wwPDB EM Validation Summary Report (i)

Dec 11, 2022 – 06:36 pm GMT

PDB ID	:	6SZS
EMDB ID	:	EMD-10353
Title	:	Release factor-dependent ribosome rescue by BrfA in the Gram-positive bacterium Bacillus subtilis
Authors	:	Muller, C.; Beckert, B.; Wilson, D.N.
Deposited on	:	2019-10-02
Resolution	:	3.06 Å(reported)
Based on initial model	:	5MGP

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 (i) 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 (i)) were used in the production of this report:

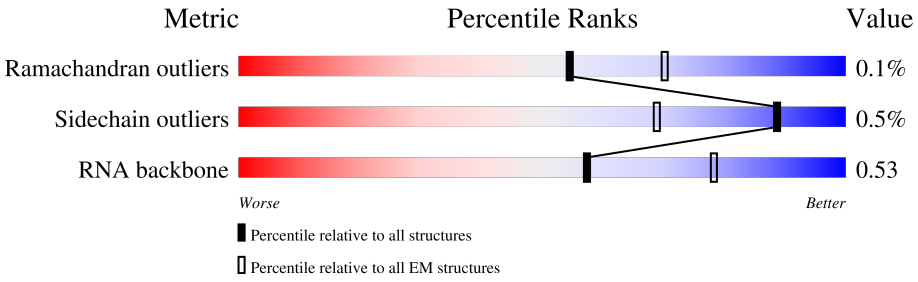
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance

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

The reported resolution of this entry is 3.06 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	0	57	9% 96%
2	1	55	18% 91% 9%
3	2	46	100%
4	3	65	97%
5	4	38	5% 97%
6	5	70	29% 93% 7%
7	A	2903	74% 23%
8	B	120	76% 21%

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Mol	Chain	Length	Quality of chain
9	C	273	5% 99%
10	D	209	6% 100%
11	E	201	11% 100%
12	F	179	9% 99%
13	G	177	12% 97%
14	H	149	70% 98%
15	J	142	6% 99%
16	K	123	14% 99%
17	L	144	8% 99%
18	M	136	10% 97%
19	N	127	93% 7%
20	O	117	99%
21	P	115	10% 99%
22	Q	118	99%
23	R	103	9% 100%
24	S	110	10% 100%
25	T	100	7% 89% 11%
26	U	104	13% 98%
27	V	94	13% 100%
28	W	85	88% 12%
29	X	78	12% 99%
30	Y	63	17% 100%
31	Z	59	8% 97%
32	a	1540	79% 20%
33	b	241	45% 93% 7%

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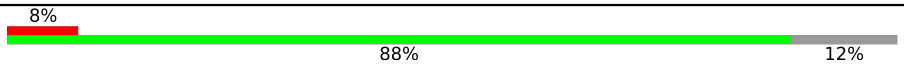
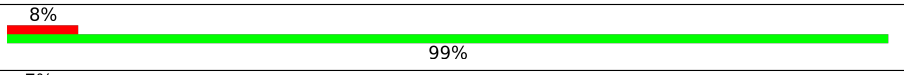
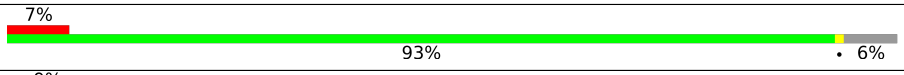
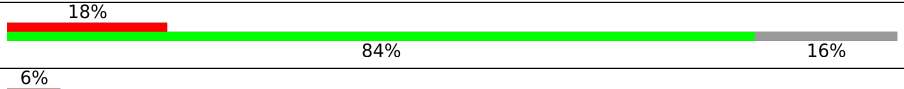
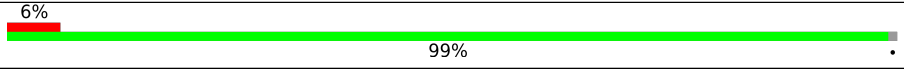
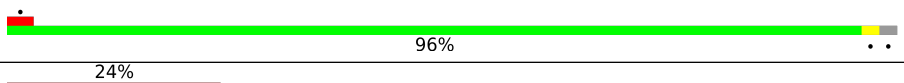
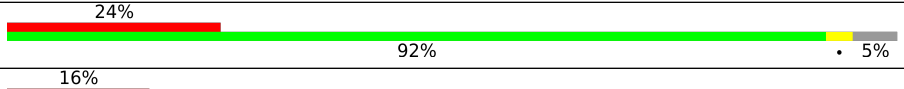
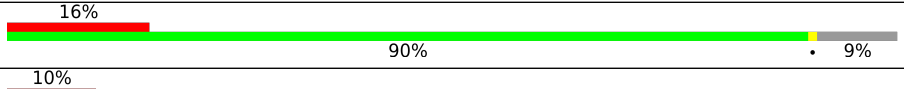
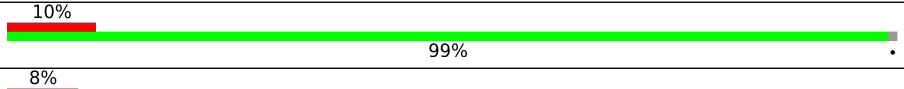
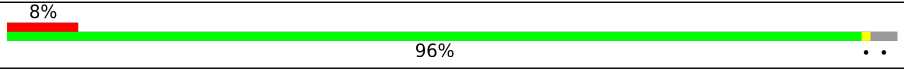
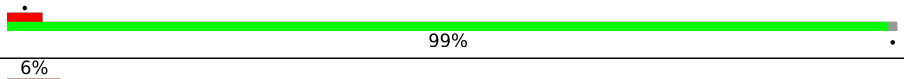
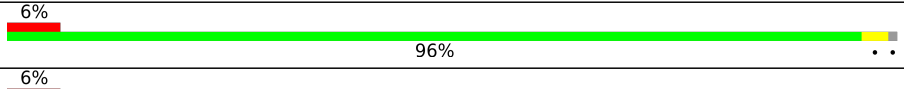
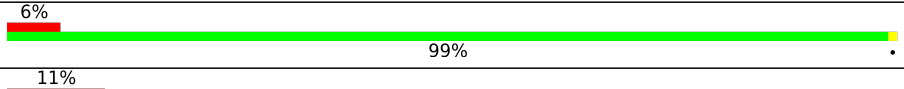
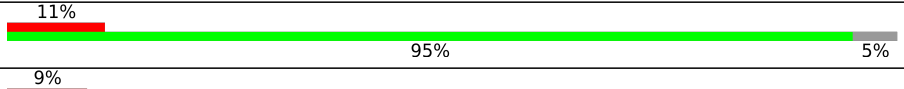
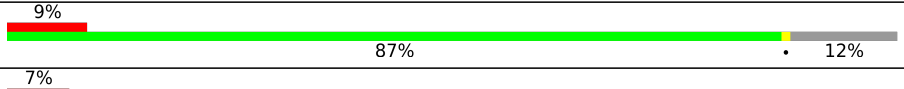
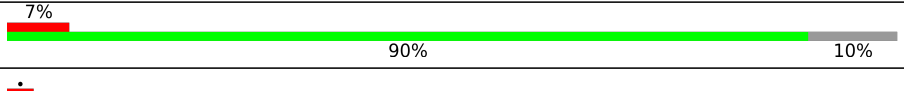
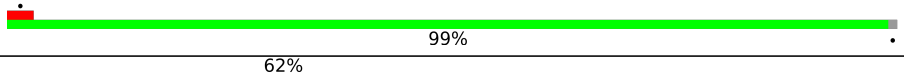
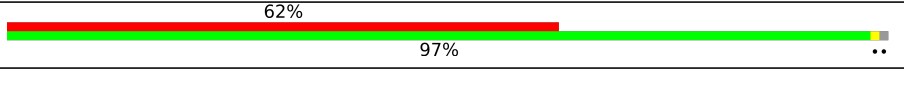
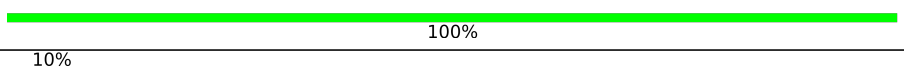
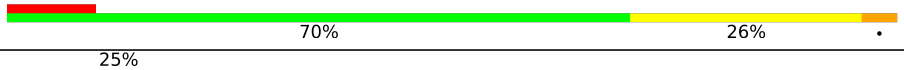
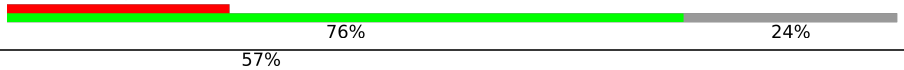
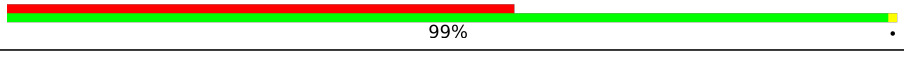
Mol	Chain	Length	Quality of chain
34	c	233	
35	d	206	
36	e	167	
37	f	135	
38	g	179	
39	h	130	
40	i	130	
41	j	103	
42	k	129	
43	l	124	
44	m	118	
45	n	101	
46	o	89	
47	p	82	
48	q	84	
49	r	75	
50	s	92	
51	t	87	
52	u	71	
53	v	6	
54	x	77	
55	y	71	
56	z	362	

2 Entry composition (i)

There are 56 unique types of molecules in this entry. The entry contains 147361 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 L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	55	434	263	92	78	1	0	0

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	1	50	409	263	75	71	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	2	46	377	228	90	57	2	0	0

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	504	323	105	74	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	4	38	302	185	65	48	4	0	0

- Molecule 6 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	5	65	514	317	98	93	6	0	0

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62321	27801	11467	20150	2903		

- Molecule 8 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 9 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 10 is a protein called 50S ribosomal protein L3.

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

- Molecule 11 is a protein called 50S ribosomal protein L4.

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

- Molecule 12 is a protein called 50S ribosomal protein L5.

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

- Molecule 13 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	174	Total	C	N	O	S	0	0
			1304	820	239	243	2		

- Molecule 14 is a protein called 50S ribosomal protein L9.

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

- Molecule 15 is a protein called 50S ribosomal protein L13.

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

- Molecule 16 is a protein called 50S ribosomal protein L14.

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

- Molecule 17 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 18 is a protein called 50S ribosomal protein L16.

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

- Molecule 19 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 20 is a protein called 50S ribosomal protein L18.

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

- Molecule 21 is a protein called 50S ribosomal protein L19.

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

- Molecule 22 is a protein called 50S ribosomal protein L20.

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

- Molecule 23 is a protein called 50S ribosomal protein L21.

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

- Molecule 24 is a protein called 50S ribosomal protein L22.

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

- Molecule 25 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	T	89	Total	C	N	O	S	0	0
			709	449	133	125	2		

- Molecule 26 is a protein called 50S ribosomal protein L24.

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

- Molecule 27 is a protein called 50S ribosomal protein L25.

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

- Molecule 28 is a protein called 50S ribosomal protein L27.

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

- Molecule 29 is a protein called 50S ribosomal protein L28.

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

- Molecule 30 is a protein called 50S ribosomal protein L29.

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

- Molecule 31 is a protein called 50S ribosomal protein L30.

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

- Molecule 32 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1540	Total	C	N	O	P	0	0
			33037	14735	6057	10705	1540		

- Molecule 33 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 34 is a protein called 30S ribosomal protein S3.

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

- Molecule 35 is a protein called 30S ribosomal protein S4.

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

- Molecule 36 is a protein called 30S ribosomal protein S5.

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

- Molecule 37 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	99	Total	C	N	O	S	0	0
			811	512	147	146	6		

- Molecule 38 is a protein called 30S ribosomal protein S7.

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

- Molecule 39 is a protein called 30S ribosomal protein S8.

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

- Molecule 40 is a protein called 30S ribosomal protein S9.

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

- Molecule 41 is a protein called 30S ribosomal protein S10.

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

- Molecule 42 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	117	Total 877	C 540	N 174	O 160	S 3	0	0

- Molecule 43 is a protein called 30S ribosomal protein S12.

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

- Molecule 44 is a protein called 30S ribosomal protein S13.

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

- Molecule 45 is a protein called 30S ribosomal protein S14.

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

- Molecule 46 is a protein called 30S ribosomal protein S15.

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

- Molecule 47 is a protein called 30S ribosomal protein S16.

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

- Molecule 48 is a protein called 30S ribosomal protein S17.

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

- Molecule 49 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	66	Total	C	N	O	S	0	0
			545	344	102	98	1		

- Molecule 50 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 51 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 53 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	6	Total	C	N	O	P	0	0
			126	56	22	42	6		

- Molecule 54 is a RNA chain called P-site tRNA-Pro(CGG).

