



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 10:48 PM UTC

PDB ID : 5ZEP / pdb_00005zep
EMDB ID : EMD-6921
Title : M. smegmatis hibernating state 70S ribosome structure
Authors : Mishra, S.; Ahmed, T.; Tyagi, A.; Shi, J.; Bhushan, S.
Deposited on : 2018-02-27
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

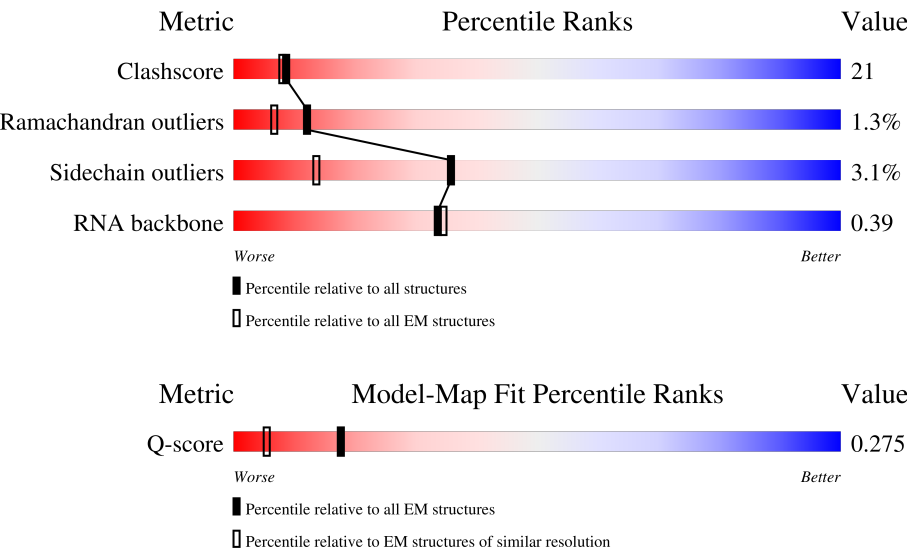
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.40 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.



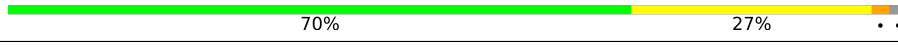
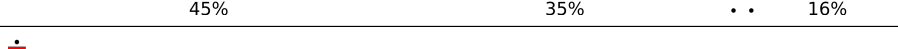
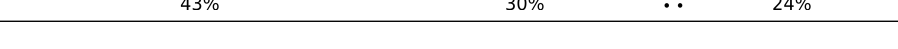
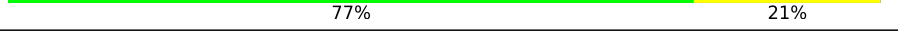
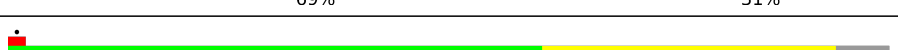
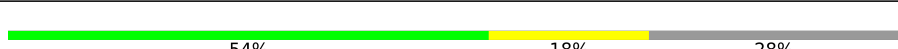
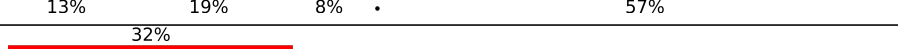
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	a	1528	46% 40% 12%
2	c	275	47% 25% 24%
3	e	214	5% 61% 30% 7%

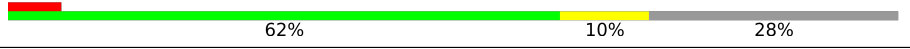
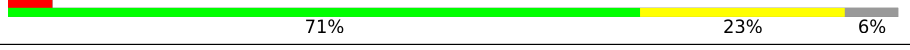
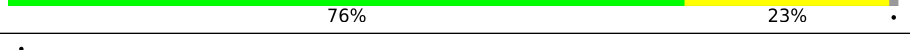
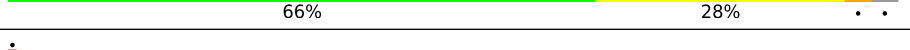
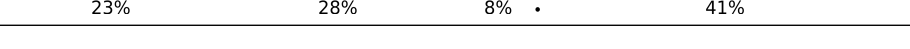
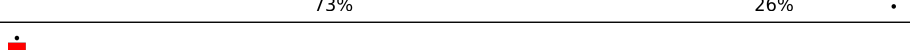
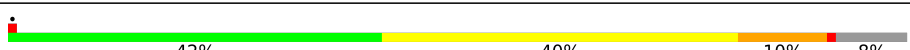
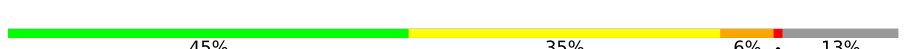
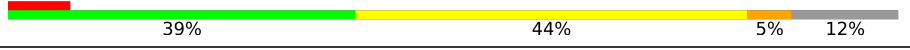
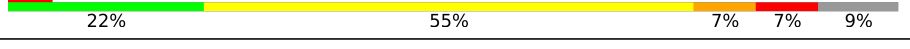
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Mol	Chain	Length	Quality of chain
4	g	156	
5	h	132	
6	i	150	
7	j	101	
8	k	138	
9	l	124	
10	o	89	
11	q	98	
12	r	84	
13	s	93	
14	t	86	
15	n	61	
16	b	277	
17	d	201	
18	f	96	
19	m	124	
20	p	156	
21	u	33	
22	w	77	
23	x	230	
24	0	479	
25	C	278	
26	D	217	
27	E	215	
28	F	187	

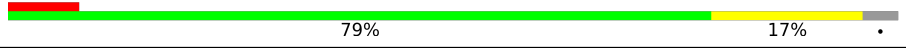
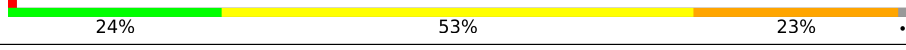
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Mol	Chain	Length	Quality of chain
29	G	179	
30	H	151	
31	I	175	
32	J	142	
33	K	147	
34	L	122	
35	M	147	
36	N	138	
37	O	199	
38	P	127	
39	Q	113	
40	R	129	
41	S	103	
42	T	153	
43	U	100	
44	V	105	
45	W	215	
46	X	88	
47	Y	64	
48	Z	77	
49	v	61	
50	y	75	
51	z	57	
52	1	55	
53	2	47	

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Mol	Chain	Length	Quality of chain
54	3	64	
55	4	37	
56	5	24	
57	B	118	
58	A	3120	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 152451 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	1506	Total	C	N	O	P	0	0
			32341	14404	5921	10510	1506		

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	210	Total	C	N	O	S	0	0
			1672	1043	324	300	5		

- Molecule 3 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	e	198	Total	C	N	O	S	0	0
			1433	885	282	262	4		

- Molecule 4 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	g	156	Total	C	N	O	S	0	0
			1240	773	242	222	3		

- Molecule 5 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	130	Total	C	N	O	S	0	0
			1003	629	188	185	1		

- Molecule 6 is a protein called 30S ribosomal protein S9.

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

- Molecule 7 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	97	Total	C	N	O	S	0	0
			775	488	143	141	3		

- Molecule 8 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	k	117	Total	C	N	O	S	0	0
			871	539	173	158	1		

- Molecule 9 is a protein called 30S ribosomal protein S12.

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

- Molecule 10 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	o	87	Total	C	N	O	0	0
			709	443	143	123		

- Molecule 11 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	q	92	Total	C	N	O	S	0	0
			730	458	138	132	2		

- Molecule 12 is a protein called 30S ribosomal protein S18 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	r	64	Total	C	N	O	S	0	0
			512	319	102	88	3		

- Molecule 13 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	s	78	Total	C	N	O	S	0	0
			630	405	117	107	1		

- Molecule 14 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	t	84	Total	C	N	O	0	0
			655	399	138	118		

- Molecule 15 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	60	Total	C	N	O	S	0	0
			477	302	97	73	5		

- Molecule 16 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	228	Total	C	N	O	S	0	0
			1793	1132	322	330	9		

- Molecule 17 is a protein called 30S ribosomal protein S4.

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

- Molecule 18 is a protein called 30S ribosomal protein S6.

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

- Molecule 19 is a protein called 30S ribosomal protein S13.

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

- Molecule 20 is a protein called 30S ribosomal protein S16.

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

- Molecule 21 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	u	32	Total	C	N	O	S	0	0
			280	172	71	36	1		

- Molecule 22 is a RNA chain called E-tRNA^fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	w	77	Total	C	N	O	P	0	0
			1643	732	297	537	77		

- Molecule 23 is a protein called Ribosome hibernation promoting factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	x	100	Total	C	N	O	S	0	0
			831	513	167	149	2		

- Molecule 24 is a protein called bS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	0	262	Total	C	N	O	S	0	0
			1310	786	262	262			

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	C	273	Total	C	N	O	S	0	0
			2097	1290	435	368	4		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	E	207	Total	C	N	O	S	0	0
			1553	959	292	300	2		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	F	181	Total	C	N	O	S	0	0
			1437	903	269	259	6		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	K	147	Total	C	N	O	S	0	0
			1138	727	208	201	2		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	L	121	Total	C	N	O	S	0	0
			930	580	178	169	3		

- Molecule 35 is a protein called 50S ribosomal protein L15.

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

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	N	134	Total	C	N	O	S	0	0
			1074	680	211	181	2		

- Molecule 37 is a protein called 50S ribosomal protein L17.

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

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	P	126	Total	C	N	O		0	0
			956	586	199	171			

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	R	124	Total	C	N	O		0	0
			988	613	203	172			

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	S	102	Total	C	N	O		0	0
			768	487	140	141			

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
42	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	U	94	Total	C	N	O	0	0
			739	469	135	135		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	V	97	Total	C	N	O	S	0	0
			731	456	137	136	2		

- Molecule 45 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
45	W	186	Total	C	N	O	0	0
			1389	859	249	281		

- Molecule 46 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
46	X	82	Total	C	N	O	0	0
			604	372	127	105		

- Molecule 47 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 48 is a protein called 50S ribosomal protein L29.

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

- Molecule 49 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	v	60	Total	C	N	O	0	0
			483	298	97	88		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	y	66	Total	C	N	O	S	0	0
			510	316	93	96	5		

- Molecule 51 is a protein called 50S ribosomal protein L32.

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

- Molecule 52 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	1	50	Total	C	N	O	S	0	0
			416	254	86	72	4		

- Molecule 53 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	2	45	Total	C	N	O	S	0	0
			372	222	96	53	1		

- Molecule 54 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	3	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 55 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	4	37	Total	C	N	O	S	0	0
			298	181	66	46	5		

- Molecule 56 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	5	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 57 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B	117	Total	C	N	O	P	0	0
			2501	1116	462	806	117		

