97 (100%)	0	100	100
21	Ag	259/275 (94%)	253 (98%)	6 (2%)	44	64
22	AU	94/107 (88%)	89 (95%)	5 (5%)	20	42
23	AK	86/136 (63%)	82 (95%)	4 (5%)	23	45
24	AS	119/132 (90%)	117 (98%)	2 (2%)	53	68
25	Ad	47/49 (96%)	47 (100%)	0	100	100
26	AR	95/122 (78%)	93 (98%)	2 (2%)	47	65
27	AP	113/130 (87%)	108 (96%)	5 (4%)	25	47
28	AT	112/115 (97%)	107 (96%)	5 (4%)	24	47
29	AZ	66/103 (64%)	66 (100%)	0	100	100
30	Ac	57/62 (92%)	57 (100%)	0	100	100
31	AD	190/202 (94%)	183 (96%)	7 (4%)	30	51
32	AF	161/170 (95%)	154 (96%)	7 (4%)	26	48
33	AQ	117/121 (97%)	115 (98%)	2 (2%)	53	68
34	CO	171/174 (98%)	169 (99%)	2 (1%)	63	74
35	CL	170/177 (96%)	169 (99%)	1 (1%)	78	81
36	CV	100/107 (94%)	97 (97%)	3 (3%)	36	57
37	CM	118/161 (73%)	116 (98%)	2 (2%)	53	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	Ca	120/121 (99%)	117 (98%)	3 (2%)	42	62
39	CN	171/172 (99%)	165 (96%)	6 (4%)	32	54
40	CI	172/181 (95%)	164 (95%)	8 (5%)	23	45
41	CD	243/250 (97%)	233 (96%)	10 (4%)	27	49
42	CQ	164/165 (99%)	158 (96%)	6 (4%)	30	51
43	CA	197/199 (99%)	192 (98%)	5 (2%)	42	62
44	CS	156/157 (99%)	151 (97%)	5 (3%)	34	56
45	CT	139/140 (99%)	138 (99%)	1 (1%)	76	79
46	CP	133/163 (82%)	129 (97%)	4 (3%)	36	57
47	CU	92/115 (80%)	91 (99%)	1 (1%)	65	74
48	CX	109/133 (82%)	104 (95%)	5 (5%)	24	46
49	CY	123/135 (91%)	120 (98%)	3 (2%)	43	63
50	CZ	117/118 (99%)	117 (100%)	0	100	100
51	Cr	119/121 (98%)	108 (91%)	11 (9%)	8	27
52	Ch	110/110 (100%)	108 (98%)	2 (2%)	51	67
53	Cb	58/126 (46%)	56 (97%)	2 (3%)	32	55
54	CB	343/349 (98%)	325 (95%)	18 (5%)	21	43
55	CF	198/215 (92%)	193 (98%)	5 (2%)	42	62
56	Cc	85/97 (88%)	85 (100%)	0	100	100
57	Cd	102/110 (93%)	101 (99%)	1 (1%)	68	76
58	Ce	115/121 (95%)	109 (95%)	6 (5%)	21	43
59	Cf	88/89 (99%)	86 (98%)	2 (2%)	44	64
60	Cg	98/100 (98%)	95 (97%)	3 (3%)	35	56
61	Ci	87/89 (98%)	84 (97%)	3 (3%)	32	55
62	Cj	74/80 (92%)	71 (96%)	3 (4%)	27	49
63	Ck	64/65 (98%)	62 (97%)	2 (3%)	35	56
64	Cl	46/48 (96%)	42 (91%)	4 (9%)	9	29
65	CC	299/348 (86%)	286 (96%)	13 (4%)	26	48
66	Cm	47/48 (98%)	43 (92%)	4 (8%)	10	30
67	Cn	24/24 (100%)	24 (100%)	0	100	100
68	Cp	74/75 (99%)	72 (97%)	2 (3%)	39	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Co	89/94 (95%)	88 (99%)	1 (1%)	65	74
70	CJ	142/149 (95%)	137 (96%)	5 (4%)	32	54
71	CH	170/171 (99%)	164 (96%)	6 (4%)	32	54
72	CE	224/252 (89%)	211 (94%)	13 (6%)	18	40
73	CG	209/223 (94%)	204 (98%)	5 (2%)	43	63
All	All	9416/10310 (91%)	9105 (97%)	311 (3%)	34	55

5 of 311 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	CB	347	LEU
70	CJ	169	LYS
57	Cd	27	ILE
64	Cl	16	LYS
72	CE	130	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
65	CC	48	ASN
70	CJ	104	ASN
72	CE	284	HIS
27	AP	114	HIS
27	AP	103	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	B2	1752/1803 (97%)	410 (23%)	53 (3%)
74	A5	3736/4010 (93%)	878 (23%)	150 (4%)
75	A7	120/121 (99%)	18 (15%)	1 (0%)
76	A8	155/157 (98%)	39 (25%)	7 (4%)
77	Cw	76/77 (98%)	19 (25%)	0
78	Dd	6/7 (85%)	3 (50%)	0
All	All	5845/6175 (94%)	1367 (23%)	211 (3%)

5 of 1367 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	B2	3	C
19	B2	4	C
19	B2	25	A
19	B2	26	U
19	B2	33	G

5 of 211 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
74	A5	1440	U
74	A5	2260	C
74	A5	4991	U
74	A5	1481	C
74	A5	2088	A

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
74	A5	4
19	B2	1

All chain breaks are listed below:



Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	698:G	O3'	730:C	P	20.24
1	A5	3292:G	O3'	3572:G	P	18.88
1	A5	4795:C	O3'	4837:G	P	18.31
1	A5	763:C	O3'	886:C	P	18.27
1	A5	2133:C	O3'	2238:G	P	16.40

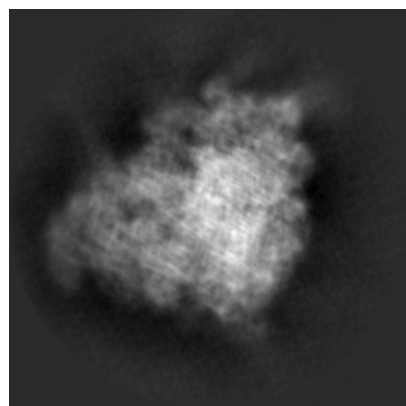
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-72483. These allow visual inspection of the internal detail of the map and identification of artifacts.