Mol	Chain	Residues	Atoms					AltConf	Trace
54	x	77	Total	C	N	O	P	0	0
			1646	733	295	541	77		

- Molecule 55 is a protein called Uncharacterized protein YqkK.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	y	54	Total	C	N	O	S	0	0
			434	264	95	74	1		

- Molecule 56 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	z	362	Total	C	N	O	S	0	0
			2742	1701	495	534	12		

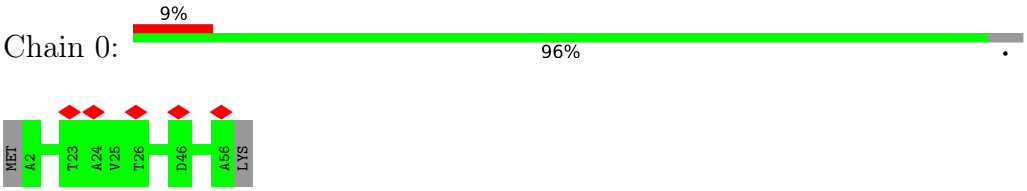
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	251	PRO	GLN	engineered mutation	UNP P28367

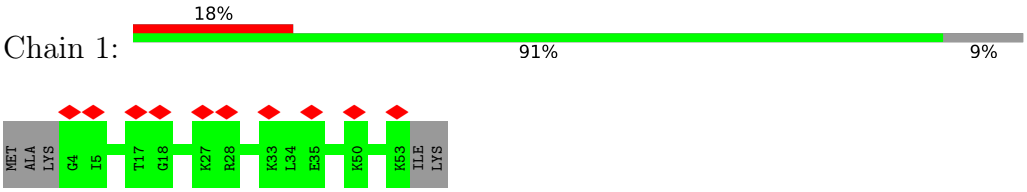
3 Residue-property plots (i)

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

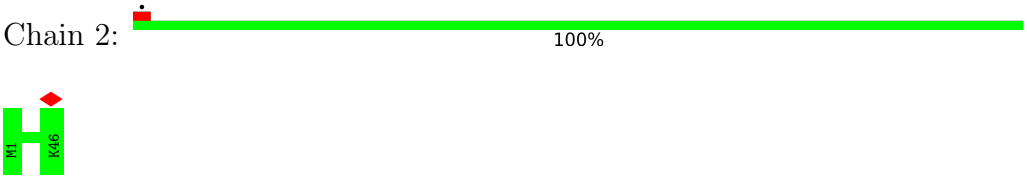
• Molecule 1: 50S ribosomal protein L32



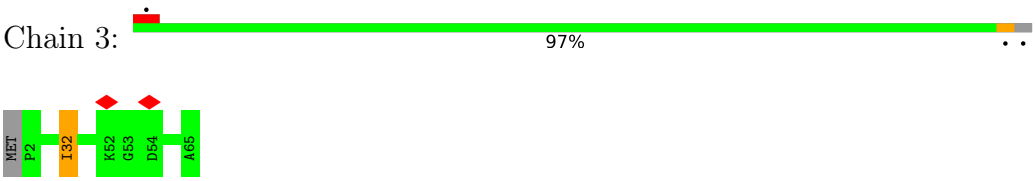
• Molecule 2: 50S ribosomal protein L33



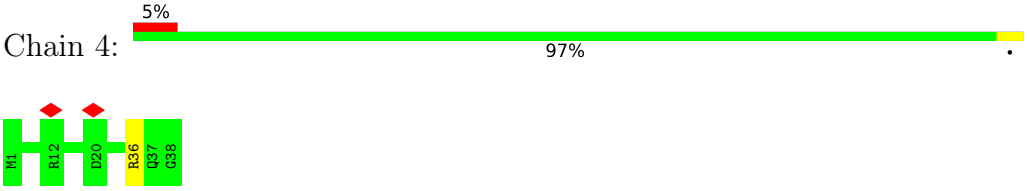
• Molecule 3: 50S ribosomal protein L34



• Molecule 4: 50S ribosomal protein L35

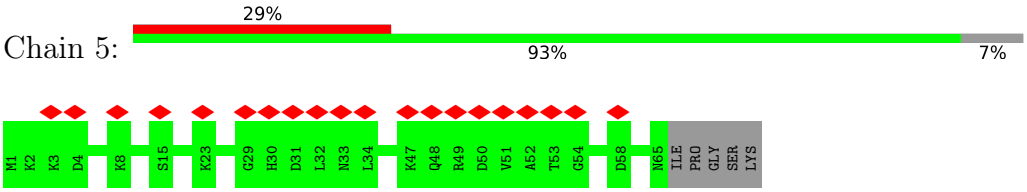


• Molecule 5: 50S ribosomal protein L36



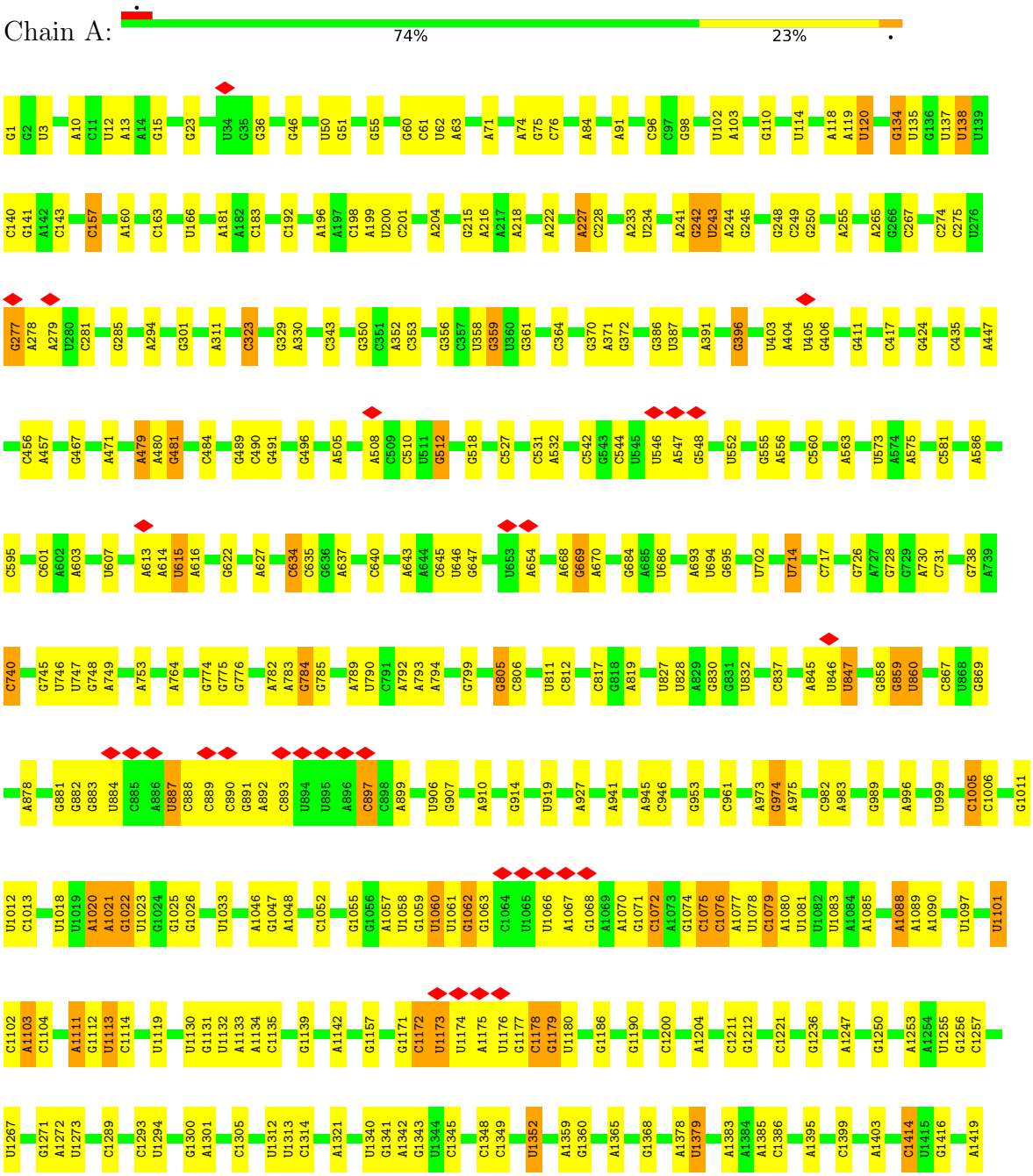
• Molecule 6: 50S ribosomal protein L31

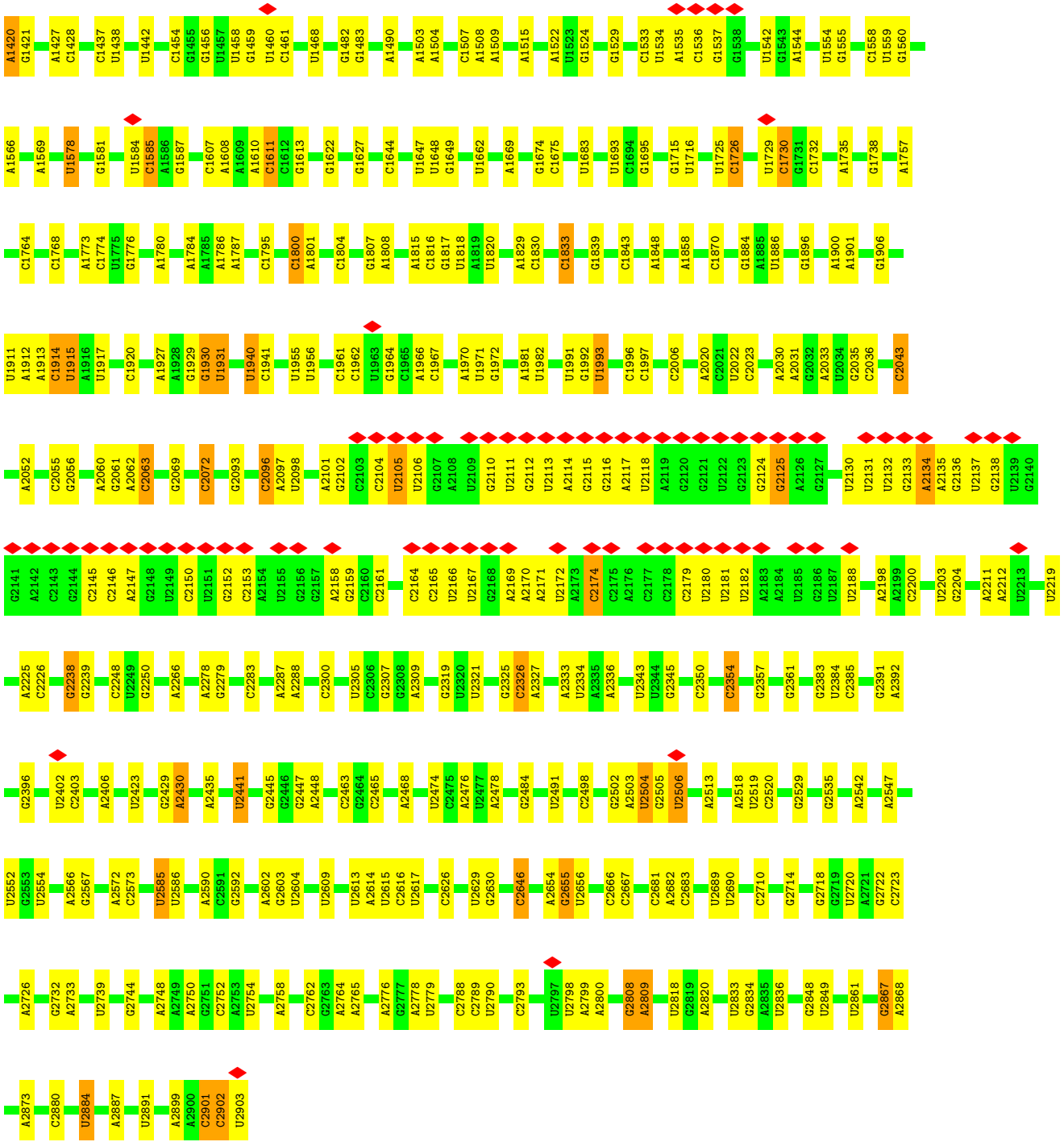
Chain 5:



• Molecule 7: 23S ribosomal RNA

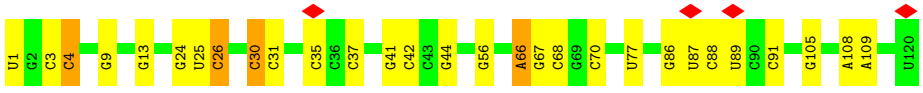
Chain A:





