



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 07:22 AM UTC

PDB ID : 6OGG / pdb_00006ogg
EMDB ID : EMD-20057
Title : 70S termination complex with RF2 bound to the UGA codon. Rotated ribosome with RF2 bound (Structure IV).
Authors : Svidritskiy, E.; Demo, G.; Loveland, A.B.; Xu, C.; Korostelev, A.A.
Deposited on : 2019-04-02
Resolution : 4.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

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

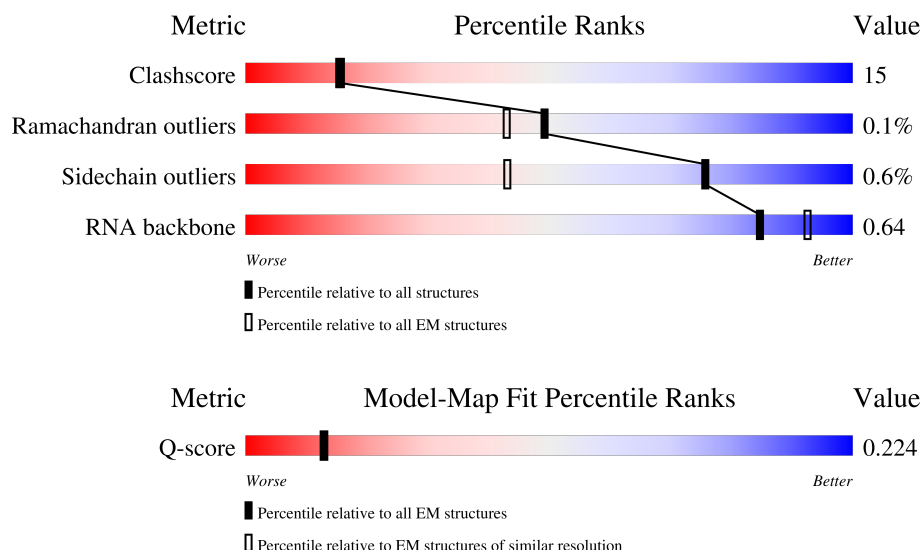
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



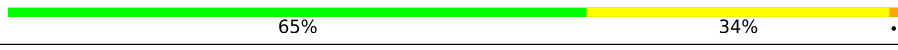
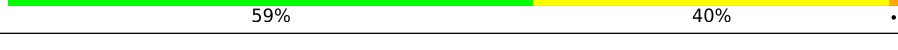
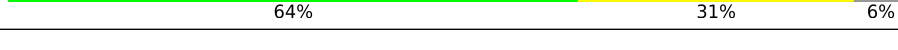
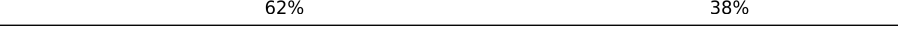
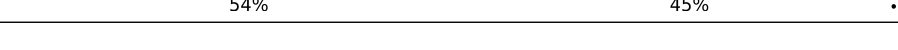
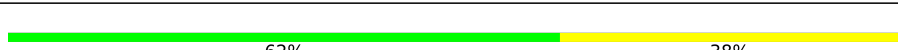
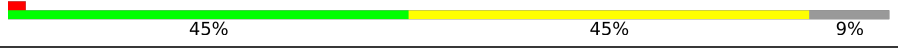
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

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

Mol	Chain	Length	Quality of chain
1	b	273	
2	c	209	
3	d	201	

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Mol	Chain	Length	Quality of chain
4	e	179	
5	f	177	
6	g	149	
7	j	142	
8	k	123	
9	l	144	
10	m	136	
11	n	127	
12	o	117	
13	p	115	
14	q	118	
15	r	103	
16	s	110	
17	t	100	
18	u	104	
19	v	94	
20	w	85	
21	x	78	
22	y	63	
23	z	59	
24	B	57	
25	C	55	
26	D	46	
27	E	65	
28	F	38	

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Mol	Chain	Length	Quality of chain
29	G	241	
30	H	233	
31	I	206	
32	J	167	
33	K	131	
34	L	156	
35	M	130	
36	N	130	
37	O	103	
38	P	129	
39	Q	124	
40	R	118	
41	S	101	
42	T	89	
43	U	82	
44	V	84	
45	W	75	
46	X	92	
47	Y	87	
48	Z	71	
49	a	234	
50	3	1539	
51	1	2903	
52	2	120	
53	5	77	

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Mol	Chain	Length	Quality of chain
54	4	27	44% 22% 7% 26%
55	8	371	37% 61% 36% ..

2 Entry composition

There are 55 unique types of molecules in this entry. The entry contains 147733 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	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 10 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	m	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	p	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	r	103	Total	C	N	O	S	0
			816	516	153	145	2	0

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	s	110	Total	C	N	O	S	0
			857	532	166	156	3	0

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	t	93	Total	C	N	O	S	0
			738	466	139	131	2	0

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	u	102	Total	C	N	O		0
			779	492	146	141		0

- Molecule 19 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	v	94	Total	C	N	O	S	0
			753	479	137	134	3	0

- Molecule 20 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	w	75	Total	C	N	O	S	0
			575	356	116	102	1	0

- Molecule 21 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	x	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 23 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 24 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 25 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	C	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 26 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 27 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 28 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 29 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 31 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 32 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 33 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

- Molecule 34 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 35 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	M	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 36 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 37 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 38 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 39 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 40 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 41 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 42 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 43 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	U	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 44 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 45 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 46 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 47 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 48 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Z	65	Total	C	N	O	S	0	0
			544	335	117	91	1		

- Molecule 49 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 50 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 1036415628

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	expression tag	GB 1370526515

- Molecule 53 is a RNA chain called tRNA^{fMet}.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	73	Total	C	N	O	P	0	0
			1556	694	281	509	72		

- Molecule 54 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	4	20	Total	C	N	O	P	0	0
			437	197	91	130	19		

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	8	361	Total	C	N	O	S	0	0
			2860	1758	503	589	10		

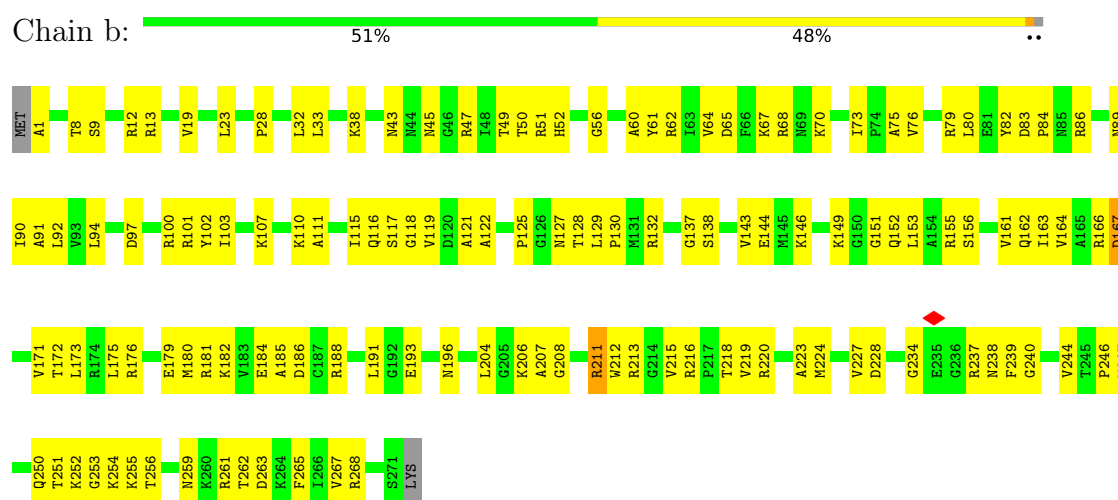
There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	-5	MET	-	initiating methionine	UNP A0A2S5ZJX2
8	-4	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-3	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-2	HIS	-	expression tag	UNP A0A2S5ZJX2
8	-1	HIS	-	expression tag	UNP A0A2S5ZJX2
8	0	HIS	-	expression tag	UNP A0A2S5ZJX2
8	1	HIS	-	expression tag	UNP A0A2S5ZJX2

3 Residue-property plots

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

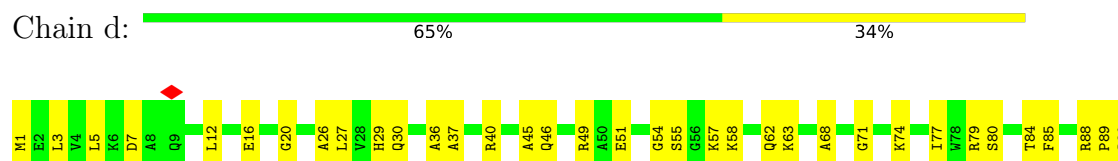
• Molecule 1: 50S ribosomal protein L2

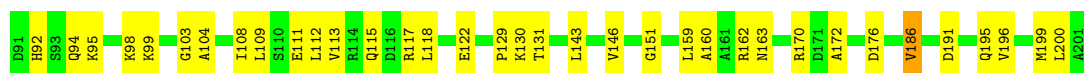


• Molecule 2: 50S ribosomal protein L3

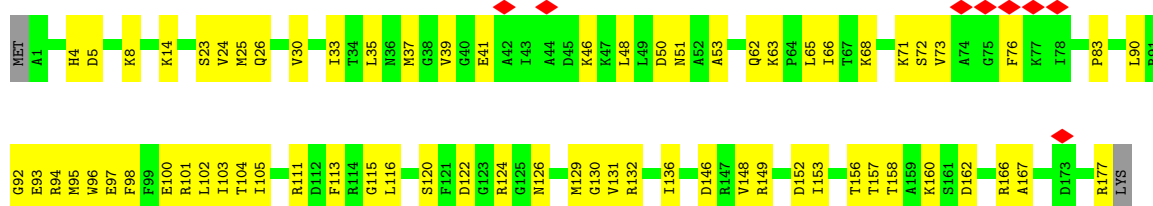


• Molecule 3: 50S ribosomal protein L4

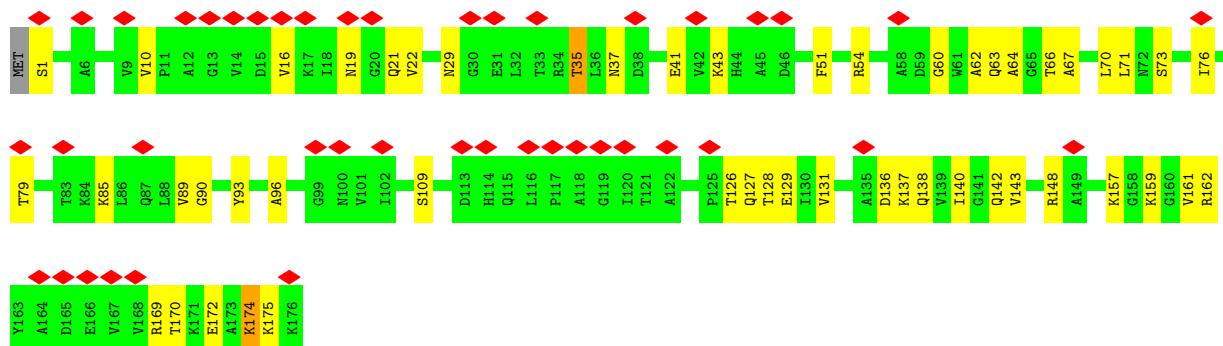




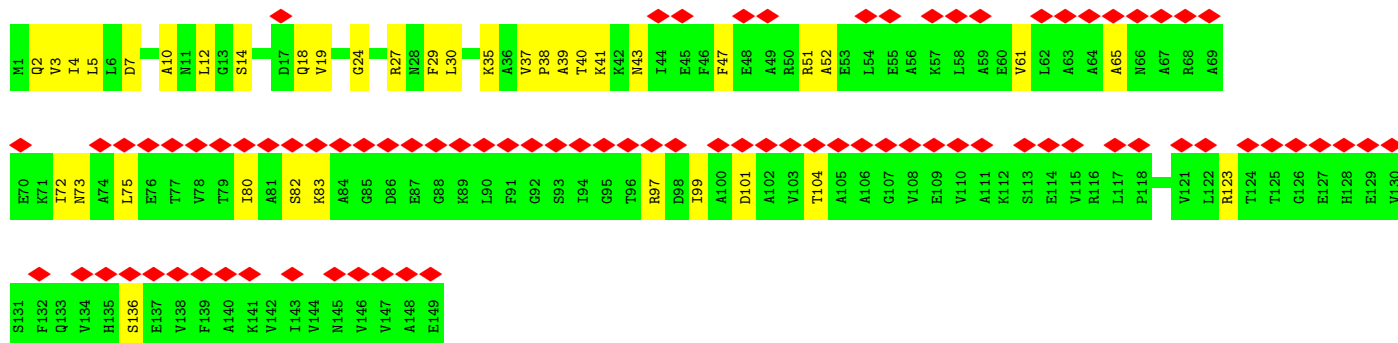
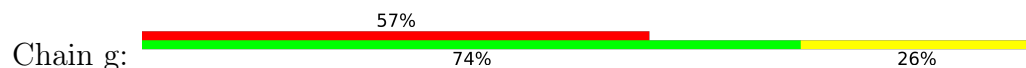
• Molecule 4: 50S ribosomal protein L5