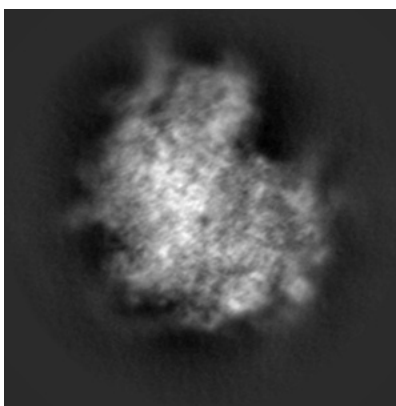
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

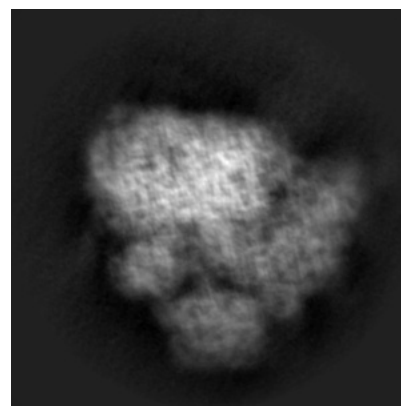
#### 6.1.1 Primary map



X

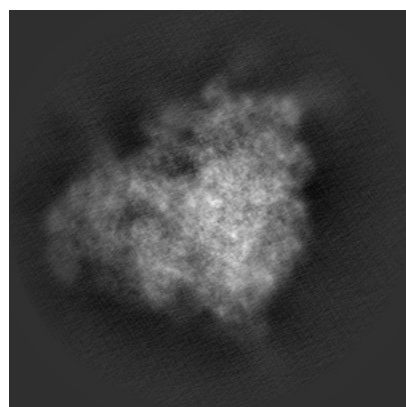


Y

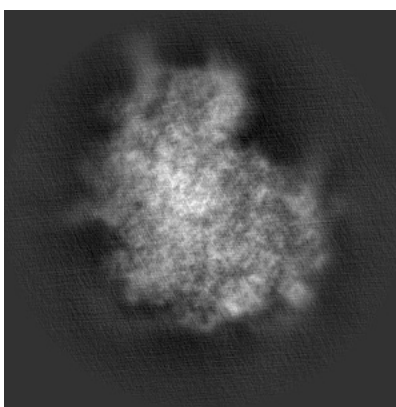


Z

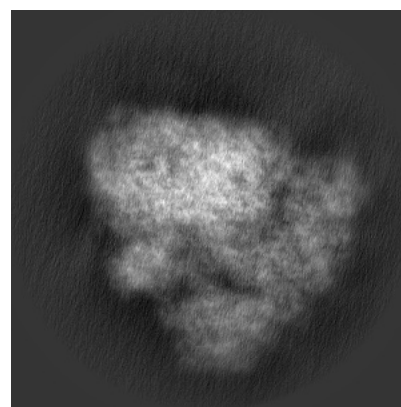
#### 6.1.2 Raw map



X



Y

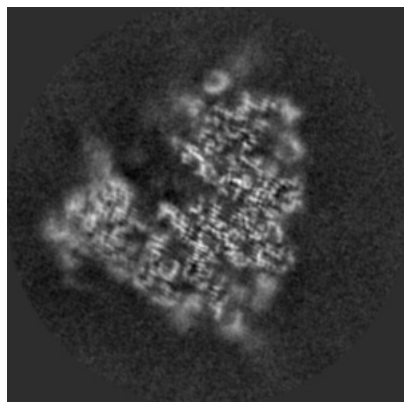


Z

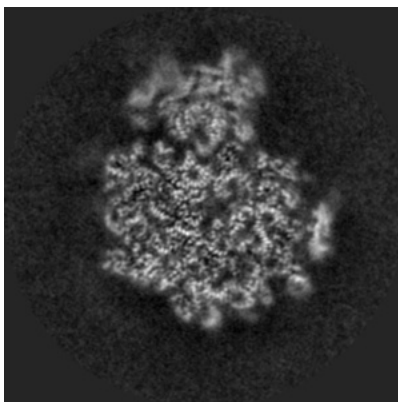
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

