



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:21 PM UTC

PDB ID : 6Q8Y / pdb_00006q8y
EMDB ID : EMD-4474
Title : Cryo-EM structure of the mRNA translating and degrading yeast 80S ribosome-Xrn1 nuclease complex
Authors : Tesina, P.; Heckel, E.; Cheng, J.; Buschauer, R.; Kater, L.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2018-12-16
Resolution : 3.10 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:

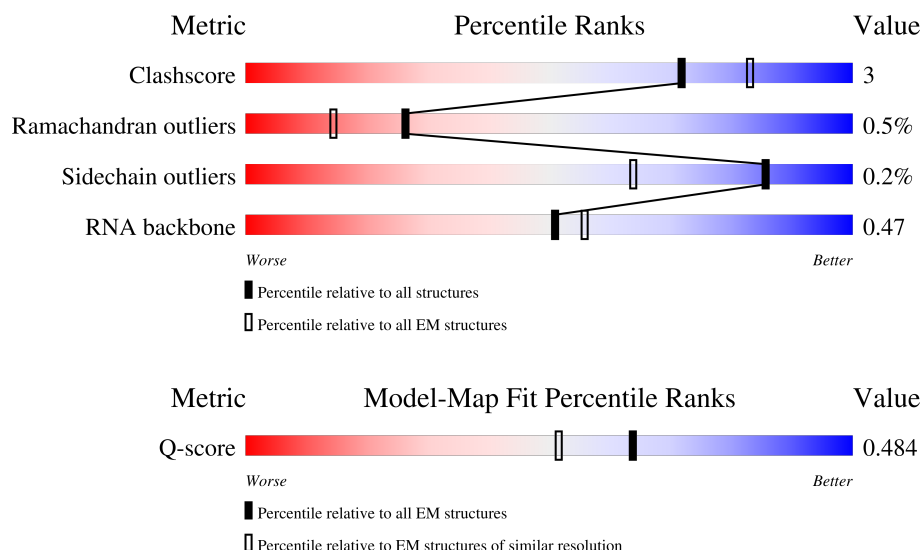
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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.



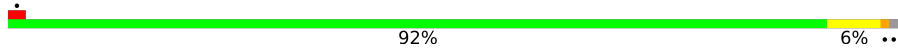
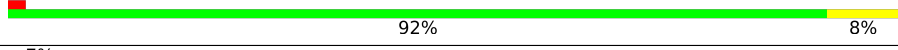
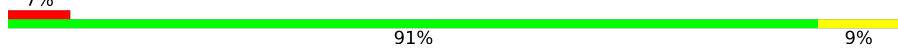
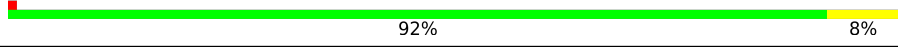
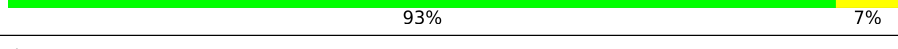
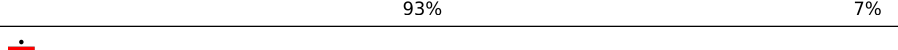
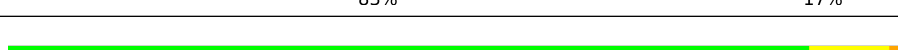
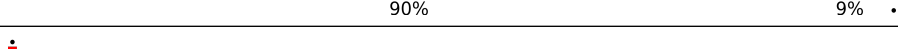
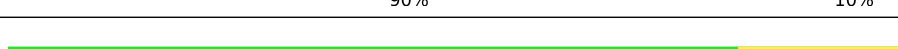
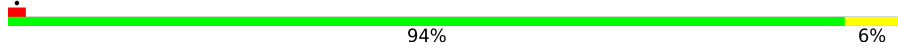
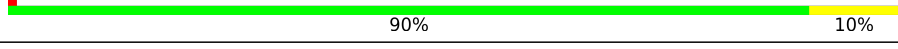
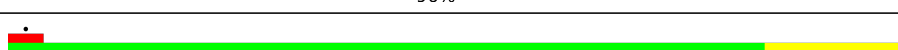
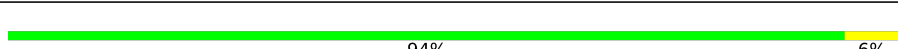
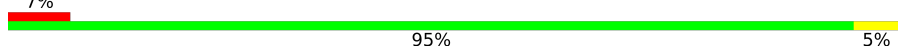
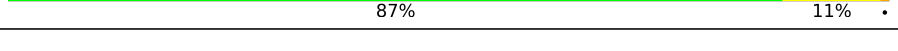
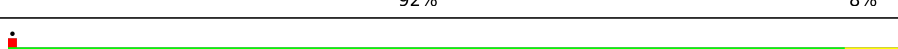
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	2	1797	
2	AA	233	
3	AB	136	

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Mol	Chain	Length	Quality of chain
4	AC	100	 92% 6% ..
5	AD	191	 92% 8%
6	AE	67	 7% 91% 9%
7	AF	87	 92% 8%
8	AG	169	 93% 7%
9	AH	121	 93% 7%
10	AI	77	 83% 17%
11	AJ	193	 90% 9% .
12	AK	126	 90% 10%
13	AL	50	 82% 18%
14	AM	136	 90% 10%
15	AN	135	 88% 12%
16	AO	52	 94% 6%
17	AP	105	 90% 10%
18	AQ	203	 88% 12%
19	AR	148	 89% 10% .
20	AS	25	 96% .
21	AT	91	 85% 15%
22	AU	197	 94% 6%
23	AV	58	 7% 95% 5%
24	AW	252	 88% 12%
25	AX	183	 5% 89% 11%
26	a	87	 87% 11% .
27	b	129	 92% 8%
28	c	144	 94% 6%

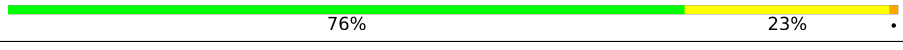
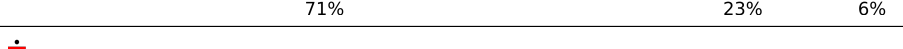
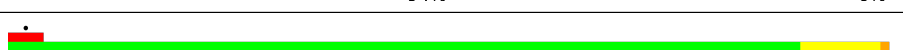
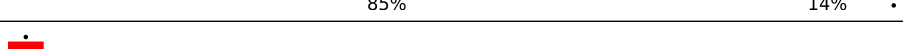
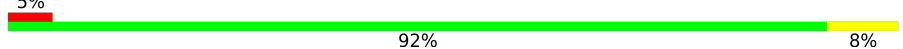
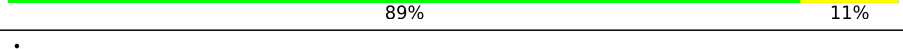
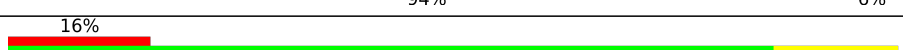
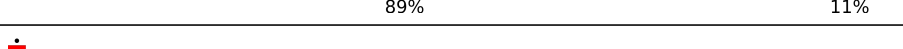
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Mol	Chain	Length	Quality of chain
29	d	132	
30	e	97	
31	f	81	
32	g	60	
33	z	916	
34	l	17	
35	n	76	
36	m	75	
37	AY	97	
38	BA	386	
39	BB	185	
40	BC	109	
41	BD	220	
42	BE	361	
43	BF	188	
44	BG	127	
45	BH	172	
46	BI	296	
47	BJ	159	
48	BK	106	
49	BL	100	
50	BM	175	
51	BN	112	
52	BO	222	
53	BP	119	

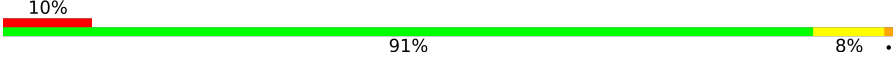
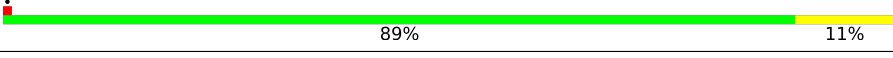
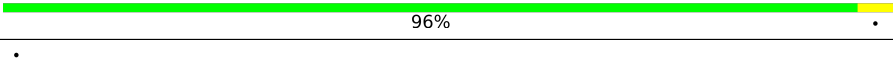
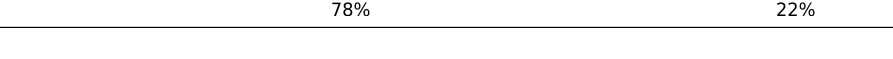
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Mol	Chain	Length	Quality of chain
54	BQ	3396	
55	BR	121	
56	BS	158	
57	A	223	
58	B	206	
59	C	96	
60	D	121	
61	E	121	
62	F	141	
63	G	125	
64	H	139	
65	J	107	
66	K	70	
67	L	63	
68	M	53	
69	N	51	
70	O	318	
71	P	219	
72	Q	214	
73	R	220	
74	S	260	
75	T	226	
76	U	184	
77	V	199	
78	W	178	

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Mol	Chain	Length	Quality of chain
79	X	155	 10% 91% 8% .
80	Y	150	 1% 89% 11% .
81	Z	127	 0% 96% 4% .
82	I	143	 2% 78% 22% .