• Molecule 5: 50S ribosomal protein L6

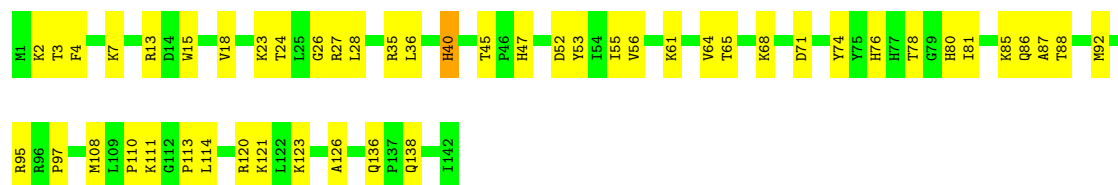


• Molecule 6: 50S ribosomal protein L9



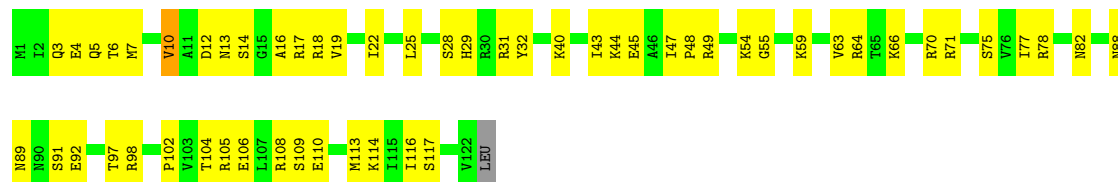
• Molecule 7: 50S ribosomal protein L13





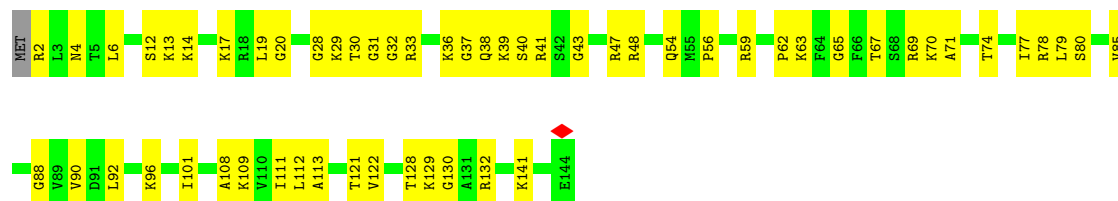
- Molecule 8: 50S ribosomal protein L14

Chain k: 54% 44% ..



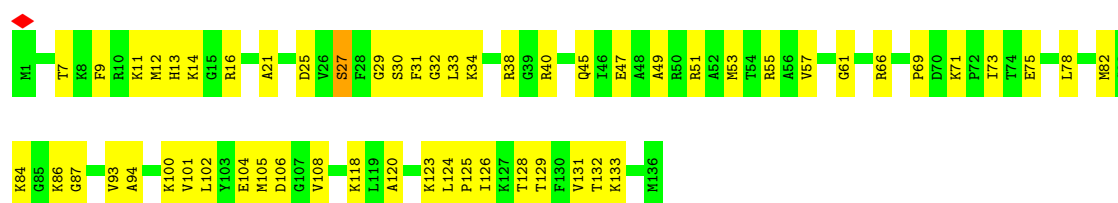
- Molecule 9: 50S ribosomal protein L15

Chain l: 60% 40% .



- Molecule 10: 50S ribosomal protein L16

Chain m: 59% 40% .

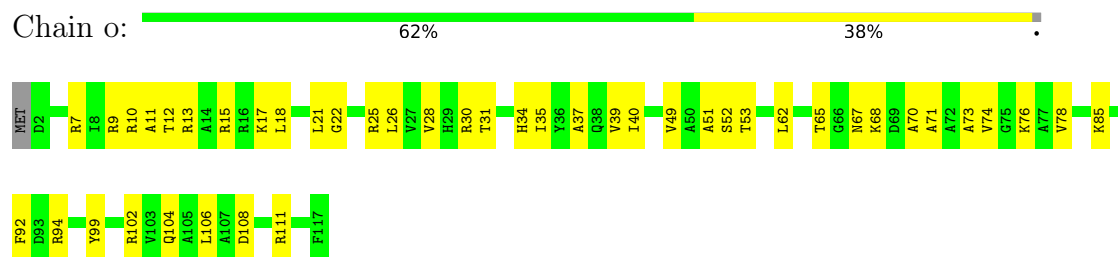


- Molecule 11: 50S ribosomal protein L17

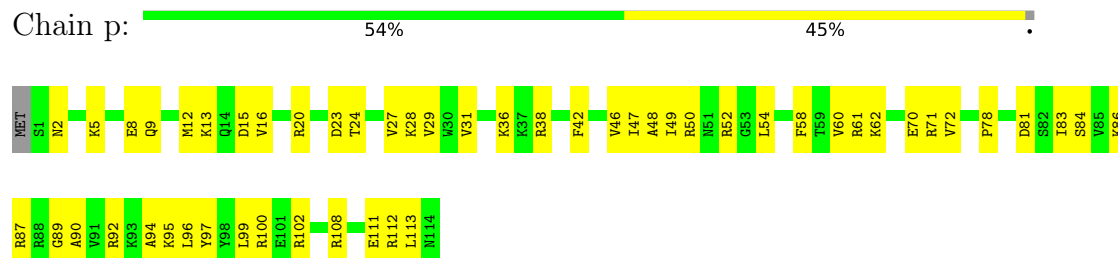
Chain n: 64% 31% 6%



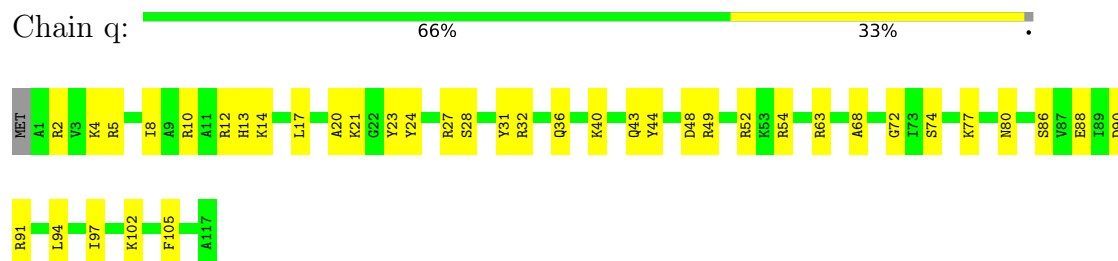
- Molecule 12: 50S ribosomal protein L18



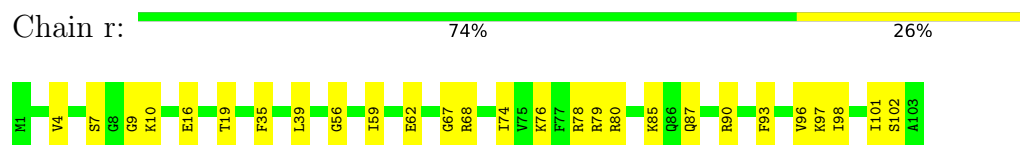
- Molecule 13: 50S ribosomal protein L19



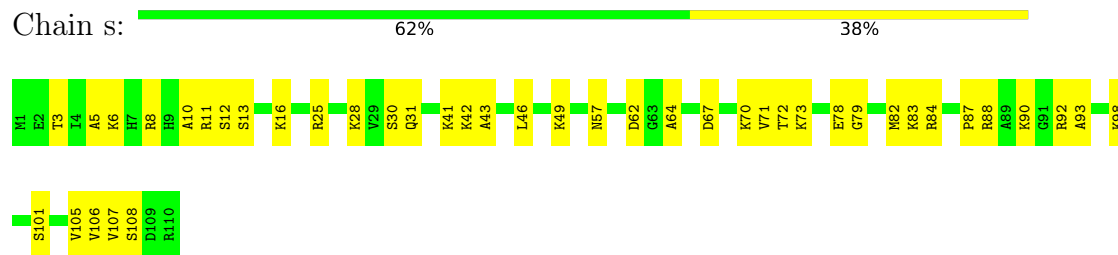
- Molecule 14: 50S ribosomal protein L20



- Molecule 15: 50S ribosomal protein L21

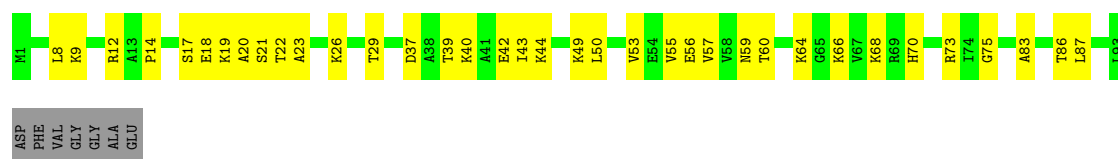


- Molecule 16: 50S ribosomal protein L22

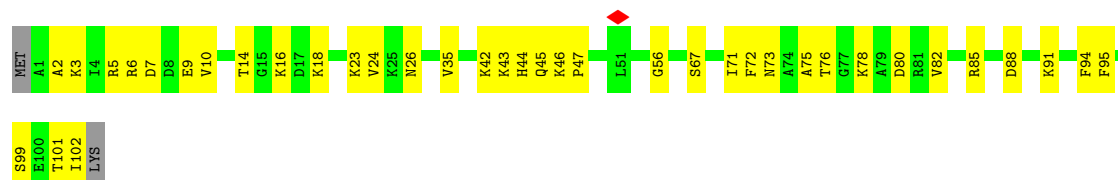


- Molecule 17: 50S ribosomal protein L23





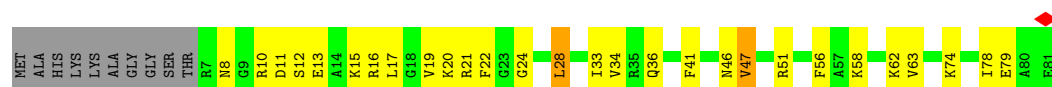
- Molecule 18: 50S ribosomal protein L24



- Molecule 19: 50S ribosomal protein L25



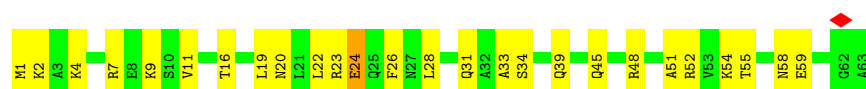
- Molecule 20: 50S ribosomal protein L27



- Molecule 21: 50S ribosomal protein L28

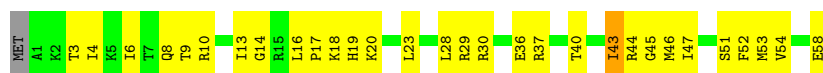


- Molecule 22: 50S ribosomal protein L29



- Molecule 23: 50S ribosomal protein L30





- Molecule 24: 50S ribosomal protein L32



- Molecule 25: 50S ribosomal protein L33



- Molecule 26: 50S ribosomal protein L34



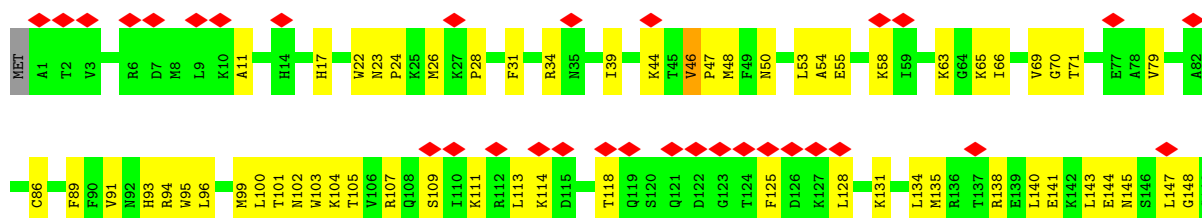
- Molecule 27: 50S ribosomal protein L35