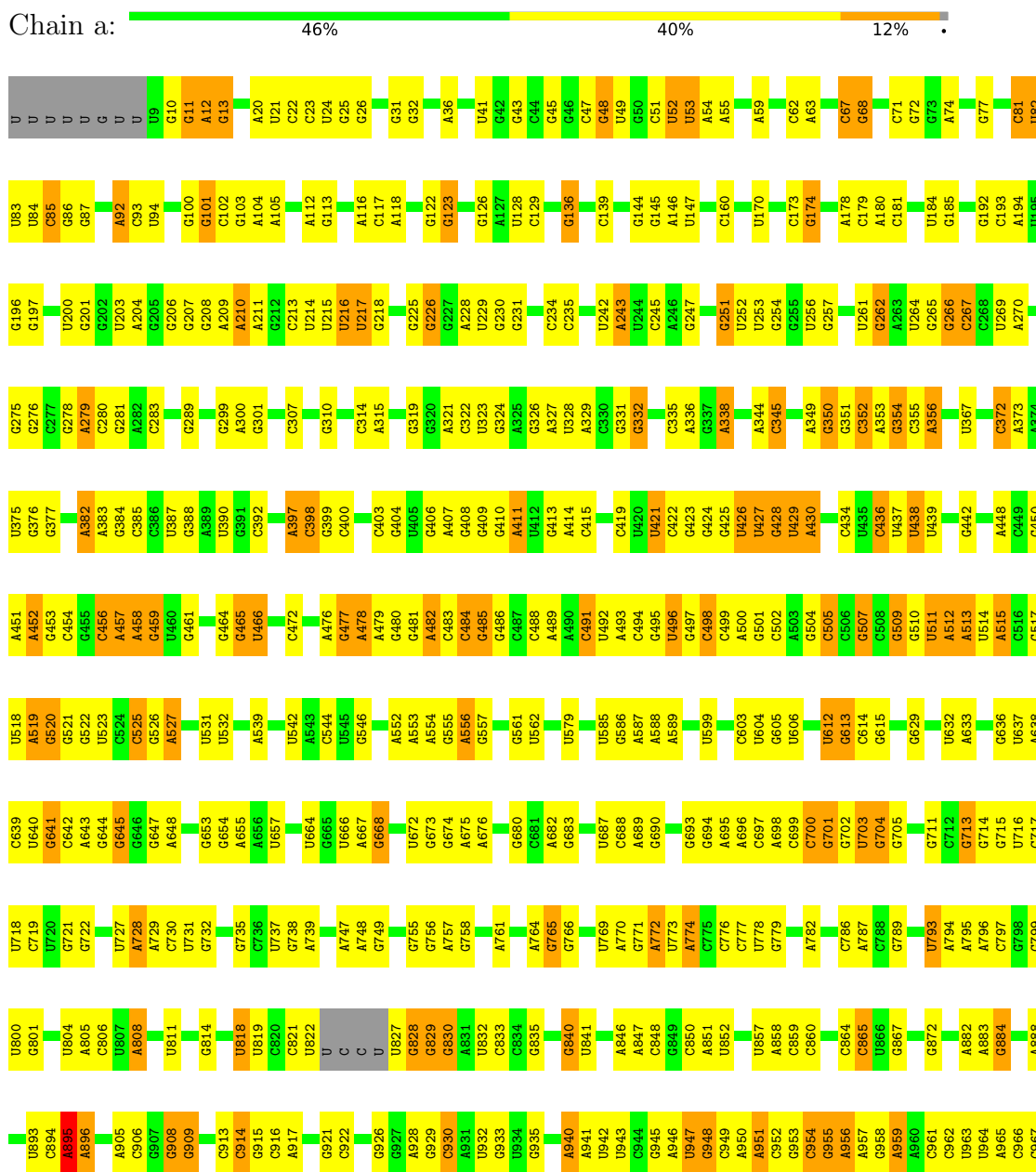
- Molecule 58 is a RNA chain called 23S rRNA.

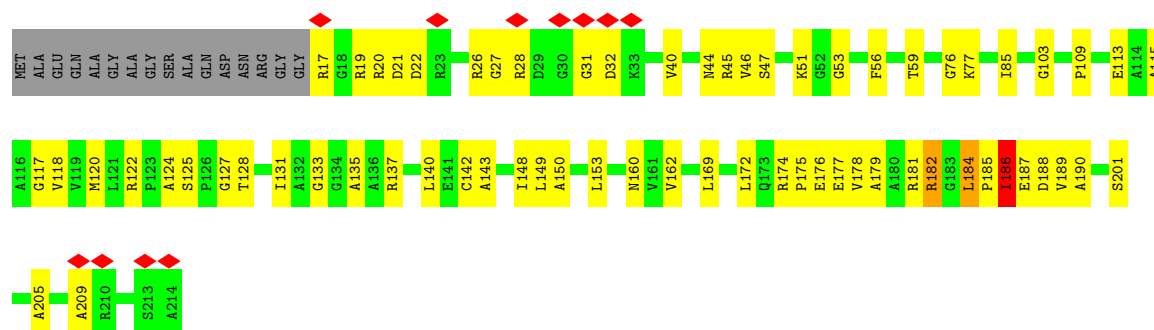
Mol	Chain	Residues	Atoms					AltConf	Trace
58	A	3102	Total	C	N	O	P	0	0
			66623	29694	12253	21574	3102		

3 Residue-property plots

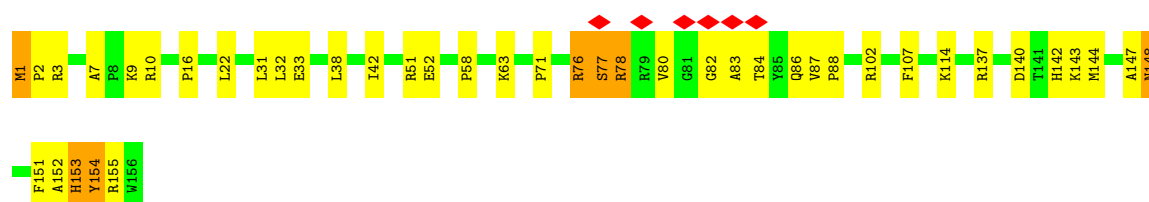
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S rRNA

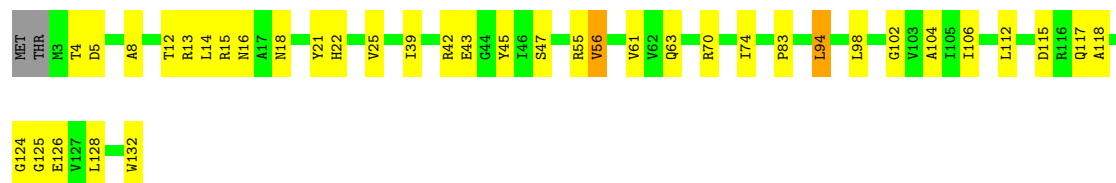




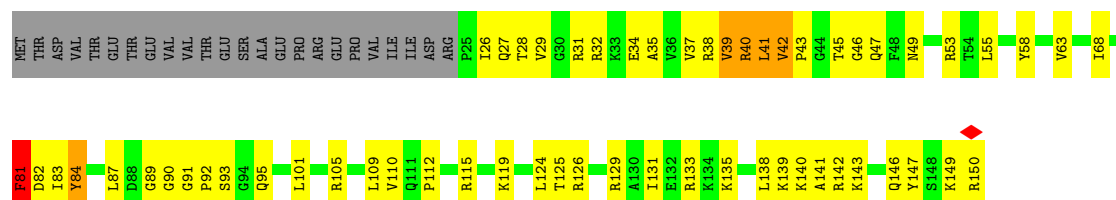
• Molecule 4: 30S ribosomal protein S7



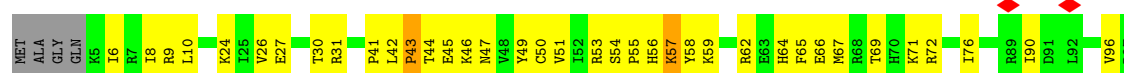
• Molecule 5: 30S ribosomal protein S8



• Molecule 6: 30S ribosomal protein S9

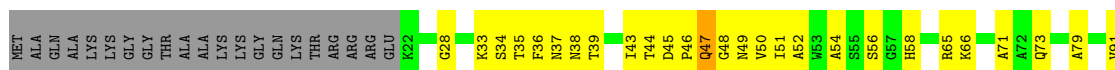


• Molecule 7: 30S ribosomal protein S10

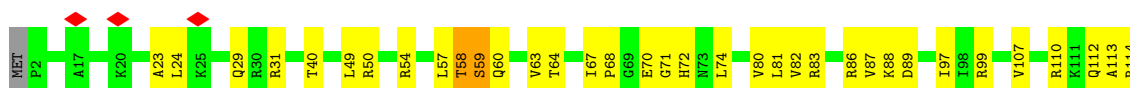




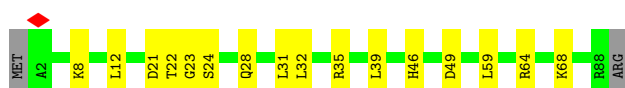
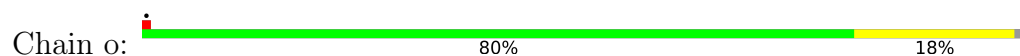
- Molecule 8: 30S ribosomal protein S11



- Molecule 9: 30S ribosomal protein S12



- Molecule 10: 30S ribosomal protein S15



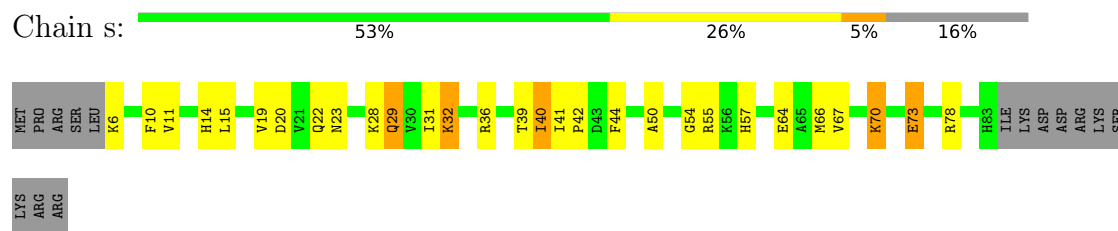
- Molecule 11: 30S ribosomal protein S17



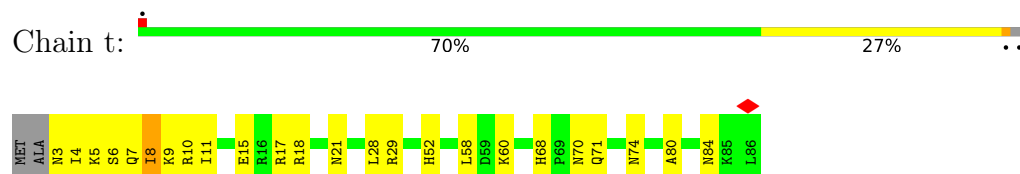
- Molecule 12: 30S ribosomal protein S18 2



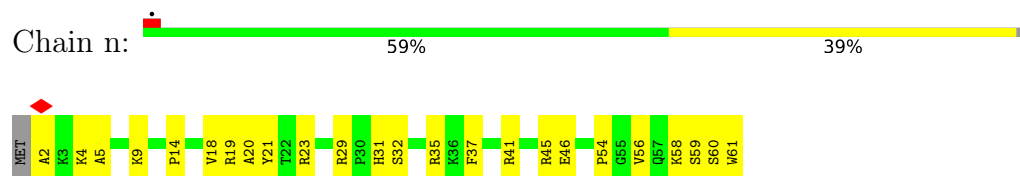
- Molecule 13: 30S ribosomal protein S19



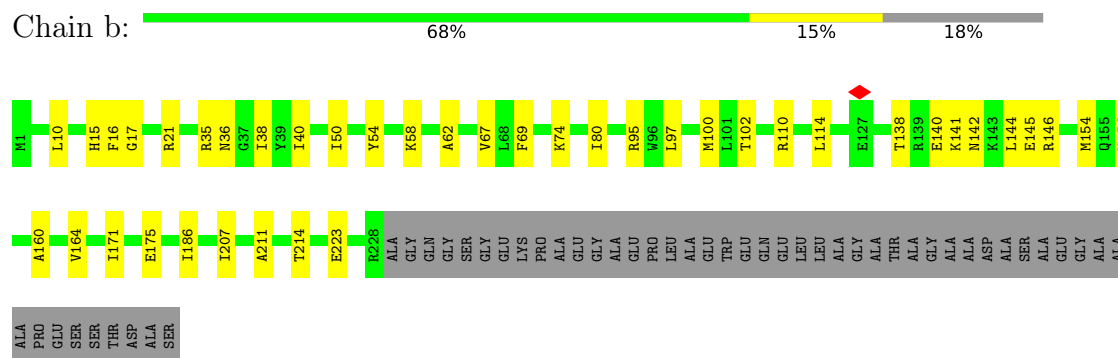
- Molecule 14: 30S ribosomal protein S20



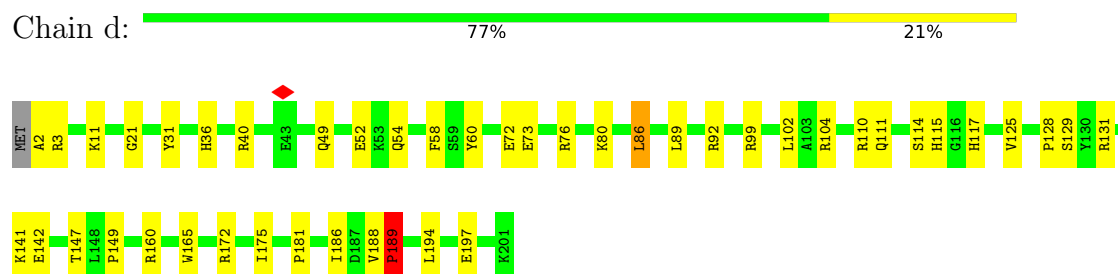
- Molecule 15: 30S ribosomal protein S14 type Z



- Molecule 16: 30S ribosomal protein S2



- Molecule 17: 30S ribosomal protein S4



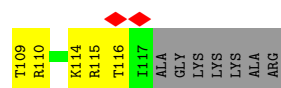
- Molecule 18: 30S ribosomal protein S6

Chain f:  69% 31%



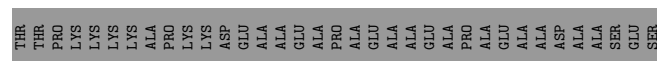
- Molecule 19: 30S ribosomal protein S13