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 209410 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1767	Total	C	N	O	P	0	0
			37645	16830	6656	12392	1767		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1570	G	A	conflict	GB 1329886537

- Molecule 2 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AA	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 3 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AB	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 4 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AC	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 5 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AD	191	Total	C	N	O	S	0	0
			1518	963	274	277	4		

- Molecule 6 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	67	Total	C	N	O	S	0	0
			543	349	106	87	1		

- Molecule 7 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AF	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 8 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AG	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 9 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AH	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 10 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	AI	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 11 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	AJ	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 13 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AL	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 15 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AN	135	Total	C	N	O	S	0	0
			1092	710	202	180			

- Molecule 16 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AO	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 17 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AP	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AQ	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 19 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AR	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 20 is a protein called 60S ribosomal protein L41-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 21 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 22 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AU	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 23 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AV	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 24 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AW	252	Total	C	N	O	S	0	0
			1914	1191	388	334	1		

- Molecule 25 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AX	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 26 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 27 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	b	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 28 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	c	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 29 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	132	Total	C	N	O	S	0	0
			1060	669	206	185			

- Molecule 30 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	e	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 33 is a protein called 5'-3' exoribonuclease 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	874	Total	C	N	O	S	0	0
			7181	4639	1194	1320	28		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	17	Total	C	N	O	P	0	0
			367	164	70	116	17		

- Molecule 35 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	76	Total	C	N	O	P	0	0
			1621	723	291	531	76		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	74	C	-	insertion	GB 1329886529
n	75	C	-	insertion	GB 1329886529
n	76	A	-	insertion	GB 1329886529

- Molecule 36 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	11	C	U	conflict	GB 176418

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AY	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 38 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BA	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 39 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BB	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 40 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BC	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 41 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BD	220	Total	C	N	O	S	0	0
			1770	1121	335	307	7		

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BE	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 43 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BF	188	Total	C	N	O	S	0	0
			1521	935	326	260			

- Molecule 44 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BG	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 45 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BH	172	Total	C	N	O	S	0	0
			1445	930	267	244	4		

- Molecule 46 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BI	296	Total	C	N	O	S	0	0
			2375	1501	414	458	2		

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BJ	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 48 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BK	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 49 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BL	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 50 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BM	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 51 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BN	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 52 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BO	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 53 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BP	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 54 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BQ	3161	Total	C	N	O	P	0	0
			67610	30200	12186	22063	3161		

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BR	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 56 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BS	158	Total	C	N	O	P	0	0
			3352	1500	586	1108	158		

- Molecule 57 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 58 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B	206	Total	C	N	O	S	0	0
			1603	1004	297	299	3		

- Molecule 59 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	C	96	Total	C	N	O	S	0	0
			813	527	133	151	2		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	D	121	Total	C	N	O	S	0	0
			877	552	153	170	2		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	E	121	Total	C	N	O	S	0	0
			957	611	176	163	7		

- Molecule 62 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	F	141	Total	C	N	O	S	0	0
			1099	704	202	193			

- Molecule 63 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	G	125	Total	C	N	O	S	0	0
			1001	625	188	186	2		

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	H	139	Total	C	N	O	S	0	0
			1143	716	222	203	2		

- Molecule 65 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 66 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	K	70	Total	C	N	O	S	0	0
			563	360	104	99			

- Molecule 67 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 68 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	M	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 69 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 70 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 71 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	P	219	Total	C	N	O	S	0	0
			1691	1082	296	311	2		

- Molecule 72 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 73 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 74 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	S	260	Total	C	N	O	S	0	0
			2061	1309	389	360	3		

- Molecule 75 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 76 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	U	179	Total	C	N	O	S	0	0
			1442	926	259	257			

- Molecule 77 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 78 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	W	178	Total	C	N	O	S	0	0
			1434	905	276	252	1		

- Molecule 79 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 80 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Y	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 81 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 82 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	I	143	Total	C	N	O	S	0	0
			1101	688	204	207	2		

- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	AF	1	Total	Zn	0
			1	1	
83	AO	1	Total	Zn	0
			1	1	
83	AP	1	Total	Zn	0
			1	1	
83	AT	1	Total	Zn	0
			1	1	
83	e	1	Total	Zn	0
			1	1	
83	BN	1	Total	Zn	0
			1	1	
83	M	1	Total	Zn	0
			1	1	
83	N	1	Total	Zn	0
			1	1	

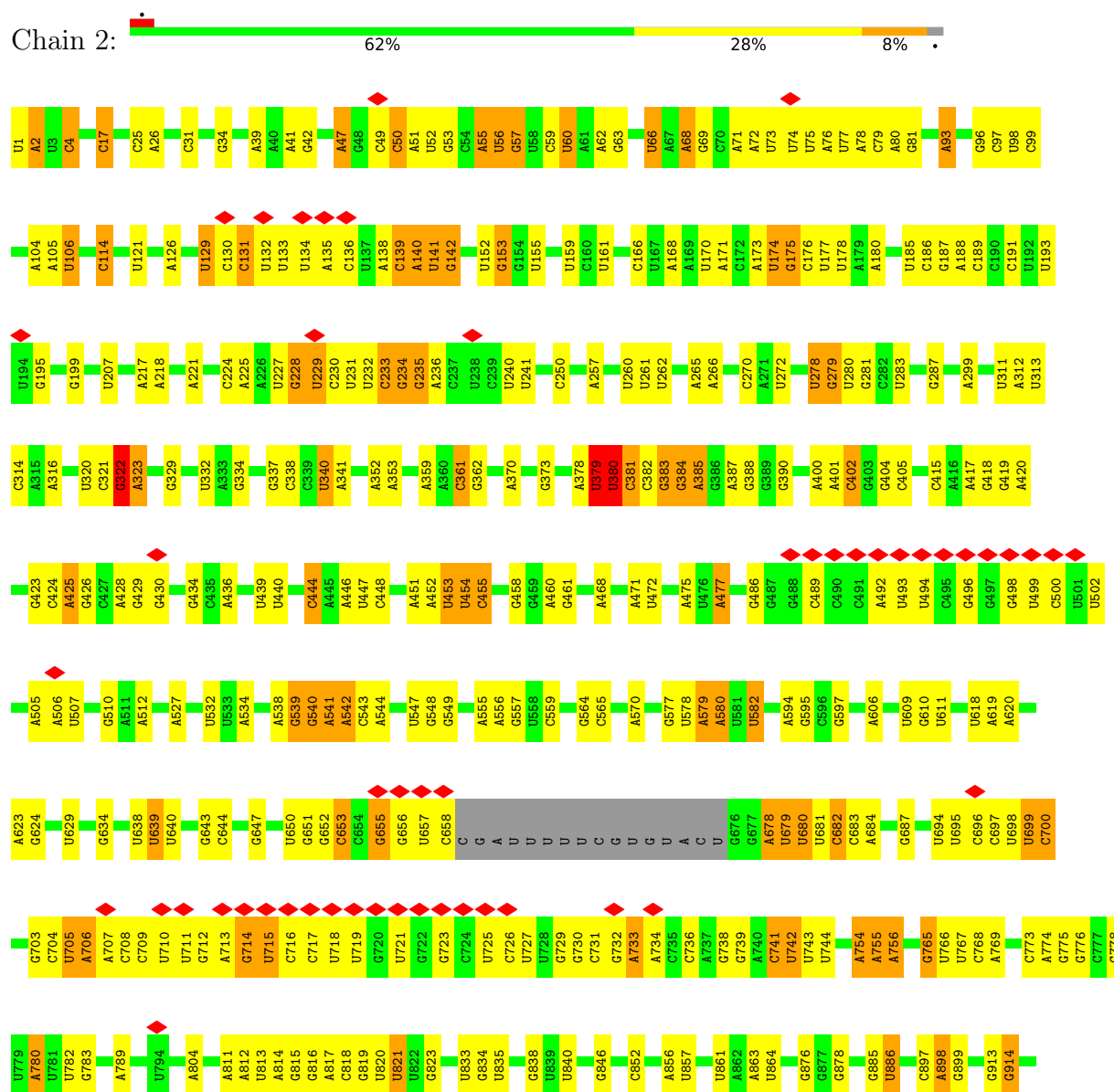
- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

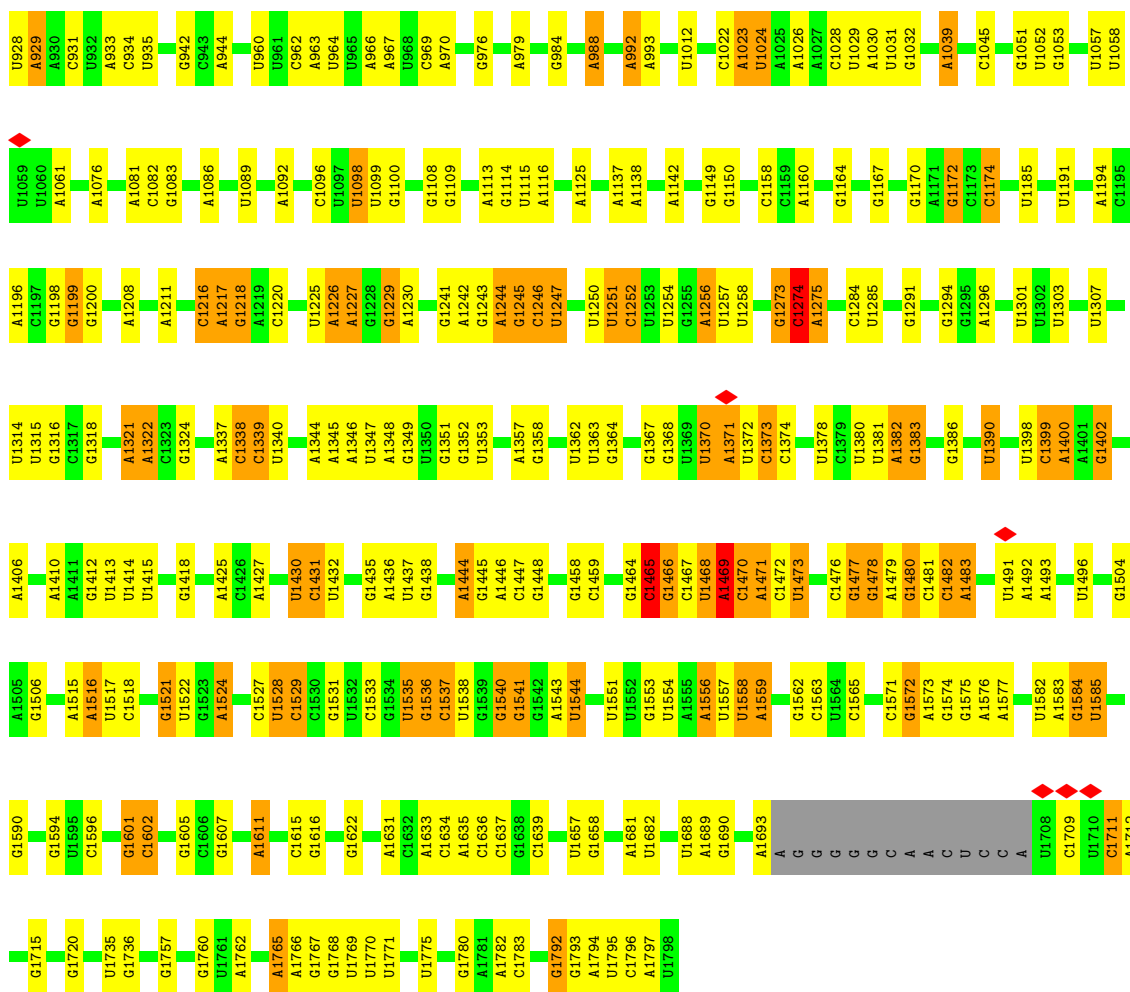
Mol	Chain	Residues	Atoms		AltConf
84	z	1	Total	Mg	0
			1	1	
84	l	1	Total	Mg	0
			1	1	