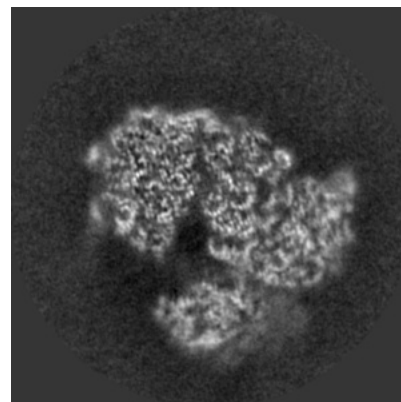
### 6.2.1 Primary map



X Index: 200

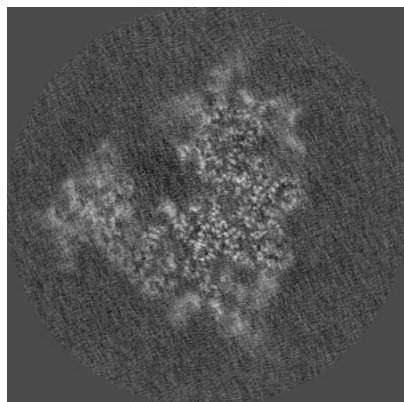


Y Index: 200

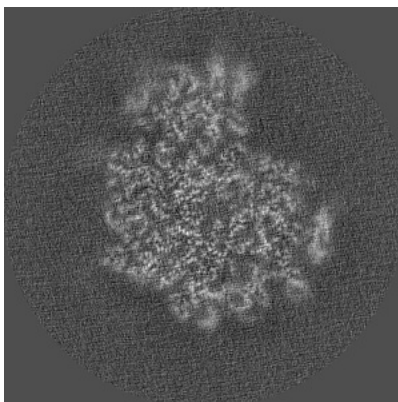


Z Index: 200

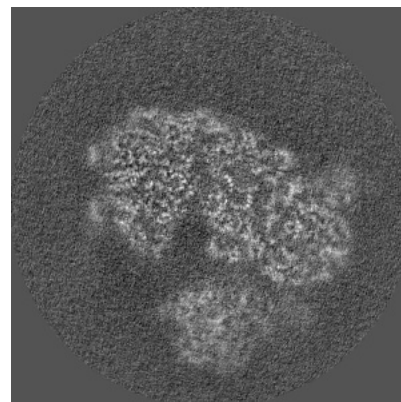
### 6.2.2 Raw map



X Index: 200



Y Index: 200

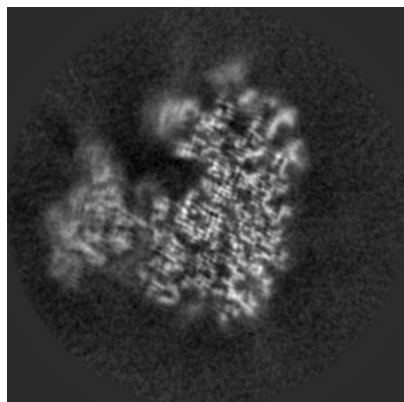


Z Index: 200

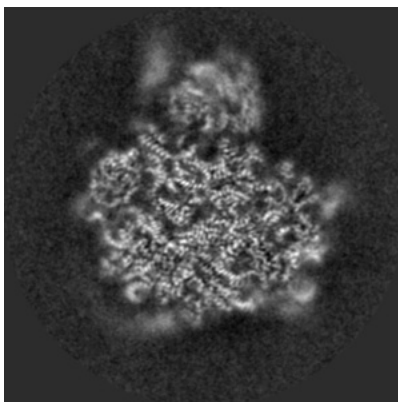
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