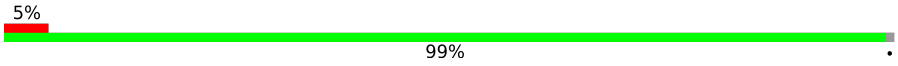
• Molecule 8: 5S ribosomal RNA

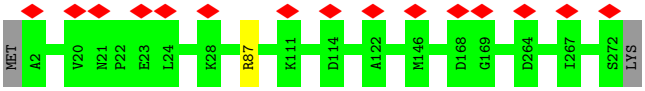
Chain B:



• Molecule 9: 50S ribosomal protein L2

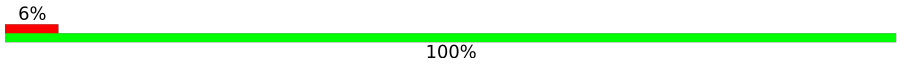
Chain C:

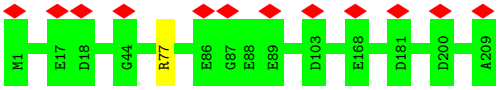




• Molecule 10: 50S ribosomal protein L3

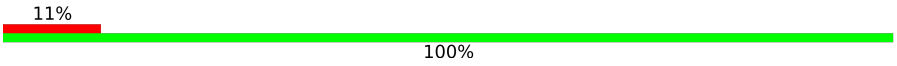
Chain D:

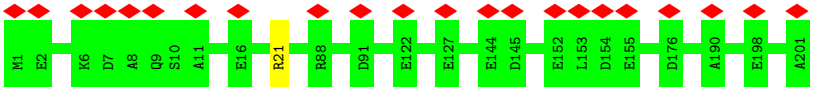




• Molecule 11: 50S ribosomal protein L4

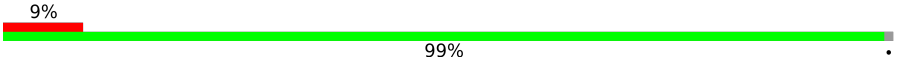
Chain E:

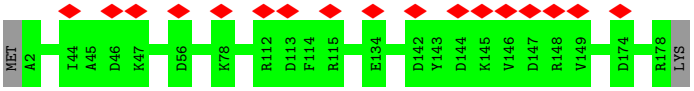




• Molecule 12: 50S ribosomal protein L5

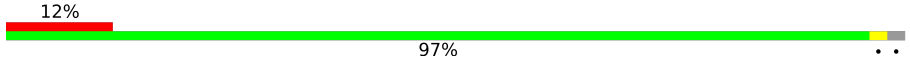
Chain F:

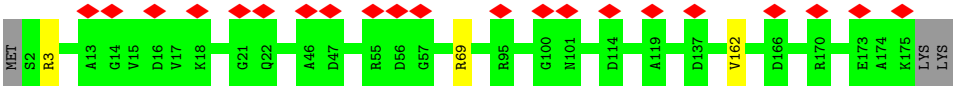




• Molecule 13: 50S ribosomal protein L6

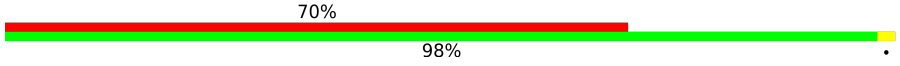
Chain G:

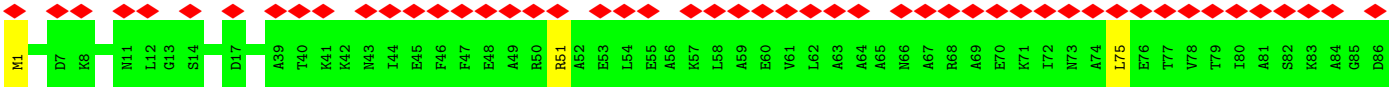


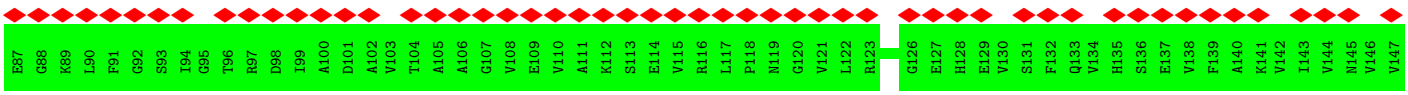


• Molecule 14: 50S ribosomal protein L9

Chain H:

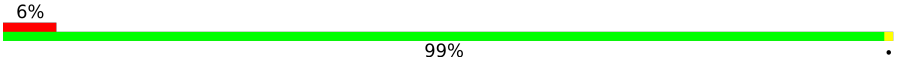


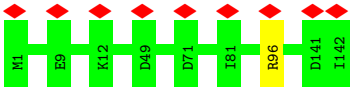




• Molecule 15: 50S ribosomal protein L13

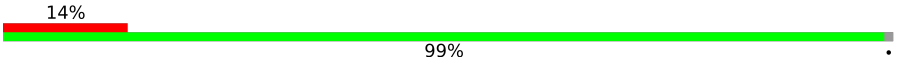
Chain J:

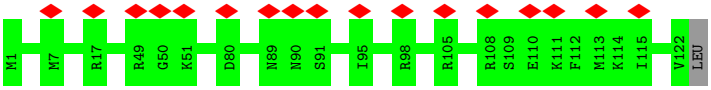




• Molecule 16: 50S ribosomal protein L14

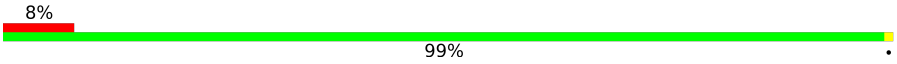
Chain K:

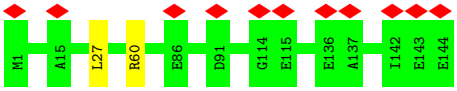




• Molecule 17: 50S ribosomal protein L15

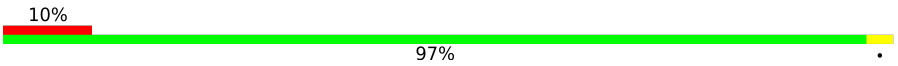
Chain L:

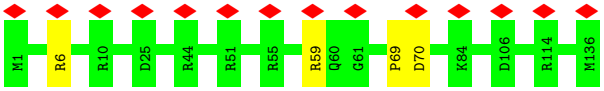




• Molecule 18: 50S ribosomal protein L16

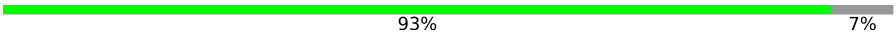
Chain M:





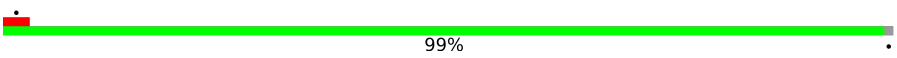
• Molecule 19: 50S ribosomal protein L17

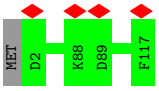
Chain N:



• Molecule 20: 50S ribosomal protein L18

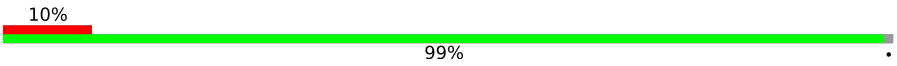
Chain O:

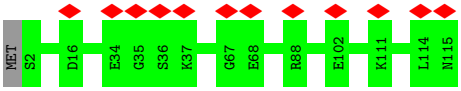




• Molecule 21: 50S ribosomal protein L19

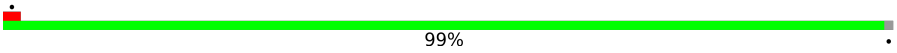
Chain P:

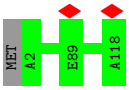




• Molecule 22: 50S ribosomal protein L20

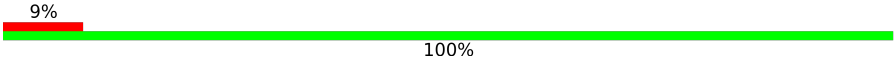
Chain Q:

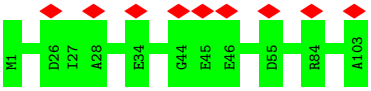




• Molecule 23: 50S ribosomal protein L21

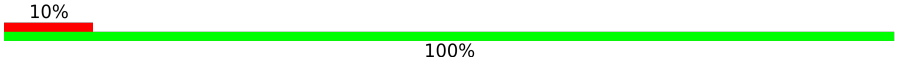
Chain R:

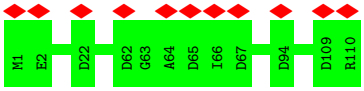




• Molecule 24: 50S ribosomal protein L22

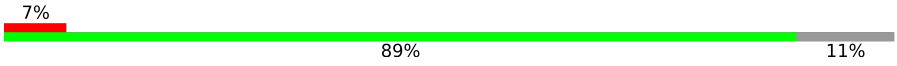
Chain S:

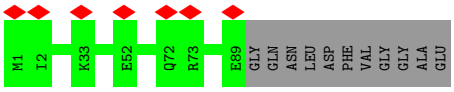




• Molecule 25: 50S ribosomal protein L23

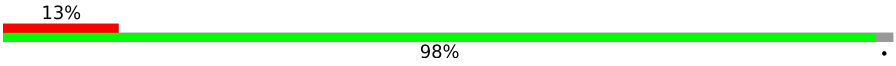
Chain T:

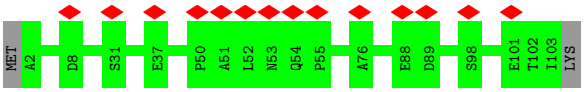




• Molecule 26: 50S ribosomal protein L24

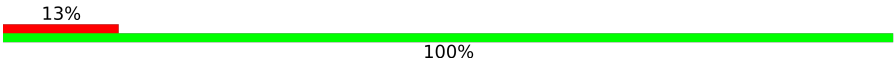
Chain U:

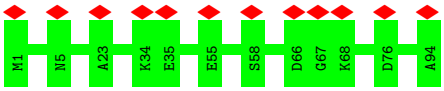




• Molecule 27: 50S ribosomal protein L25

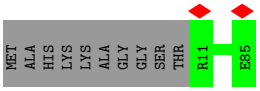
Chain V:





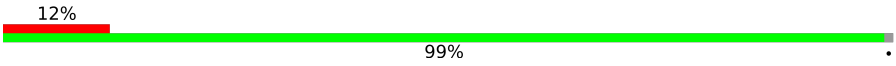
• Molecule 28: 50S ribosomal protein L27

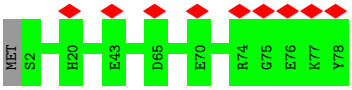
Chain W:



• Molecule 29: 50S ribosomal protein L28

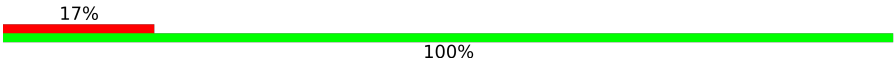
Chain X:

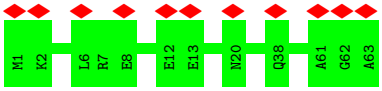




• Molecule 30: 50S ribosomal protein L29

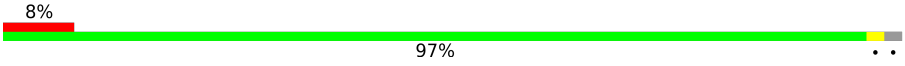
Chain Y:

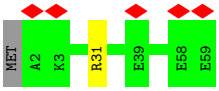




• Molecule 31: 50S ribosomal protein L30

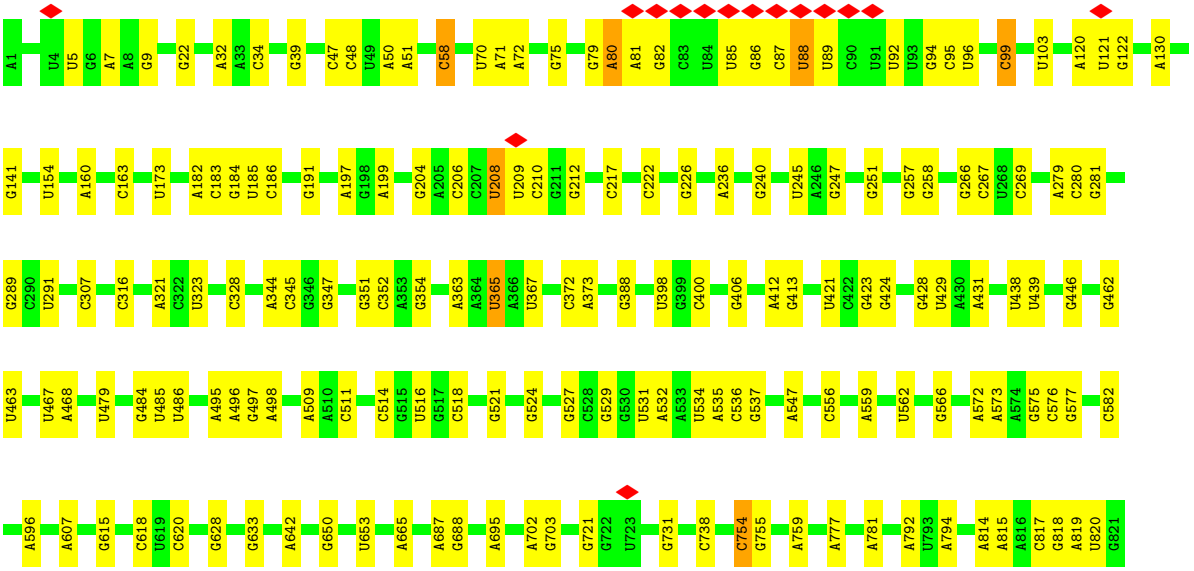
Chain Z:

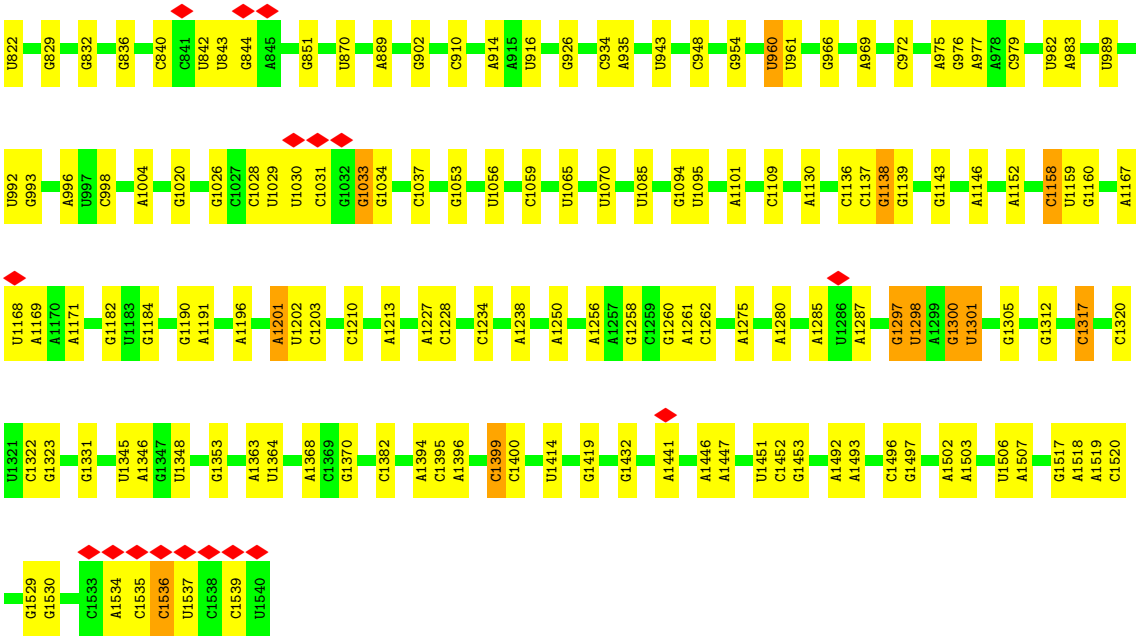




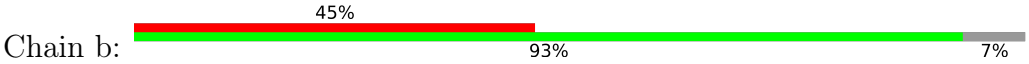
• Molecule 32: 16S ribosomal RNA

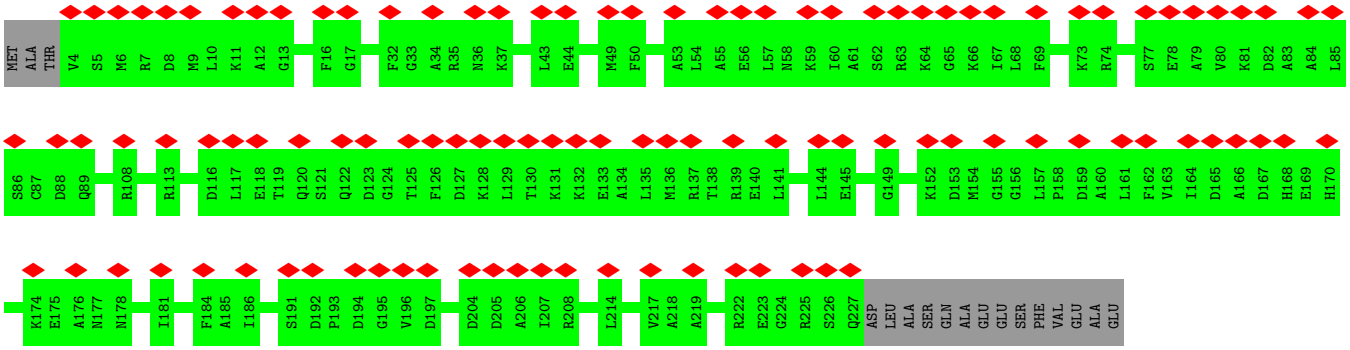
Chain a:



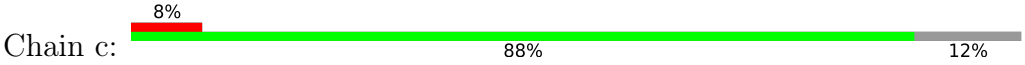


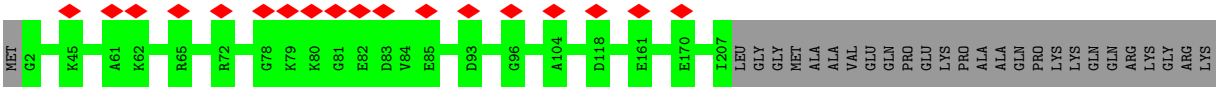
• Molecule 33: 30S ribosomal protein S2



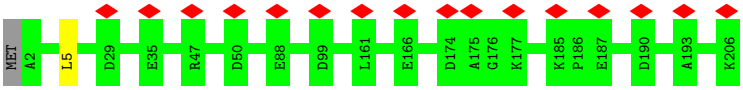


• Molecule 34: 30S ribosomal protein S3



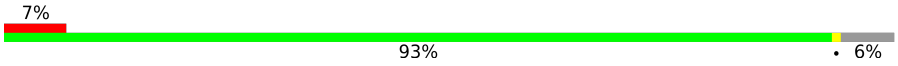


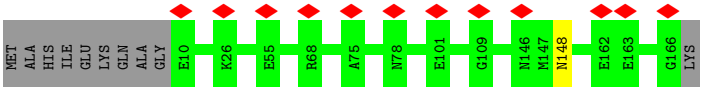
• Molecule 35: 30S ribosomal protein S4



• Molecule 36: 30S ribosomal protein S5

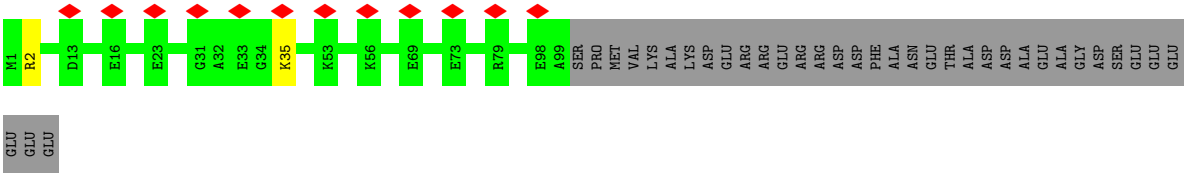
Chain e:





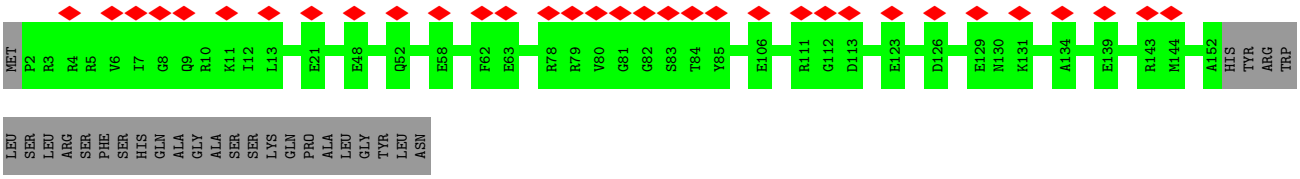
• Molecule 37: 30S ribosomal protein S6

Chain f:



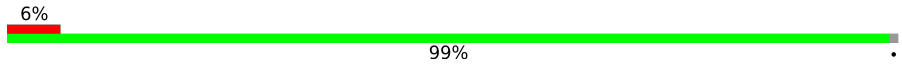
• Molecule 38: 30S ribosomal protein S7

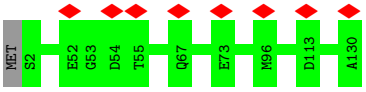
Chain g:



• Molecule 39: 30S ribosomal protein S8

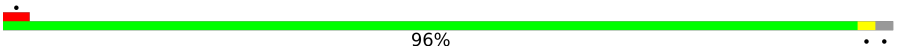
Chain h:

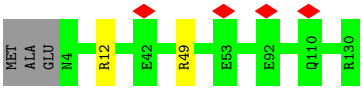




• Molecule 40: 30S ribosomal protein S9

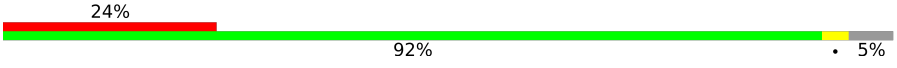
Chain i:

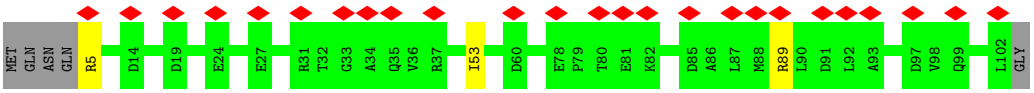




• Molecule 41: 30S ribosomal protein S10

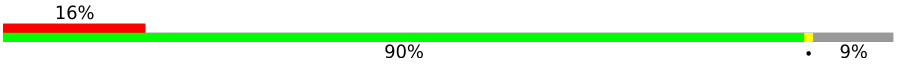
Chain j:

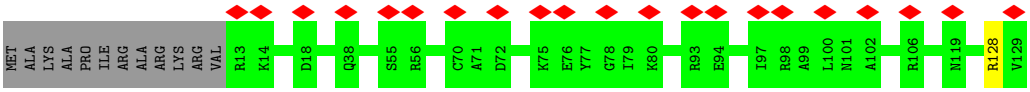




• Molecule 42: 30S ribosomal protein S11

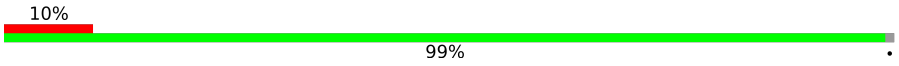
Chain k:

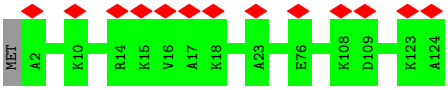




• Molecule 43: 30S ribosomal protein S12

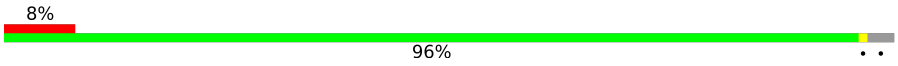
Chain l:





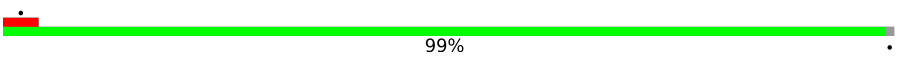
• Molecule 44: 30S ribosomal protein S13

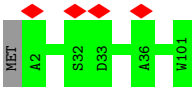
Chain m:



• Molecule 45: 30S ribosomal protein S14

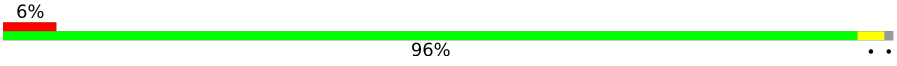
Chain n:

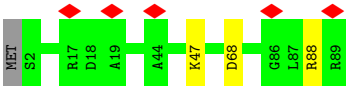




• Molecule 46: 30S ribosomal protein S15

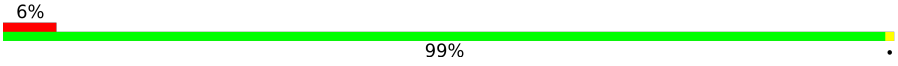
Chain o:

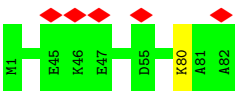




• Molecule 47: 30S ribosomal protein S16

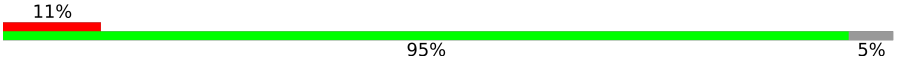
Chain p:

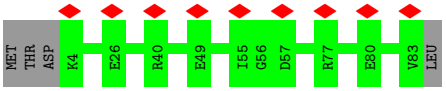




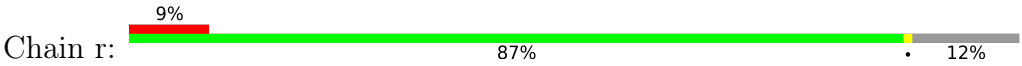
• Molecule 48: 30S ribosomal protein S17

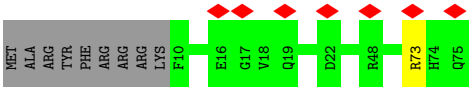
Chain q:



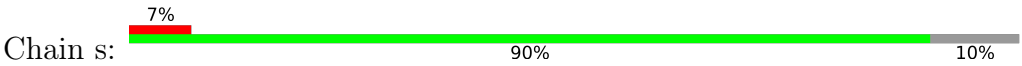


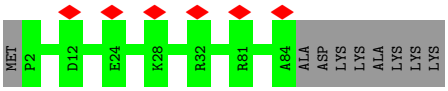
• Molecule 49: 30S ribosomal protein S18



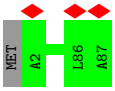


• Molecule 50: 30S ribosomal protein S19

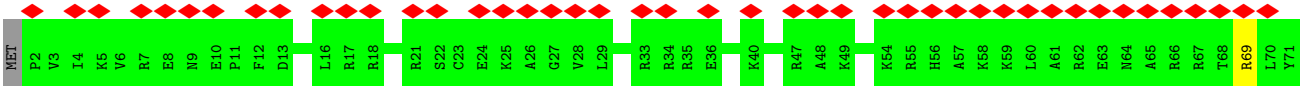




• Molecule 51: 30S ribosomal protein S20



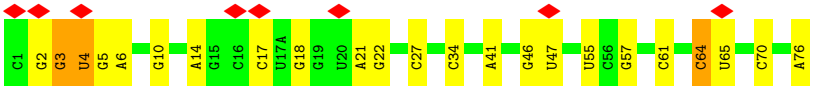
• Molecule 52: 30S ribosomal protein S21



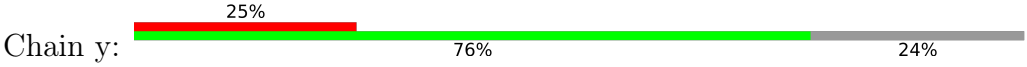
• Molecule 53: mRNA

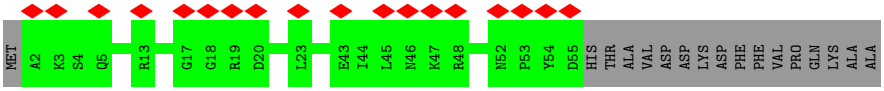
There are no outlier residues recorded for this chain.

• Molecule 54: P-site tRNA-Pro(CGG)

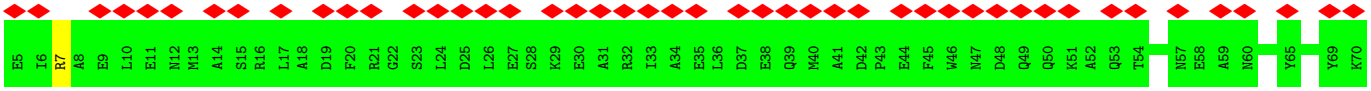


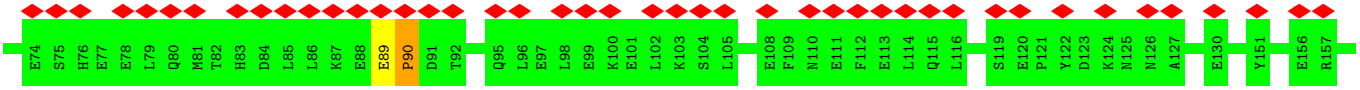
• Molecule 55: Uncharacterized protein YqkK

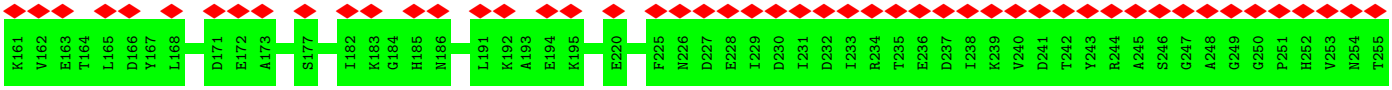


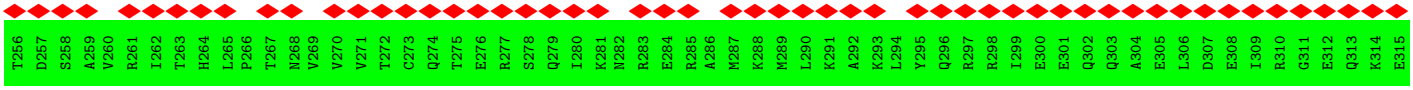


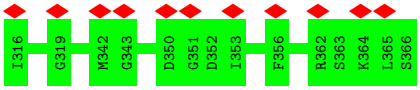
• Molecule 56: Peptide chain release factor 2











4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	154405	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 ($e^-/Å^2$)	83.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.187	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.0387	Depositor
Map size (Å)	391.92, 391.92, 391.92	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.065, 1.065, 1.065	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	0	0.44	0/440	0.53	0/588
2	1	0.45	0/416	0.53	0/554
3	2	0.44	0/380	0.54	0/498
4	3	0.46	0/513	0.60	0/676
5	4	0.48	0/303	0.57	0/397
6	5	0.38	0/523	0.56	0/698
7	A	0.92	2/69800 (0.0%)	1.11	352/108892 (0.3%)
8	B	0.82	1/2873 (0.0%)	1.14	20/4478 (0.4%)
9	C	0.49	0/2121	0.59	0/2852
10	D	0.48	0/1586	0.60	0/2134
11	E	0.43	0/1571	0.55	0/2113
12	F	0.39	0/1434	0.57	0/1926
13	G	0.36	0/1324	0.55	0/1794
14	H	0.34	0/1122	0.67	1/1515 (0.1%)
15	J	0.42	0/1152	0.52	0/1551
16	K	0.46	0/947	0.62	0/1268
17	L	0.43	0/1062	0.62	1/1413 (0.1%)
18	M	0.43	0/1093	0.64	1/1460 (0.1%)
19	N	0.44	0/958	0.57	0/1281
20	O	0.40	0/902	0.55	0/1209
21	P	0.46	0/929	0.52	0/1242
22	Q	0.48	0/960	0.52	0/1278
23	R	0.44	0/829	0.56	0/1107
24	S	0.39	0/864	0.54	0/1156
25	T	0.37	0/715	0.55	0/955
26	U	0.40	0/787	0.58	0/1051
27	V	0.42	0/766	0.55	0/1025
28	W	0.45	0/582	0.49	0/769
29	X	0.43	0/635	0.52	0/848
30	Y	0.34	0/510	0.49	0/677
31	Z	0.36	0/453	0.52	0/605
32	a	0.92	0/36991	1.08	127/57705 (0.2%)
33	b	0.36	0/1784	0.59	0/2403
34	c	0.43	0/1651	0.58	0/2225

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	d	0.44	0/1665	0.59	1/2227 (0.0%)
36	e	0.44	0/1169	0.60	1/1573 (0.1%)
37	f	0.43	0/829	0.58	0/1120
38	g	0.38	0/1195	0.59	0/1602
39	h	0.43	0/989	0.53	0/1326
40	i	0.43	0/1034	0.62	0/1375
41	j	0.46	1/796 (0.1%)	0.68	0/1077
42	k	0.40	0/893	0.55	0/1205
43	l	0.48	0/969	0.59	0/1300
44	m	0.41	0/892	0.64	1/1193 (0.1%)
45	n	0.42	0/817	0.54	0/1088
46	o	0.37	0/722	0.62	1/964 (0.1%)
47	p	0.45	0/659	0.61	0/884
48	q	0.42	0/657	0.57	0/881
49	r	0.42	0/554	0.53	0/743
50	s	0.41	0/680	0.57	0/915
51	t	0.37	0/676	0.47	0/895
52	u	0.37	0/598	0.47	0/792
53	v	0.75	0/139	1.29	0/214
54	x	0.71	0/1839	1.17	13/2866 (0.5%)
55	y	0.37	0/440	0.57	0/579
56	z	0.37	0/2786	0.59	1/3764 (0.0%)
All	All	0.80	4/159974 (0.0%)	0.99	520/238926 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1	G	OP3-P	-10.58	1.48	1.61
8	B	1	U	OP3-P	-10.53	1.48	1.61
41	j	53	ILE	C-N	-5.64	1.21	1.34
7	A	1800	C	N1-C6	-5.11	1.34	1.37

The worst 5 of 520 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	2164	C	N1-C2-O2	13.10	126.76	118.90
7	A	2164	C	C2-N1-C1'	12.70	132.77	118.80
7	A	12	U	N3-C2-O2	-12.63	113.36	122.20
32	a	95	C	C2-N1-C1'	12.04	132.05	118.80
7	A	12	U	N1-C2-O2	11.79	131.06	122.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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
1	0	53/57 (93%)	50 (94%)	3 (6%)	0	100 100
2	1	48/55 (87%)	43 (90%)	5 (10%)	0	100 100
3	2	44/46 (96%)	43 (98%)	1 (2%)	0	100 100
4	3	62/65 (95%)	56 (90%)	5 (8%)	1 (2%)	9 33
5	4	36/38 (95%)	34 (94%)	2 (6%)	0	100 100
6	5	63/70 (90%)	54 (86%)	9 (14%)	0	100 100
9	C	269/273 (98%)	247 (92%)	22 (8%)	0	100 100
10	D	207/209 (99%)	188 (91%)	19 (9%)	0	100 100
11	E	199/201 (99%)	192 (96%)	7 (4%)	0	100 100
12	F	175/179 (98%)	163 (93%)	12 (7%)	0	100 100
13	G	172/177 (97%)	153 (89%)	19 (11%)	0	100 100
14	H	147/149 (99%)	121 (82%)	26 (18%)	0	100 100
15	J	140/142 (99%)	134 (96%)	6 (4%)	0	100 100
16	K	120/123 (98%)	110 (92%)	10 (8%)	0	100 100
17	L	142/144 (99%)	132 (93%)	10 (7%)	0	100 100
18	M	134/136 (98%)	129 (96%)	4 (3%)	1 (1%)	22 52
19	N	116/127 (91%)	105 (90%)	11 (10%)	0	100 100
20	O	114/117 (97%)	108 (95%)	6 (5%)	0	100 100
21	P	112/115 (97%)	104 (93%)	8 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	Q	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
23	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
24	S	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
25	T	87/100 (87%)	81 (93%)	6 (7%)	0	100	100
26	U	100/104 (96%)	86 (86%)	14 (14%)	0	100	100
27	V	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
28	W	73/85 (86%)	70 (96%)	3 (4%)	0	100	100
29	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
30	Y	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
31	Z	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
33	b	222/241 (92%)	203 (91%)	19 (9%)	0	100	100
34	c	204/233 (88%)	191 (94%)	13 (6%)	0	100	100
35	d	203/206 (98%)	190 (94%)	13 (6%)	0	100	100
36	e	155/167 (93%)	142 (92%)	13 (8%)	0	100	100
37	f	97/135 (72%)	92 (95%)	5 (5%)	0	100	100
38	g	149/179 (83%)	141 (95%)	8 (5%)	0	100	100
39	h	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
40	i	125/130 (96%)	112 (90%)	13 (10%)	0	100	100
41	j	96/103 (93%)	86 (90%)	10 (10%)	0	100	100
42	k	115/129 (89%)	105 (91%)	10 (9%)	0	100	100
43	l	121/124 (98%)	108 (89%)	13 (11%)	0	100	100
44	m	112/118 (95%)	97 (87%)	15 (13%)	0	100	100
45	n	98/101 (97%)	93 (95%)	5 (5%)	0	100	100
46	o	86/89 (97%)	80 (93%)	5 (6%)	1 (1%)	13	40
47	p	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
48	q	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
49	r	64/75 (85%)	64 (100%)	0	0	100	100
50	s	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
51	t	84/87 (97%)	82 (98%)	2 (2%)	0	100	100
52	u	68/71 (96%)	66 (97%)	2 (3%)	0	100	100
55	y	52/71 (73%)	46 (88%)	6 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
56	z	360/362 (99%)	324 (90%)	34 (9%)	2 (1%)	25 55
All	All	5998/6346 (94%)	5546 (92%)	447 (8%)	5 (0%)	54 81