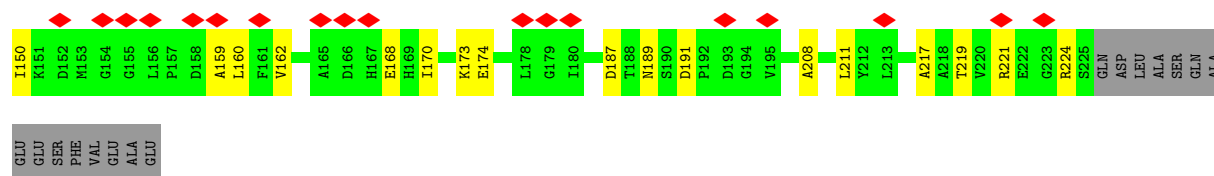


- Molecule 28: 50S ribosomal protein L36

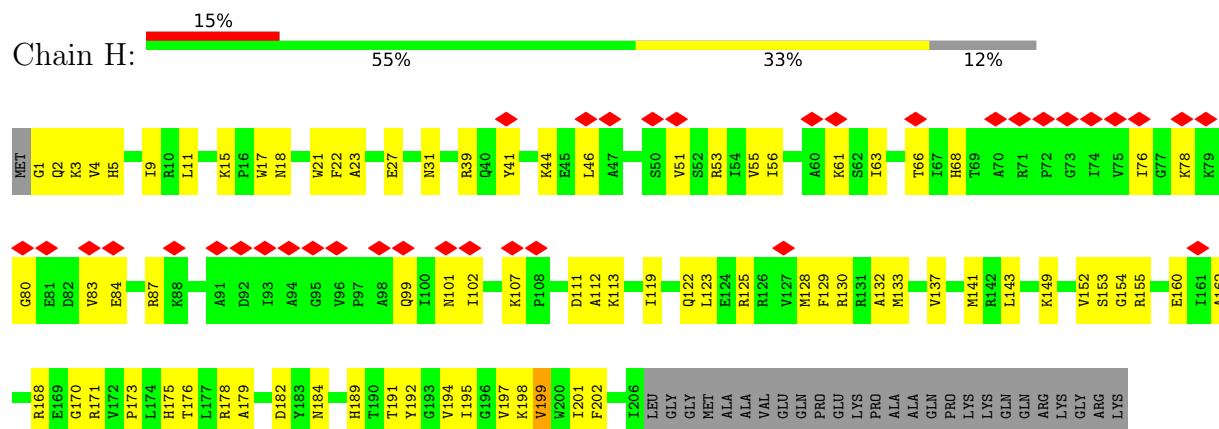


- Molecule 29: 30S ribosomal protein S2

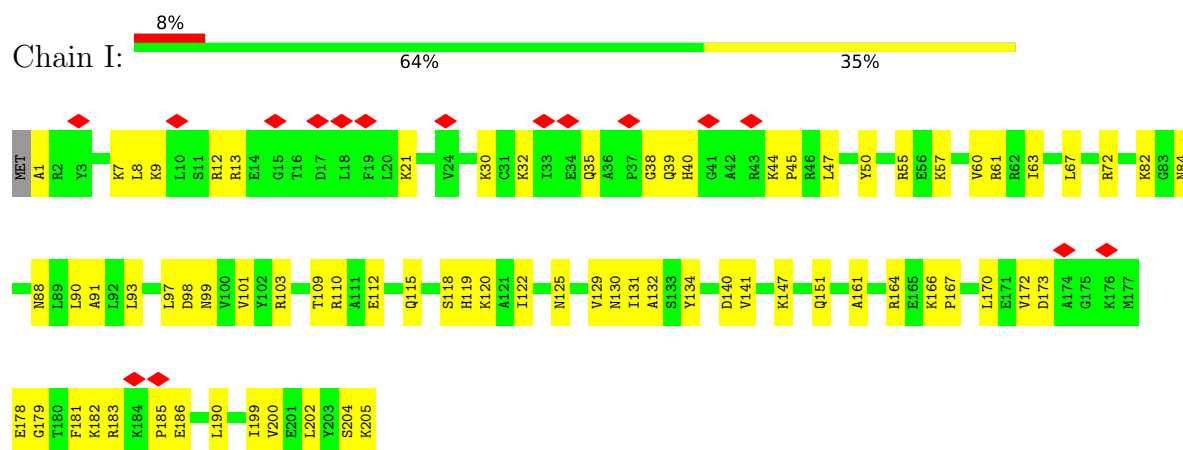




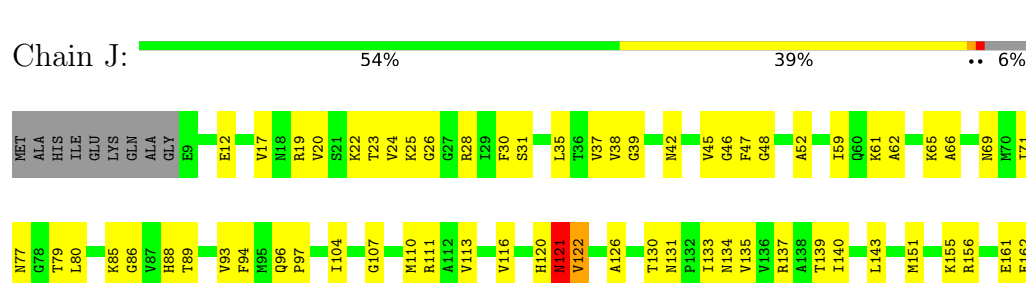
• Molecule 30: 30S ribosomal protein S3



• Molecule 31: 30S ribosomal protein S4

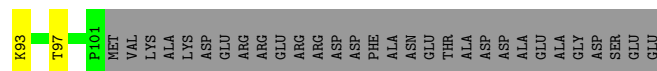


• Molecule 32: 30S ribosomal protein S5

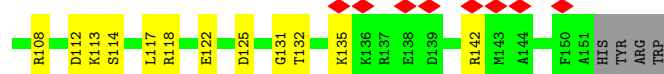


• Molecule 33: 30S ribosomal protein S6





Chain L:



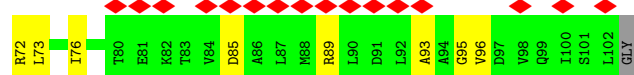
Chain M: 61% 38%



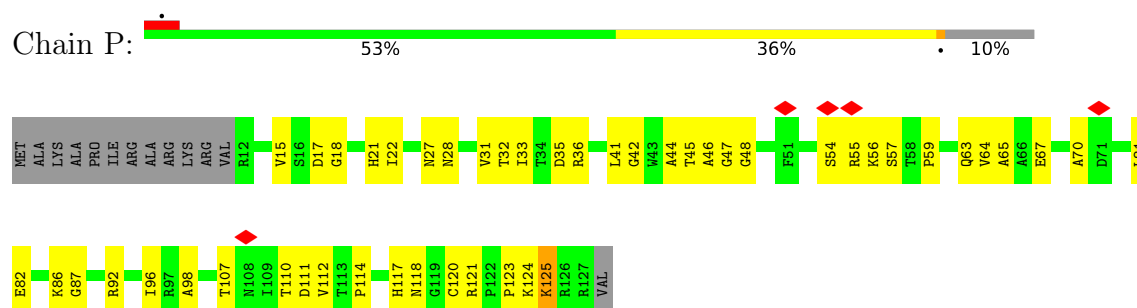
Chain N: 63% 34% .



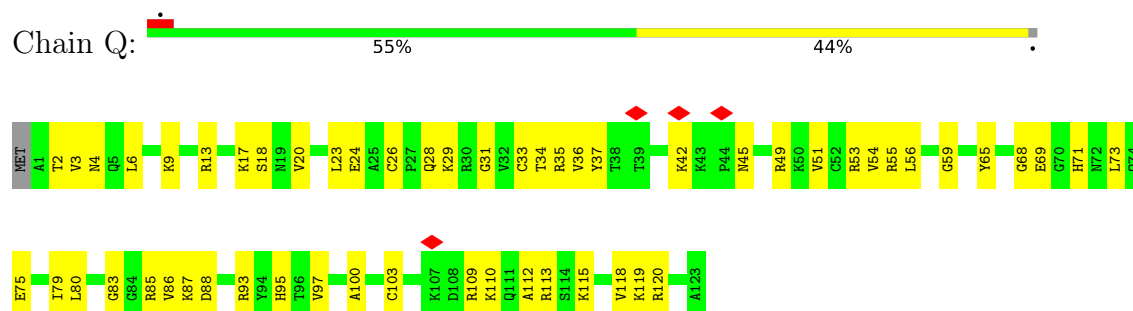
Chain O: 26% 59% 35% 5%



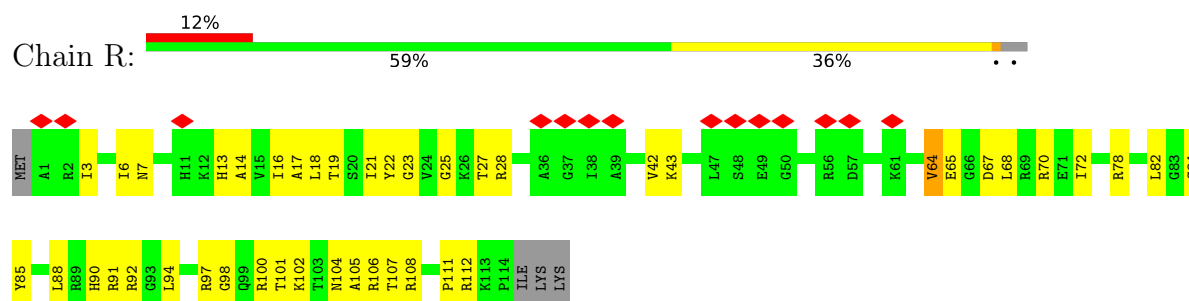
- Molecule 38: 30S ribosomal protein S11



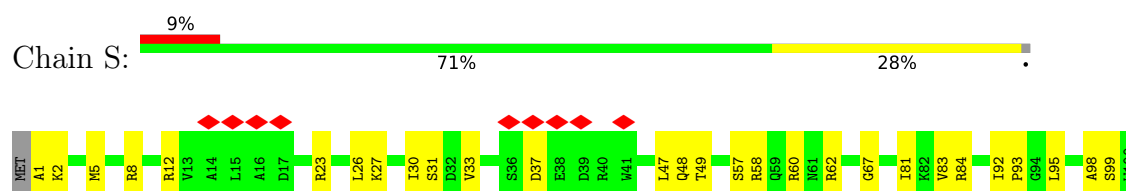
- Molecule 39: 30S ribosomal protein S12



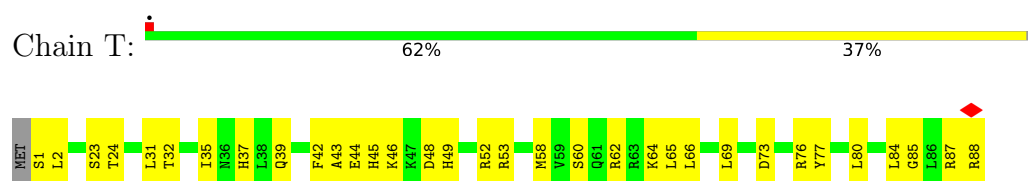
- Molecule 40: 30S ribosomal protein S13



- Molecule 41: 30S ribosomal protein S14



- Molecule 42: 30S ribosomal protein S15



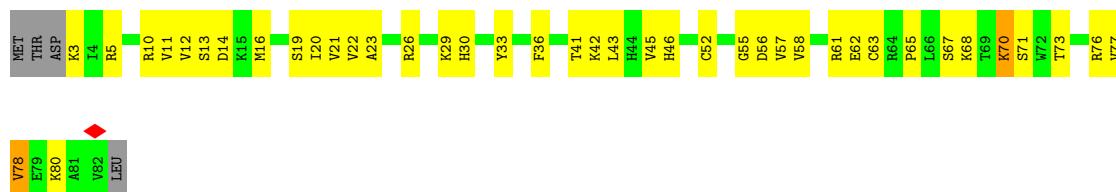
- Molecule 43: 30S ribosomal protein S16

Chain U:  68% 32%



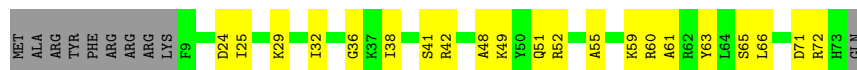
- Molecule 44: 30S ribosomal protein S17

Chain V:  46% 46% 5%



- Molecule 45: 30S ribosomal protein S18

Chain W:  59% 28% 13%



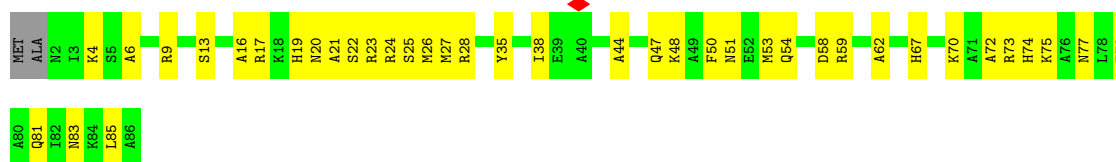
- Molecule 46: 30S ribosomal protein S19