Chain m:  60% 33% 6%



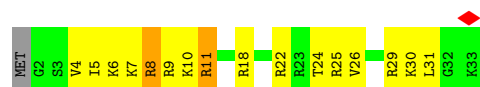
- Molecule 20: 30S ribosomal protein S16

Chain p:  54% 18% 28%



- Molecule 21: Conserved domain protein

Chain u:  48% 42% 6%



- Molecule 22: E-tRNA^{fMet}

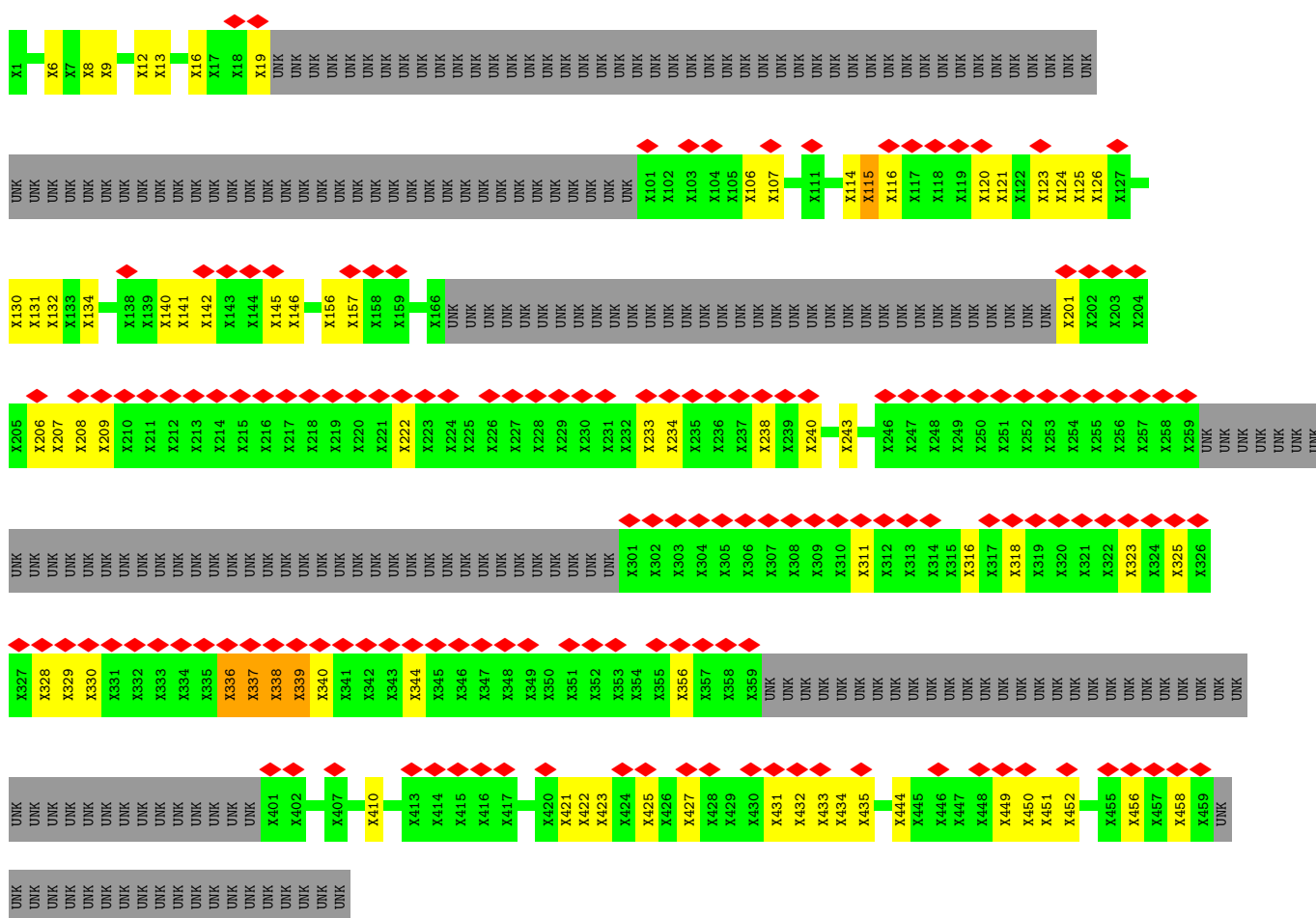
Chain w:  17% 48% 52%



- Molecule 23: Ribosome hibernation promoting factor

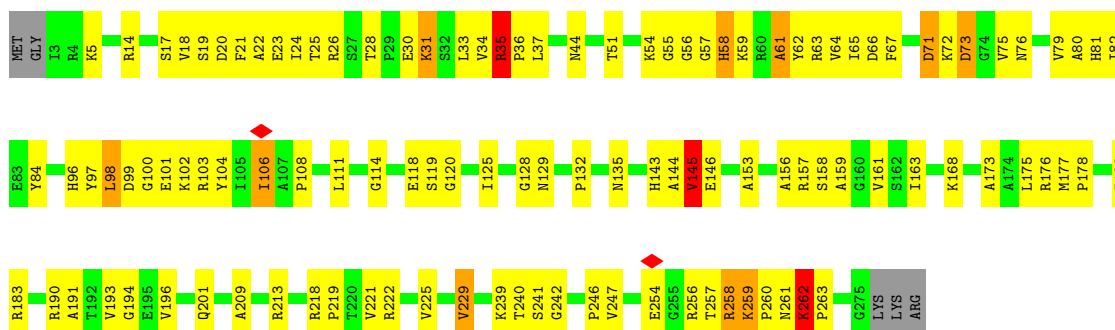
Chain x:  35% 13% 19% 8% 57%

- Molecule 24: bS1



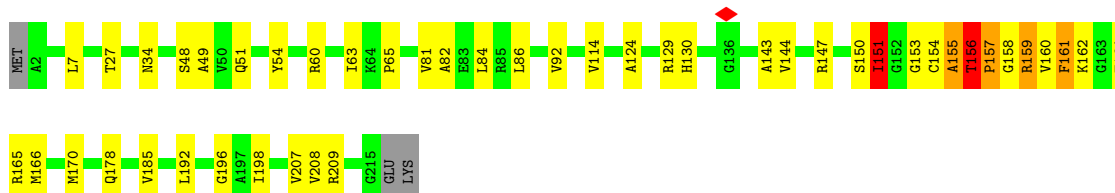
- Molecule 25: 50S ribosomal protein L2





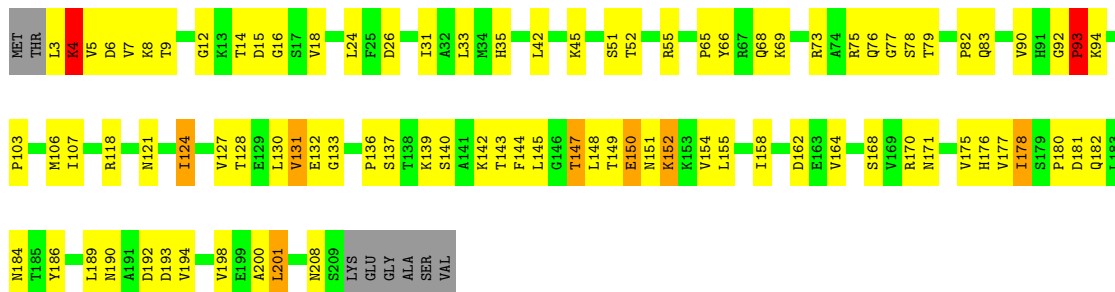
- Molecule 26: 50S ribosomal protein L3

Chain D: 77% 18% ...



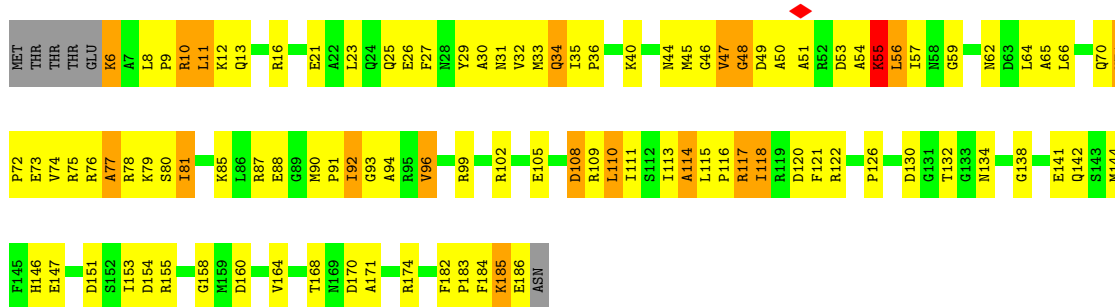
- Molecule 27: 50S ribosomal protein L4

Chain E: 54% 38% ...



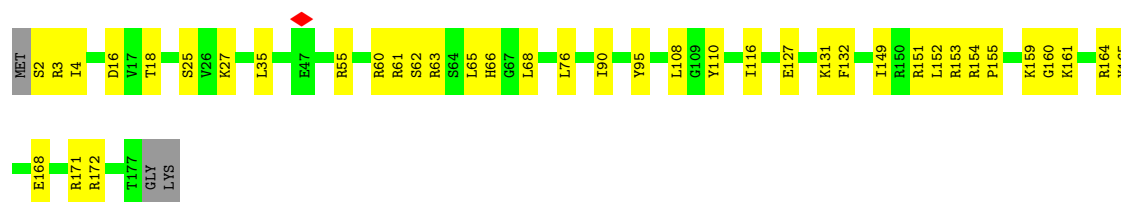
- Molecule 28: 50S ribosomal protein L5

Chain F: 42% 45% 10% ...



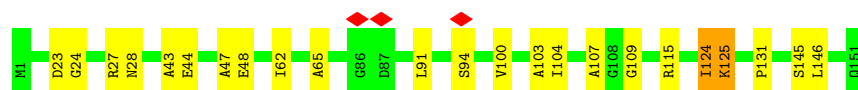
- Molecule 29: 50S ribosomal protein L6

Chain G:  77% 22%



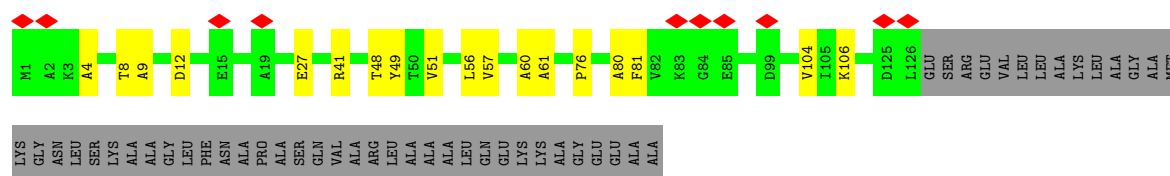
- Molecule 30: 50S ribosomal protein L9

Chain H:  85% 14%



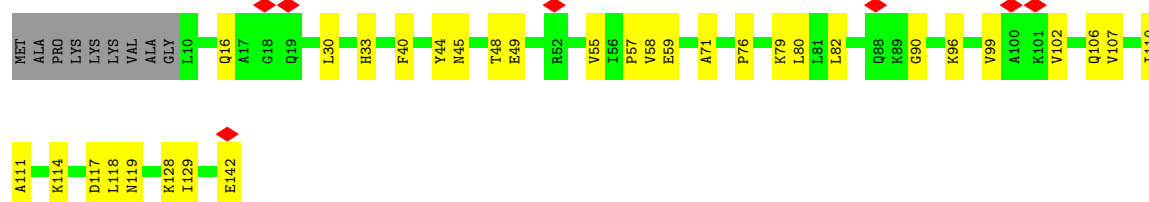
- Molecule 31: 50S ribosomal protein L10

Chain I:  6% 62% 10% 28%



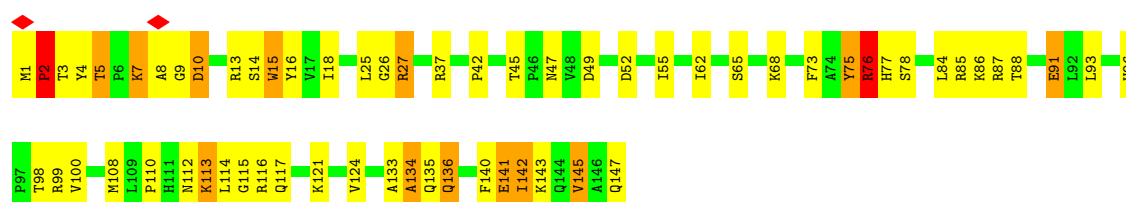
- Molecule 32: 50S ribosomal protein L11