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
56	z	90	PRO
46	o	47	LYS
56	z	89	GLU
18	M	69	PRO
4	3	32	ILE

5.3.2 Protein sidechains (i)

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	0	46/48 (96%)	46 (100%)	0	100 100
2	1	45/49 (92%)	45 (100%)	0	100 100
3	2	38/38 (100%)	38 (100%)	0	100 100
4	3	51/52 (98%)	50 (98%)	1 (2%)	55 78
5	4	34/34 (100%)	33 (97%)	1 (3%)	42 70
6	5	58/62 (94%)	58 (100%)	0	100 100
9	C	216/218 (99%)	215 (100%)	1 (0%)	88 94
10	D	164/164 (100%)	163 (99%)	1 (1%)	86 93
11	E	165/165 (100%)	164 (99%)	1 (1%)	86 93
12	F	148/150 (99%)	148 (100%)	0	100 100
13	G	135/138 (98%)	132 (98%)	3 (2%)	52 76
14	H	114/114 (100%)	112 (98%)	2 (2%)	59 80
15	J	116/116 (100%)	115 (99%)	1 (1%)	78 90
16	K	103/104 (99%)	103 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
17	L	103/103 (100%)	102 (99%)	1 (1%)	76 89
18	M	109/109 (100%)	107 (98%)	2 (2%)	59 80
19	N	98/103 (95%)	98 (100%)	0	100 100
20	O	86/87 (99%)	86 (100%)	0	100 100
21	P	99/100 (99%)	99 (100%)	0	100 100
22	Q	89/90 (99%)	89 (100%)	0	100 100
23	R	84/84 (100%)	84 (100%)	0	100 100
24	S	93/93 (100%)	93 (100%)	0	100 100
25	T	77/84 (92%)	77 (100%)	0	100 100
26	U	83/85 (98%)	83 (100%)	0	100 100
27	V	78/78 (100%)	78 (100%)	0	100 100
28	W	57/63 (90%)	57 (100%)	0	100 100
29	X	67/68 (98%)	67 (100%)	0	100 100
30	Y	55/55 (100%)	55 (100%)	0	100 100
31	Z	48/49 (98%)	47 (98%)	1 (2%)	53 77
33	b	186/199 (94%)	186 (100%)	0	100 100
34	c	170/190 (90%)	170 (100%)	0	100 100
35	d	172/173 (99%)	172 (100%)	0	100 100
36	e	119/126 (94%)	119 (100%)	0	100 100
37	f	86/116 (74%)	84 (98%)	2 (2%)	50 75
38	g	124/147 (84%)	124 (100%)	0	100 100
39	h	104/105 (99%)	104 (100%)	0	100 100
40	i	105/107 (98%)	103 (98%)	2 (2%)	57 79
41	j	86/90 (96%)	84 (98%)	2 (2%)	50 75
42	k	90/99 (91%)	89 (99%)	1 (1%)	73 88
43	l	103/104 (99%)	103 (100%)	0	100 100
44	m	92/96 (96%)	92 (100%)	0	100 100
45	n	83/84 (99%)	83 (100%)	0	100 100
46	o	76/77 (99%)	75 (99%)	1 (1%)	69 86
47	p	65/65 (100%)	64 (98%)	1 (2%)	65 83
48	q	74/78 (95%)	74 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	r	57/65 (88%)	56 (98%)	1 (2%)	59 80
50	s	72/79 (91%)	72 (100%)	0	100 100
51	t	65/66 (98%)	65 (100%)	0	100 100
52	u	60/61 (98%)	59 (98%)	1 (2%)	60 82
55	y	47/61 (77%)	47 (100%)	0	100 100
56	z	267/319 (84%)	266 (100%)	1 (0%)	91 95
All	All	4962/5210 (95%)	4935 (100%)	27 (0%)	89 94

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	Z	31	ARG
40	i	12	ARG
49	r	73	ARG
37	f	35	LYS
40	i	49	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
23	R	66	HIS
50	s	69	HIS
30	Y	15	ASN
50	s	14	HIS
56	z	252	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	a	1539/1540 (99%)	271 (17%)	0
53	v	5/6 (83%)	0	0
54	x	76/77 (98%)	18 (23%)	0
7	A	2902/2903 (99%)	622 (21%)	28 (0%)
8	B	119/120 (99%)	19 (15%)	3 (2%)
All	All	4641/4646 (99%)	930 (20%)	31 (0%)

5 of 930 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	3	U
7	A	10	A
7	A	13	A
7	A	15	G
7	A	23	G

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	A	1111	A
7	A	2901	C
7	A	1190	G
8	B	86	G
7	A	2326	C

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 monosaccharides 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.

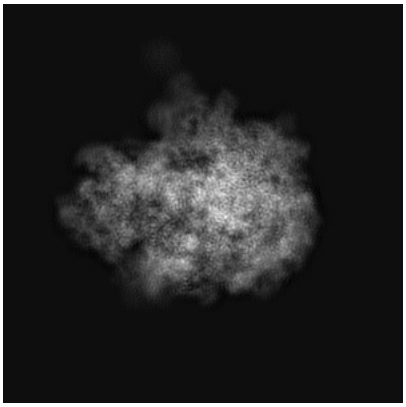
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10353. These allow visual inspection of the internal detail of the map and identification of artifacts.

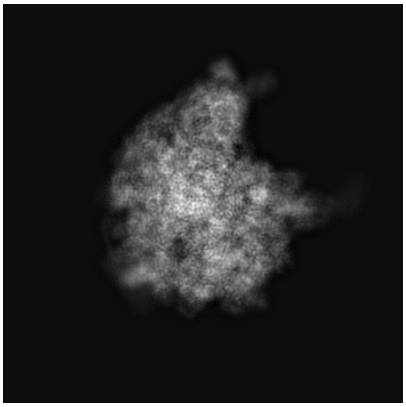
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

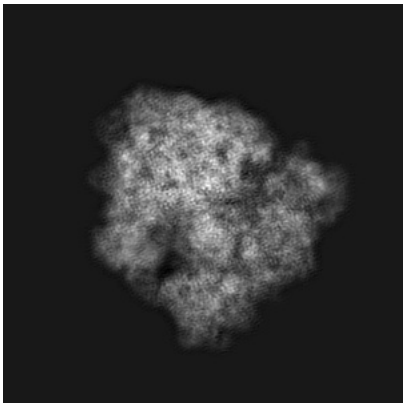
6.1.1 Primary map



X



Y

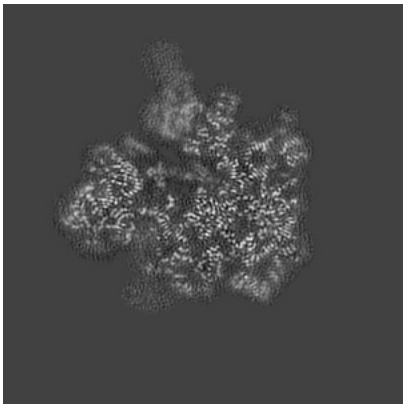


Z

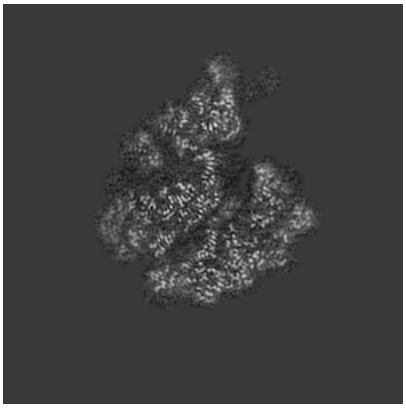
The images above show the map projected in three orthogonal directions.

6.2 Central slices

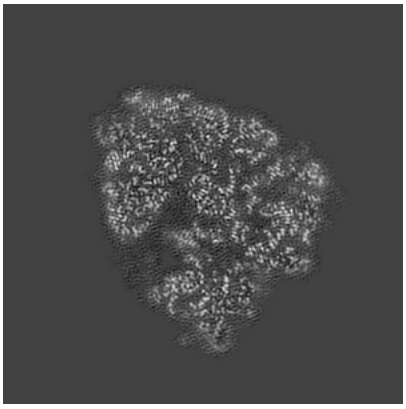
6.2.1 Primary map



X Index: 184



Y Index: 184

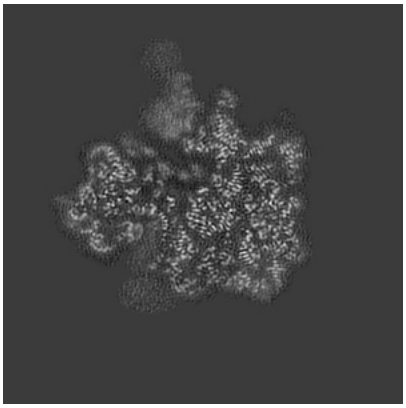


Z Index: 184

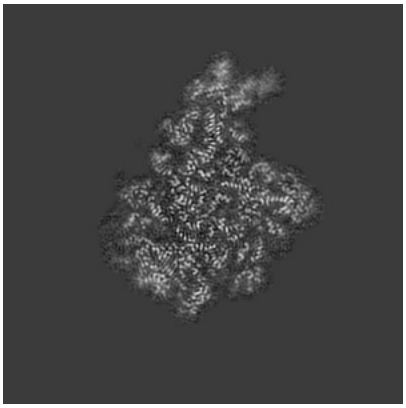
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

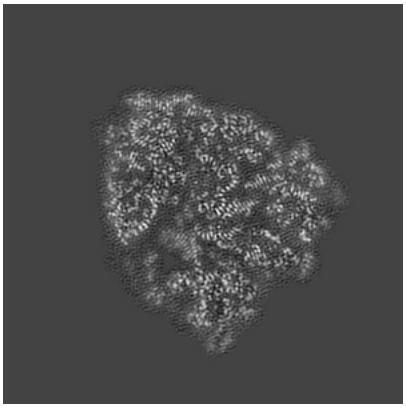
6.3.1 Primary map



X Index: 188



Y Index: 200

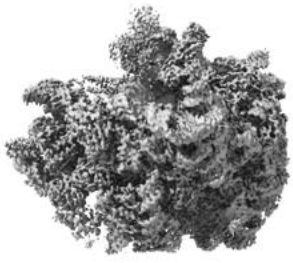


Z Index: 188

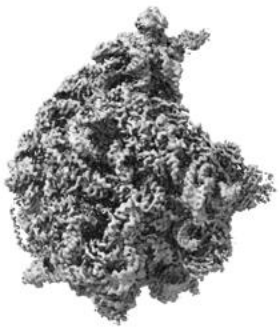
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

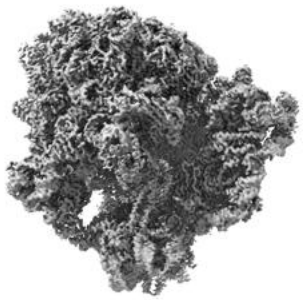
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0387. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