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: 18S ribosomal RNA

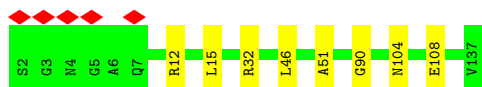




- Molecule 2: 60S ribosomal protein L8-A



- Molecule 3: 60S ribosomal protein L23-A



- Molecule 4: 60S ribosomal protein L36-A





- Molecule 5: 60S ribosomal protein L9-A



- Molecule 6: 60S ribosomal protein L24-A



- Molecule 7: 60S ribosomal protein L37-A



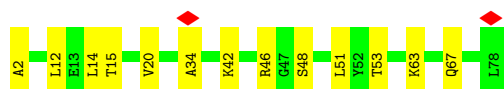
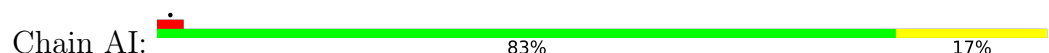
- Molecule 8: 60S ribosomal protein L11-B



- Molecule 9: 60S ribosomal protein L25



- Molecule 10: 60S ribosomal protein L38

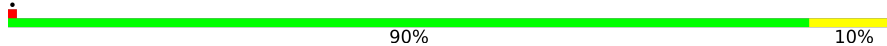


- Molecule 11: 60S ribosomal protein L13-A

Chain AJ:  90% 9%



- Molecule 12: 60S ribosomal protein L26-A

Chain AK:  90% 10%

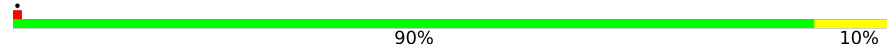


- Molecule 13: 60S ribosomal protein L39

Chain AL:  82% 18%



- Molecule 14: 60S ribosomal protein L14-A

Chain AM:  90% 10%

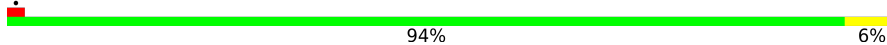


- Molecule 15: 60S ribosomal protein L27-A

Chain AN:  88% 12%



- Molecule 16: Ubiquitin-60S ribosomal protein L40

Chain AO:  94% 6%



- Molecule 17: 60S ribosomal protein L42-A

Chain AP:  90% 10%



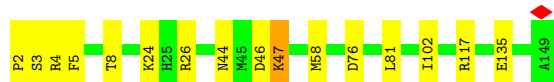
- Molecule 18: 60S ribosomal protein L15-A

Chain AQ:  88% 12%

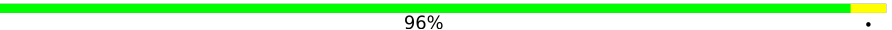


- Molecule 19: 60S ribosomal protein L28

Chain AR:  89% 10%



- Molecule 20: 60S ribosomal protein L41-B

Chain AS:  96%

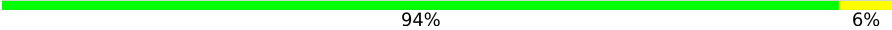


- Molecule 21: 60S ribosomal protein L43-A

Chain AT:  85% 15%



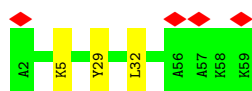
- Molecule 22: 60S ribosomal protein L16-A

Chain AU:  94% 6%



- Molecule 23: 60S ribosomal protein L29

Chain AV:  7% 95% 5%



- Molecule 24: 60S ribosomal protein L2-A

Chain AW:  88% 12%





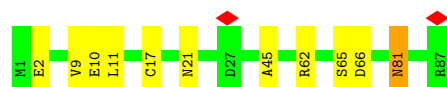
- Molecule 25: 60S ribosomal protein L17-A

Chain AX: 5% 89% 11%



- Molecule 26: 40S ribosomal protein S21-A

Chain a: 87% 11%



- Molecule 27: 40S ribosomal protein S22-A

Chain b: 92% 8%



- Molecule 28: 40S ribosomal protein S23-A

Chain c: 94% 6%



- Molecule 29: 40S ribosomal protein S24-A

Chain d: 10% 83% 14%



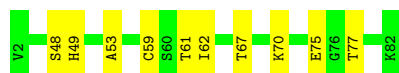
- Molecule 30: 40S ribosomal protein S26-B

Chain e: 9% 71% 25%



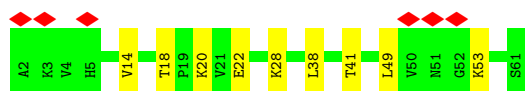
- Molecule 31: 40S ribosomal protein S27-A

Chain f:  88% 12%



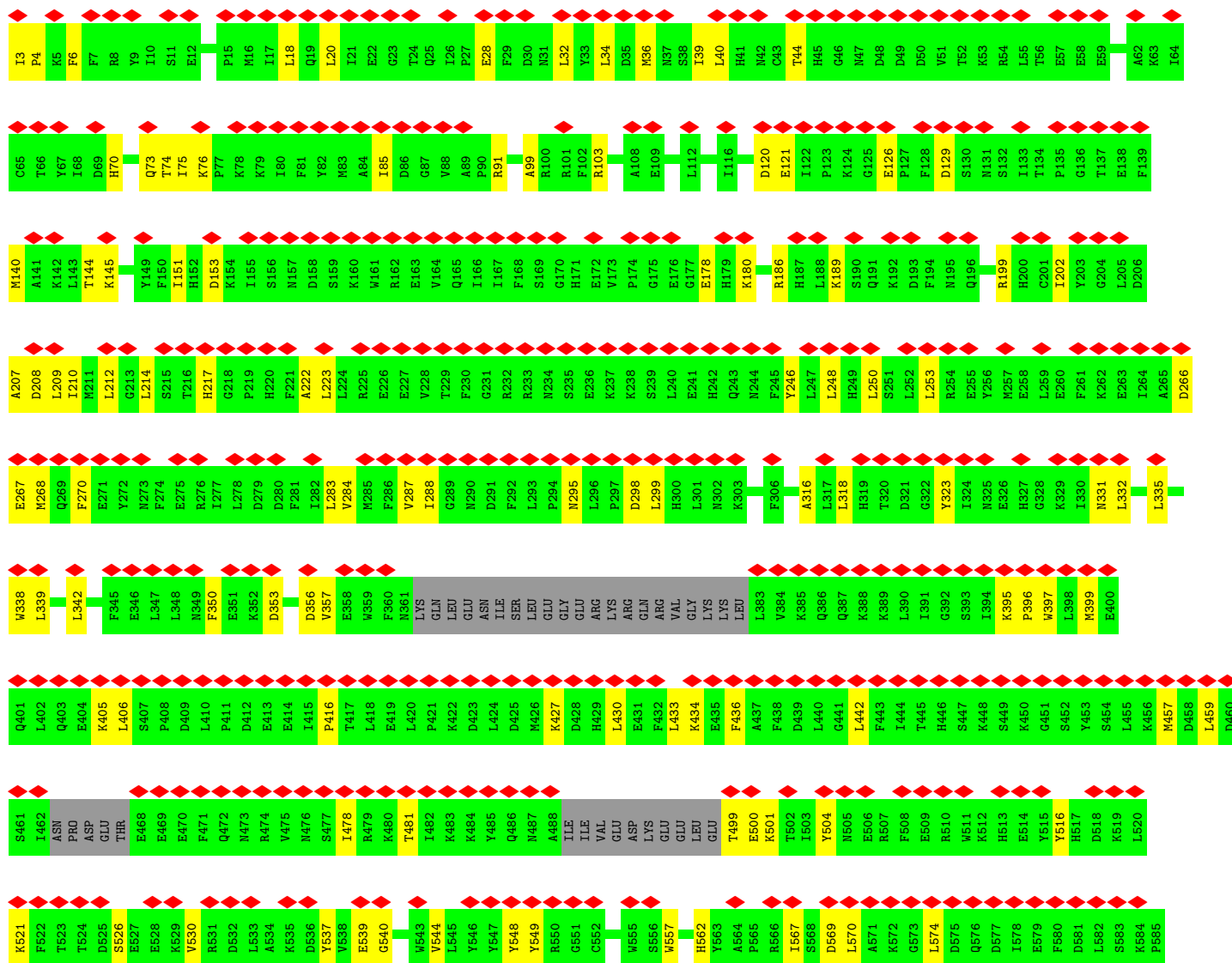
- Molecule 32: 40S ribosomal protein S30-A