Chain J:  5% 71% 23% 6%



- Molecule 33: 50S ribosomal protein L13

Chain K:  57% 33% 9%



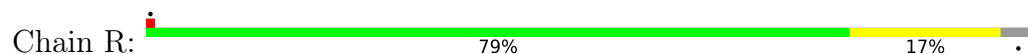
- Molecule 34: 50S ribosomal protein L14



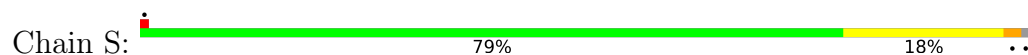
- Molecule 39: 50S ribosomal protein L19



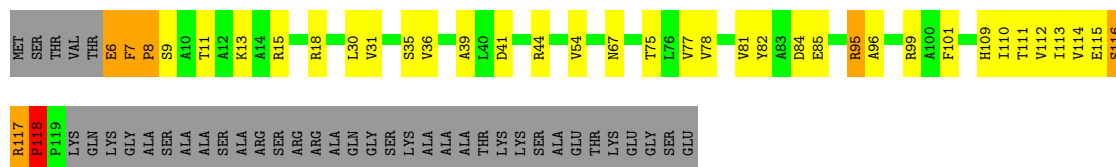
- Molecule 40: 50S ribosomal protein L20



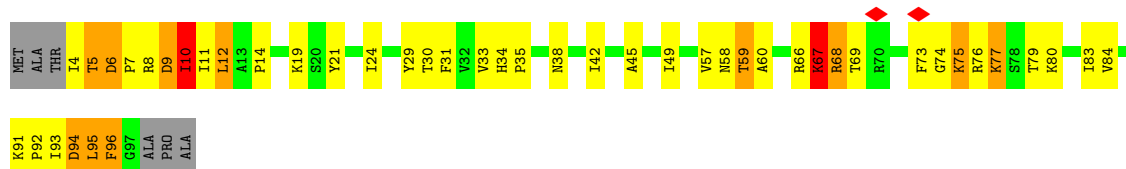
- Molecule 41: 50S ribosomal protein L21



- Molecule 42: 50S ribosomal protein L22

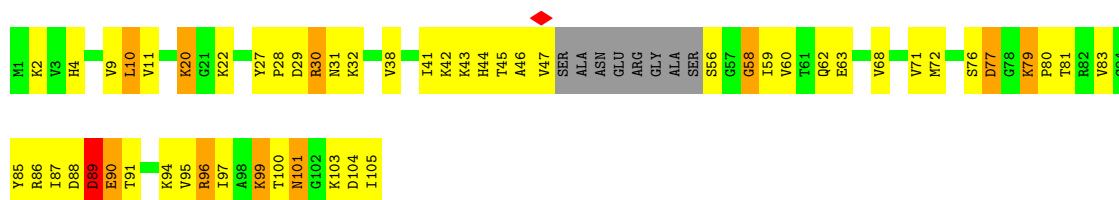


- Molecule 43: 50S ribosomal protein L23



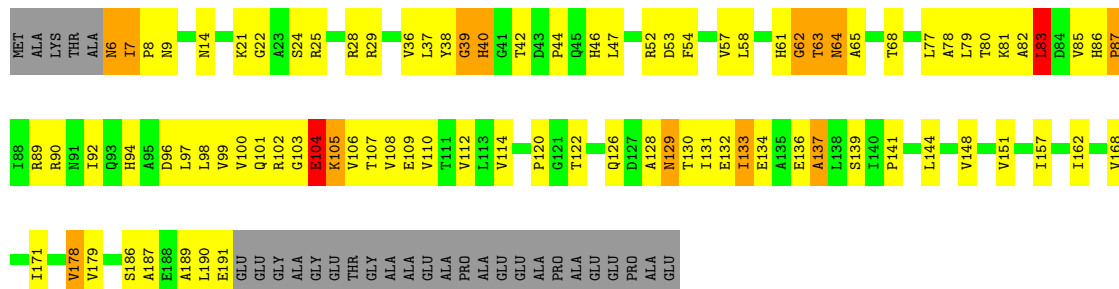
- Molecule 44: 50S ribosomal protein L24





- Molecule 45: 50S ribosomal protein L25

Chain W: 45% 35% 6% 13%



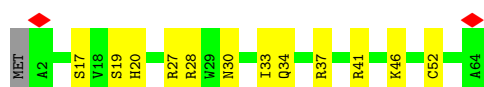
- Molecule 46: 50S ribosomal protein L27

Chain X: 5% 56% 31% 6% 7%



- Molecule 47: 50S ribosomal protein L28

Chain Y: 80% 19%



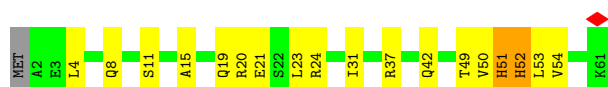
- Molecule 48: 50S ribosomal protein L29

Chain Z: 51% 26% 5% 18%

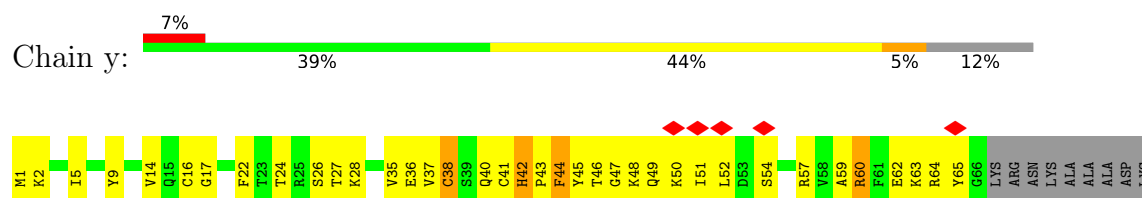


- Molecule 49: 50S ribosomal protein L30

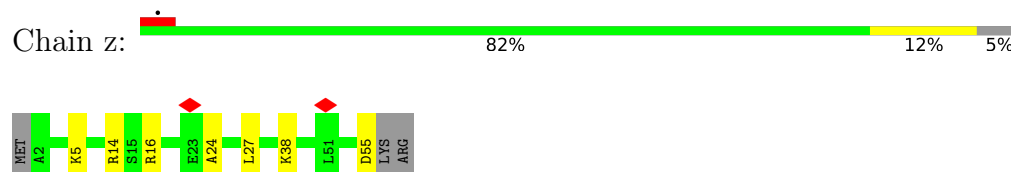
Chain v: 69% 26%



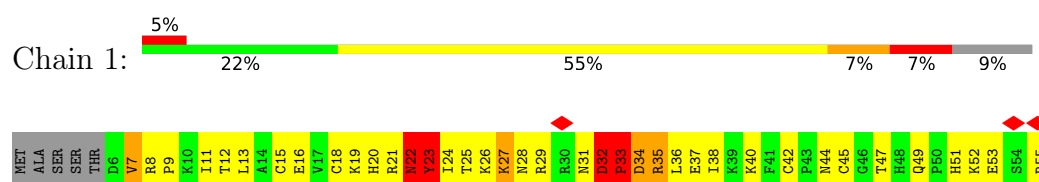
- Molecule 50: 50S ribosomal protein L31



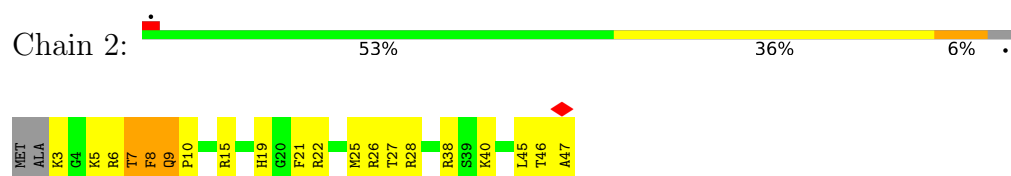
- Molecule 51: 50S ribosomal protein L32



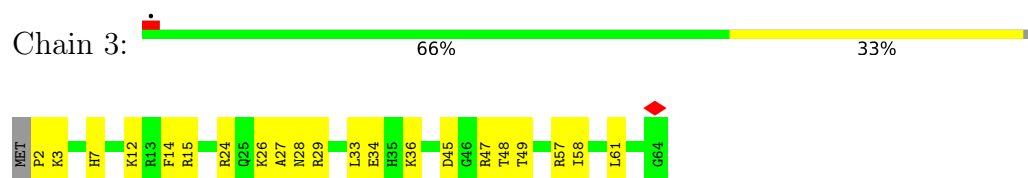
- Molecule 52: 50S ribosomal protein L33 1



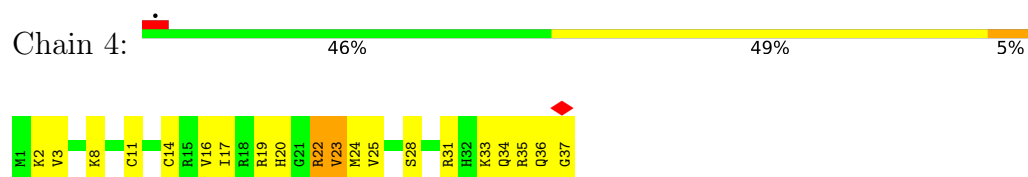
- Molecule 53: 50S ribosomal protein L34



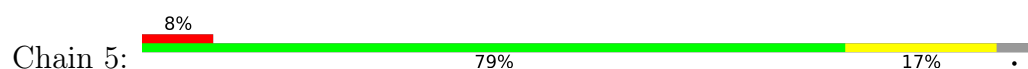
- Molecule 54: 50S ribosomal protein L35

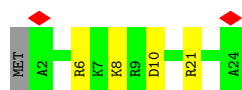


- Molecule 55: 50S ribosomal protein L36



- Molecule 56: Uncharacterized protein





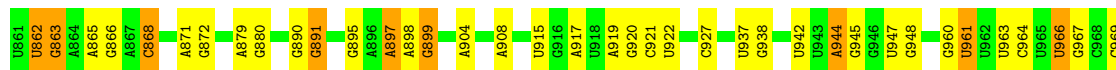
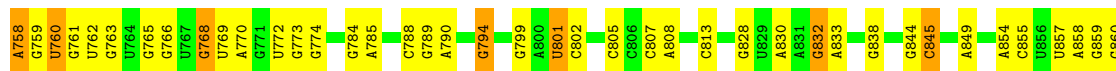
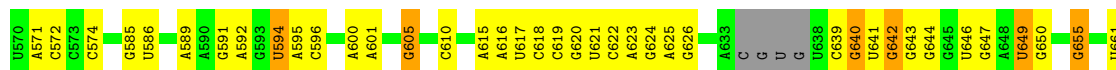
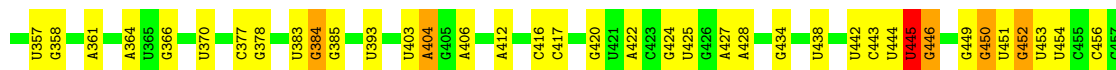
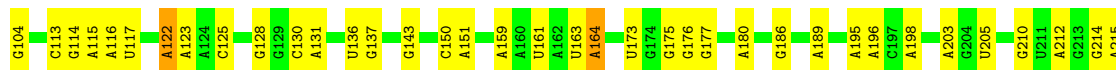
• Molecule 57: 5S rRNA