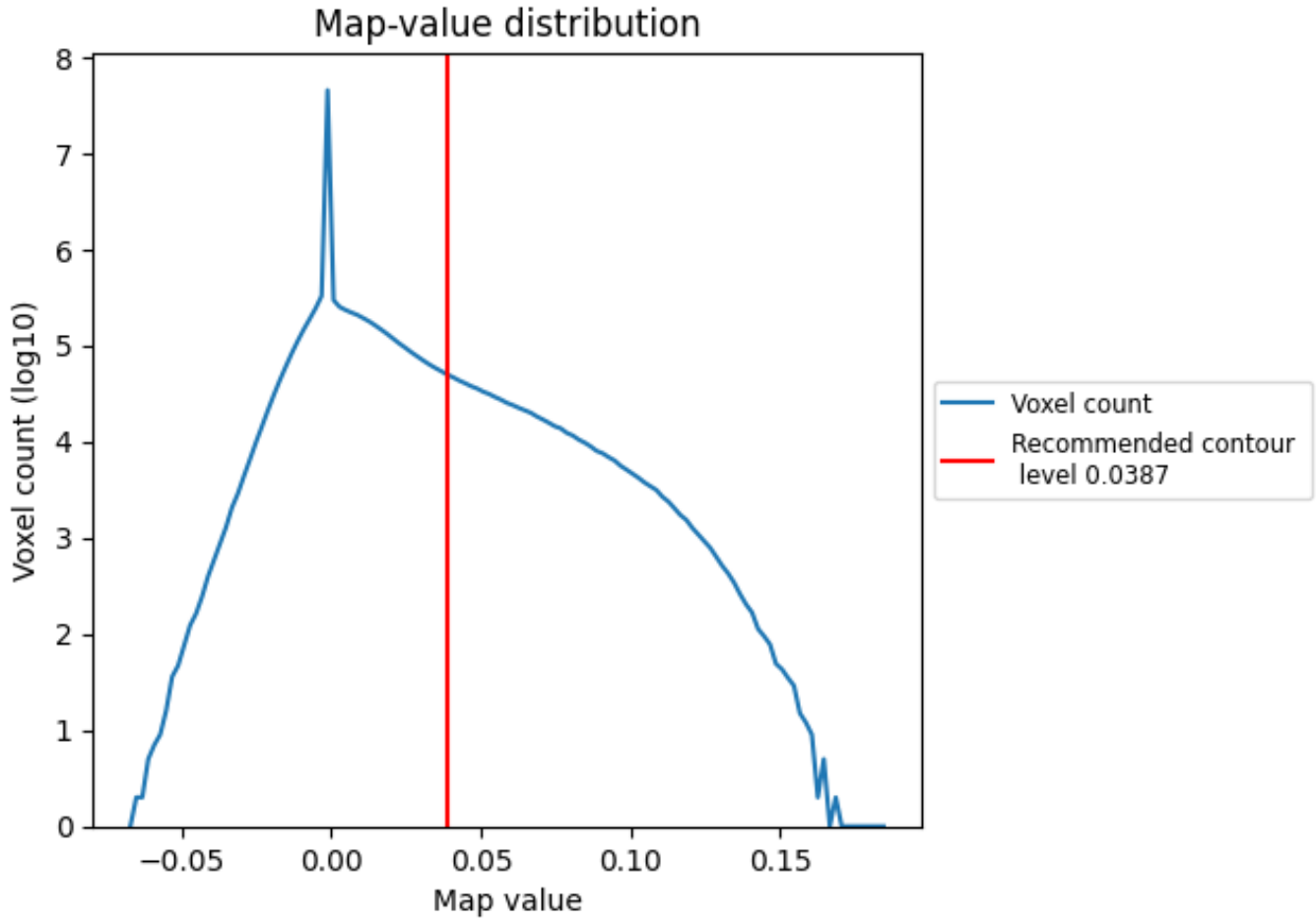
6.5 Mask visualisation (i)

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

7 Map analysis

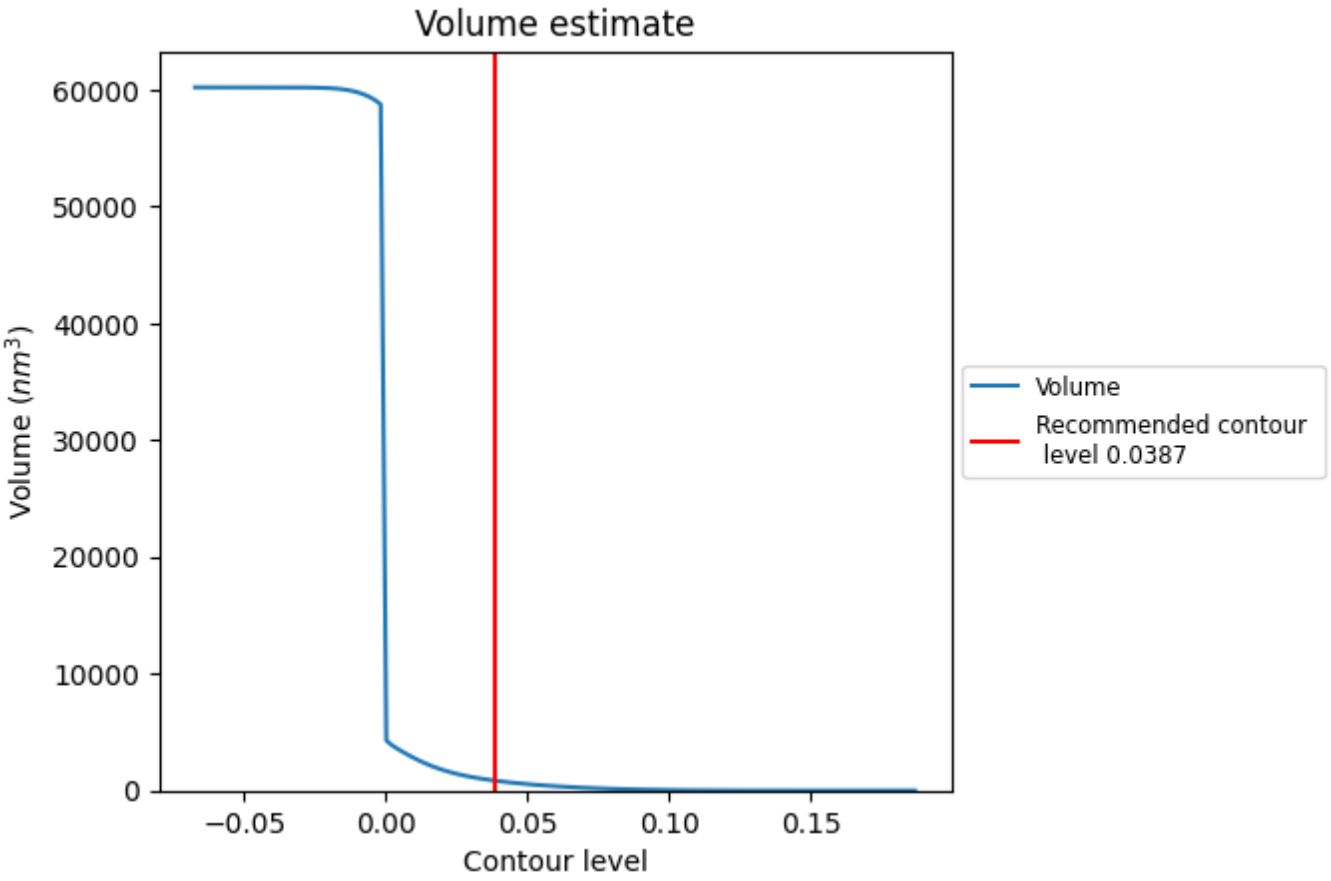
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

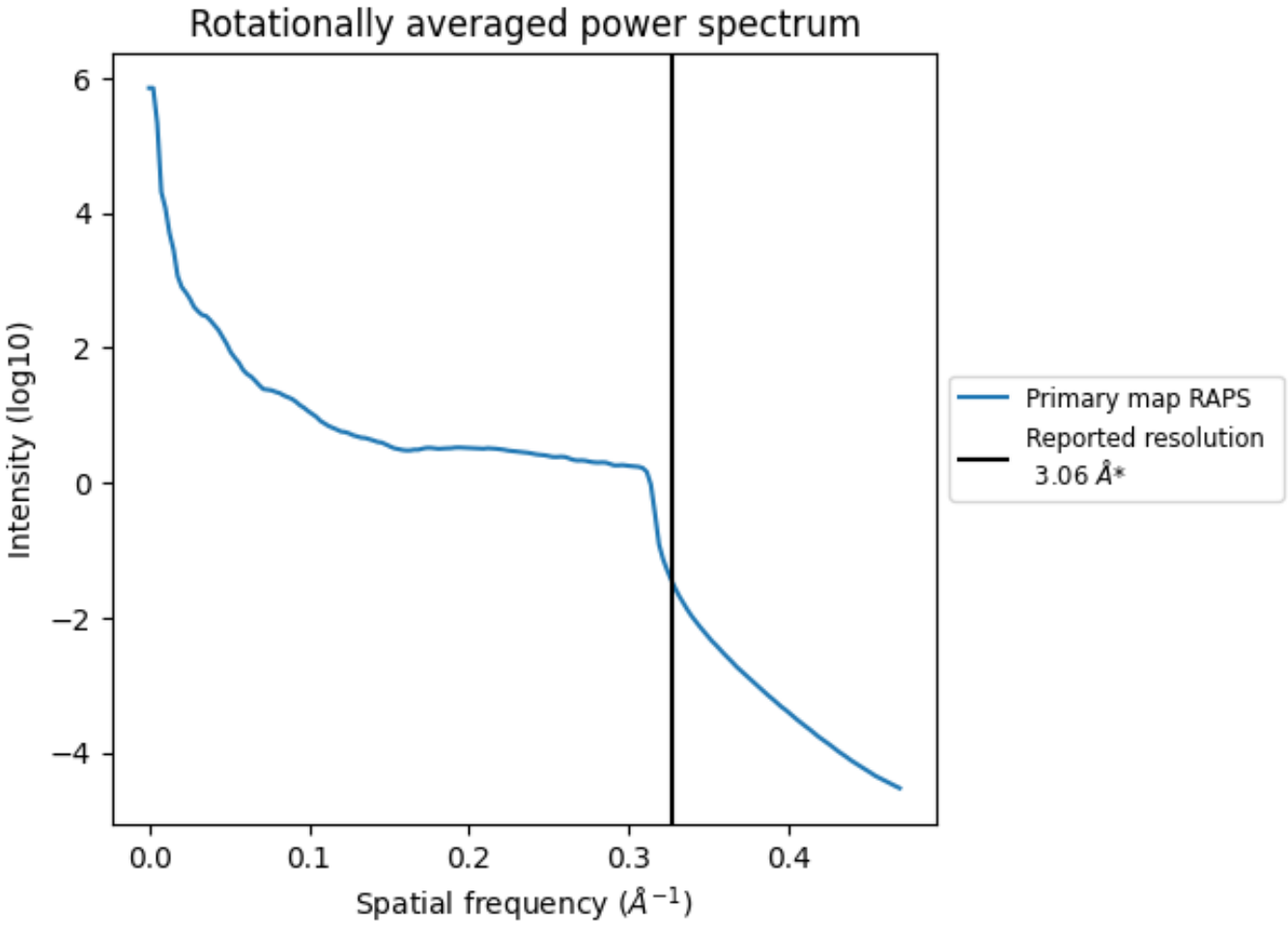
7.2 Volume estimate (i)



The volume at the recommended contour level is 842 nm^3; this corresponds to an approximate mass of 760 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 (i)