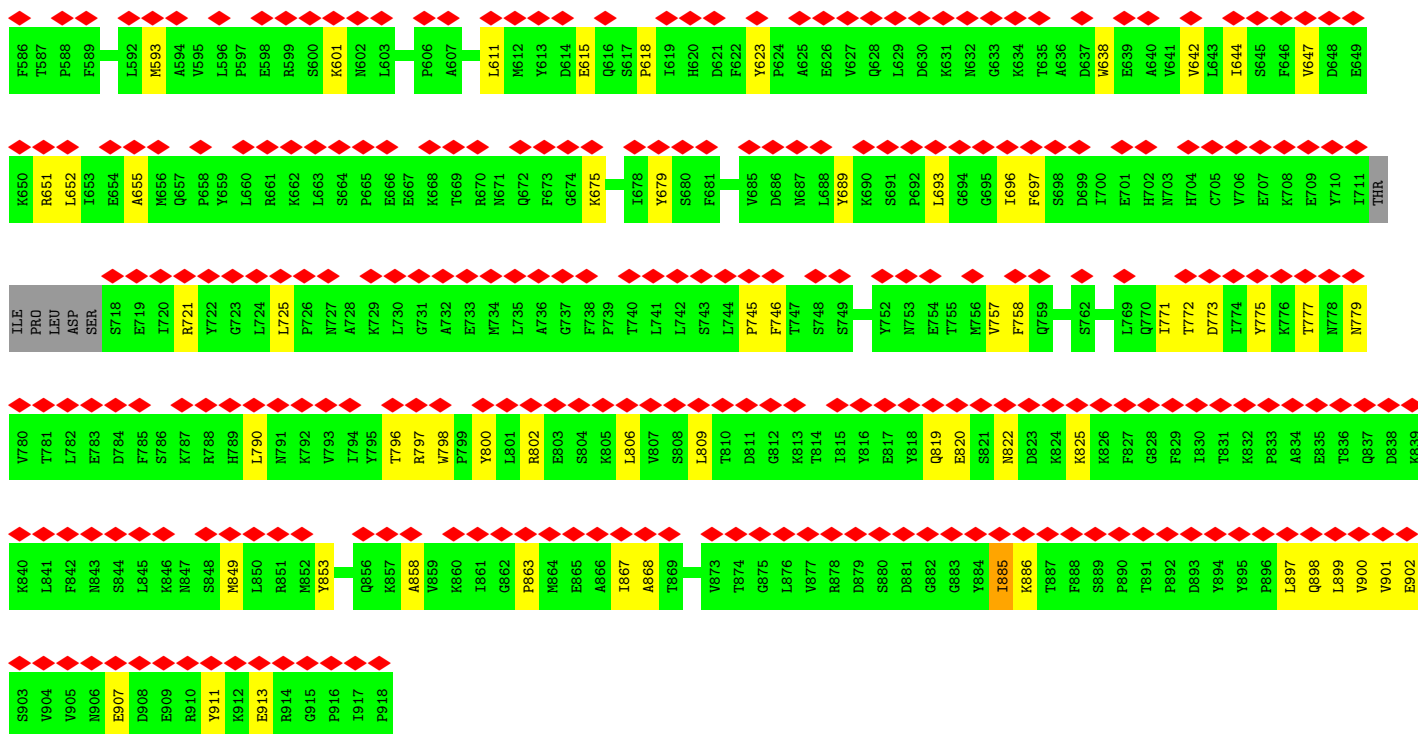
Chain g:  10% 85% 15%



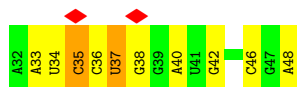
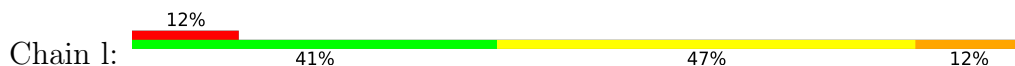
- Molecule 33: 5'-3' exoribonuclease 1

Chain z:  72% 77% 18% 5%

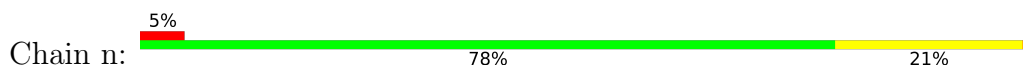




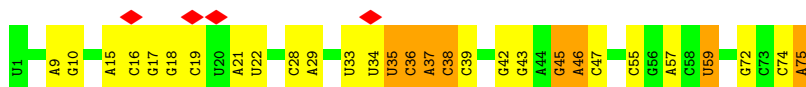
- Molecule 34: mRNA



- Molecule 35: P-site tRNA



- Molecule 36: E-site tRNA

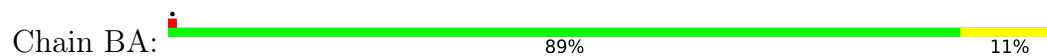


- Molecule 37: 60S ribosomal protein L30





- Molecule 38: 60S ribosomal protein L3



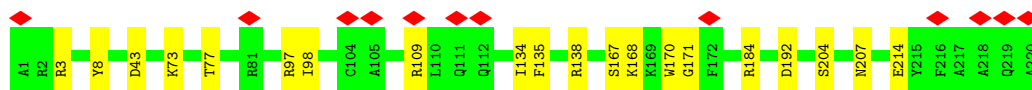
- Molecule 39: 60S ribosomal protein L18-A



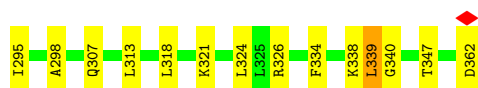
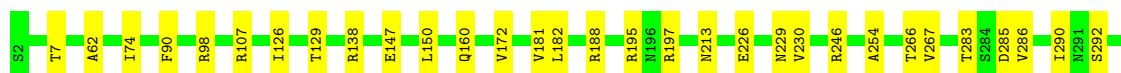
- Molecule 40: 60S ribosomal protein L31-A



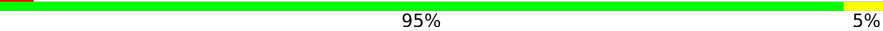
- Molecule 41: 60S ribosomal protein L10



- Molecule 42: 60S ribosomal protein L4-A



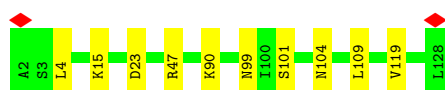
- Molecule 43: 60S ribosomal protein L19-A

Chain BF:  95% 5%



- Molecule 44: 60S ribosomal protein L32

Chain BG:  92% 8%



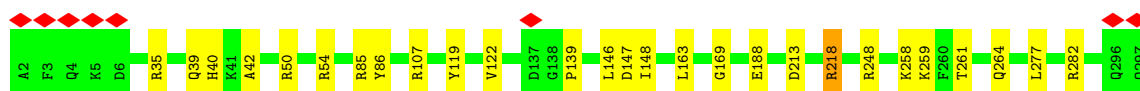
- Molecule 45: 60S ribosomal protein L20-A

Chain BH:  91% 9%



- Molecule 46: 60S ribosomal protein L5

Chain BI:  91% 9%



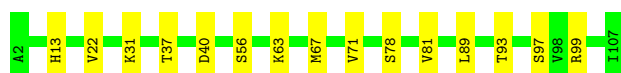
- Molecule 47: 60S ribosomal protein L21-A

Chain BJ:  87% 13%



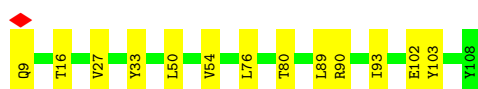
- Molecule 48: 60S ribosomal protein L33-A

Chain BK:  86% 14%

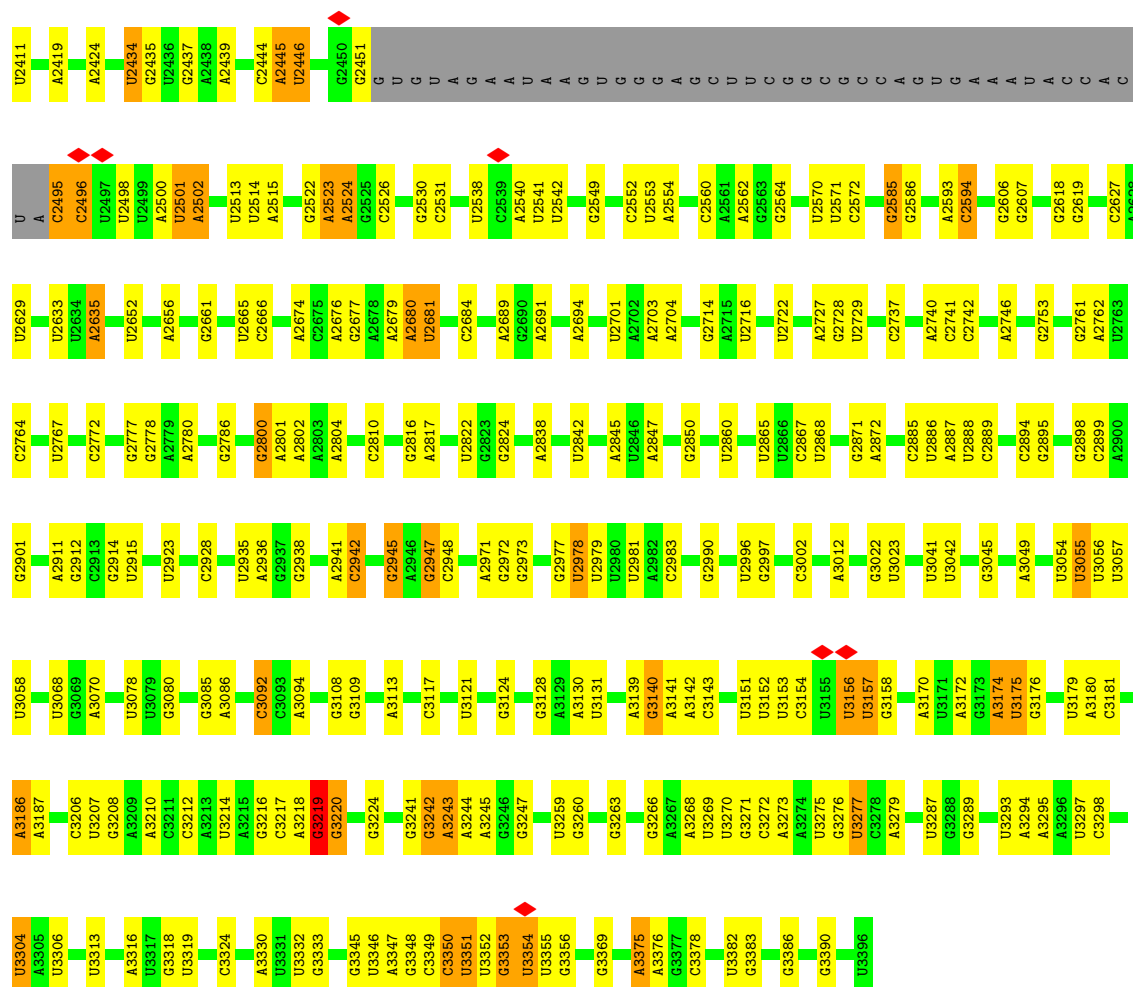


- Molecule 49: 60S ribosomal protein L22-A

Chain BL:  87% 13%







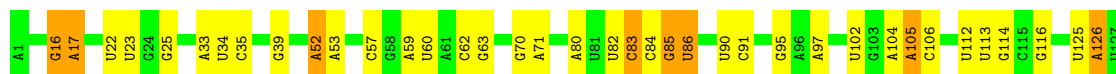
- Molecule 55: 5S ribosomal RNA

Chain BR: 76% 23% .