Chain B: 24% 53% 23%



• Molecule 58: 23S rRNA

Chain A: 58% 34% 7%



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A2257	A2142	G2045	G1933	G1803	G1711	U1619	C1558	A1480	G1363	A1246	A1164	G1069	G972
U2261	C2144	A2046	G1938	A1804	G1712	U1620	U1560	A1481	U1364	G1249	A1169	C1068	G973
G2262	A2151	G2052	U1939	G1805	U1713	C1621	C1561	A1482	G1365	U1250	G1170	G1069	G974
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C3088	U2980	G2665	C2764	U2877	C3088	U2381	C2472	U2567	G2665	C2764	U2877	C3088	U2980	C3088
A3093	A2981	C2668	G2761	A2878	A3093	U2382	C2473	C2571	C2668	G2761	A2878	A3093	A2981	A3093
A3094	A2982	G2669	C2762	C2881	A3094	U2387	G2476	C2574	G2669	C2762	C2881	A3094	A2982	A3094
C3095	G2985	U2670	C2763	C2882	C3095	U2388	C2485	G2575	U2670	C2763	C2882	C3095	G2985	C3095
U3096	A2989	G2671	G2764	U2885	U3096	U2389	U2486	A2578	G2671	G2764	U2885	U3096	A2989	U3096
C3101	A2990	A2672	U2765	A2886	C3101	U2390	C2487	A2582	A2672	U2765	A2886	C3101	A2990	C3101
U3102	C2993	U2673	U2767	G2887	U3102	U2391	G2487	A2582	U2673	U2767	G2887	U3102	C2993	U3102
C3106	U2993	C2676	U2768	C2891	C3106	U2392	A2490	A2582	C2676	U2768	C2891	C3106	U2993	C3106
G3107	C2994	A2677	A2769	G2892	G3107	U2393	A2497	U2585	A2677	A2769	G2892	G3107	C2994	G3107
A3112	U2995	G2678	A2790	G2893	A3112	U2394	A2498	G2586	G2678	A2790	G2893	A3112	U2995	A3112
A3113	G3001	G2682	C2792	G2894	A3113	U2404	C2499	A2593	G2682	C2792	G2894	A3113	G3001	A3113
A3114	C3003	U2686	G2793	C2895	A3114	U2405	G2500	G2594	U2686	G2793	C2895	A3114	C3003	A3114
A3115	C3004	U2687	G2794	G2897	A3115	U2406	G2501	G2595	U2687	G2794	G2897	A3115	C3004	A3115
C	A3005	C2900	A2796	C2900	C	U2407	G2503	G2596	C2900	A2796	C2900	C	A3005	A3115
	U3009	U2906	C2797	U2906		U2408	G2506	A2601	U2906	C2797	U2906		U3009	
	U3010	C2907	G2798	C2907		U2409	C2507	G2607	U3010	C2907	C2907		U3010	
	C3011	U2908	C2799	A2693		U2410	C2508	G2608	C3011	U2908	A2693		C3011	
	U3012	G2909	G2800	G2694		U2411	C2509	A2609	U3012	G2909	G2694		U3012	
	C3013	G2909	G2802	C2698		U2412	A2510	C2610	C3013	G2909	C2698		C3013	
	A3014	U2913	C2803	C2699		U2413	A2511	U2611	A3014	U2913	C2699		A3014	
	C3015	A2914	U2810	A2700		U2414	A2512	A2612	C3015	A2914	A2700		C3015	
	C3017	C2915	U2811	A2702		U2418	U2515	U2613	C3017	C2915	A2702		C3017	
	A3021	U2922	A2814	G2705		A2421	C2517	G2615	A3021	U2922	G2705		A3021	
	G3022	C2923	C2815	G2709		A2422	A2522	A2616	G3022	C2923	G2709		G3022	
	G3023	A2926	A2826	U2827		A2427	G2527	U2626	G3023	A2926	U2827		G3023	
	A3024	G2932	U2828	U2828		A2431	C2431	U2628	A3024	G2932	U2828		A3024	
	G3025					A2432	G2432		G3025				G3025	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	391837	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.253	Depositor
Minimum map value	-0.087	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	419.84, 419.84, 419.84	wwPDB
Map dimensions	328, 328, 328	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.28, 1.28, 1.28	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	a	0.40	0/36201	0.52	5/56488 (0.0%)
2	c	0.31	0/1696	0.77	2/2276 (0.1%)
3	e	0.38	0/1449	0.77	3/1949 (0.2%)
4	g	0.31	0/1260	0.72	1/1701 (0.1%)
5	h	0.44	0/1018	0.92	4/1375 (0.3%)
6	i	0.34	0/1012	0.80	1/1362 (0.1%)
7	j	0.31	0/789	0.71	2/1069 (0.2%)
8	k	0.31	0/889	0.75	2/1201 (0.2%)
9	l	0.41	0/969	0.95	1/1294 (0.1%)
10	o	0.31	0/718	0.66	1/963 (0.1%)
11	q	0.39	0/741	0.74	2/993 (0.2%)
12	r	0.30	0/517	0.72	2/691 (0.3%)
13	s	0.33	0/647	0.88	4/871 (0.5%)
14	t	0.35	0/658	0.68	0/875
15	n	0.46	0/488	0.67	0/650
16	b	0.26	0/1822	0.63	0/2457
17	d	0.34	0/1672	0.75	2/2251 (0.1%)
18	f	0.35	0/782	0.69	2/1059 (0.2%)
19	m	0.33	0/942	0.73	0/1260
20	p	0.39	0/908	0.69	0/1226
21	u	0.58	0/280	0.93	0/359
22	w	0.40	0/1835	0.62	0/2857
23	x	0.59	0/843	1.18	6/1127 (0.5%)
25	C	1.00	0/2140	1.15	16/2879 (0.6%)
26	D	0.51	0/1609	0.74	2/2165 (0.1%)
27	E	0.86	0/1576	1.06	3/2132 (0.1%)
28	F	0.61	0/1459	1.12	14/1962 (0.7%)
29	G	0.31	0/1369	0.60	0/1848
30	H	0.29	0/1027	0.69	2/1398 (0.1%)
31	I	0.22	0/925	0.56	0/1246
32	J	0.27	0/1006	0.71	0/1364
33	K	0.80	0/1165	1.21	16/1578 (1.0%)
34	L	0.89	0/938	1.11	6/1257 (0.5%)
35	M	0.49	0/1091	0.71	0/1457

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
36	N	0.91	0/1100	1.07	3/1482 (0.2%)
37	O	0.85	2/936 (0.2%)	1.35	20/1256 (1.6%)
38	P	0.38	0/966	0.62	0/1298
39	Q	0.46	0/921	0.70	0/1236
40	R	0.51	0/1000	0.64	0/1341
41	S	0.44	0/778	0.63	0/1048
42	T	0.95	1/887 (0.1%)	1.16	7/1204 (0.6%)
43	U	0.76	0/749	1.11	6/1006 (0.6%)
44	V	0.66	0/737	1.05	4/987 (0.4%)
45	W	0.61	1/1404 (0.1%)	1.09	5/1917 (0.3%)
46	X	0.95	1/613 (0.2%)	1.10	3/821 (0.4%)
47	Y	0.52	0/478	0.78	0/641
48	Z	0.69	0/530	0.92	0/708
49	v	0.85	0/486	1.00	1/651 (0.2%)
50	y	0.40	0/520	0.84	1/698 (0.1%)
51	z	0.54	0/427	0.70	0/572
52	1	0.71	0/424	1.07	4/567 (0.7%)
53	2	0.95	0/375	1.34	4/493 (0.8%)
54	3	1.01	0/507	1.03	1/672 (0.1%)
55	4	0.79	0/302	0.90	0/401
56	5	0.46	0/191	0.76	0/247
57	B	0.28	0/2797	0.49	0/4357
58	A	0.47	0/74597	0.50	4/116386 (0.0%)
All	All	0.49	5/164166 (0.0%)	0.63	162/245629 (0.1%)

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
2	c	0	1
3	e	0	1
4	g	0	3
5	h	0	2
7	j	0	1
8	k	0	2
9	l	0	2
11	q	0	1
12	r	0	1
13	s	0	2
17	d	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
23	x	0	11
24	0	0	8
25	C	0	5
26	D	0	2
27	E	0	5
28	F	0	1
33	K	0	1
36	N	0	2
37	O	0	2
42	T	0	1
43	U	0	1
45	W	0	2
52	1	0	2
All	All	0	60

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
45	W	7	ILE	C-N	6.26	1.39	1.33
37	O	84	GLY	C-N	6.17	1.42	1.34
42	T	117	ARG	C-N	5.86	1.40	1.33
37	O	45	ARG	C-N	5.50	1.40	1.34
46	X	81	VAL	C-N	5.03	1.39	1.33

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	W	62	GLY	N-CA-C	19.02	133.81	111.93
5	h	94	LEU	N-CA-C	-15.74	85.11	109.04
45	W	61	HIS	CA-C-N	11.61	131.13	120.10
45	W	61	HIS	C-N-CA	11.61	131.13	120.10
28	F	117	ARG	N-CA-C	10.58	122.81	111.28

There are no chirality outliers.

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	c	62	ARG	Peptide
3	e	186	ILE	Peptide
4	g	1	MET	Peptide
4	g	32	LEU	Peptide

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Mol	Chain	Res	Type	Group
4	g	76	ARG	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	32341	0	16263	1139	0
2	c	1672	0	1720	178	0
3	e	1433	0	1485	156	0
4	g	1240	0	1293	121	0
5	h	1003	0	1039	54	0
6	i	994	0	1048	163	0
7	j	775	0	808	57	0
8	k	871	0	885	107	0
9	l	958	0	1045	36	0
10	o	709	0	747	30	0
11	q	730	0	772	37	0
12	r	512	0	543	35	0
13	s	630	0	639	90	0
14	t	655	0	707	98	0
15	n	477	0	501	59	0
16	b	1793	0	1839	71	0
17	d	1641	0	1668	67	0
18	f	771	0	797	42	0
19	m	935	0	985	55	0
20	p	891	0	933	34	0
21	u	280	0	342	10	0
22	w	1643	0	834	296	0
23	x	831	0	835	396	0
24	0	1310	0	305	117	0
25	C	2097	0	2147	198	0
26	D	1587	0	1629	85	0
27	E	1553	0	1587	145	0
28	F	1437	0	1463	233	0
29	G	1348	0	1399	28	0
30	H	1018	0	988	15	0
31	I	918	0	959	13	0
32	J	990	0	1020	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	K	1138	0	1174	119	0
34	L	930	0	989	57	0
35	M	1078	0	1151	48	0
36	N	1074	0	1116	60	0
37	O	919	0	959	135	0
38	P	956	0	990	58	0
39	Q	907	0	938	33	0
40	R	988	0	1038	20	0
41	S	768	0	820	47	0
42	T	873	0	909	54	0
43	U	739	0	775	101	0
44	V	731	0	782	112	0
45	W	1389	0	1411	217	0
46	X	604	0	622	59	0
47	Y	470	0	484	8	0
48	Z	527	0	537	61	0
49	v	483	0	513	22	0
50	y	510	0	501	108	0
51	z	423	0	463	12	0
52	1	416	0	421	101	0
53	2	372	0	406	36	0
54	3	502	0	541	32	0
55	4	298	0	321	47	0
56	5	189	0	205	4	0
57	B	2501	0	1270	249	0
58	A	66623	0	33513	1110	0
All	All	152451	0	102074	5320	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 21.

The worst 5 of 5320 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)
6:i:26:ILE:HB	6:i:41:LEU:CD2	1.19	1.66
6:i:26:ILE:CB	6:i:41:LEU:HD23	1.23	1.64
43:U:83:ILE:HD11	58:A:1456:G:C2	1.14	1.63
1:a:1034:C:C5	23:x:75:ARG:CA	1.78	1.62
12:r:32:TYR:CE1	18:f:91:LEU:HD11	1.34	1.59