Chain X:  12% 54% 32% 14%



- Molecule 47: 30S ribosomal protein S20

Chain Y:  53% 45%

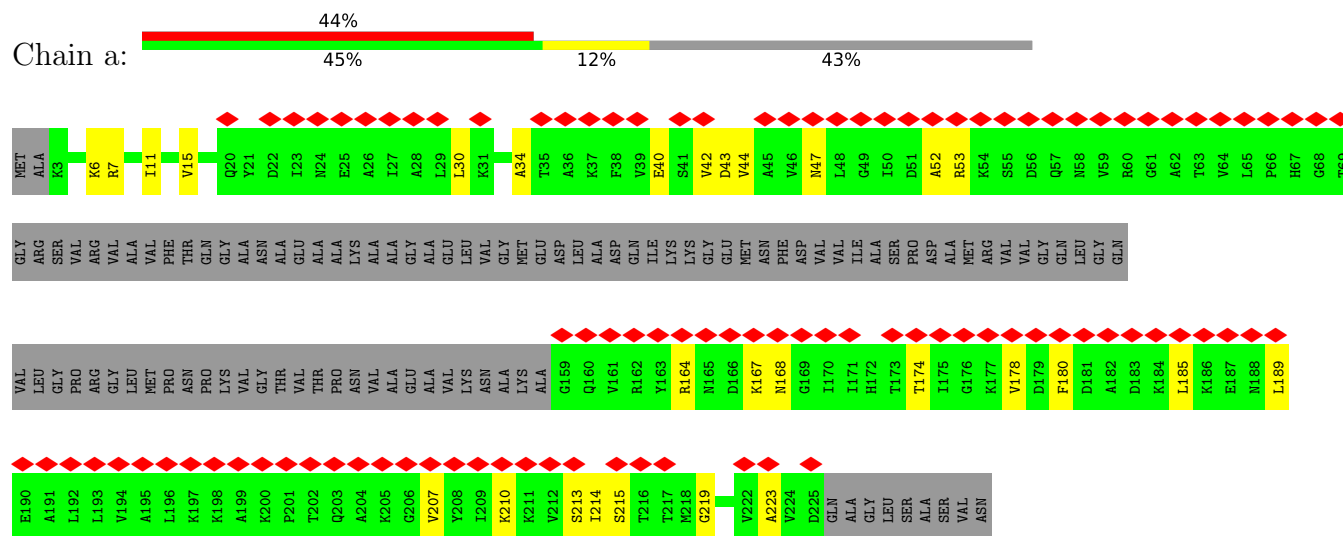


- Molecule 48: 30S ribosomal protein S21

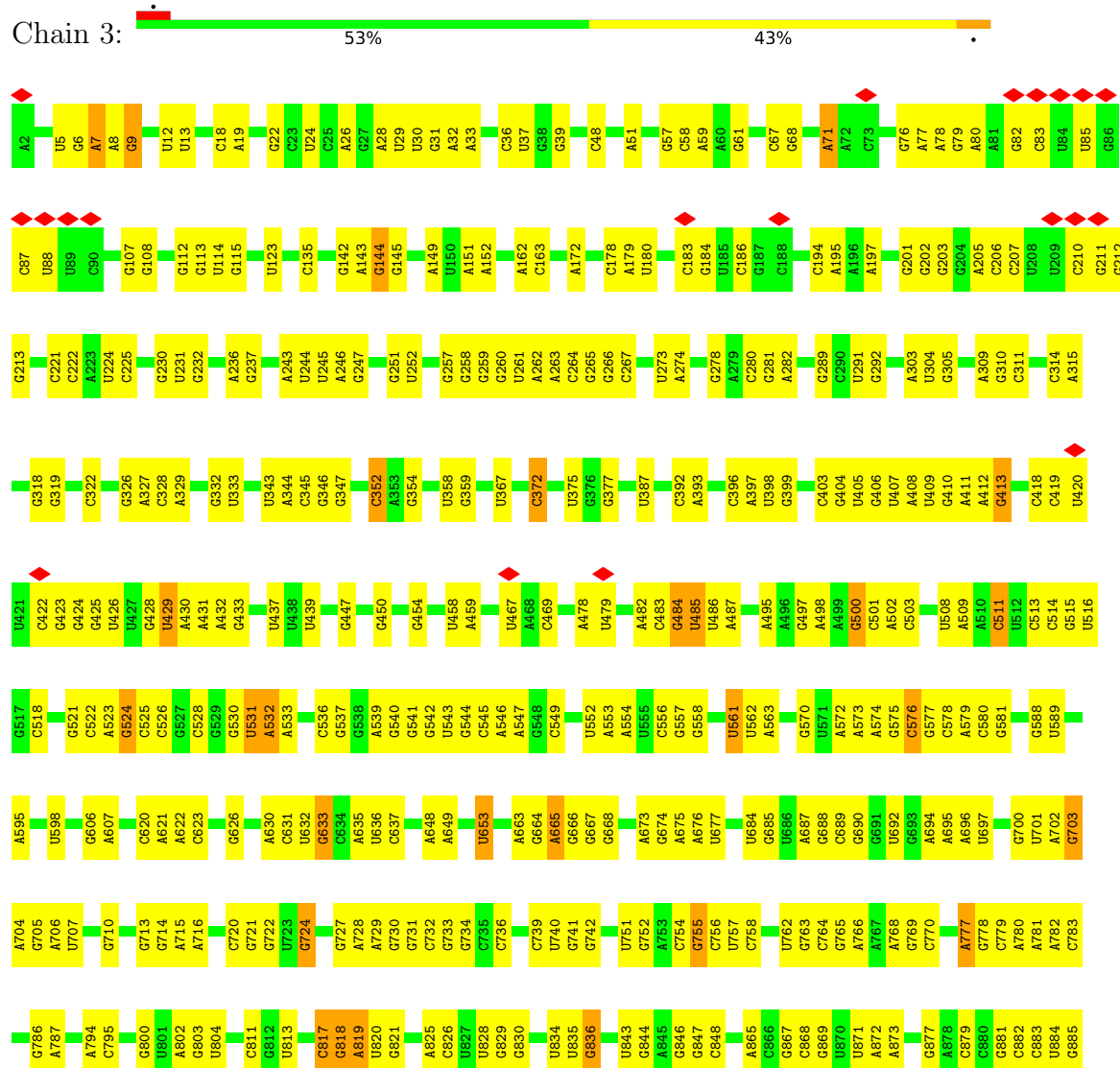
Chain Z:  11% 55% 35% 8%

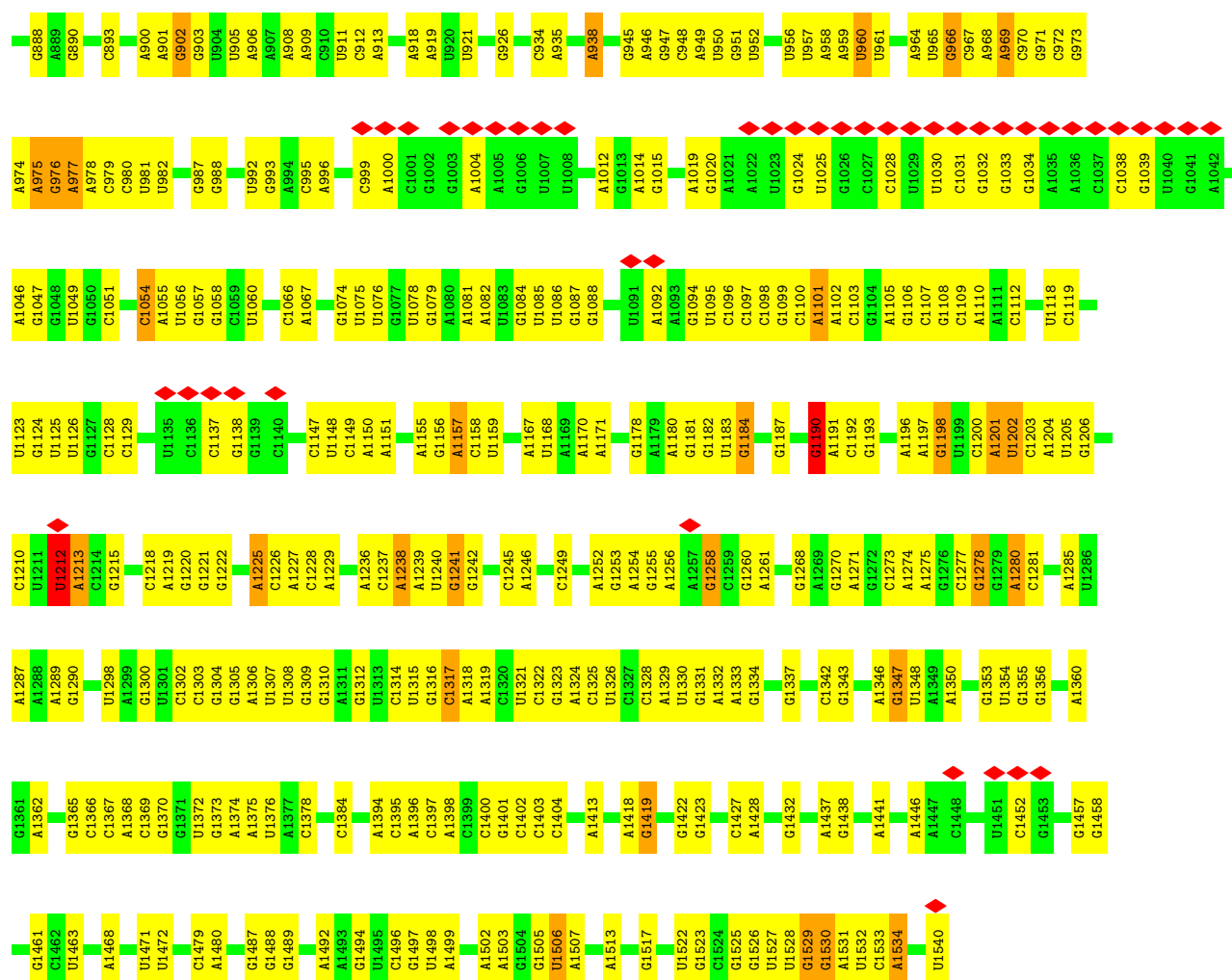


Chain a:

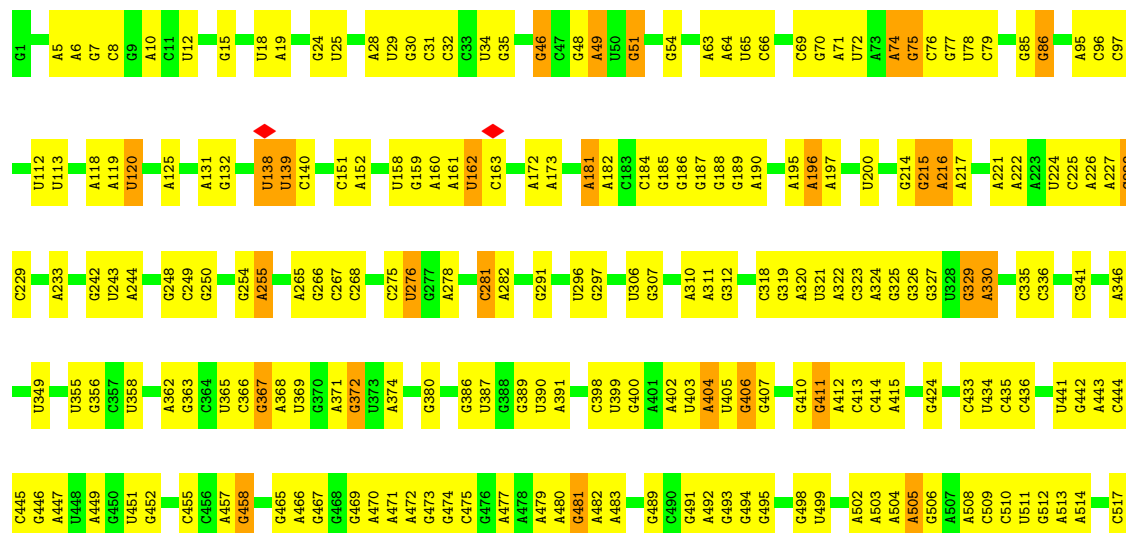


Chain 3:





• Molecule 51: 23S ribosomal RNA

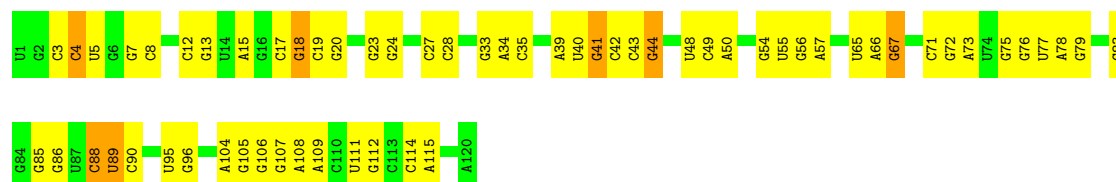




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C2023	G2024	U2025	U2026	U2027	U2028	U2029	U2030	U2031	C2036	U2037	U2038	U2039	U2040	C2043	U2044	C2045	C2050	A2051	A2052	U2053	U2054	U2055	U2056	U2060	U2061	C2064	C2065	U2066	U2067	U2068	U2069	U2070	U2071	U2074	U2075	U2076	U2077	U2078	U2079	U2080	U2081	C2091	U2092	U2093	A2101	G2102	C2103	C2104	U2105	U2106	U2107																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
U2108	U2109	U2110	U2111	U2112	U2113	U2114	U2115	U2116	U2117	U2118	U2119	U2120	U2121	U2122	U2123	U2124	U2125	U2126	U2127	U2128	U2129	U2130	U2131	U2132	U2133	U2136	U2137	U2138	U2139	U2140	U2141	U2142	U2143	U2144	U2145	U2146	U2147	U2148	U2149	U2150	U2151	U2152	U2153	U2154	U2155	U2156	U2157	U2158	U2159	U2160	U2161	U2162	U2163	U2164	U2165	U2166	U2167	U2168																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
U2169	U2170	U2171	U2172	U2173	U2174	U2175	U2176	U2177	U2178	U2179	U2180	U2181	U2184	U2185	U2189	U2190	U2191	U2192	U2193	U2194	U2195	U2196	U2197	U2198	U2199	U2200	U2201	U2202	U2203	U2204	U2205	U2206	U2207	U2208	U2209	U2210	U2211	U2212	U2213	U2214	U2215	U2216	U2217	U2220	U2221	U2222	U2223	U2224	U2225	U2226	U2227	U2228	U2229	U2230	U2231	U2232	U2233	U2234	U2235	U2236	U2237	U2238	U2239	U2240	U2241	U2242	U2243	U2244	U2245	U2246	U2247	U2248	U2249	U2250	U2251	U2252	U2253	U2254	U2255	U2256	U2257																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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- Molecule 52: 5S ribosomal RNA

Chain 2: 



- Molecule 53: tRNA^{fMet}

Chain 5: 



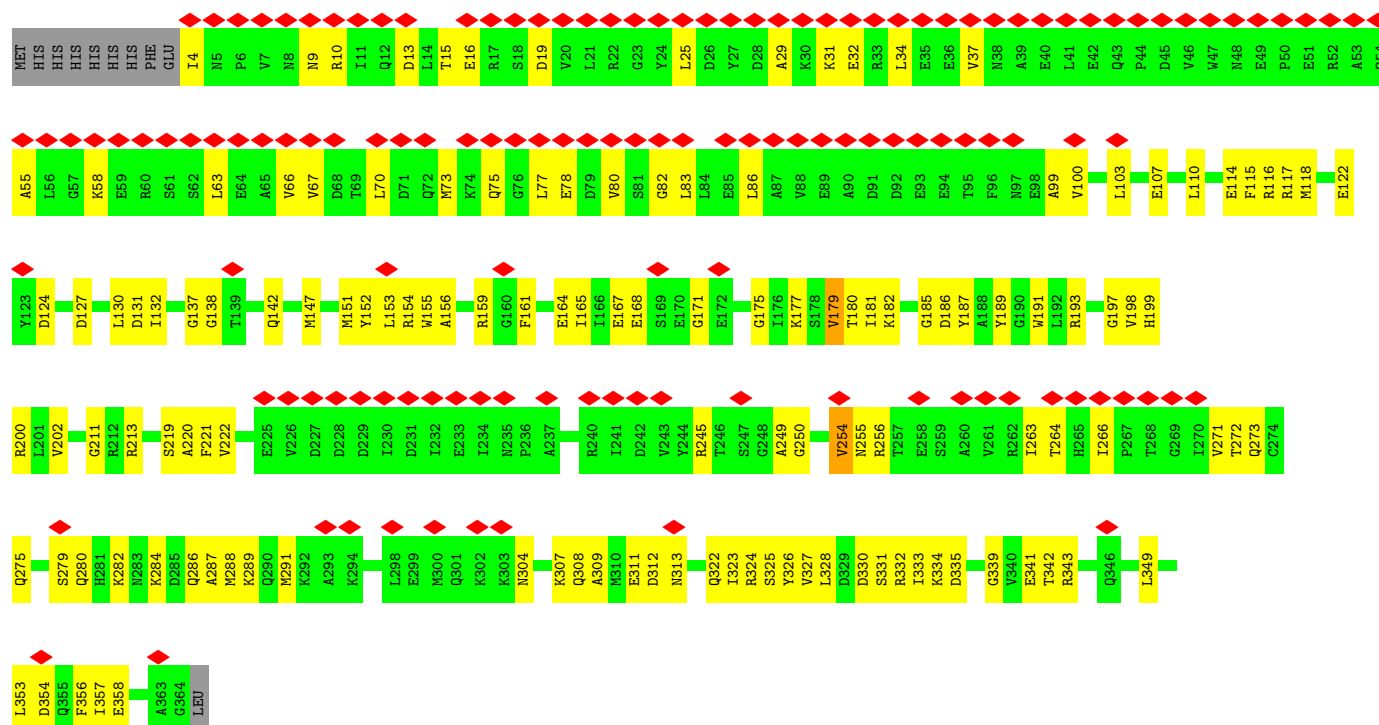
- Molecule 54: mRNA

Chain 4: 



- Molecule 55: Peptide chain release factor 2

Chain 8: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	5881	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.429	Depositor
Minimum map value	-2.704	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.455	Depositor
Recommended contour level	0.9	Depositor
Map size (Å)	416.208, 416.208, 416.208	wwPDB
Map dimensions	312, 312, 312	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.334, 1.334, 1.334	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	b	0.40	0/2121	0.79	2/2852 (0.1%)
2	c	0.39	0/1586	0.75	0/2134
3	d	0.36	0/1571	0.70	0/2113
4	e	0.31	0/1434	0.74	0/1926
5	f	0.31	0/1343	0.69	0/1816
6	g	0.29	0/1122	0.82	3/1515 (0.2%)
7	j	0.37	0/1152	0.66	1/1551 (0.1%)
8	k	0.39	0/947	0.72	0/1268
9	l	0.38	0/1054	0.76	0/1403
10	m	0.40	0/1093	0.77	0/1460
11	n	0.37	0/973	0.78	0/1301
12	o	0.29	0/902	0.69	0/1209
13	p	0.40	0/929	0.68	0/1242
14	q	0.35	0/960	0.60	0/1278
15	r	0.36	0/829	0.71	0/1107
16	s	0.36	0/864	0.73	2/1156 (0.2%)
17	t	0.34	0/744	0.67	0/994
18	u	0.36	0/787	0.74	0/1051
19	v	0.39	0/766	0.69	0/1025
20	w	0.35	0/582	0.69	0/769
21	x	0.36	0/635	0.71	0/848
22	y	0.29	0/510	0.63	0/677
23	z	0.39	0/453	0.69	1/605 (0.2%)
24	B	0.37	0/450	0.75	0/599
25	C	0.35	0/416	0.66	0/554
26	D	0.40	0/380	0.69	0/498
27	E	0.43	0/513	0.82	0/676
28	F	0.32	0/303	0.70	0/397
29	G	0.28	0/1787	0.74	2/2408 (0.1%)
30	H	0.27	0/1651	0.67	0/2225
31	I	0.31	0/1665	0.75	0/2227
32	J	0.29	0/1169	0.83	4/1573 (0.3%)
33	K	0.42	2/843 (0.2%)	0.73	0/1140
34	L	0.27	0/1195	0.74	1/1602 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	M	0.28	0/989	0.66	0/1326
36	N	0.29	0/1034	0.78	0/1375
37	O	0.32	0/796	0.73	0/1077
38	P	0.31	0/885	0.83	2/1195 (0.2%)
39	Q	0.39	0/969	0.90	2/1300 (0.2%)
40	R	0.26	0/892	0.79	2/1193 (0.2%)
41	S	0.26	0/817	0.63	0/1088
42	T	0.27	0/722	0.75	2/964 (0.2%)
43	U	0.29	0/659	0.66	0/884
44	V	0.33	0/657	0.71	0/881
45	W	0.28	0/544	0.77	2/731 (0.3%)
46	X	0.32	0/652	0.77	0/877
47	Y	0.29	0/671	0.65	0/888
48	Z	0.34	0/550	0.97	4/728 (0.5%)
49	a	0.28	0/1033	0.67	0/1387
50	3	0.39	0/36963	0.46	2/57662 (0.0%)
51	1	0.39	0/69796	0.46	1/108888 (0.0%)
52	2	0.40	0/2872	0.46	0/4479
53	5	0.39	0/1738	0.47	0/2709
54	4	0.39	0/493	0.47	0/769
55	8	0.34	1/2900 (0.0%)	0.76	1/3908 (0.0%)
All	All	0.37	3/160361 (0.0%)	0.55	34/239508 (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
5	f	0	1
6	g	0	1
10	m	0	2
13	p	0	1
27	E	0	1
32	J	0	1
44	V	0	1
48	Z	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
33	K	10	VAL	C-N	6.17	1.42	1.33
33	K	18	VAL	C-N	6.16	1.41	1.34
55	8	266	ILE	C-N	5.22	1.38	1.33

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	z	13	ILE	N-CA-C	-6.94	106.29	112.12
1	b	211	ARG	CA-C-N	-6.35	111.63	122.56
1	b	211	ARG	C-N-CA	-6.35	111.63	122.56
32	J	121	ASN	CA-C-N	6.21	133.14	121.97
32	J	121	ASN	C-N-CA	6.21	133.14	121.97

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	f	174	LYS	Peptide
6	g	10	ALA	Peptide
10	m	27	SER	Peptide
10	m	57	VAL	Peptide
13	p	15	ASP	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	b	2082	0	2157	139	0
2	c	1565	0	1616	100	0
3	d	1552	0	1619	86	0
4	e	1410	0	1447	61	0
5	f	1323	0	1374	49	0
6	g	1111	0	1148	26	0
7	j	1129	0	1162	63	0
8	k	938	0	1012	58	0
9	l	1045	0	1117	83	0
10	m	1074	0	1157	52	0
11	n	960	0	1000	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	o	892	0	923	38	0
13	p	917	0	965	62	0
14	q	947	0	1022	43	0
15	r	816	0	839	23	0
16	s	857	0	922	61	0
17	t	738	0	807	37	0
18	u	779	0	834	46	0
19	v	753	0	780	26	0
20	w	575	0	592	36	0
21	x	625	0	655	41	0
22	y	509	0	543	28	0
23	z	449	0	491	24	0
24	B	444	0	461	32	0
25	C	409	0	440	33	0
26	D	377	0	418	27	0
27	E	504	0	574	35	0
28	F	302	0	343	20	0
29	G	1756	0	1787	78	0
30	H	1624	0	1699	65	0
31	I	1643	0	1710	81	0
32	J	1156	0	1199	60	0
33	K	824	0	815	25	0
34	L	1181	0	1240	39	0
35	M	979	0	1034	42	0
36	N	1022	0	1070	61	0
37	O	786	0	828	33	0
38	P	869	0	878	84	0
39	Q	955	0	1019	63	0
40	R	883	0	944	61	0
41	S	805	0	847	37	0
42	T	714	0	737	26	0
43	U	649	0	666	29	0
44	V	648	0	691	35	0
45	W	535	0	552	28	0
46	X	637	0	665	47	0
47	Y	665	0	714	43	0
48	Z	544	0	579	31	0
49	a	1026	0	1092	32	0
50	3	33012	0	16618	901	0
51	1	62317	0	31346	1446	0
52	2	2568	0	1303	74	0
53	5	1556	0	793	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	4	437	0	219	20	0
55	8	2860	0	2758	120	0
All	All	147733	0	100221	3623	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 15.