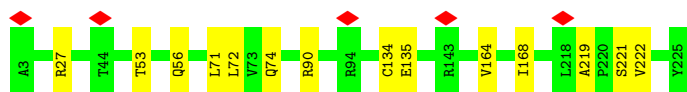
- Molecule 56: 5.8S ribosomal RNA

Chain BS: 71% 23% 6%

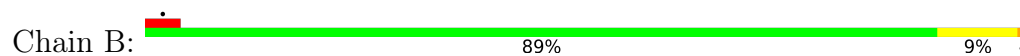


- Molecule 57: 40S ribosomal protein S3

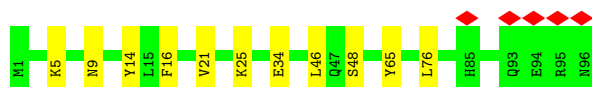
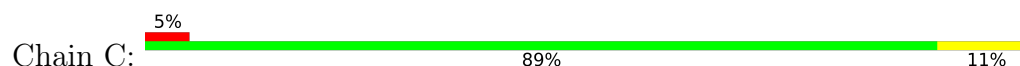
Chain A: 94% 6%



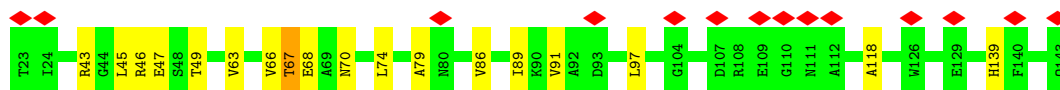
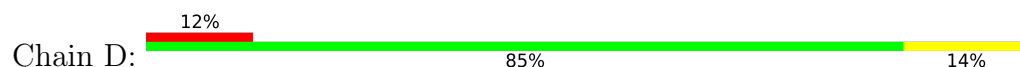
- Molecule 58: Rps5p



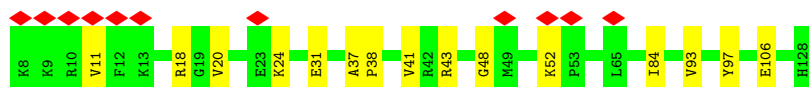
- Molecule 59: 40S ribosomal protein S10-A



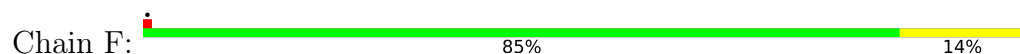
- Molecule 60: 40S ribosomal protein S12



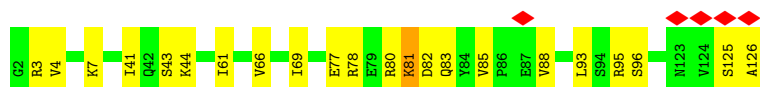
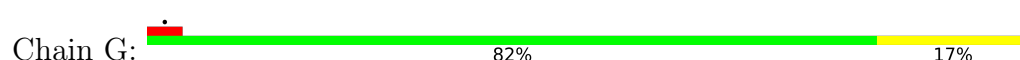
- Molecule 61: 40S ribosomal protein S15



- Molecule 62: 40S ribosomal protein S16-A

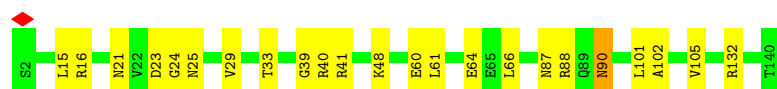


- Molecule 63: 40S ribosomal protein S17-A



- Molecule 64: 40S ribosomal protein S18-A

Chain H:  83% 16%



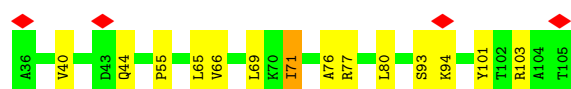
- Molecule 65: 40S ribosomal protein S20

Chain J:  5% 92% 8%



- Molecule 66: 40S ribosomal protein S25-A

Chain K:  6% 80% 19%

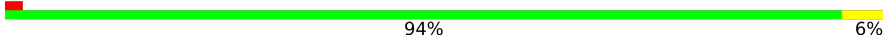


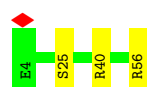
- Molecule 67: 40S ribosomal protein S28-A

Chain L:  6% 89% 11%



- Molecule 68: 40S ribosomal protein S29-A

Chain M:  94% 6%



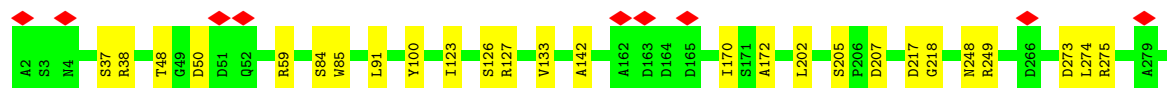
- Molecule 69: Ubiquitin-40S ribosomal protein S31

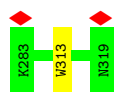
Chain N:  16% 86% 14%



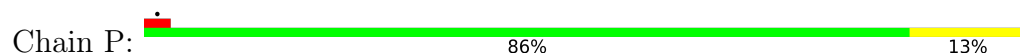
- Molecule 70: Guanine nucleotide-binding protein subunit beta-like protein

Chain O:  92% 8%

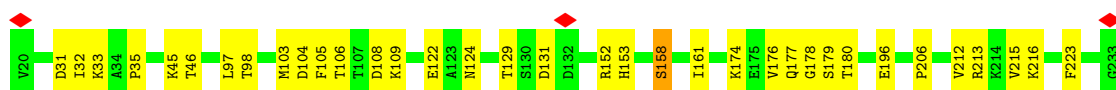
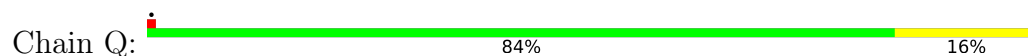




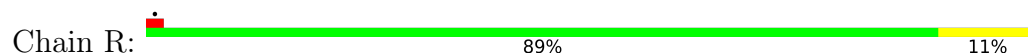
- Molecule 71: 40S ribosomal protein S0-A



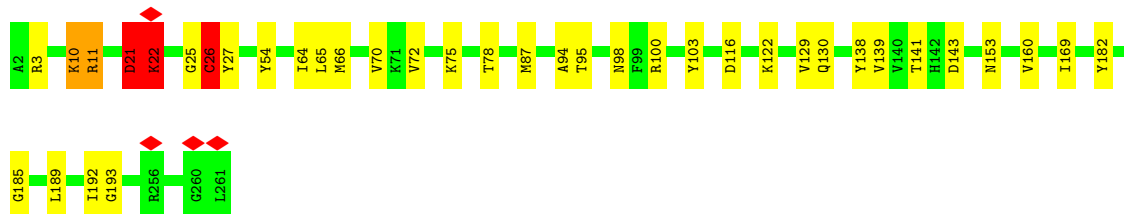
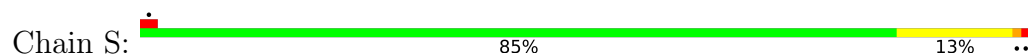
- Molecule 72: 40S ribosomal protein S1-A



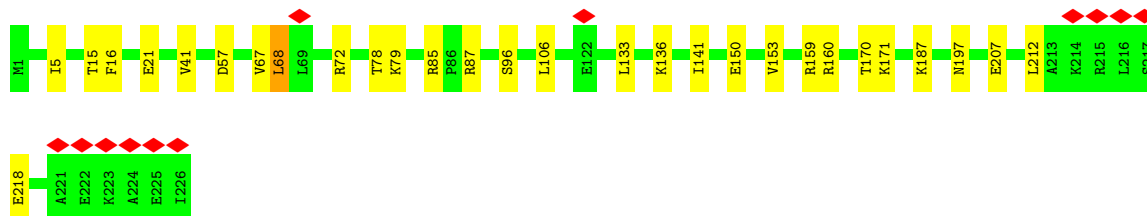
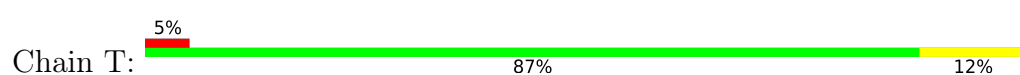
- Molecule 73: 40S ribosomal protein S2



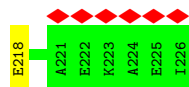
- Molecule 74: 40S ribosomal protein S4-A



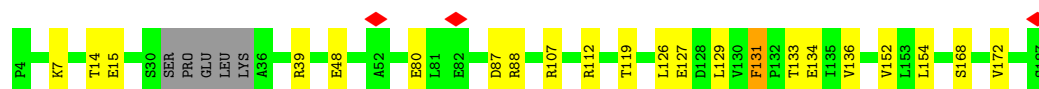
- Molecule 75: 40S ribosomal protein S6-A



- Molecule 76: 40S ribosomal protein S7-A

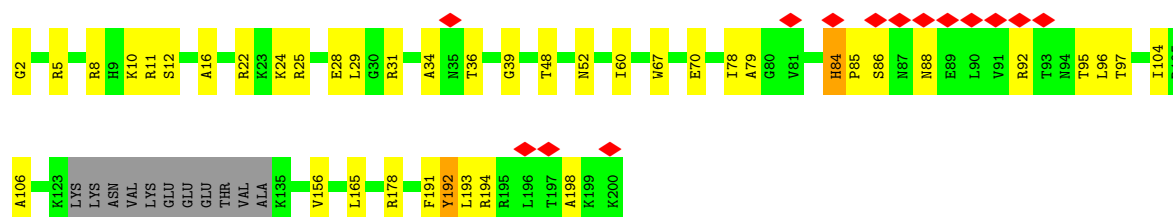


Chain U:  85% 11% ..