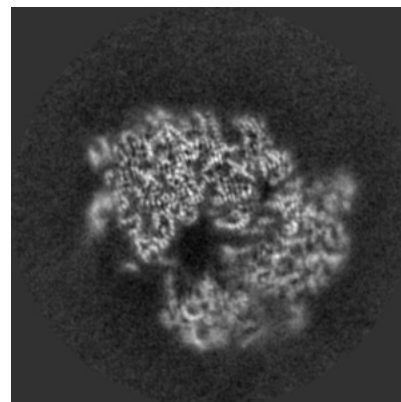
### 6.3.1 Primary map



X Index: 213

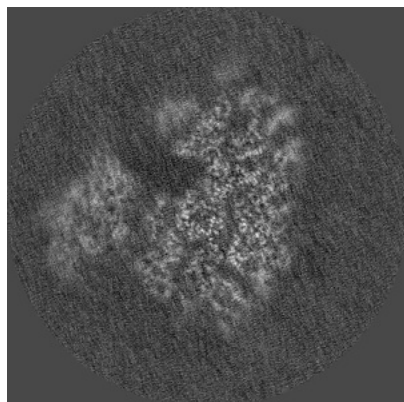


Y Index: 218

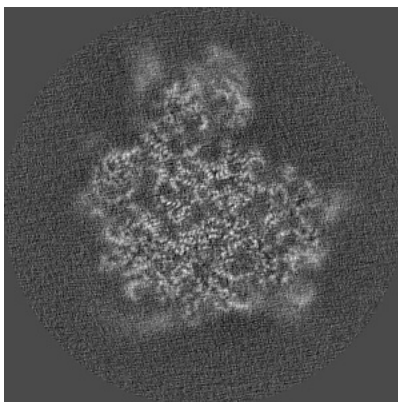


Z Index: 208

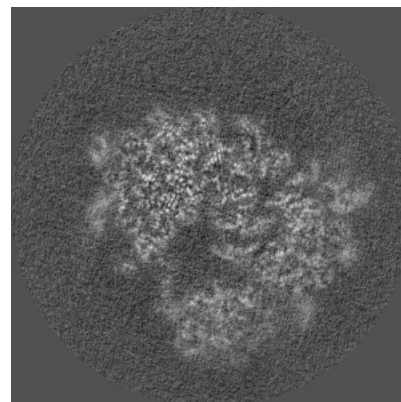
### 6.3.2 Raw map



X Index: 211



Y Index: 217



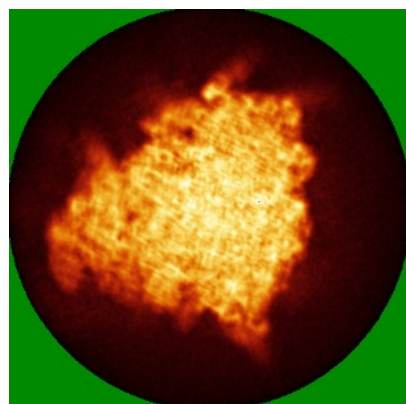
Z Index: 208

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

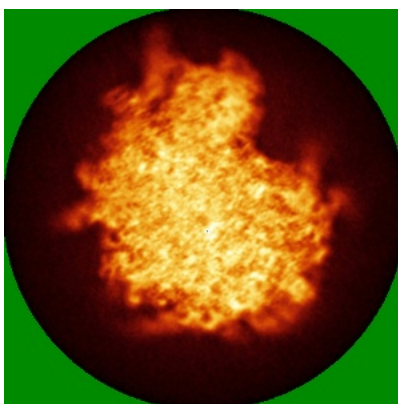


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

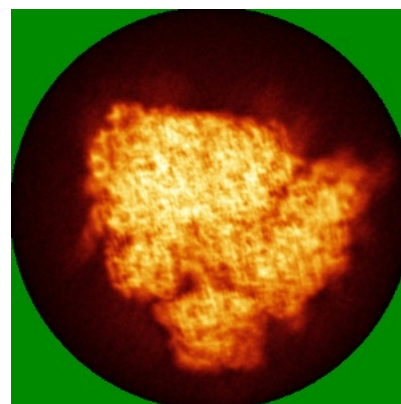
### 6.4.1 Primary map



X

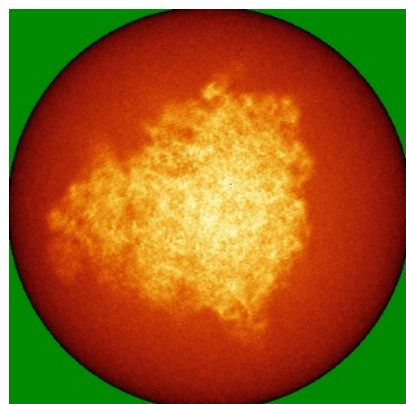


Y

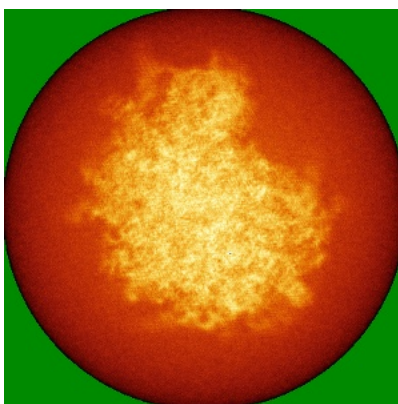


Z

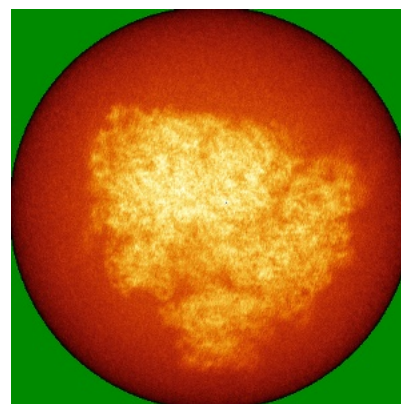
### 6.4.2 Raw map



X



Y

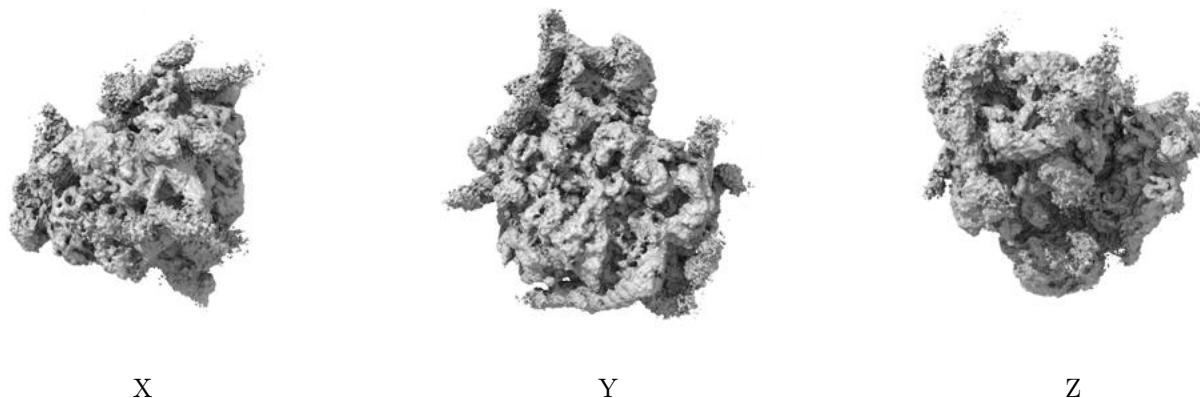


Z

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

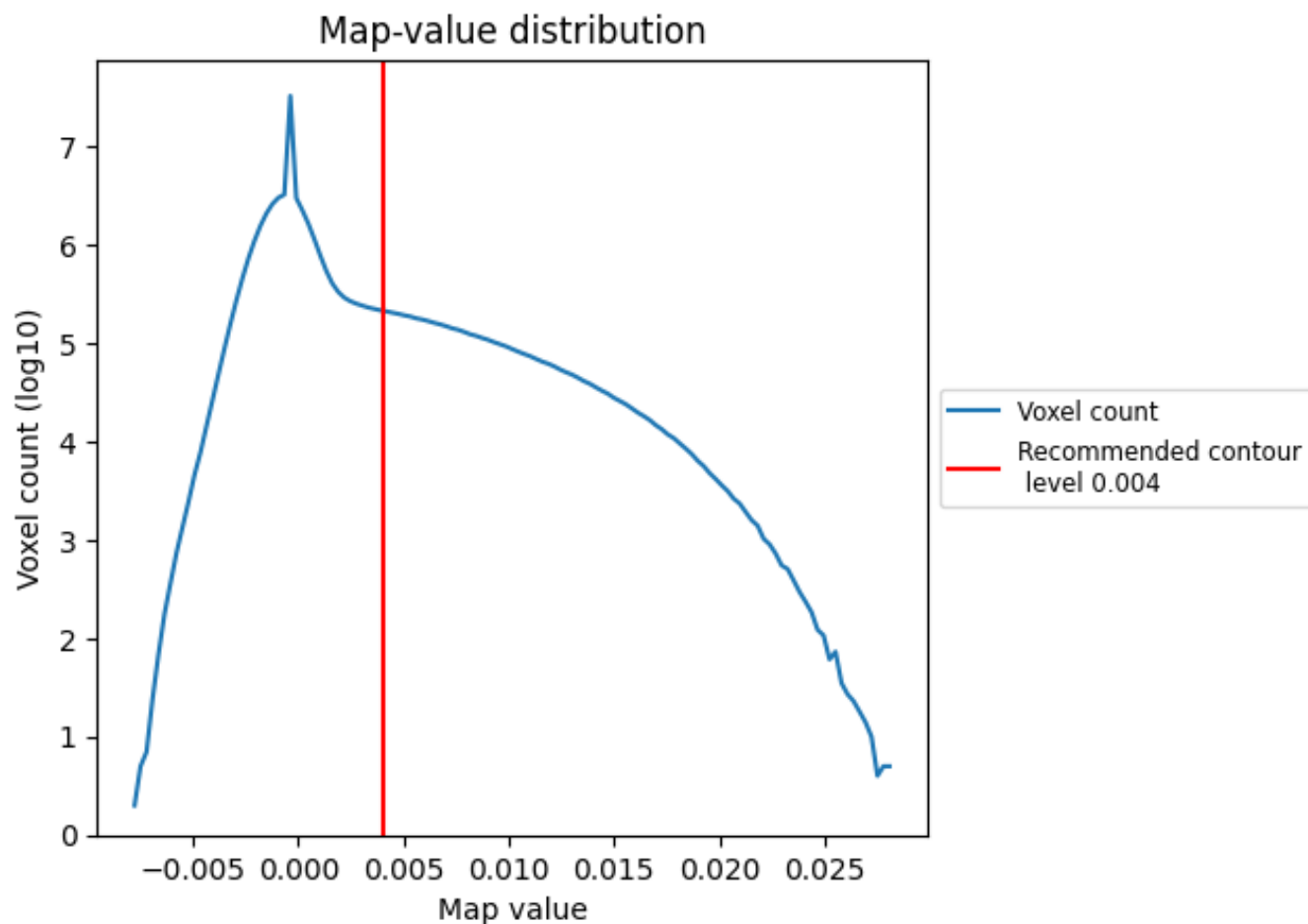
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