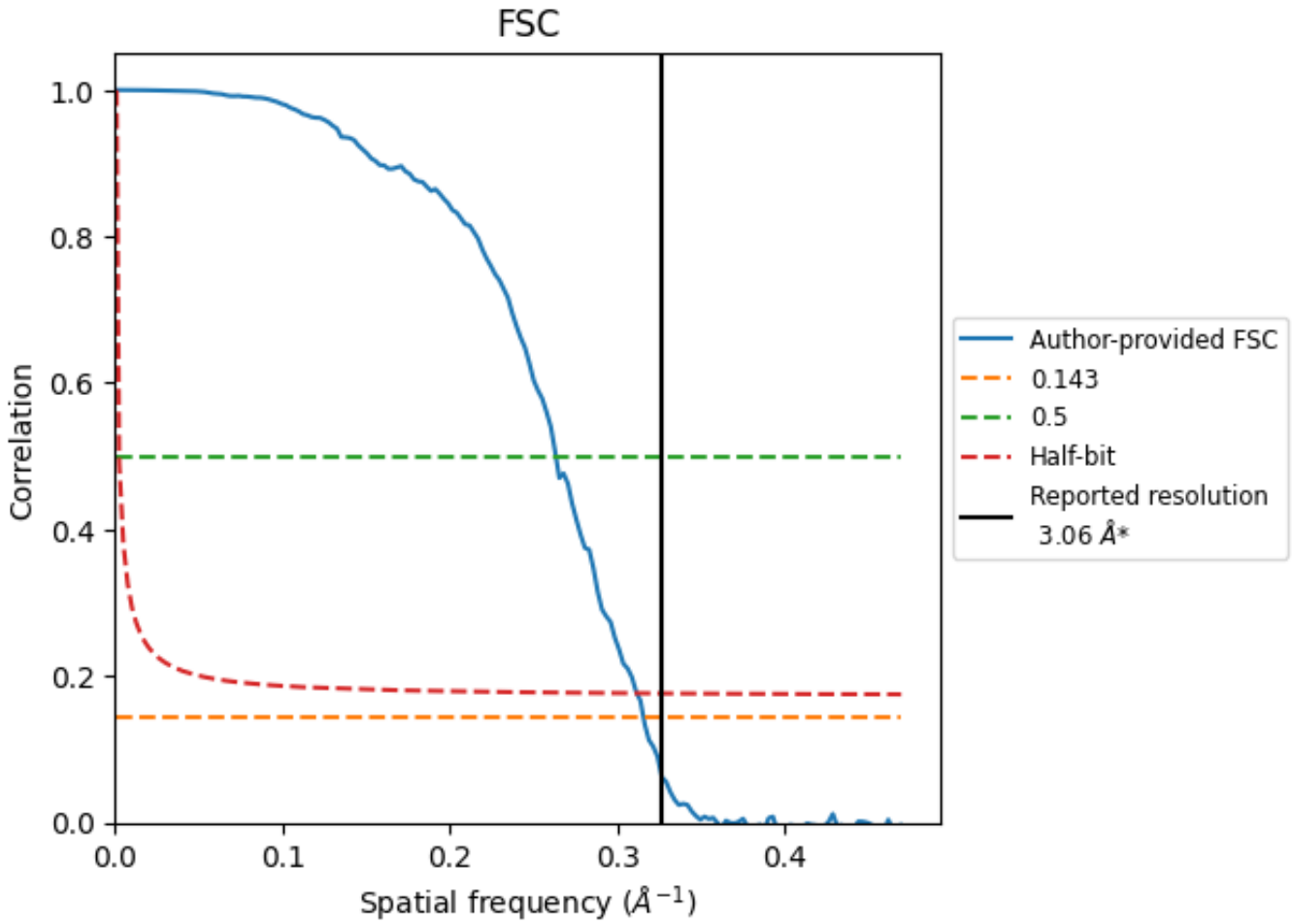


*Reported resolution corresponds to spatial frequency of 0.327 Å^{-1}

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.327 Å^{-1}

8.2 Resolution estimates (i)

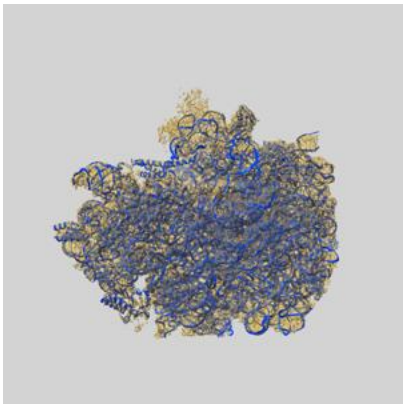
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.06	-	-
Author-provided FSC curve	3.17	3.80	3.21
Unmasked-calculated*	-	-	-

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

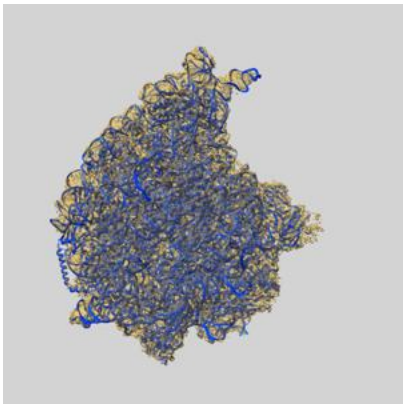
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10353 and PDB model 6SZS. Per-residue inclusion information can be found in section 3 on page 14.

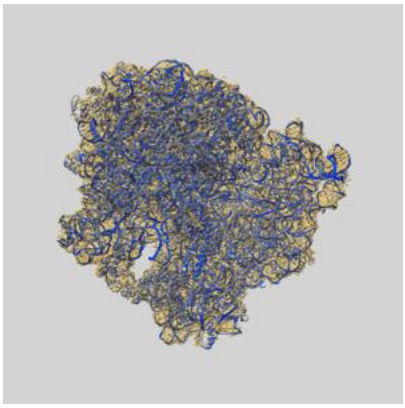
9.1 Map-model overlay



X



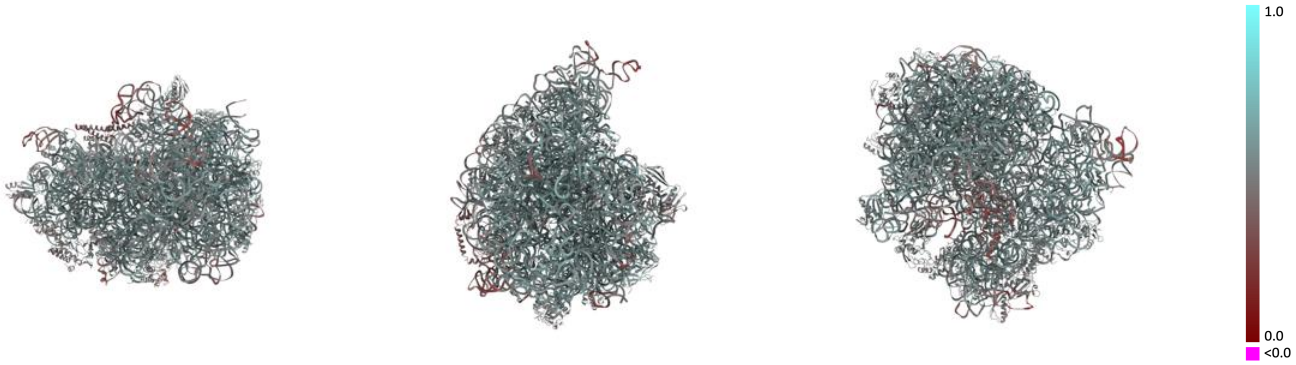
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0387 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.

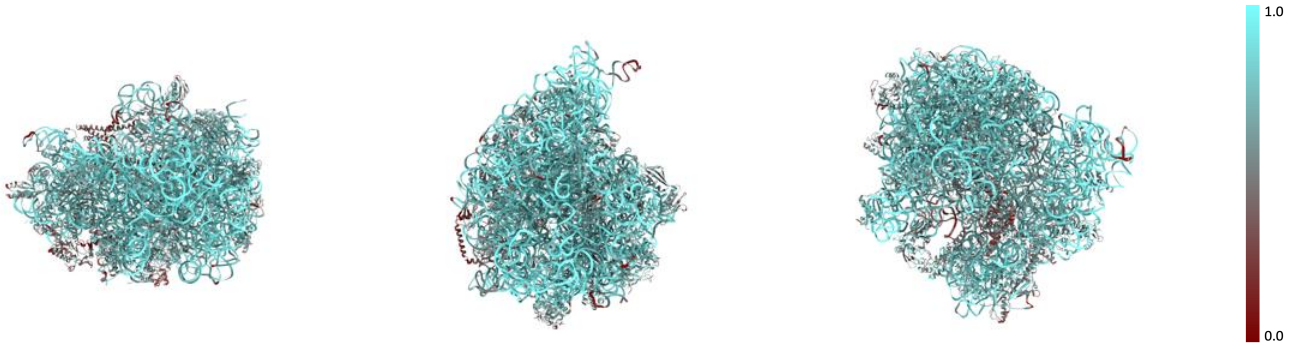
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

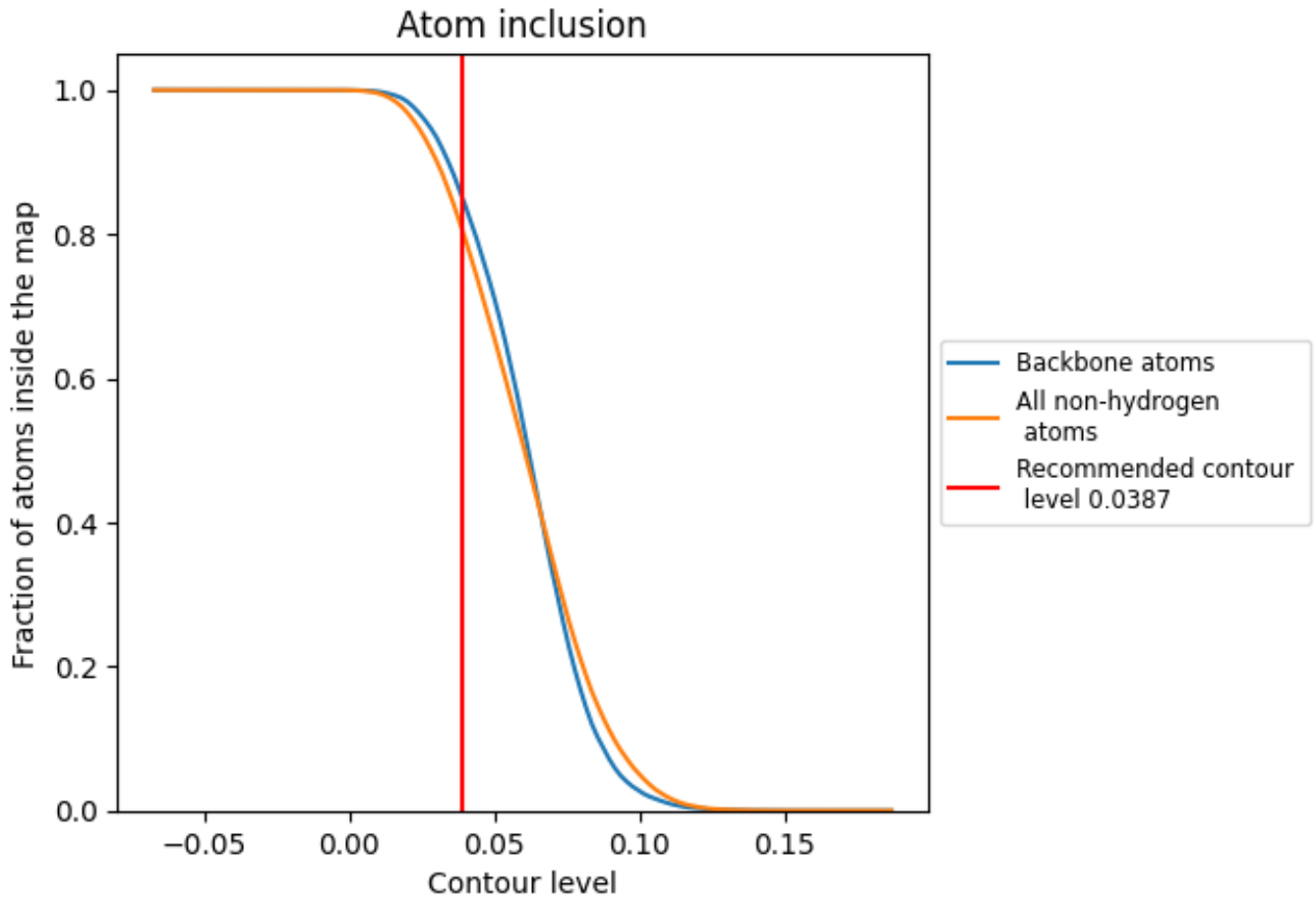
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.0387).

9.4 Atom inclusion (i)



At the recommended contour level, 85% of all backbone atoms, 81% 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 (0.0387) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8082	0.5350
0	0.7201	0.5610
1	0.6758	0.5510
2	0.7437	0.5870
3	0.7800	0.5850
4	0.7021	0.5650
5	0.5606	0.4760
A	0.8823	0.5380
B	0.9152	0.5320
C	0.6875	0.5710
D	0.6983	0.5650
E	0.6493	0.5340
F	0.6351	0.5060
G	0.6072	0.5000
H	0.2929	0.4060
J	0.7436	0.5570
K	0.6298	0.5610
L	0.6885	0.5490
M	0.6344	0.5600
N	0.7817	0.5700
O	0.7381	0.5340
P	0.6622	0.5620
Q	0.7566	0.5600
R	0.6838	0.5590
S	0.6579	0.5520
T	0.6162	0.5410
U	0.6232	0.5160
V	0.6762	0.5400
W	0.7138	0.5780
X	0.7121	0.5540
Y	0.6177	0.5030
Z	0.6728	0.5530
a	0.9073	0.5390
b	0.4065	0.4690
c	0.6736	0.5350

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Chain	Atom inclusion	Q-score
d	0.7113	0.5320
e	0.6825	0.5460
f	0.6532	0.5180
g	0.5682	0.5020
h	0.7115	0.5520
i	0.7293	0.5250
j	0.5848	0.5060
k	0.6084	0.5320
l	0.6678	0.5630
m	0.6910	0.5220
n	0.7300	0.5450
o	0.6826	0.5170
p	0.7640	0.5410
q	0.6487	0.5290
r	0.6641	0.5270
s	0.7002	0.5420
t	0.7282	0.5290
u	0.3482	0.4730
v	0.7619	0.5430
x	0.7017	0.4860
y	0.5251	0.5390
z	0.3826	0.4520