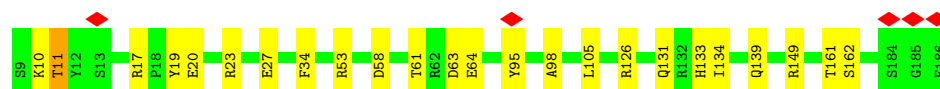
- Molecule 77: 40S ribosomal protein S8-A

Chain V:  74% 20% • 6%

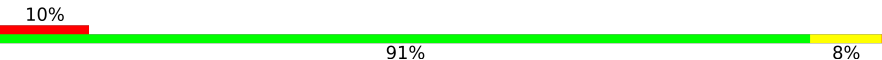


- Molecule 78: 40S ribosomal protein S9-A

Chain W:  87% 13% ..



- Molecule 79: 40S ribosomal protein S11-A

Chain X:  91% 8% • 10%

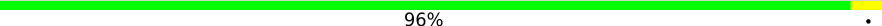


- Molecule 80: 40S ribosomal protein S13

Chain Y:  89% 11%



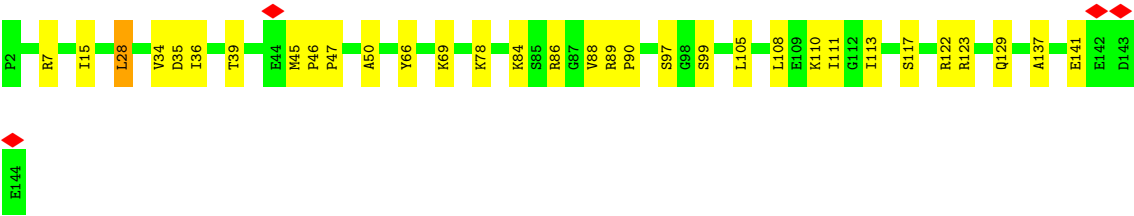
- Molecule 81: 40S ribosomal protein S14-B

Chain Z:  96% .



- Molecule 82: 40S ribosomal protein S19-A

Chain I:  78% 22% •



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	217000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.5	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	0.470	Depositor
Minimum map value	-0.232	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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	2	0.50	0/42103	0.48	6/65603 (0.0%)
2	AA	0.57	0/1836	0.61	0/2481
3	AB	0.67	0/1018	0.62	0/1369
4	AC	0.53	0/778	0.57	0/1034
5	AD	0.51	0/1539	0.58	0/2073
6	AE	0.63	0/555	0.57	0/738
7	AF	0.81	0/696	0.85	0/923
8	AG	0.42	0/1374	0.57	0/1842
9	AH	0.63	0/979	0.61	0/1321
10	AI	0.51	0/618	0.55	0/826
11	AJ	0.67	0/1568	0.74	0/2106
12	AK	0.64	0/1004	0.58	0/1341
13	AL	0.79	0/443	0.73	0/588
14	AM	0.55	0/1068	0.57	0/1438
15	AN	0.59	0/1118	0.60	0/1497
16	AO	0.54	0/423	0.55	0/562
17	AP	0.64	0/860	0.58	0/1136
18	AQ	0.83	0/1757	0.75	1/2354 (0.0%)
19	AR	0.73	0/1204	0.74	2/1612 (0.1%)
20	AS	0.71	0/234	0.74	0/300
21	AT	0.68	0/701	0.76	0/934
22	AU	0.67	0/1585	0.58	0/2128
23	AV	0.57	0/473	0.59	0/629
24	AW	0.79	0/1948	0.76	1/2617 (0.0%)
25	AX	0.68	0/1443	0.66	0/1944
26	a	0.51	0/693	0.68	0/935
27	b	0.68	0/1038	0.57	0/1395
28	c	0.61	0/1139	0.66	0/1518
29	d	0.42	0/1074	0.66	1/1431 (0.1%)
30	e	0.66	0/782	1.01	5/1047 (0.5%)
31	f	0.50	0/620	0.54	0/838
32	g	0.40	0/481	0.59	0/640

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	z	0.32	0/7362	0.70	0/9944
34	l	0.33	0/411	0.47	0/639
35	n	0.34	0/1811	0.38	0/2821
36	m	0.26	0/1773	0.43	0/2759
37	AY	0.59	0/750	0.61	0/1008
38	BA	0.70	0/3146	0.66	0/4228
39	BB	0.67	0/1465	0.69	0/1965
40	BC	0.64	0/890	0.62	0/1196
41	BD	0.54	0/1807	0.62	0/2425
42	BE	0.70	0/2800	0.65	0/3790
43	BF	0.65	0/1538	0.67	0/2050
44	BG	0.68	0/1041	0.60	0/1394
45	BH	0.62	0/1481	0.60	0/1990
46	BI	0.49	0/2425	0.55	0/3271
47	BJ	0.61	0/1300	0.64	0/1743
48	BK	0.76	0/868	0.61	0/1168
49	BL	0.44	0/812	0.55	1/1099 (0.1%)
50	BM	0.50	0/1260	0.50	0/1694
51	BN	0.73	0/890	0.61	0/1189
52	BO	0.67	0/1821	0.62	0/2451
53	BP	0.60	0/978	0.65	0/1301
54	BQ	0.64	0/75679	0.52	13/117989 (0.0%)
55	BR	0.48	0/2883	0.42	0/4491
56	BS	0.66	0/3745	0.50	0/5829
57	A	0.40	0/1759	0.52	0/2368
58	B	0.41	0/1623	0.62	0/2195
59	C	0.30	0/833	0.53	0/1126
60	D	0.31	0/885	0.70	0/1202
61	E	0.31	0/978	0.65	0/1315
62	F	0.46	0/1119	0.66	0/1503
63	G	0.42	0/1011	0.67	0/1355
64	H	0.34	0/1162	0.58	0/1564
65	J	0.40	0/865	0.56	0/1169
66	K	0.36	0/571	0.71	0/768
67	L	0.39	0/499	0.53	0/670
68	M	0.46	0/452	0.51	0/600
69	N	0.27	0/404	0.59	0/542
70	O	0.30	0/2489	0.48	0/3389
71	P	0.46	0/1732	0.62	1/2371 (0.0%)
72	Q	0.49	0/1735	0.68	1/2335 (0.0%)
73	R	0.59	0/1702	0.60	0/2310
74	S	0.52	0/2102	0.66	6/2829 (0.2%)
75	T	0.39	0/1823	0.60	0/2439

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	U	0.42	0/1465	0.57	0/1971
77	V	0.60	0/1514	0.79	1/2021 (0.0%)
78	W	0.52	0/1456	0.72	0/1949
79	X	0.64	0/1239	0.62	0/1673
80	Y	0.59	0/1215	0.65	0/1638
81	Z	0.61	0/901	0.69	0/1217
82	I	0.41	0/1119	0.70	2/1504 (0.1%)
All	All	0.58	0/224741	0.56	41/329657 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AA	0	3
4	AC	0	2
5	AD	0	1
10	AI	0	1
11	AJ	0	1
18	AQ	0	1
19	AR	0	1
21	AT	0	1
26	a	0	1
27	b	0	1
29	d	0	3
30	e	0	7
33	z	0	5
40	BC	0	1
41	BD	0	3
42	BE	0	1
46	BI	0	1
52	BO	0	1
53	BP	0	2
57	A	0	1
58	B	0	2
61	E	0	1
64	H	0	1
66	K	0	1
71	P	0	2
72	Q	0	2
74	S	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
75	T	0	3
76	U	0	1
77	V	0	6
78	W	0	2
79	X	0	1
80	Y	0	1
All	All	0	62

There are no bond length outliers.

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	BQ	1303	A	C1'-C2'-O2'	-17.58	82.04	108.40
54	BQ	1307	G	C2'-C3'-O3'	9.39	123.59	109.50
1	2	1465	C	C2'-C3'-O3'	8.80	126.90	113.70
54	BQ	1580	A	C2'-C3'-O3'	7.55	120.83	109.50
54	BQ	1303	A	C4'-C3'-O3'	-7.17	102.25	113.00

There are no chirality outliers.

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AA	156	ASP	Peptide
2	AA	74	THR	Peptide
2	AA	76	ALA	Peptide
4	AC	26	ILE	Peptide
4	AC	32	ALA	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	2	37645	0	18939	248	0
2	AA	1804	0	1877	16	0
3	AB	1003	0	1048	8	0
4	AC	771	0	849	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	AD	1518	0	1587	10	0
6	AE	543	0	564	4	0
7	AF	681	0	683	5	0
8	AG	1353	0	1383	9	0
9	AH	964	0	1025	8	0
10	AI	612	0	682	7	0
11	AJ	1543	0	1608	13	0
12	AK	993	0	1081	10	0
13	AL	436	0	475	7	0
14	AM	1053	0	1149	9	0
15	AN	1092	0	1155	12	0
16	AO	417	0	455	2	0
17	AP	847	0	914	7	0
18	AQ	1720	0	1779	16	0
19	AR	1173	0	1215	11	0
20	AS	233	0	284	1	0
21	AT	694	0	734	11	0
22	AU	1555	0	1659	9	0
23	AV	462	0	491	3	0
24	AW	1914	0	1981	27	0
25	AX	1420	0	1437	14	0
26	a	684	0	672	7	0
27	b	1021	0	1060	6	0
28	c	1121	0	1196	5	0
29	d	1060	0	1123	14	0
30	e	769	0	814	17	0
31	f	610	0	633	6	0
32	g	473	0	518	5	0
33	z	7181	0	7071	99	0
34	l	367	0	185	3	0
35	n	1621	0	822	3	0
36	m	1589	0	810	12	0
37	AY	742	0	797	8	0
38	BA	3075	0	3142	31	0
39	BB	1441	0	1543	18	0
40	BC	876	0	912	5	0
41	BD	1770	0	1808	9	0
42	BE	2748	0	2859	29	0
43	BF	1521	0	1617	7	0
44	BG	1020	0	1090	7	0
45	BH	1445	0	1487	11	0
46	BI	2375	0	2325	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
47	BJ	1276	0	1323	13	0
48	BK	850	0	880	11	0
49	BL	796	0	812	9	0
50	BM	1239	0	1326	14	0
51	BN	880	0	941	9	0
52	BO	1784	0	1862	15	0
53	BP	969	0	1078	1	0
54	BQ	67610	0	33962	262	0
55	BR	2579	0	1304	5	0
56	BS	3352	0	1695	15	0
57	A	1734	0	1817	8	0
58	B	1603	0	1664	16	0
59	C	813	0	800	7	0
60	D	877	0	883	13	0
61	E	957	0	981	9	0
62	F	1099	0	1151	19	0
63	G	1001	0	1063	15	0
64	H	1143	0	1168	23	0
65	J	855	0	917	6	0
66	K	563	0	603	8	0
67	L	497	0	535	7	0
68	M	442	0	429	3	0
69	N	397	0	397	7	0
70	O	2436	0	2386	16	0
71	P	1691	0	1673	15	0
72	Q	1709	0	1784	22	0
73	R	1671	0	1768	16	0
74	S	2061	0	2135	27	0
75	T	1799	0	1879	23	0
76	U	1442	0	1529	16	0
77	V	1489	0	1525	25	0
78	W	1434	0	1511	16	0
79	X	1213	0	1257	10	0
80	Y	1192	0	1255	10	0
81	Z	891	0	883	4	0
82	I	1101	0	1102	39	0
83	AF	1	0	0	0	0
83	AO	1	0	0	0	0
83	AP	1	0	0	0	0
83	AT	1	0	0	0	0
83	BN	1	0	0	0	0
83	M	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	N	1	0	0	0	0
83	e	1	0	0	0	0
84	l	1	0	0	0	0
84	z	1	0	0	0	0
All	All	209410	0	155816	1211	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 3.