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
2	c	208/275 (76%)	184 (88%)	17 (8%)	7 (3%)	3	17
3	e	196/214 (92%)	176 (90%)	19 (10%)	1 (0%)	24	54
4	g	154/156 (99%)	144 (94%)	9 (6%)	1 (1%)	21	50
5	h	128/132 (97%)	119 (93%)	8 (6%)	1 (1%)	16	44
6	i	124/150 (83%)	108 (87%)	13 (10%)	3 (2%)	4	22
7	j	95/101 (94%)	84 (88%)	10 (10%)	1 (1%)	11	38
8	k	115/138 (83%)	103 (90%)	10 (9%)	2 (2%)	7	28
9	l	120/124 (97%)	93 (78%)	26 (22%)	1 (1%)	16	44
10	o	85/89 (96%)	81 (95%)	4 (5%)	0	100	100
11	q	90/98 (92%)	79 (88%)	11 (12%)	0	100	100
12	r	62/84 (74%)	54 (87%)	8 (13%)	0	100	100
13	s	76/93 (82%)	68 (90%)	8 (10%)	0	100	100
14	t	82/86 (95%)	77 (94%)	5 (6%)	0	100	100
15	n	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
16	b	226/277 (82%)	211 (93%)	15 (7%)	0	100	100
17	d	198/201 (98%)	185 (93%)	12 (6%)	1 (0%)	24	54
18	f	94/96 (98%)	90 (96%)	4 (4%)	0	100	100
19	m	114/124 (92%)	102 (90%)	12 (10%)	0	100	100
20	p	111/156 (71%)	104 (94%)	7 (6%)	0	100	100
21	u	30/33 (91%)	28 (93%)	2 (7%)	0	100	100
23	x	98/230 (43%)	80 (82%)	15 (15%)	3 (3%)	3	18
25	C	271/278 (98%)	234 (86%)	33 (12%)	4 (2%)	8	30
26	D	212/217 (98%)	197 (93%)	10 (5%)	5 (2%)	4	22
27	E	205/215 (95%)	179 (87%)	20 (10%)	6 (3%)	3	19
28	F	179/187 (96%)	163 (91%)	14 (8%)	2 (1%)	11	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	G	174/179 (97%)	166 (95%)	8 (5%)	0	100	100
30	H	149/151 (99%)	139 (93%)	9 (6%)	1 (1%)	18	47
31	I	124/175 (71%)	118 (95%)	6 (5%)	0	100	100
32	J	131/142 (92%)	118 (90%)	13 (10%)	0	100	100
33	K	145/147 (99%)	132 (91%)	10 (7%)	3 (2%)	5	24
34	L	119/122 (98%)	106 (89%)	10 (8%)	3 (2%)	4	21
35	M	143/147 (97%)	128 (90%)	15 (10%)	0	100	100
36	N	132/138 (96%)	111 (84%)	20 (15%)	1 (1%)	16	44
37	O	115/199 (58%)	101 (88%)	11 (10%)	3 (3%)	4	21
38	P	124/127 (98%)	119 (96%)	5 (4%)	0	100	100
39	Q	111/113 (98%)	102 (92%)	9 (8%)	0	100	100
40	R	122/129 (95%)	120 (98%)	2 (2%)	0	100	100
41	S	100/103 (97%)	94 (94%)	5 (5%)	1 (1%)	12	40
42	T	112/153 (73%)	103 (92%)	6 (5%)	3 (3%)	4	20
43	U	92/100 (92%)	76 (83%)	11 (12%)	5 (5%)	1	10
44	V	93/105 (89%)	83 (89%)	8 (9%)	2 (2%)	5	24
45	W	184/215 (86%)	156 (85%)	22 (12%)	6 (3%)	3	17
46	X	80/88 (91%)	61 (76%)	14 (18%)	5 (6%)	1	7
47	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
48	Z	61/77 (79%)	59 (97%)	1 (2%)	1 (2%)	7	29
49	v	58/61 (95%)	53 (91%)	5 (9%)	0	100	100
50	y	64/75 (85%)	60 (94%)	3 (5%)	1 (2%)	7	29
51	z	52/57 (91%)	51 (98%)	1 (2%)	0	100	100
52	1	48/55 (87%)	40 (83%)	5 (10%)	3 (6%)	1	7
53	2	43/47 (92%)	41 (95%)	2 (5%)	0	100	100
54	3	61/64 (95%)	54 (88%)	7 (12%)	0	100	100
55	4	35/37 (95%)	29 (83%)	5 (14%)	1 (3%)	3	19
56	5	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
All	All	6085/6909 (88%)	5493 (90%)	515 (8%)	77 (1%)	12	33

5 of 77 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	c	138	GLN
2	c	143	GLN
2	c	144	PRO
4	g	154	TYR
8	k	116	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	c	171/212 (81%)	165 (96%)	6 (4%)	32	56
3	e	139/147 (95%)	137 (99%)	2 (1%)	59	70
4	g	132/132 (100%)	129 (98%)	3 (2%)	44	63
5	h	106/108 (98%)	106 (100%)	0	100	100
6	i	102/125 (82%)	97 (95%)	5 (5%)	22	49
7	j	88/90 (98%)	87 (99%)	1 (1%)	65	74
8	k	91/105 (87%)	90 (99%)	1 (1%)	65	74
9	l	103/105 (98%)	103 (100%)	0	100	100
10	o	75/77 (97%)	75 (100%)	0	100	100
11	q	78/83 (94%)	76 (97%)	2 (3%)	40	61
12	r	55/72 (76%)	53 (96%)	2 (4%)	31	56
13	s	69/84 (82%)	68 (99%)	1 (1%)	59	70
14	t	69/70 (99%)	68 (99%)	1 (1%)	59	70
15	n	49/50 (98%)	49 (100%)	0	100	100
16	b	191/218 (88%)	191 (100%)	0	100	100
17	d	175/176 (99%)	174 (99%)	1 (1%)	78	80
18	f	85/85 (100%)	85 (100%)	0	100	100
19	m	99/104 (95%)	99 (100%)	0	100	100
20	p	92/118 (78%)	92 (100%)	0	100	100
21	u	30/31 (97%)	23 (77%)	7 (23%)	1	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	x	88/199 (44%)	67 (76%)	21 (24%)	1	2
25	C	214/218 (98%)	206 (96%)	8 (4%)	30	55
26	D	160/163 (98%)	157 (98%)	3 (2%)	50	66
27	E	167/173 (96%)	158 (95%)	9 (5%)	20	47
28	F	150/156 (96%)	138 (92%)	12 (8%)	11	36
29	G	148/150 (99%)	147 (99%)	1 (1%)	76	78
30	H	90/116 (78%)	90 (100%)	0	100	100
31	I	89/120 (74%)	89 (100%)	0	100	100
32	J	102/108 (94%)	102 (100%)	0	100	100
33	K	120/120 (100%)	116 (97%)	4 (3%)	33	57
34	L	99/100 (99%)	98 (99%)	1 (1%)	68	75
35	M	112/114 (98%)	111 (99%)	1 (1%)	70	76
36	N	112/116 (97%)	109 (97%)	3 (3%)	39	60
37	O	96/158 (61%)	89 (93%)	7 (7%)	13	39
38	P	93/94 (99%)	93 (100%)	0	100	100
39	Q	100/100 (100%)	99 (99%)	1 (1%)	68	75
40	R	97/99 (98%)	97 (100%)	0	100	100
41	S	82/83 (99%)	81 (99%)	1 (1%)	63	72
42	T	90/117 (77%)	88 (98%)	2 (2%)	45	63
43	U	82/85 (96%)	72 (88%)	10 (12%)	5	19
44	V	81/86 (94%)	71 (88%)	10 (12%)	4	18
45	W	152/168 (90%)	144 (95%)	8 (5%)	20	47
46	X	59/63 (94%)	55 (93%)	4 (7%)	14	40
47	Y	50/51 (98%)	50 (100%)	0	100	100
48	Z	58/66 (88%)	55 (95%)	3 (5%)	21	48
49	v	53/54 (98%)	52 (98%)	1 (2%)	50	66
50	y	57/63 (90%)	54 (95%)	3 (5%)	20	47
51	z	43/46 (94%)	43 (100%)	0	100	100
52	1	48/52 (92%)	41 (85%)	7 (15%)	3	12
53	2	35/36 (97%)	34 (97%)	1 (3%)	37	60
54	3	53/54 (98%)	53 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	4	35/35 (100%)	34 (97%)	1 (3%)	37	60
56	5	18/19 (95%)	18 (100%)	0	100	100
All	All	5032/5574 (90%)	4878 (97%)	154 (3%)	36	59

5 of 154 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
43	U	96	PHE
50	y	44	PHE
44	V	30	ARG
45	W	104	GLU
52	1	37	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 132 such sidechains are listed below:

Mol	Chain	Res	Type
48	Z	52	GLN
49	v	51	HIS
55	4	36	GLN
23	x	85	HIS
23	x	84	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	a	1504/1528 (98%)	398 (26%)	0
22	w	76/77 (98%)	41 (53%)	0
57	B	116/118 (98%)	33 (28%)	1 (0%)
58	A	3096/3120 (99%)	785 (25%)	28 (0%)
All	All	4792/4843 (98%)	1257 (26%)	29 (0%)

5 of 1257 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	a	11	G
1	a	12	A
1	a	13	G
1	a	26	G
1	a	36	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
58	A	1010	U
58	A	2350	G
58	A	1186	G
58	A	2085	C
58	A	1117	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 [i](#)

There are no chain breaks in this entry.

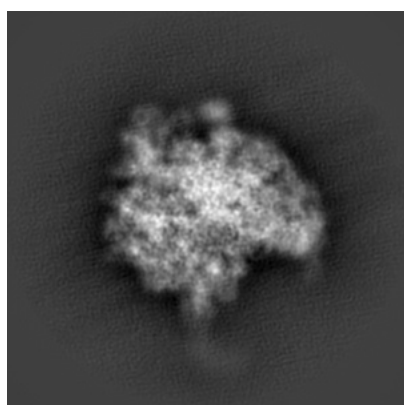
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-6921. These allow visual inspection of the internal detail of the map and identification of artifacts.

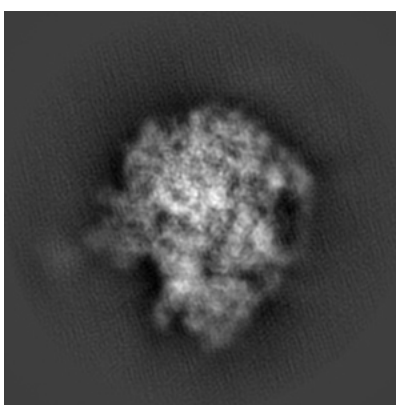
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

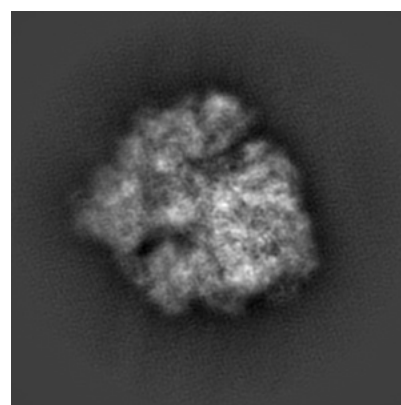
6.1.1 Primary map



X



Y

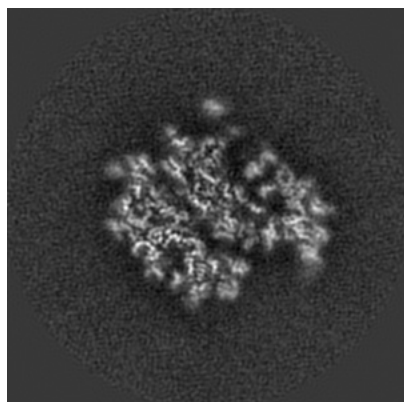


Z

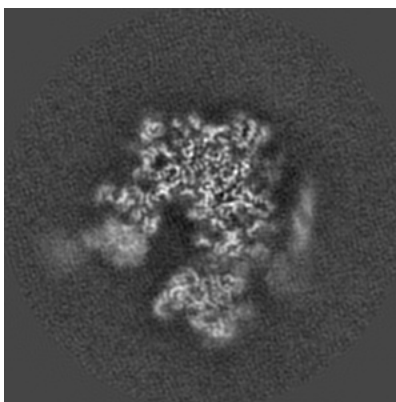
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

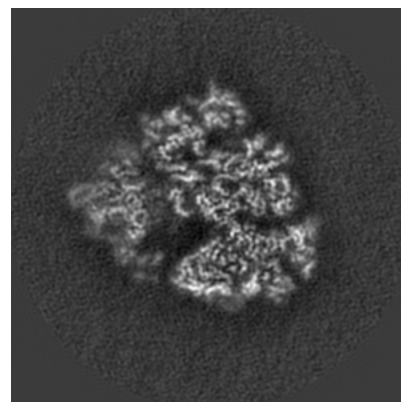
6.2.1 Primary map



X Index: 164



Y Index: 164

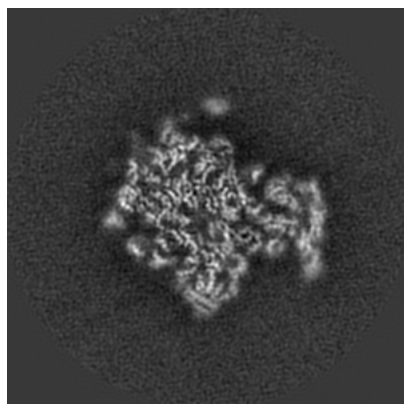


Z Index: 164

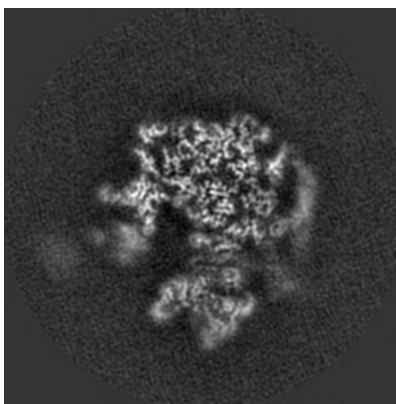
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

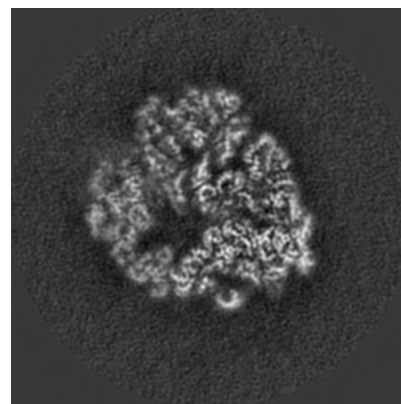
6.3.1 Primary map



X Index: 171



Y Index: 169

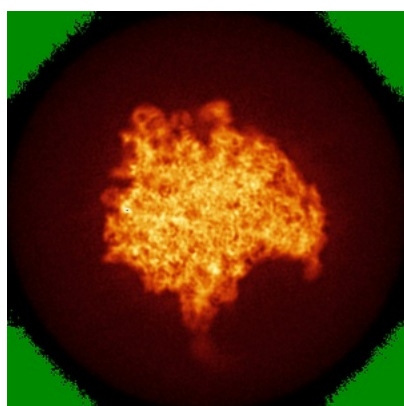


Z Index: 157

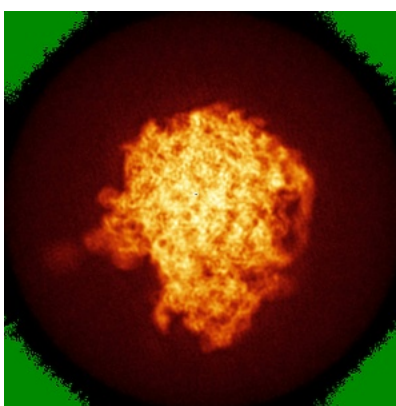
The images above show the largest variance slices of the map in three orthogonal directions.