The worst 5 of 3623 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)
7:j:114:LEU:HD12	51:1:558:U:H5'	1.24	1.15
51:1:1915:U:H1'	55:8:308:GLN:HG2	1.29	1.14
13:p:52:ARG:NH2	51:1:2720:U:H5''	1.64	1.10
38:P:41:LEU:HD13	50:3:685:G:H5''	1.16	1.10
50:3:959:A:H2'	50:3:960:U:H4'	1.34	1.09

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	b	269/273 (98%)	239 (89%)	30 (11%)	0	100	100
2	c	207/209 (99%)	187 (90%)	20 (10%)	0	100	100
3	d	199/201 (99%)	183 (92%)	16 (8%)	0	100	100
4	e	175/179 (98%)	152 (87%)	22 (13%)	1 (1%)	21	58
5	f	174/177 (98%)	154 (88%)	20 (12%)	0	100	100
6	g	147/149 (99%)	123 (84%)	24 (16%)	0	100	100
7	j	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
8	k	120/123 (98%)	108 (90%)	12 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	l	141/144 (98%)	131 (93%)	10 (7%)	0	100	100
10	m	134/136 (98%)	116 (87%)	18 (13%)	0	100	100
11	n	118/127 (93%)	104 (88%)	14 (12%)	0	100	100
12	o	114/117 (97%)	104 (91%)	10 (9%)	0	100	100
13	p	112/115 (97%)	99 (88%)	13 (12%)	0	100	100
14	q	115/118 (98%)	112 (97%)	3 (3%)	0	100	100
15	r	101/103 (98%)	90 (89%)	11 (11%)	0	100	100
16	s	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
17	t	91/100 (91%)	85 (93%)	6 (7%)	0	100	100
18	u	100/104 (96%)	89 (89%)	11 (11%)	0	100	100
19	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
20	w	73/85 (86%)	63 (86%)	10 (14%)	0	100	100
21	x	75/78 (96%)	71 (95%)	4 (5%)	0	100	100
22	y	61/63 (97%)	59 (97%)	1 (2%)	1 (2%)	7	37
23	z	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
24	B	54/57 (95%)	46 (85%)	8 (15%)	0	100	100
25	C	48/55 (87%)	47 (98%)	1 (2%)	0	100	100
26	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
27	E	62/65 (95%)	52 (84%)	9 (14%)	1 (2%)	7	37
28	F	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
29	G	223/241 (92%)	210 (94%)	13 (6%)	0	100	100
30	H	204/233 (88%)	186 (91%)	18 (9%)	0	100	100
31	I	203/206 (98%)	181 (89%)	21 (10%)	1 (0%)	24	62
32	J	155/167 (93%)	137 (88%)	16 (10%)	2 (1%)	9	41
33	K	99/131 (76%)	83 (84%)	16 (16%)	0	100	100
34	L	149/156 (96%)	135 (91%)	14 (9%)	0	100	100
35	M	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
36	N	125/130 (96%)	102 (82%)	22 (18%)	1 (1%)	16	52
37	O	96/103 (93%)	83 (86%)	12 (12%)	1 (1%)	12	47
38	P	114/129 (88%)	93 (82%)	21 (18%)	0	100	100
39	Q	121/124 (98%)	93 (77%)	28 (23%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	R	112/118 (95%)	99 (88%)	13 (12%)	0	100	100
41	S	98/101 (97%)	84 (86%)	14 (14%)	0	100	100
42	T	86/89 (97%)	79 (92%)	6 (7%)	1 (1%)	10	42
43	U	80/82 (98%)	73 (91%)	7 (9%)	0	100	100
44	V	78/84 (93%)	64 (82%)	14 (18%)	0	100	100
45	W	63/75 (84%)	55 (87%)	8 (13%)	0	100	100
46	X	77/92 (84%)	71 (92%)	6 (8%)	0	100	100
47	Y	83/87 (95%)	80 (96%)	3 (4%)	0	100	100
48	Z	63/71 (89%)	43 (68%)	20 (32%)	0	100	100
49	a	130/234 (56%)	114 (88%)	16 (12%)	0	100	100
55	8	359/371 (97%)	328 (91%)	31 (9%)	0	100	100
All	All	6011/6421 (94%)	5366 (89%)	636 (11%)	9 (0%)	49	82

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	y	24	GLU
32	J	121	ASN
32	J	122	VAL
42	T	46	LYS
4	e	111	ARG

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	b	216/218 (99%)	215 (100%)	1 (0%)	81	81
2	c	164/164 (100%)	163 (99%)	1 (1%)	78	80
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	80
4	e	148/150 (99%)	147 (99%)	1 (1%)	76	78
5	f	137/138 (99%)	136 (99%)	1 (1%)	76	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	g	114/114 (100%)	114 (100%)	0	100	100
7	j	116/116 (100%)	116 (100%)	0	100	100
8	k	103/104 (99%)	101 (98%)	2 (2%)	50	66
9	l	102/103 (99%)	102 (100%)	0	100	100
10	m	109/109 (100%)	109 (100%)	0	100	100
11	n	100/104 (96%)	100 (100%)	0	100	100
12	o	86/87 (99%)	85 (99%)	1 (1%)	63	73
13	p	99/100 (99%)	99 (100%)	0	100	100
14	q	89/90 (99%)	89 (100%)	0	100	100
15	r	84/84 (100%)	83 (99%)	1 (1%)	63	73
16	s	93/93 (100%)	92 (99%)	1 (1%)	65	73
17	t	80/84 (95%)	80 (100%)	0	100	100
18	u	83/85 (98%)	83 (100%)	0	100	100
19	v	78/78 (100%)	75 (96%)	3 (4%)	29	51
20	w	57/63 (90%)	55 (96%)	2 (4%)	32	53
21	x	67/68 (98%)	67 (100%)	0	100	100
22	y	55/55 (100%)	55 (100%)	0	100	100
23	z	48/49 (98%)	47 (98%)	1 (2%)	47	65
24	B	47/48 (98%)	47 (100%)	0	100	100
25	C	45/49 (92%)	44 (98%)	1 (2%)	45	64
26	D	38/38 (100%)	38 (100%)	0	100	100
27	E	51/52 (98%)	51 (100%)	0	100	100
28	F	34/34 (100%)	34 (100%)	0	100	100
29	G	186/199 (94%)	184 (99%)	2 (1%)	65	73
30	H	170/190 (90%)	169 (99%)	1 (1%)	78	80
31	I	172/173 (99%)	172 (100%)	0	100	100
32	J	119/126 (94%)	117 (98%)	2 (2%)	53	67
33	K	88/112 (79%)	88 (100%)	0	100	100
34	L	124/129 (96%)	124 (100%)	0	100	100
35	M	104/105 (99%)	103 (99%)	1 (1%)	68	75
36	N	105/107 (98%)	104 (99%)	1 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	O	86/90 (96%)	86 (100%)	0	100	100
38	P	89/99 (90%)	88 (99%)	1 (1%)	65	73
39	Q	103/104 (99%)	103 (100%)	0	100	100
40	R	92/96 (96%)	92 (100%)	0	100	100
41	S	83/84 (99%)	83 (100%)	0	100	100
42	T	76/77 (99%)	76 (100%)	0	100	100
43	U	65/65 (100%)	65 (100%)	0	100	100
44	V	74/78 (95%)	73 (99%)	1 (1%)	59	70
45	W	56/65 (86%)	56 (100%)	0	100	100
46	X	70/79 (89%)	70 (100%)	0	100	100
47	Y	65/66 (98%)	65 (100%)	0	100	100
48	Z	55/61 (90%)	54 (98%)	1 (2%)	51	66
49	a	110/181 (61%)	110 (100%)	0	100	100
55	8	307/317 (97%)	306 (100%)	1 (0%)	86	84
All	All	5007/5245 (96%)	4979 (99%)	28 (1%)	76	80

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
20	w	47	VAL
55	8	179	VAL
29	G	46	VAL
38	P	15	VAL
25	C	22	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 121 such sidechains are listed below:

Mol	Chain	Res	Type
28	F	37	GLN
47	Y	54	GLN
31	I	139	ASN
47	Y	47	GLN
55	8	280	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
50	3	1538/1539 (99%)	145 (9%)	2 (0%)
51	1	2902/2903 (99%)	365 (12%)	6 (0%)
52	2	119/120 (99%)	11 (9%)	1 (0%)
53	5	72/77 (93%)	7 (9%)	0
54	4	19/27 (70%)	3 (15%)	0
All	All	4650/4666 (99%)	531 (11%)	9 (0%)

5 of 531 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
50	3	6	G
50	3	7	A
50	3	9	G
50	3	31	G
50	3	32	A

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	1	2436	G
52	2	88	C
51	1	1738	G
51	1	2286	G
51	1	2299	U

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

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

5.5 Carbohydrates [i](#)

There are no 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
10	m	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	m	96:ILE	C	97:GLN	N	1.19

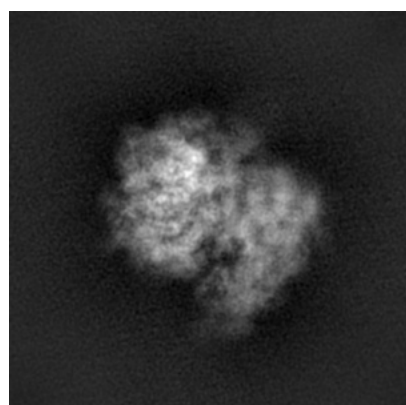
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20057. These allow visual inspection of the internal detail of the map and identification of artifacts.

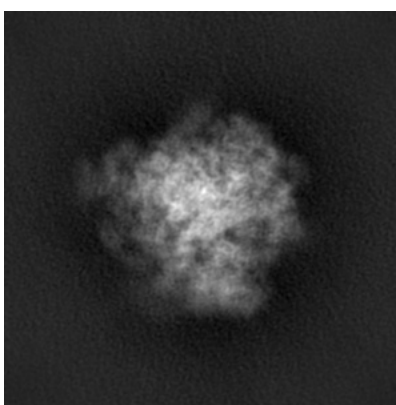
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

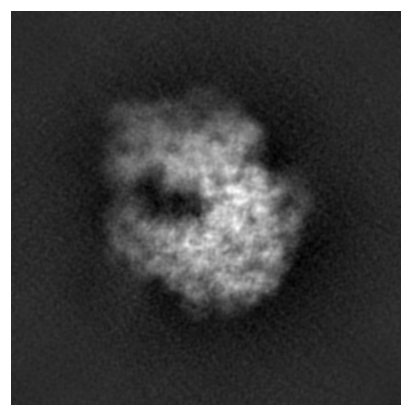
6.1.1 Primary map



X



Y

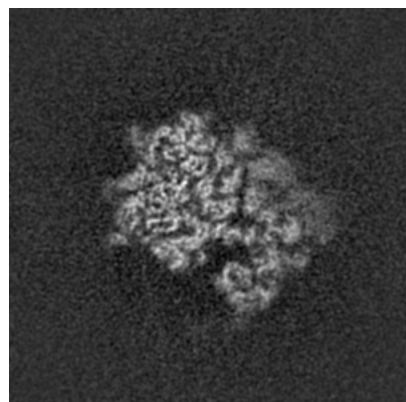


Z

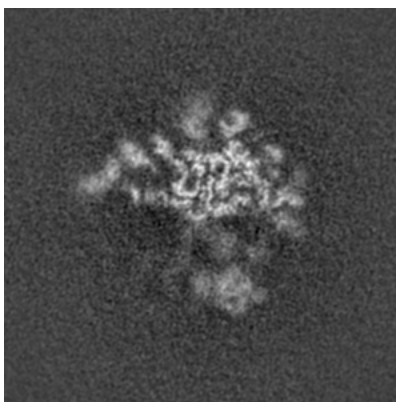
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

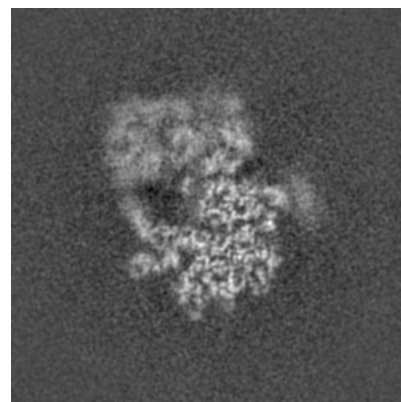
6.2.1 Primary map



X Index: 156



Y Index: 156

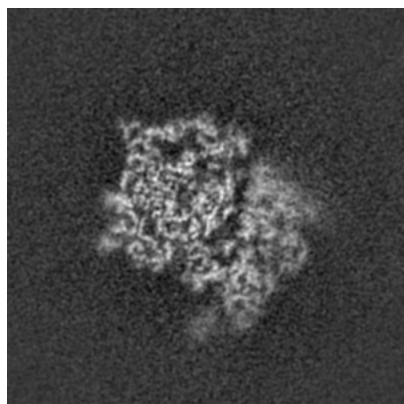


Z Index: 156

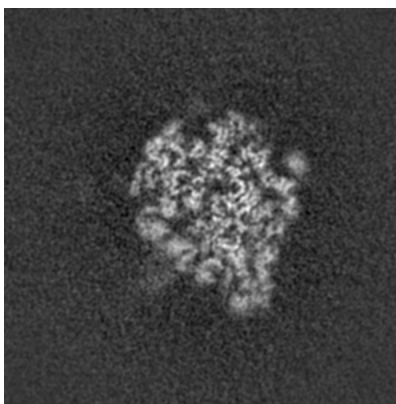
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