The worst 5 of 1211 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)
46:BI:218:ARG:HB2	46:BI:218:ARG:HH11	1.19	1.03
1:2:992:A:H2	1:2:1012:U:H3	0.97	0.96
33:z:406:LEU:HD11	33:z:459:LEU:HD11	1.49	0.95
1:2:384:G:H5'	1:2:384:G:H8	1.35	0.91
46:BI:218:ARG:HH11	46:BI:218:ARG:CB	1.88	0.87

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	231/233 (99%)	204 (88%)	25 (11%)	2 (1%)	14	44
3	AB	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
4	AC	97/100 (97%)	90 (93%)	5 (5%)	2 (2%)	5	25
5	AD	189/191 (99%)	175 (93%)	13 (7%)	1 (0%)	24	57
6	AE	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
7	AF	85/87 (98%)	77 (91%)	8 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AG	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	21	52
9	AH	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
10	AI	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
11	AJ	191/193 (99%)	168 (88%)	19 (10%)	4 (2%)	5	25
12	AK	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
13	AL	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
14	AM	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
15	AN	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
16	AO	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
17	AP	103/105 (98%)	92 (89%)	11 (11%)	0	100	100
18	AQ	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	24	57
19	AR	146/148 (99%)	125 (86%)	19 (13%)	2 (1%)	9	34
20	AS	23/25 (92%)	23 (100%)	0	0	100	100
21	AT	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
22	AU	195/197 (99%)	188 (96%)	7 (4%)	0	100	100
23	AV	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
24	AW	250/252 (99%)	238 (95%)	12 (5%)	0	100	100
25	AX	181/183 (99%)	174 (96%)	7 (4%)	0	100	100
26	a	85/87 (98%)	70 (82%)	13 (15%)	2 (2%)	4	22
27	b	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
28	c	142/144 (99%)	125 (88%)	16 (11%)	1 (1%)	18	49
29	d	130/132 (98%)	112 (86%)	16 (12%)	2 (2%)	8	32
30	e	95/97 (98%)	73 (77%)	21 (22%)	1 (1%)	11	39
31	f	79/81 (98%)	69 (87%)	10 (13%)	0	100	100
32	g	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
33	z	864/916 (94%)	783 (91%)	80 (9%)	1 (0%)	48	78
37	AY	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
38	BA	384/386 (100%)	354 (92%)	30 (8%)	0	100	100
39	BB	183/185 (99%)	169 (92%)	14 (8%)	0	100	100
40	BC	107/109 (98%)	97 (91%)	9 (8%)	1 (1%)	14	44
41	BD	218/220 (99%)	198 (91%)	19 (9%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
42	BE	359/361 (99%)	322 (90%)	35 (10%)	2 (1%)	21	52
43	BF	186/188 (99%)	173 (93%)	12 (6%)	1 (0%)	24	57
44	BG	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
45	BH	170/172 (99%)	159 (94%)	11 (6%)	0	100	100
46	BI	294/296 (99%)	271 (92%)	22 (8%)	1 (0%)	36	67
47	BJ	157/159 (99%)	140 (89%)	15 (10%)	2 (1%)	9	35
48	BK	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
49	BL	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
50	BM	152/175 (87%)	144 (95%)	8 (5%)	0	100	100
51	BN	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
52	BO	220/222 (99%)	206 (94%)	13 (6%)	1 (0%)	24	57
53	BP	117/119 (98%)	110 (94%)	5 (4%)	2 (2%)	7	30
57	A	221/223 (99%)	205 (93%)	16 (7%)	0	100	100
58	B	204/206 (99%)	167 (82%)	34 (17%)	3 (2%)	8	32
59	C	94/96 (98%)	79 (84%)	15 (16%)	0	100	100
60	D	119/121 (98%)	81 (68%)	37 (31%)	1 (1%)	16	47
61	E	119/121 (98%)	98 (82%)	21 (18%)	0	100	100
62	F	139/141 (99%)	120 (86%)	16 (12%)	3 (2%)	5	24
63	G	123/125 (98%)	103 (84%)	18 (15%)	2 (2%)	7	30
64	H	137/139 (99%)	117 (85%)	20 (15%)	0	100	100
65	J	105/107 (98%)	94 (90%)	11 (10%)	0	100	100
66	K	68/70 (97%)	56 (82%)	11 (16%)	1 (2%)	8	32
67	L	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
68	M	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
69	N	49/51 (96%)	38 (78%)	11 (22%)	0	100	100
70	O	316/318 (99%)	294 (93%)	22 (7%)	0	100	100
71	P	217/219 (99%)	191 (88%)	23 (11%)	3 (1%)	9	34
72	Q	212/214 (99%)	179 (84%)	32 (15%)	1 (0%)	24	57
73	R	218/220 (99%)	196 (90%)	21 (10%)	1 (0%)	24	57
74	S	258/260 (99%)	225 (87%)	31 (12%)	2 (1%)	16	47
75	T	224/226 (99%)	199 (89%)	24 (11%)	1 (0%)	30	61

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	U	175/184 (95%)	160 (91%)	15 (9%)	0	100	100
77	V	184/199 (92%)	158 (86%)	25 (14%)	1 (0%)	24	57
78	W	176/178 (99%)	144 (82%)	30 (17%)	2 (1%)	11	39
79	X	153/155 (99%)	140 (92%)	12 (8%)	1 (1%)	18	49
80	Y	148/150 (99%)	138 (93%)	10 (7%)	0	100	100
81	Z	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
82	I	141/143 (99%)	131 (93%)	9 (6%)	1 (1%)	18	49
All	All	11782/12024 (98%)	10635 (90%)	1093 (9%)	54 (0%)	26	57

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AA	156	ASP
2	AA	157	VAL
11	AJ	62	THR
42	BE	339	LEU
53	BP	91	ALA

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	AA	187/191 (98%)	185 (99%)	2 (1%)	65	78
3	AB	104/104 (100%)	104 (100%)	0	100	100
4	AC	81/82 (99%)	81 (100%)	0	100	100
5	AD	171/171 (100%)	171 (100%)	0	100	100
6	AE	56/59 (95%)	56 (100%)	0	100	100
7	AF	70/70 (100%)	70 (100%)	0	100	100
8	AG	147/147 (100%)	147 (100%)	0	100	100
9	AH	104/105 (99%)	104 (100%)	0	100	100
10	AI	68/68 (100%)	68 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	AJ	154/154 (100%)	154 (100%)	0	100	100
12	AK	109/109 (100%)	109 (100%)	0	100	100
13	AL	45/45 (100%)	45 (100%)	0	100	100
14	AM	107/107 (100%)	107 (100%)	0	100	100
15	AN	115/115 (100%)	115 (100%)	0	100	100
16	AO	47/47 (100%)	47 (100%)	0	100	100
17	AP	90/90 (100%)	90 (100%)	0	100	100
18	AQ	175/175 (100%)	175 (100%)	0	100	100
19	AR	118/118 (100%)	118 (100%)	0	100	100
20	AS	23/23 (100%)	23 (100%)	0	100	100
21	AT	71/71 (100%)	71 (100%)	0	100	100
22	AU	160/160 (100%)	160 (100%)	0	100	100
23	AV	46/46 (100%)	46 (100%)	0	100	100
24	AW	193/194 (100%)	192 (100%)	1 (0%)	81	85
25	AX	140/145 (97%)	139 (99%)	1 (1%)	76	82
26	a	74/74 (100%)	74 (100%)	0	100	100
27	b	110/110 (100%)	110 (100%)	0	100	100
28	c	119/119 (100%)	119 (100%)	0	100	100
29	d	111/111 (100%)	111 (100%)	0	100	100
30	e	83/83 (100%)	82 (99%)	1 (1%)	63	78
31	f	70/70 (100%)	70 (100%)	0	100	100
32	g	50/51 (98%)	50 (100%)	0	100	100
33	z	783/842 (93%)	777 (99%)	6 (1%)	73	81
37	AY	81/81 (100%)	81 (100%)	0	100	100
38	BA	320/322 (99%)	317 (99%)	3 (1%)	70	80
39	BB	150/150 (100%)	150 (100%)	0	100	100
40	BC	92/96 (96%)	92 (100%)	0	100	100
41	BD	184/186 (99%)	184 (100%)	0	100	100
42	BE	288/288 (100%)	288 (100%)	0	100	100
43	BF	153/153 (100%)	153 (100%)	0	100	100
44	BG	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	BH	156/156 (100%)	156 (100%)	0	100	100
46	BI	244/244 (100%)	243 (100%)	1 (0%)	84	86
47	BJ	136/136 (100%)	136 (100%)	0	100	100
48	BK	90/90 (100%)	90 (100%)	0	100	100
49	BL	87/87 (100%)	87 (100%)	0	100	100
50	BM	134/152 (88%)	134 (100%)	0	100	100
51	BN	95/95 (100%)	95 (100%)	0	100	100
52	BO	186/186 (100%)	185 (100%)	1 (0%)	81	85
53	BP	104/104 (100%)	104 (100%)	0	100	100
57	A	182/182 (100%)	182 (100%)	0	100	100
58	B	172/173 (99%)	172 (100%)	0	100	100
59	C	88/89 (99%)	88 (100%)	0	100	100
60	D	89/98 (91%)	88 (99%)	1 (1%)	65	78
61	E	100/103 (97%)	100 (100%)	0	100	100
62	F	115/117 (98%)	114 (99%)	1 (1%)	70	80
63	G	113/113 (100%)	113 (100%)	0	100	100
64	H	124/124 (100%)	124 (100%)	0	100	100
65	J	100/100 (100%)	100 (100%)	0	100	100
66	K	61/61 (100%)	61 (100%)	0	100	100
67	L	56/56 (100%)	56 (100%)	0	100	100
68	M	47/47 (100%)	47 (100%)	0	100	100
69	N	43/43 (100%)	43 (100%)	0	100	100
70	O	259/261 (99%)	259 (100%)	0	100	100
71	P	177/184 (96%)	175 (99%)	2 (1%)	65	78
72	Q	191/191 (100%)	190 (100%)	1 (0%)	81	85
73	R	180/180 (100%)	180 (100%)	0	100	100
74	S	219/221 (99%)	215 (98%)	4 (2%)	51	73
75	T	188/193 (97%)	188 (100%)	0	100	100
76	U	160/165 (97%)	160 (100%)	0	100	100
77	V	150/160 (94%)	150 (100%)	0	100	100
78	W	152/152 (100%)	152 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
79	X	129/136 (95%)	129 (100%)	0	100	100
80	Y	127/127 (100%)	127 (100%)	0	100	100
81	Z	81/96 (84%)	81 (100%)	0	100	100
82	I	112/115 (97%)	112 (100%)	0	100	100
All	All	10005/10178 (98%)	9980 (100%)	25 (0%)	85	89