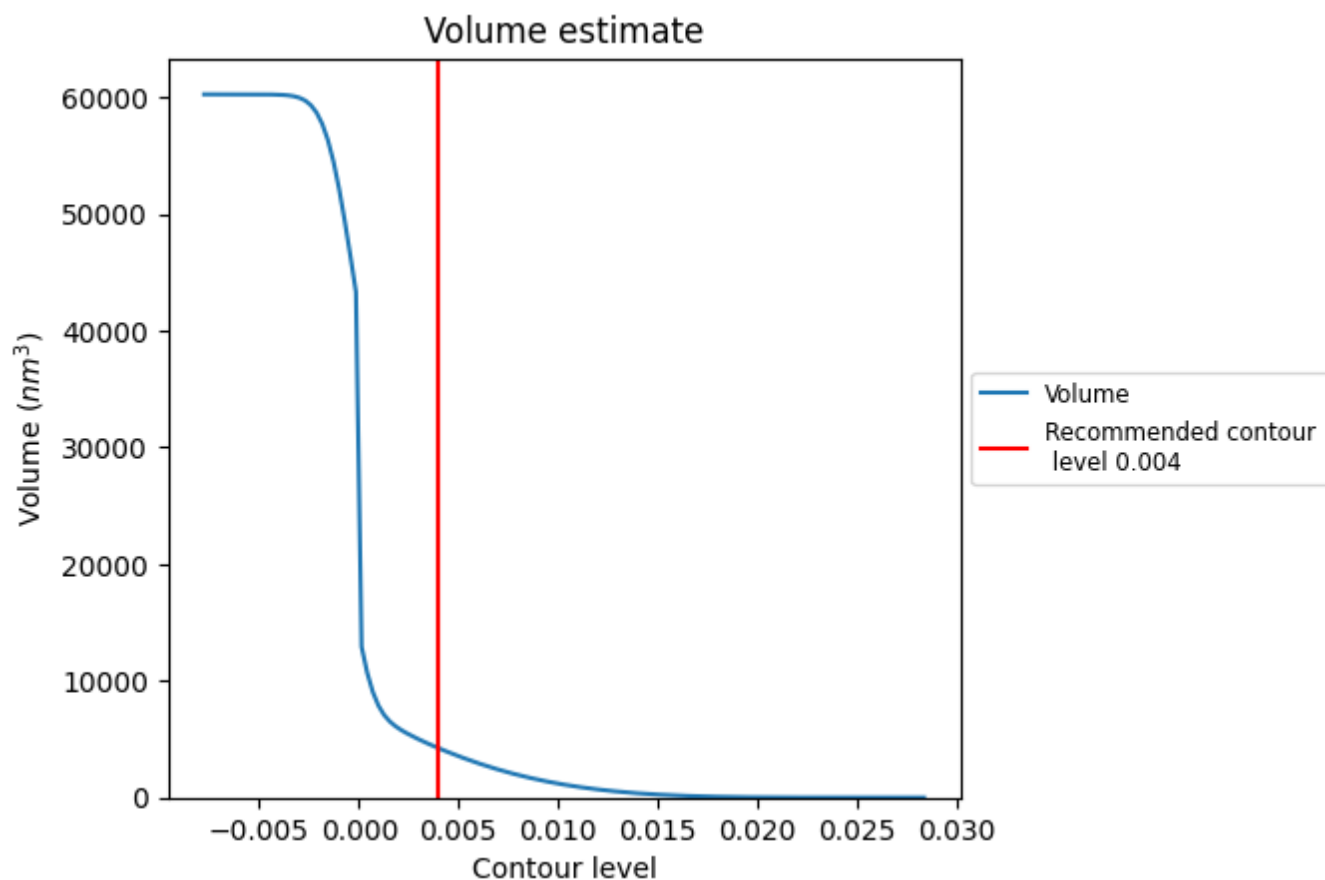
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