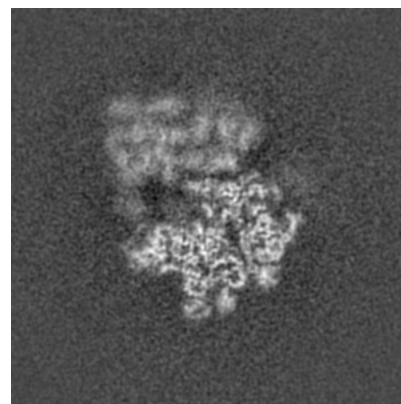
6.3.1 Primary map



X Index: 167



Y Index: 138

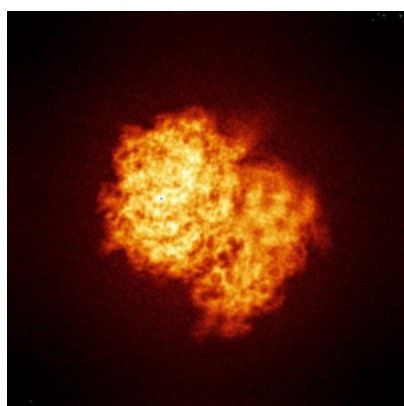


Z Index: 164

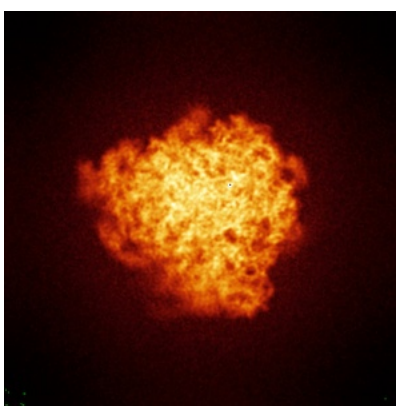
The images above show the largest variance slices of the map in three orthogonal directions.

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

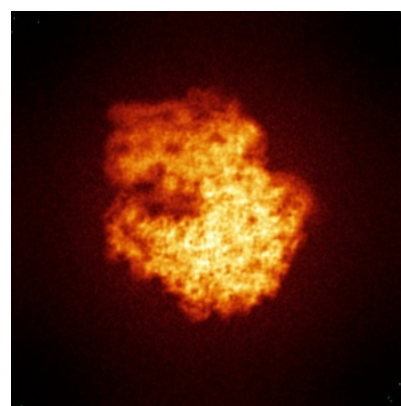
6.4.1 Primary map



X



Y

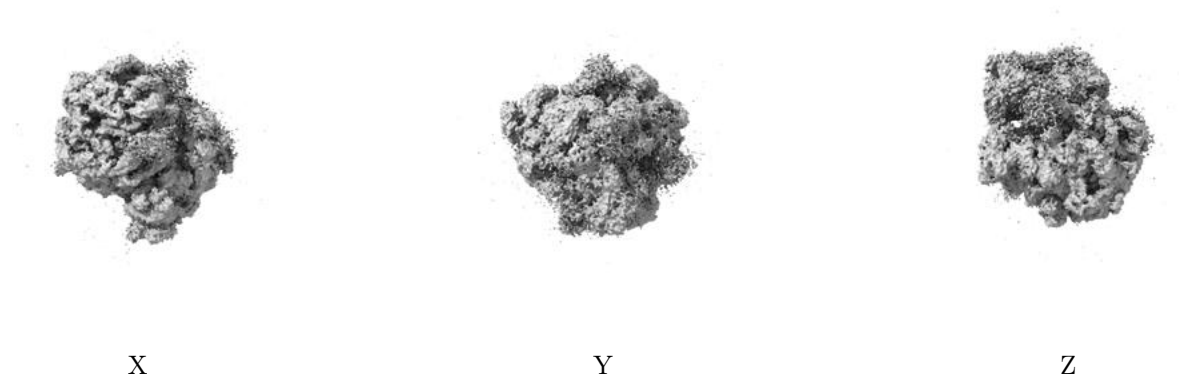


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

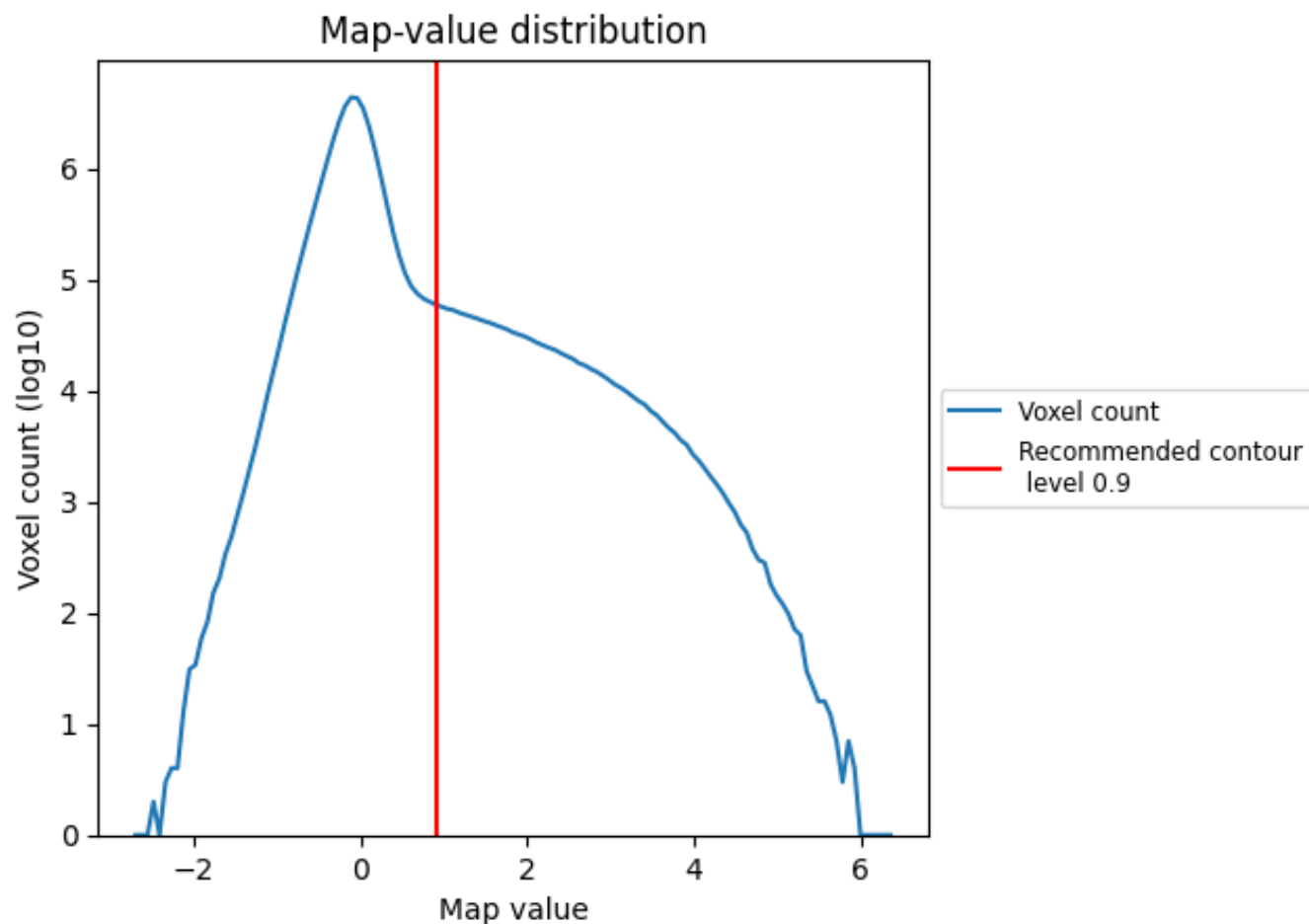
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

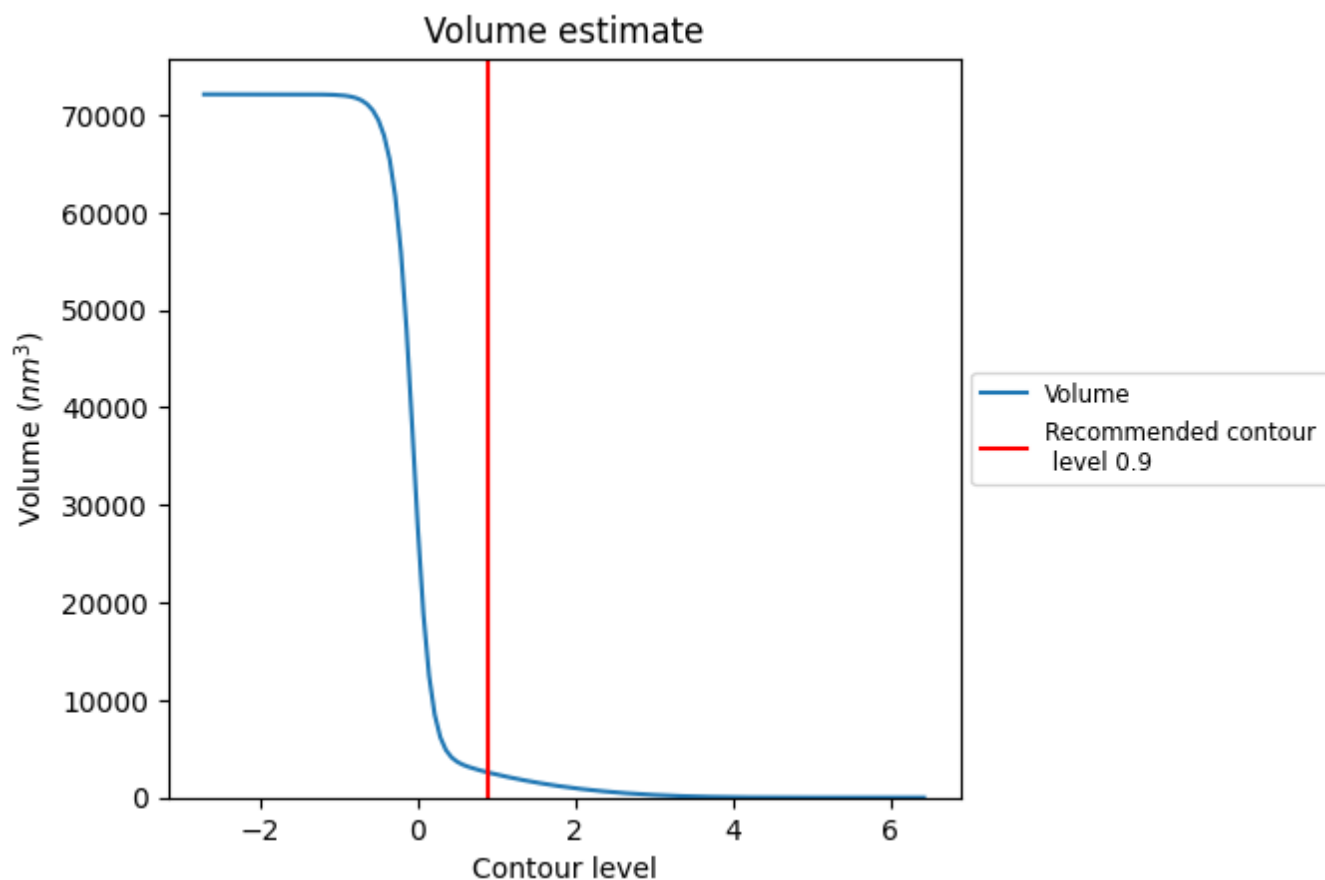
This section contains the results of statistical analysis of the map.

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.