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

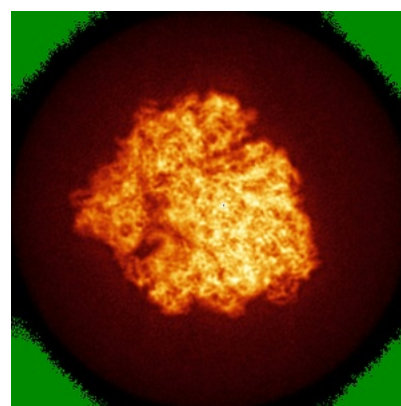
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

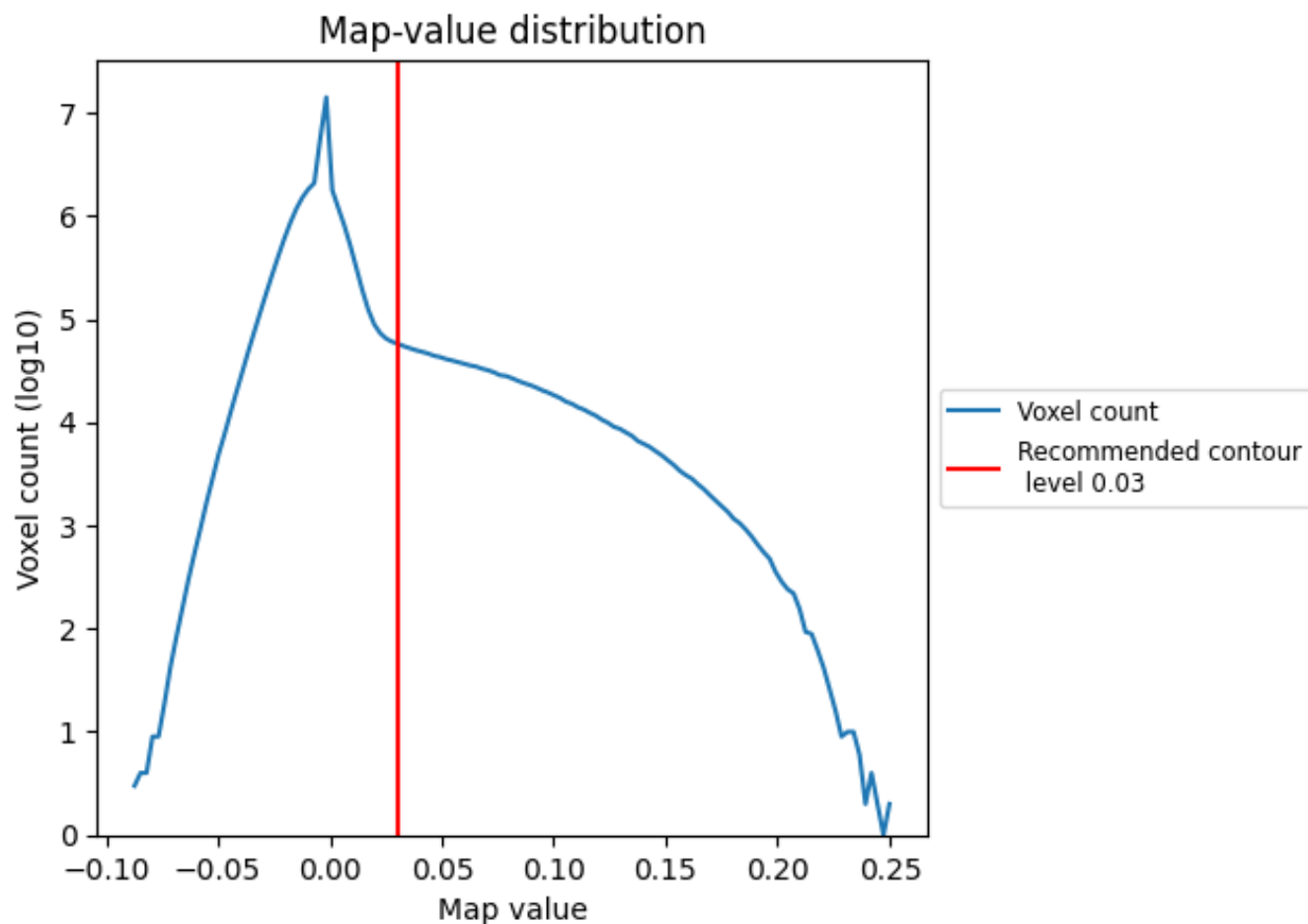
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

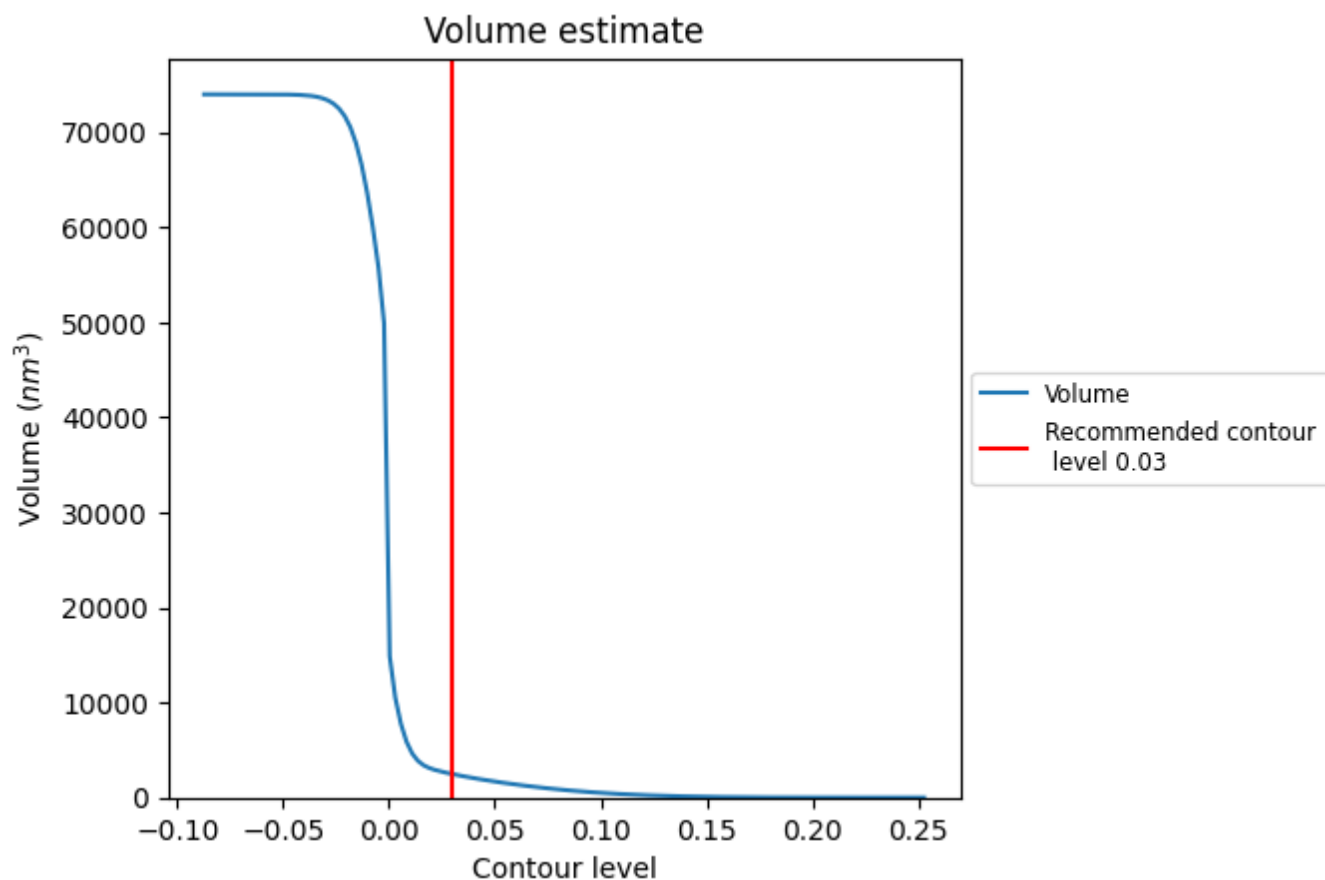
This section contains the results of statistical analysis of the map.

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.

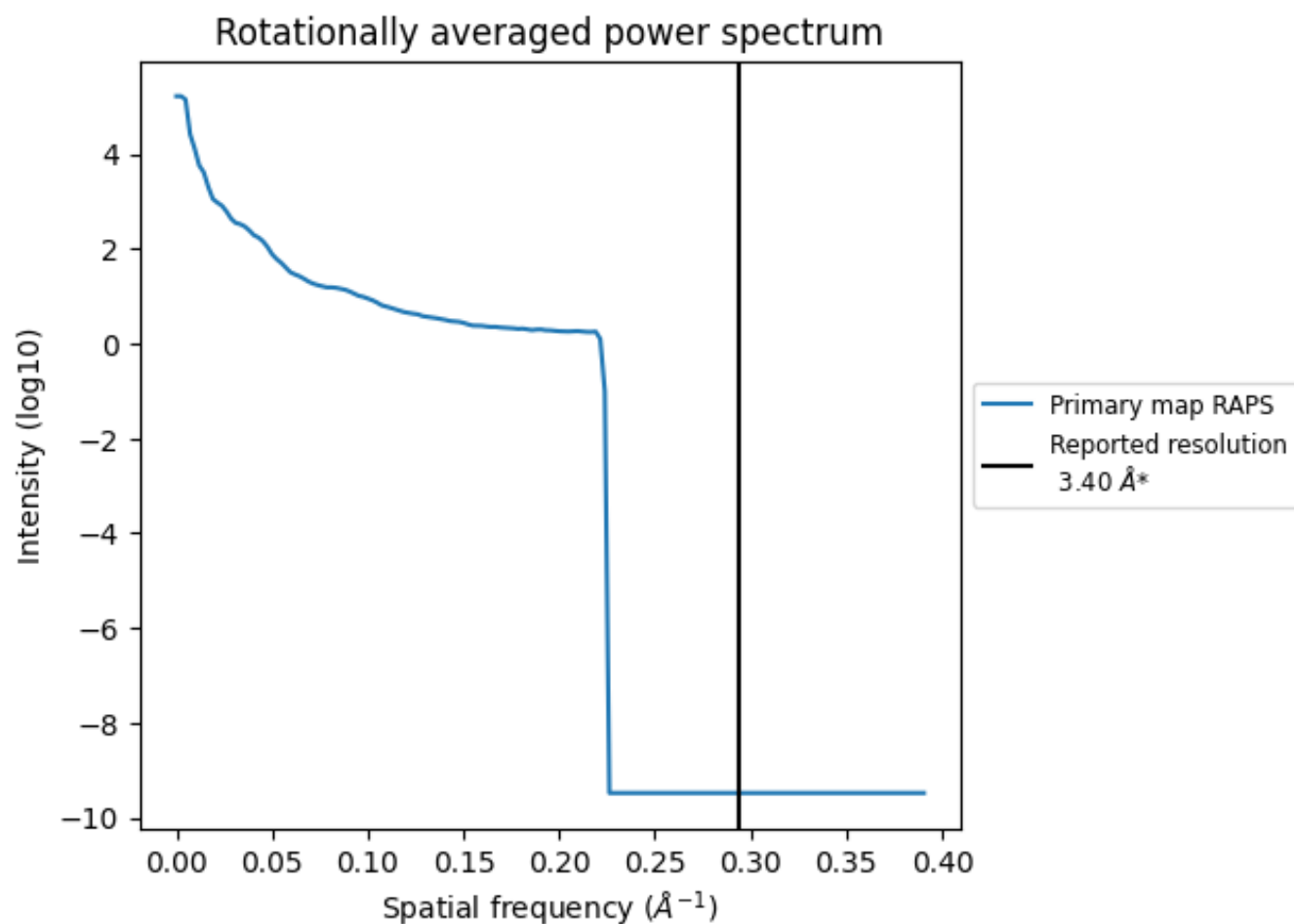
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2473 nm³; this corresponds to an approximate mass of 2234 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 0.294 Å⁻¹