## 7.2 Volume estimate [i](#)

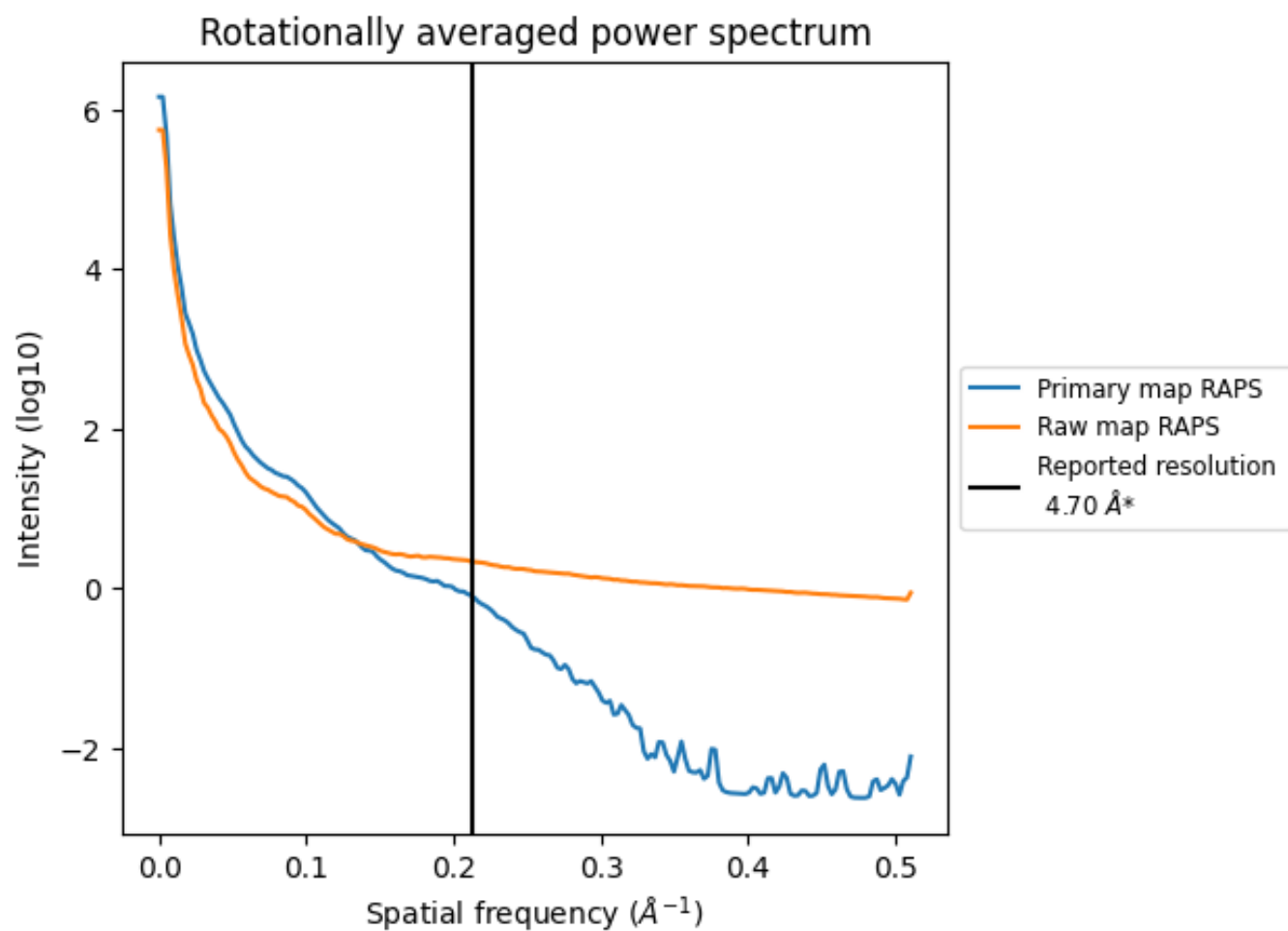


The volume at the recommended contour level is 4233 nm<sup>3</sup>; this corresponds to an approximate mass of 3824 kDa.