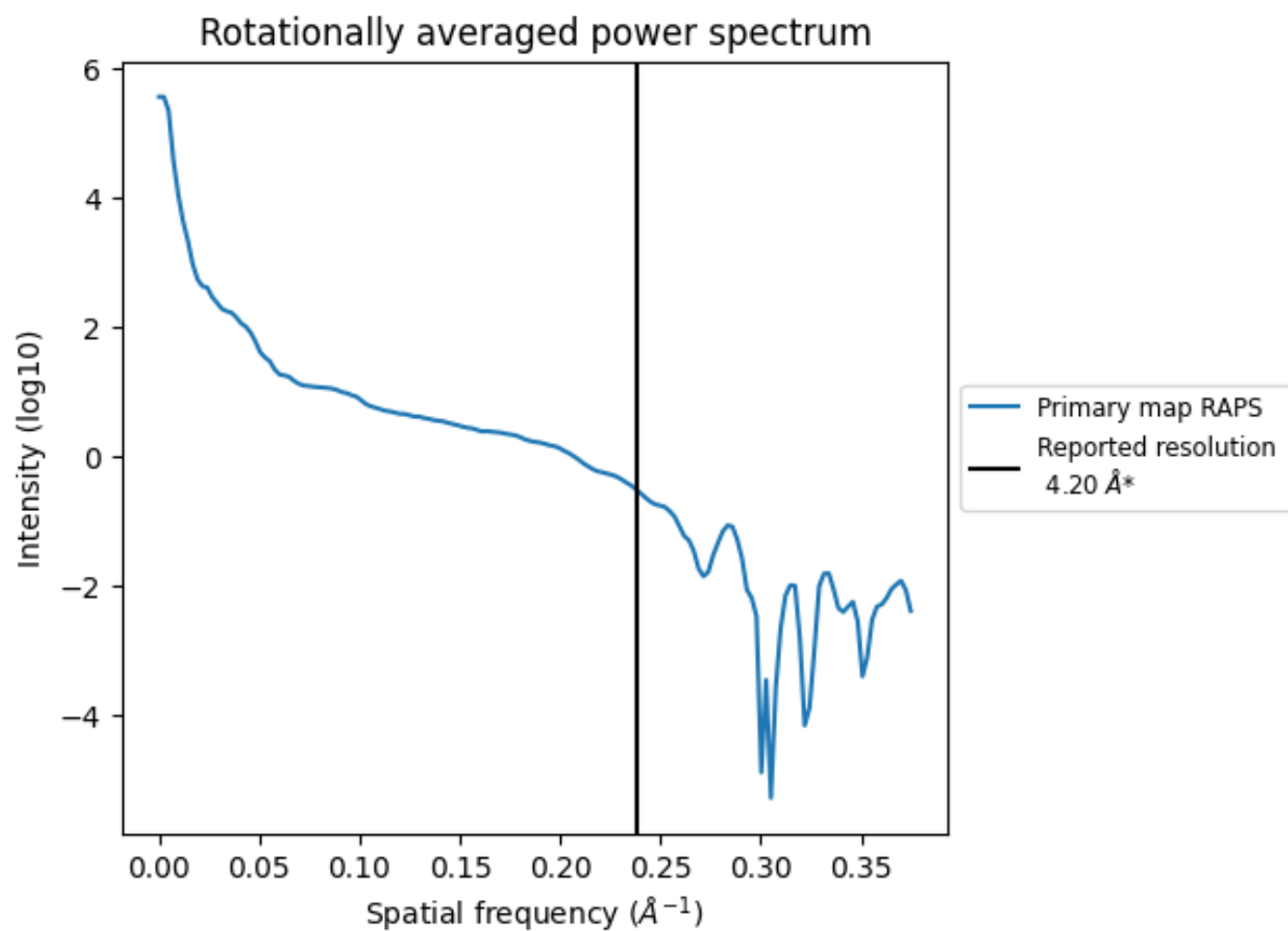
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2573 nm³; this corresponds to an approximate mass of 2324 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 0.238 Å⁻¹

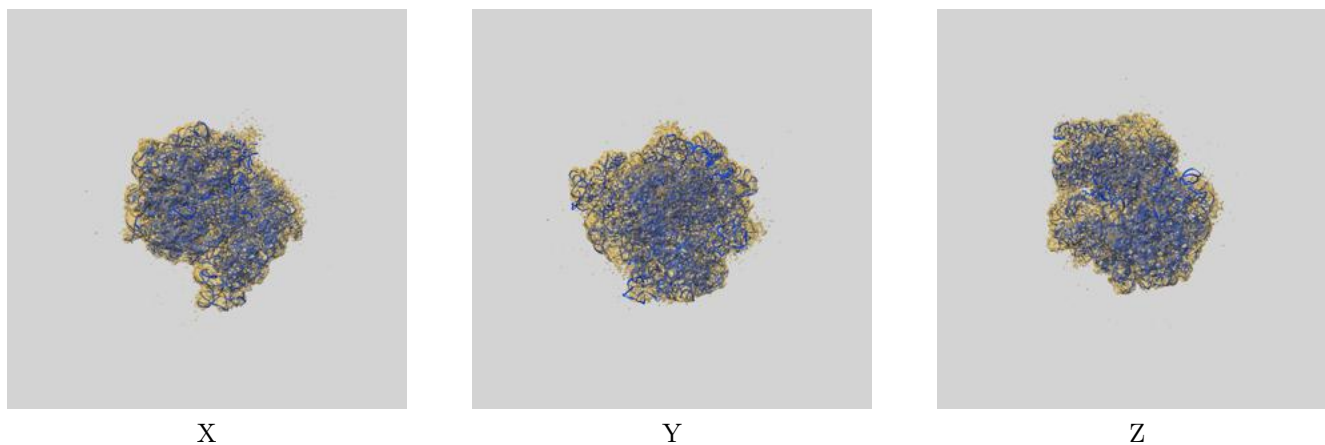
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

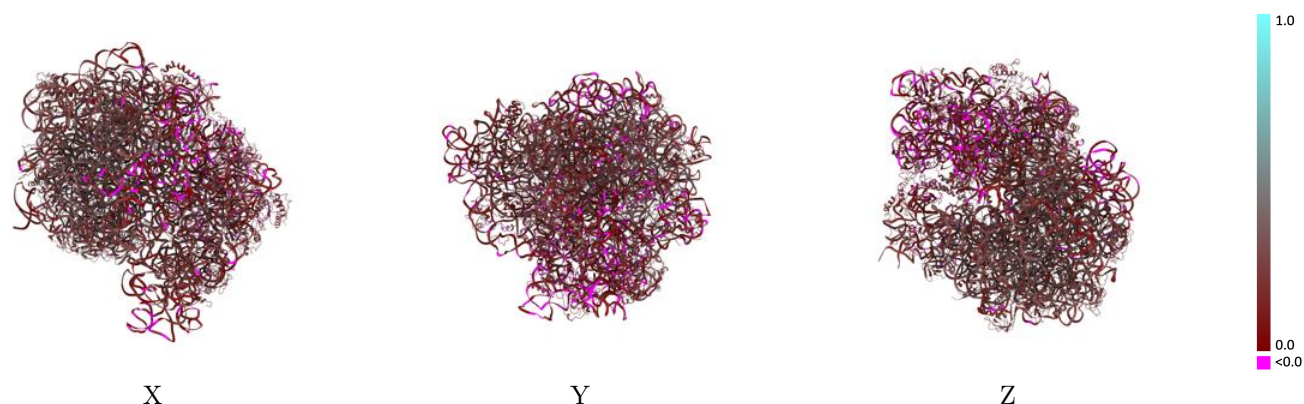
This section contains information regarding the fit between EMDB map EMD-20057 and PDB model 6OGG. Per-residue inclusion information can be found in section [3](#) on page [15](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.9 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](#)

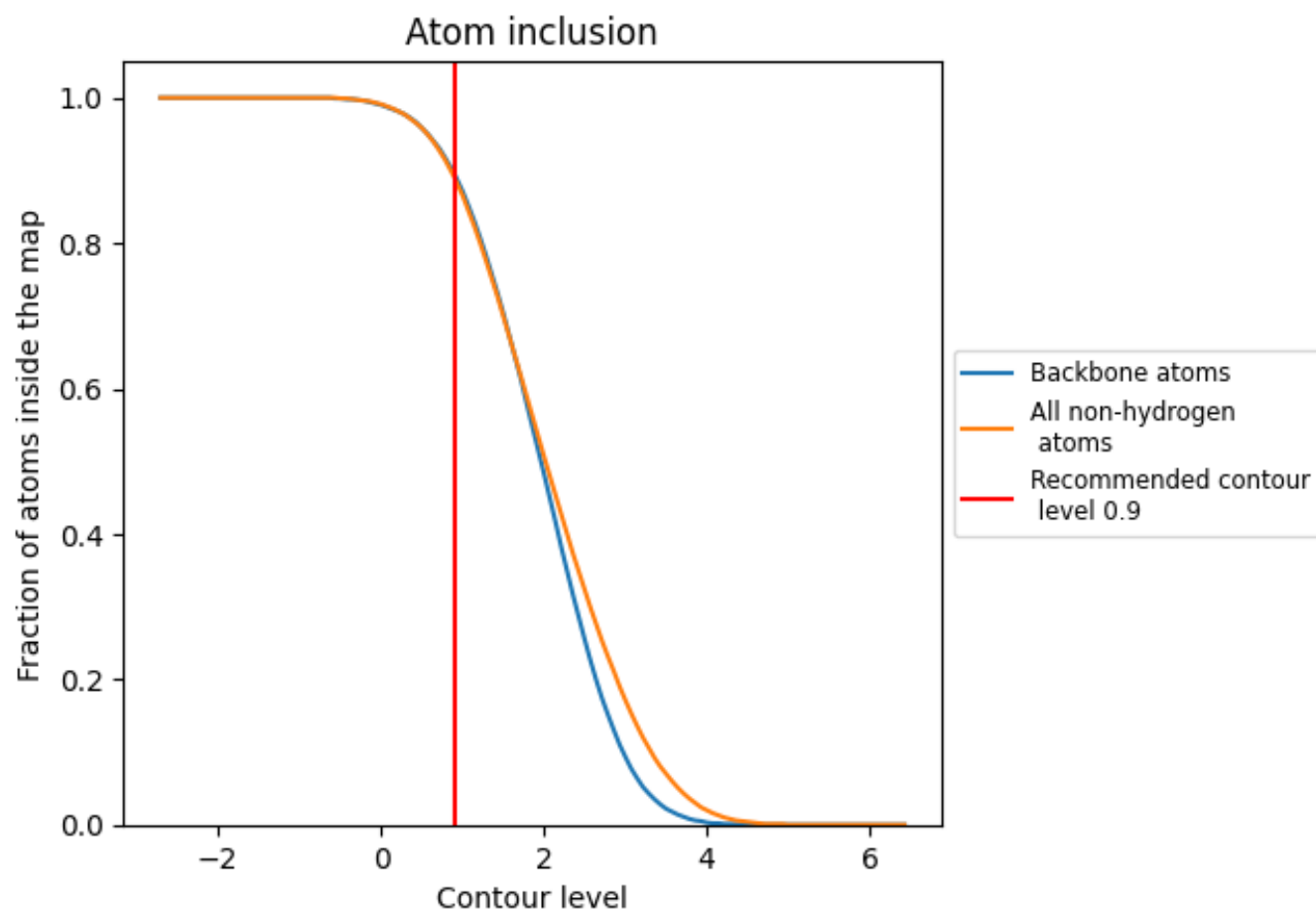


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 89% 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 (0.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.2240
1	 0.9070	 0.2460
2	 0.9720	 0.2100
3	 0.9150	 0.1580
4	 0.8920	 0.0830
5	 0.7780	 0.0890
8	 0.5660	 0.1900
B	 0.9700	 0.3210
C	 0.8600	 0.2750
D	 0.9470	 0.3110
E	 0.9630	 0.3070
F	 0.9380	 0.1780
G	 0.6850	 0.2020
H	 0.7360	 0.1980
I	 0.8400	 0.2070
J	 0.9480	 0.2500
K	 0.9500	 0.1840
L	 0.7760	 0.1760
M	 0.9490	 0.2290
N	 0.9010	 0.1530
O	 0.6480	 0.1950
P	 0.9050	 0.1660
Q	 0.8890	 0.2380
R	 0.8140	 0.1920
S	 0.8500	 0.1540
T	 0.9420	 0.2000
U	 0.9510	 0.2700
V	 0.9790	 0.2460
W	 0.9750	 0.1860
X	 0.8280	 0.1600
Y	 0.9290	 0.2280
Z	 0.7620	 0.2340
a	 0.2300	 0.2050
b	 0.9690	 0.2920
c	 0.9720	 0.3200



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Chain	Atom inclusion	Q-score
d	 0.9260	 0.3050
e	 0.8920	 0.2010
f	 0.6370	 0.2340
g	 0.4020	 0.2340
j	 0.9710	 0.3010
k	 0.9520	 0.3240
l	 0.9640	 0.3080
m	 0.9550	 0.3070
n	 0.9710	 0.3070
o	 0.9750	 0.2480
p	 0.9660	 0.3250
q	 0.9550	 0.2920
r	 0.9510	 0.3100
s	 0.9580	 0.3230
t	 0.9360	 0.2830
u	 0.9430	 0.2850
v	 0.9660	 0.2750
w	 0.9700	 0.3240
x	 0.9430	 0.2910
y	 0.9480	 0.2760
z	 0.9700	 0.3110