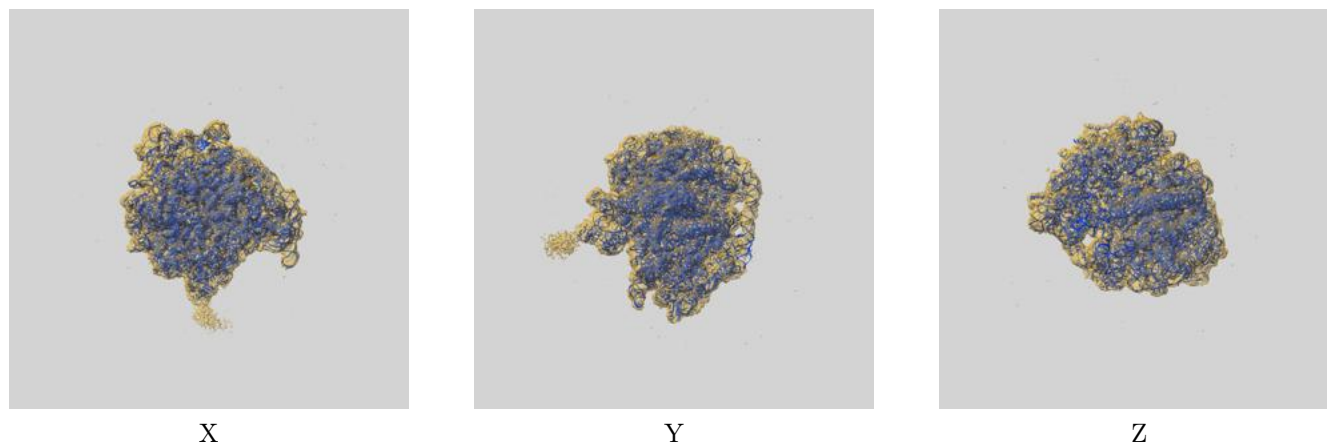
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

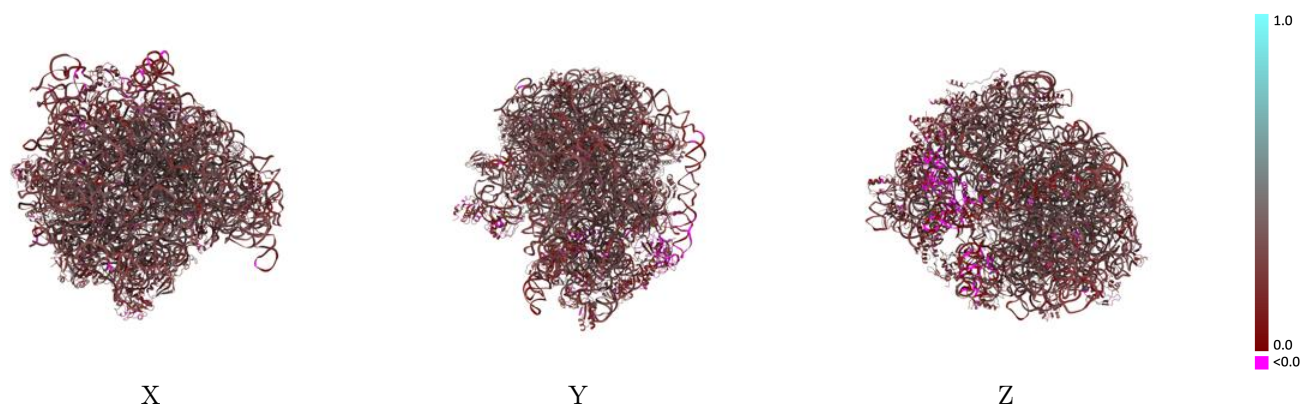
This section contains information regarding the fit between EMDB map EMD-6921 and PDB model 5ZEP. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

9.1 Map-model overlay [i](#)



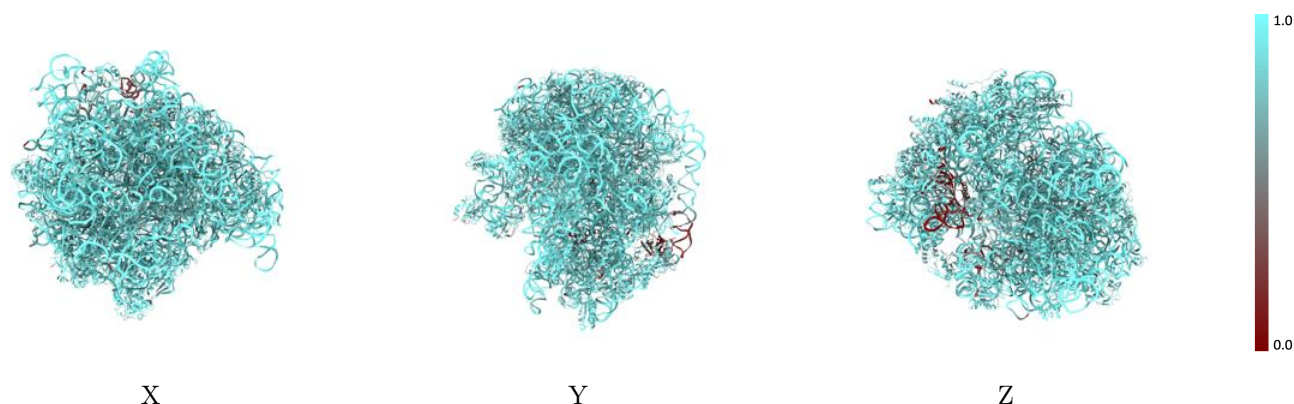
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



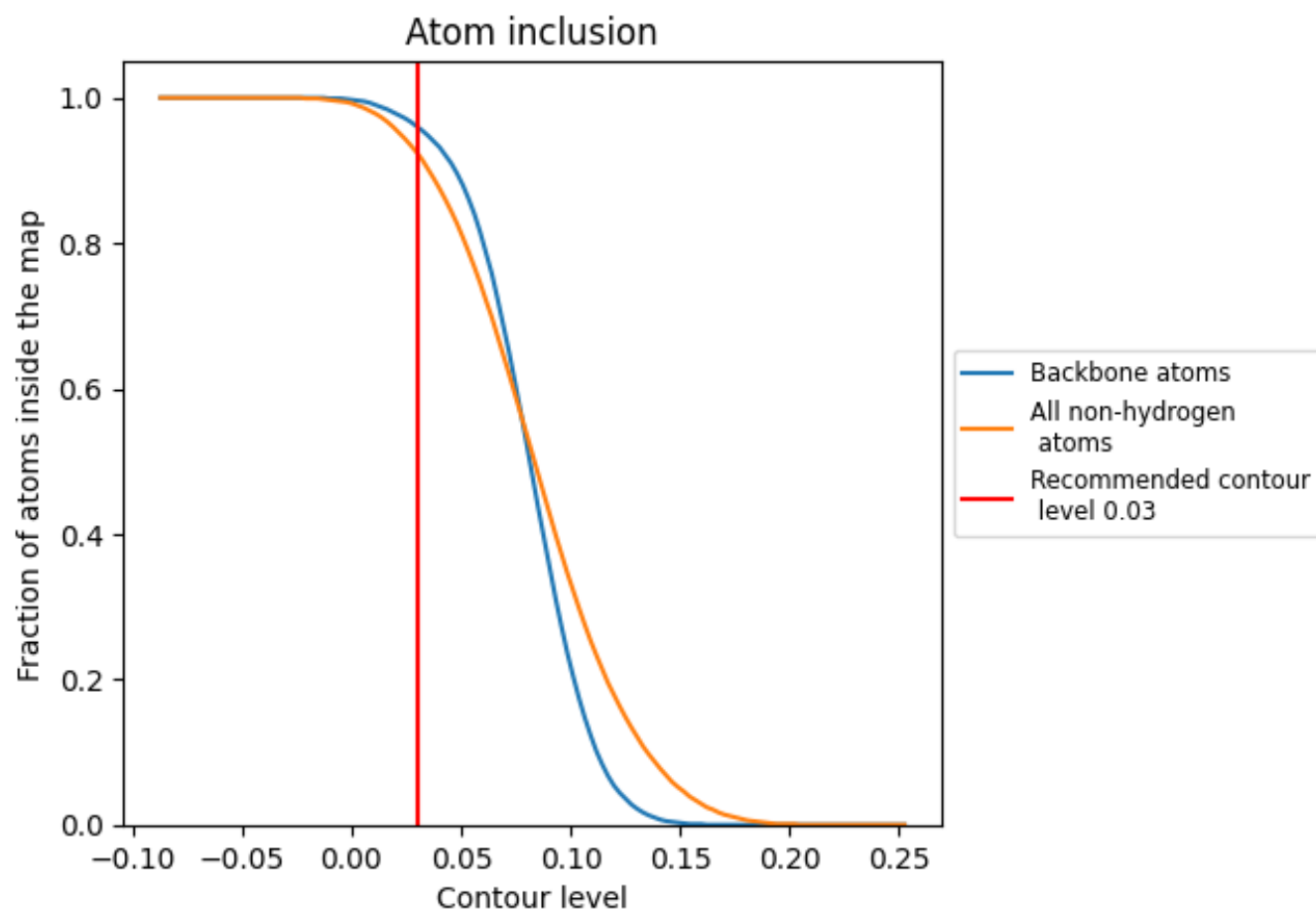
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 92% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9240	 0.2750
0	 0.4170	 0.0310
1	 0.8560	 0.2240
2	 0.8370	 0.3070
3	 0.8210	 0.2930
4	 0.8850	 0.2810
5	 0.8270	 0.2680
A	 0.9680	 0.2950
B	 0.9760	 0.2680
C	 0.8200	 0.2850
D	 0.8540	 0.2870
E	 0.8670	 0.2690
F	 0.8780	 0.2420
G	 0.9110	 0.2520
H	 0.8720	 0.2260
I	 0.8400	 0.1300
J	 0.8630	 0.1190
K	 0.8560	 0.2760
L	 0.7560	 0.2780
M	 0.8450	 0.2700
N	 0.8330	 0.2880
O	 0.8120	 0.2510
P	 0.9100	 0.2480
Q	 0.8040	 0.2540
R	 0.8550	 0.2450
S	 0.8680	 0.3080
T	 0.8290	 0.2830
U	 0.8340	 0.2990
V	 0.8780	 0.2290
W	 0.8890	 0.2550
X	 0.8060	 0.2590
Y	 0.8460	 0.3030
Z	 0.8420	 0.2110
a	 0.9860	 0.3000
b	 0.8330	 0.1980



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Chain	Atom inclusion	Q-score
c	 0.8420	 0.2040
d	 0.8530	 0.1940
e	 0.8140	 0.2510
f	 0.8650	 0.2630
g	 0.8400	 0.2020
h	 0.8760	 0.2830
i	 0.9170	 0.2300
j	 0.8770	 0.2300
k	 0.8600	 0.2540
l	 0.8090	 0.2680
m	 0.8560	 0.2020
n	 0.8420	 0.2520
o	 0.8440	 0.2410
p	 0.8680	 0.2440
q	 0.8140	 0.2600
r	 0.8850	 0.2500
s	 0.8470	 0.2270
t	 0.8300	 0.1930
u	 0.6830	 0.2450
v	 0.8310	 0.2500
w	 0.6690	 0.1340
x	 0.2420	 -0.0160
y	 0.8460	 0.2190
z	 0.8210	 0.2820