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 ⓘ

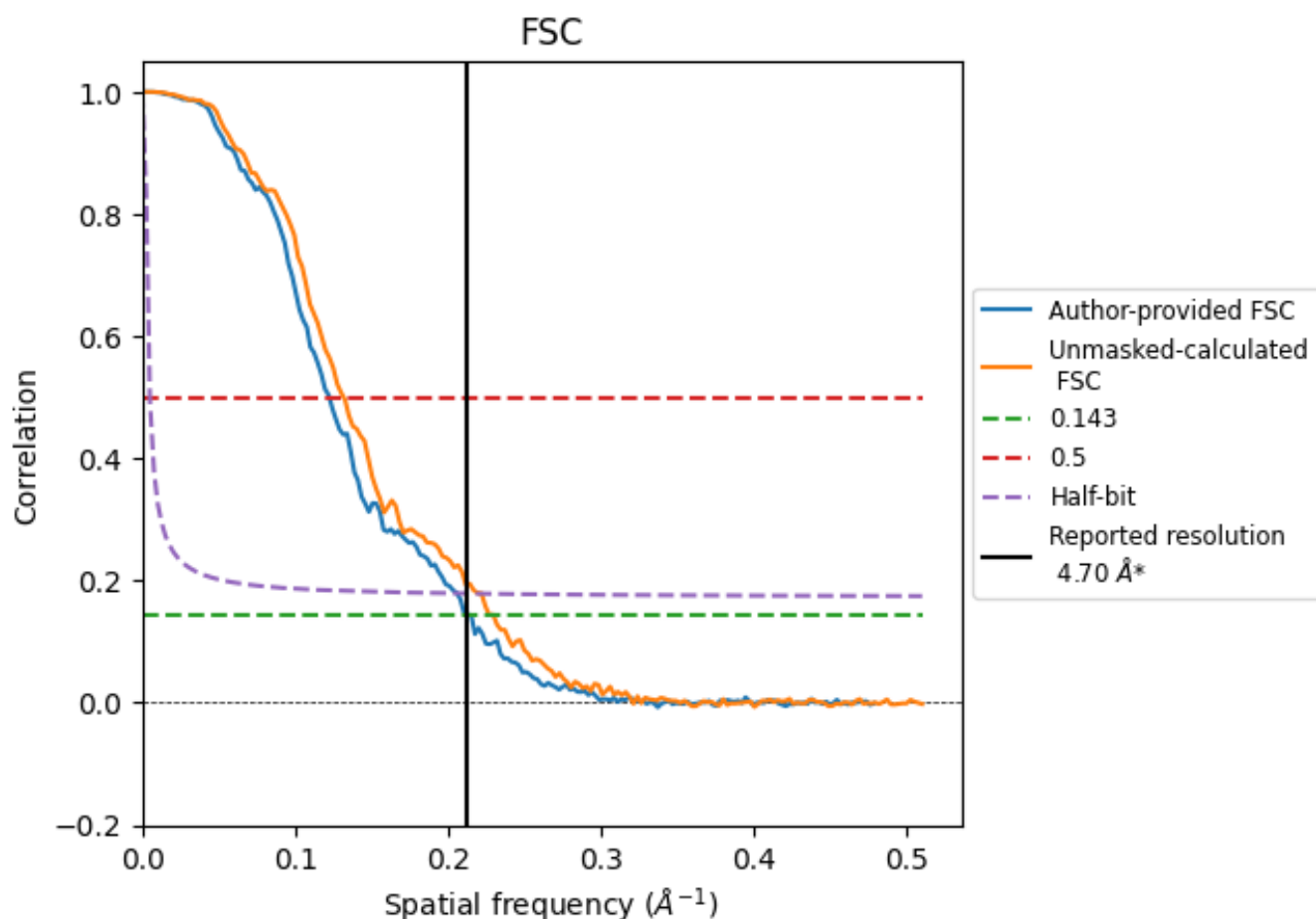


\*Reported resolution corresponds to spatial frequency of 0.213  $\text{\AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.213 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.70	-	-
Author-provided FSC curve	4.66	8.17	4.85
Unmasked-calculated*	4.35	7.59	4.50

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

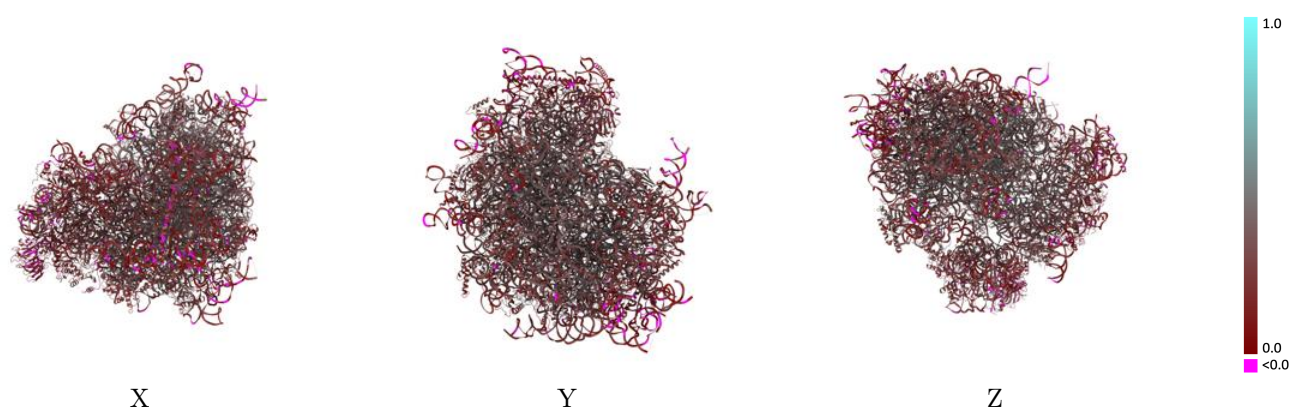
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-72483 and PDB model 9Y4H. Per-residue inclusion information can be found in section 3 on page 18.

### 9.1 Map-model overlay [i](#)

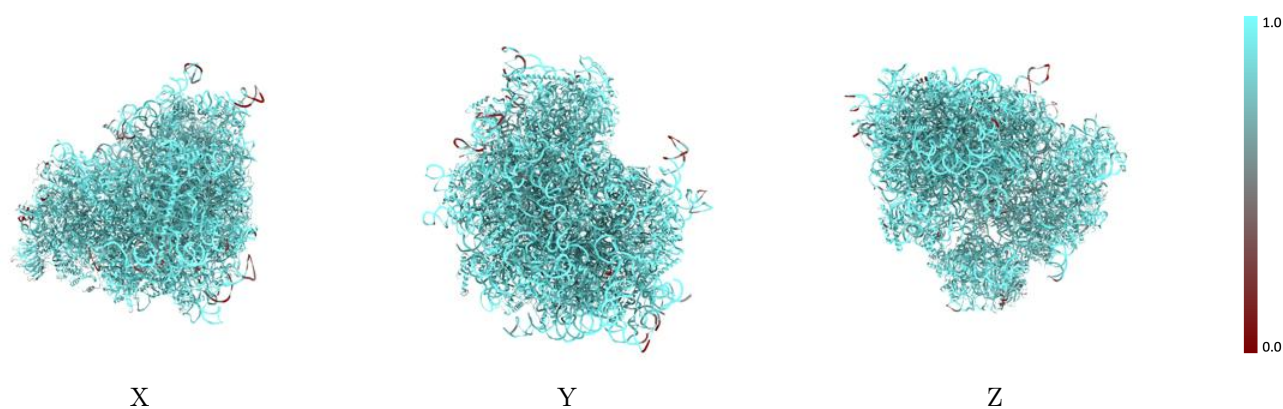
This section was not generated.

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



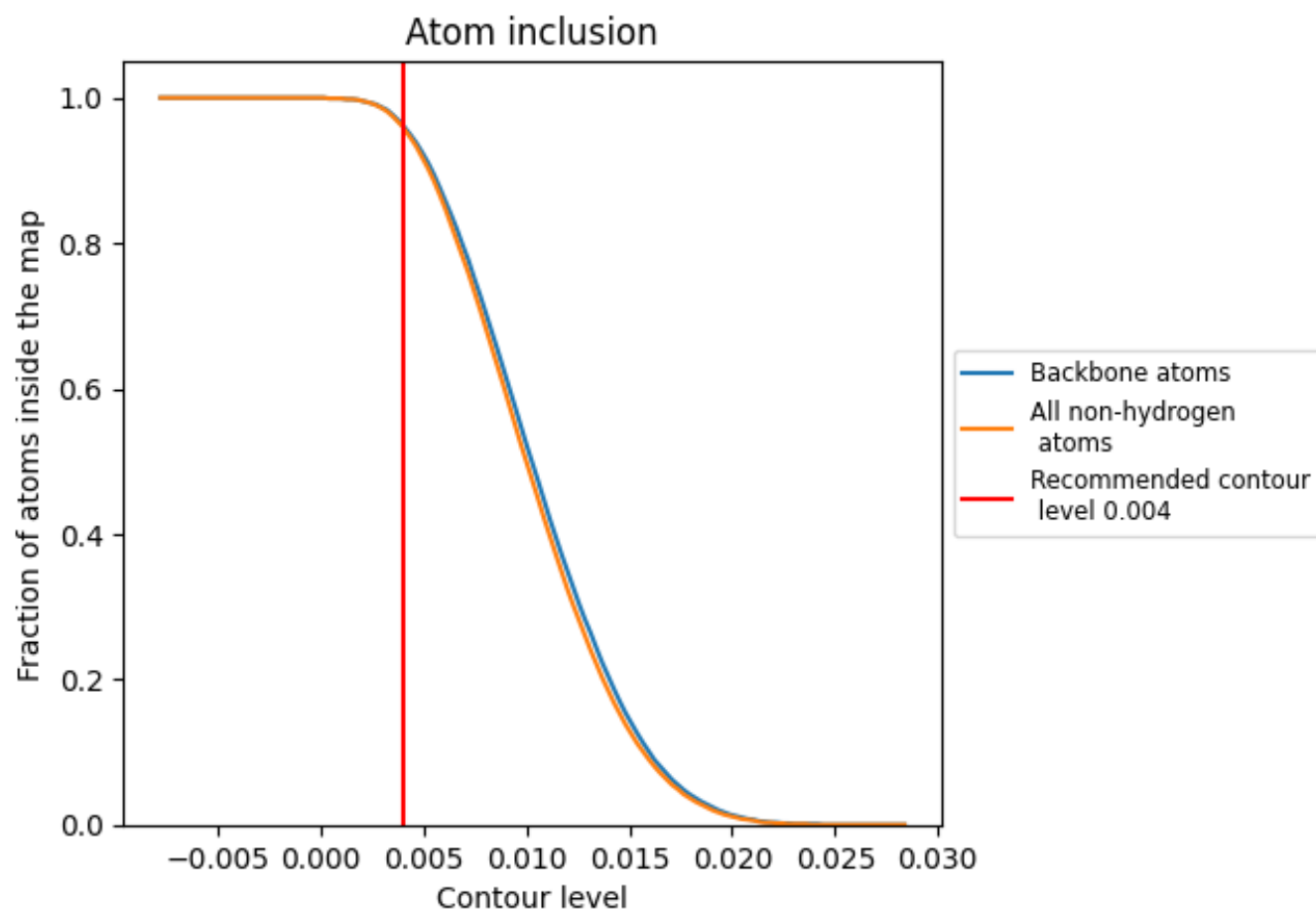
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.004).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 96% 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 (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9600	0.2880
A5	0.9810	0.3090
A7	0.9910	0.3400
A8	0.9920	0.3110
AA	0.9180	0.2710
AB	0.9440	0.2740
AC	0.9340	0.2920
AD	0.8660	0.1960
AE	0.9580	0.2350
AF	0.8900	0.2040
AG	0.9470	0.1960
AH	0.8950	0.2840
AI	0.9580	0.2890
AJ	0.9360	0.1910
AK	0.8460	0.1660
AL	0.9050	0.2900
AN	0.8980	0.2930
AO	0.9770	0.3110
AP	0.9220	0.1830
AQ	0.9160	0.1550
AR	0.8270	0.1380
AS	0.9650	0.2010
AT	0.9630	0.1850
AU	0.7940	0.1750
AV	0.9020	0.2920
AW	0.9390	0.2850
AX	0.9160	0.3100
AY	0.9690	0.1890
AZ	0.8890	0.1760
Aa	0.9570	0.2950
Ab	0.8980	0.2650
Ac	0.8150	0.1860
Ad	0.9560	0.1780
Ae	0.9010	0.2420
Ag	0.8700	0.1470







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Chain	Atom inclusion	Q-score
B2	 0.9800	 0.2580
CA	 0.9220	 0.3560
CB	 0.9510	 0.3720
CC	 0.9630	 0.3360
CD	 0.9800	 0.3170
CE	 0.9610	 0.2480
CF	 0.9440	 0.3140
CG	 0.9340	 0.2720
CH	 0.9430	 0.3120
CI	 0.9520	 0.3500
CJ	 0.9580	 0.3050
CL	 0.9550	 0.2820
CM	 0.9740	 0.2830
CN	 0.9640	 0.3440
CO	 0.9370	 0.3530
CP	 0.9630	 0.3320
CQ	 0.9590	 0.3450
CS	 0.9560	 0.2930
CT	 0.9590	 0.3370
CU	 0.9560	 0.2410
CV	 0.8990	 0.3890
CW	 0.9140	 0.2580
CX	 0.9480	 0.2750
CY	 0.9700	 0.2700
CZ	 0.9660	 0.2860
Ca	 0.9670	 0.3480
Cb	 0.9740	 0.3480
Cc	 0.9620	 0.3060
Cd	 0.9200	 0.3170
Ce	 0.9430	 0.3570
Cf	 0.9390	 0.3170
Cg	 0.9690	 0.2920
Ch	 0.9750	 0.2650
Ci	 0.9520	 0.2660
Cj	 0.9790	 0.3530
Ck	 0.9190	 0.2730
Cl	 0.9980	 0.3510
Cm	 0.9630	 0.3570
Cn	 0.9220	 0.3220
Co	 0.9550	 0.3620
Cp	 0.9340	 0.3540
Cr	 0.8930	 0.2740

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Chain	Atom inclusion	Q-score
Cw	 0.9640	 0.2540
Dd	 0.9930	 0.2180