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	BI	218	ARG
62	F	31	VAL
74	S	26	CYS
60	D	139	HIS
71	P	109	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
45	BH	138	GLN
63	G	62	GLN
47	BJ	5	HIS
53	BP	16	GLN
70	O	139	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1762/1797 (98%)	510 (28%)	66 (3%)
34	l	16/17 (94%)	8 (50%)	0
35	n	75/76 (98%)	13 (17%)	0
36	m	74/75 (98%)	22 (29%)	0
54	BQ	3158/3396 (92%)	648 (20%)	92 (2%)
55	BR	120/121 (99%)	22 (18%)	3 (2%)
56	BS	157/158 (99%)	37 (23%)	4 (2%)
All	All	5362/5640 (95%)	1260 (23%)	165 (3%)

5 of 1260 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A

5 of 165 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	BQ	1820	U
54	BQ	2971	A
54	BQ	1913	A
54	BQ	2495	C
54	BQ	3243	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

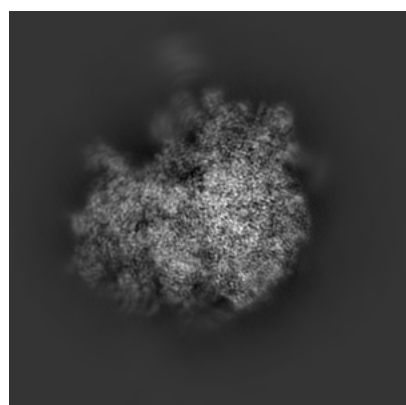
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4474. These allow visual inspection of the internal detail of the map and identification of artifacts.

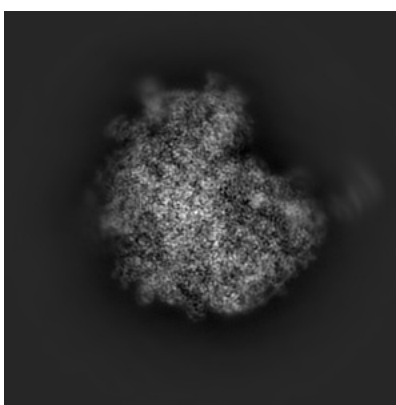
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

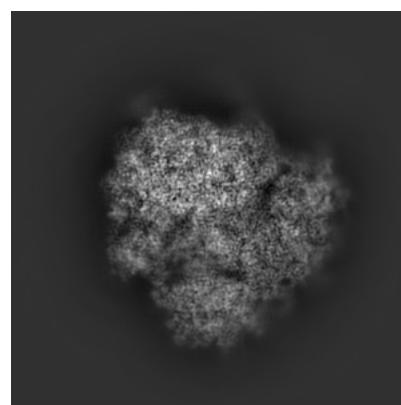
6.1.1 Primary map



X



Y

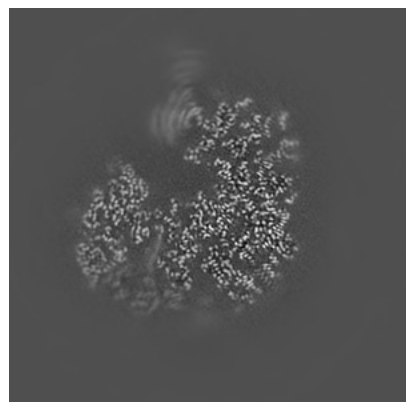


Z

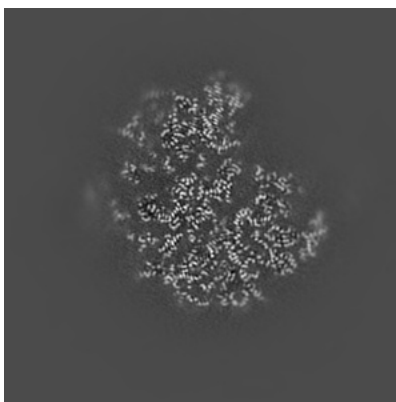
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

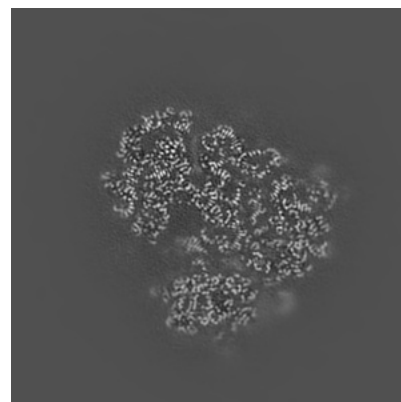
6.2.1 Primary map



X Index: 200



Y Index: 200

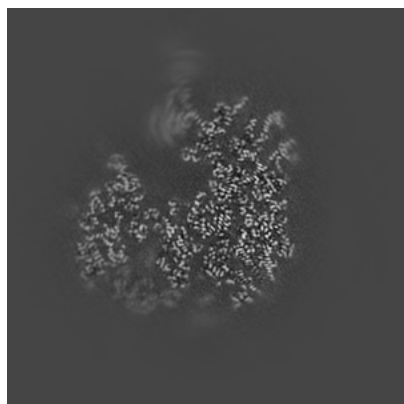


Z Index: 200

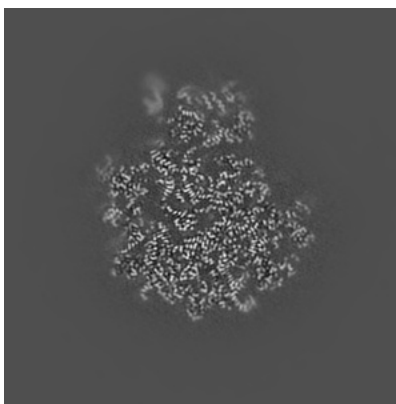
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

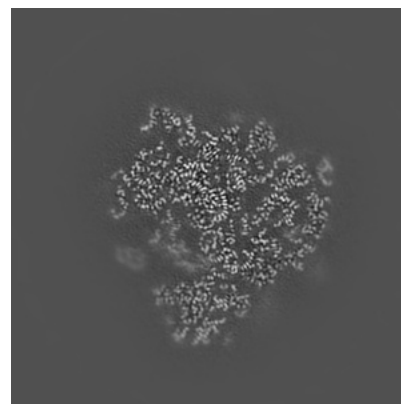
6.3.1 Primary map



X Index: 203



Y Index: 226

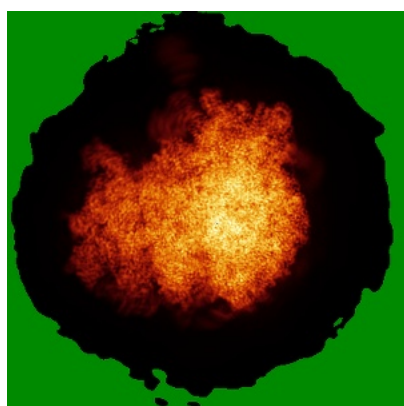


Z Index: 180

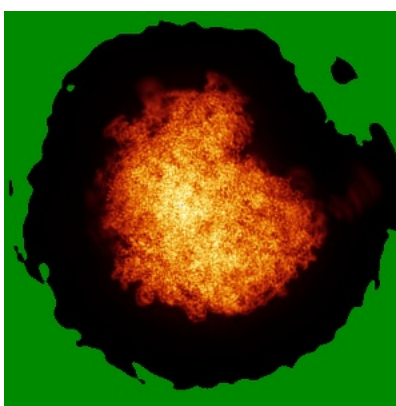
The images above show the largest variance slices of the map in three orthogonal directions.

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

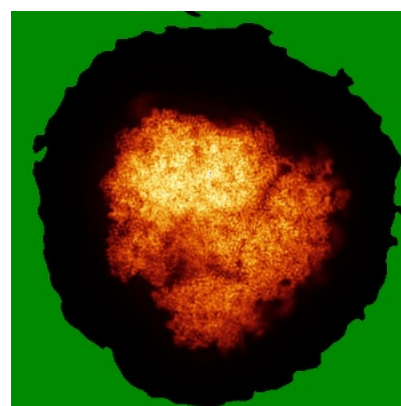
6.4.1 Primary map



X



Y

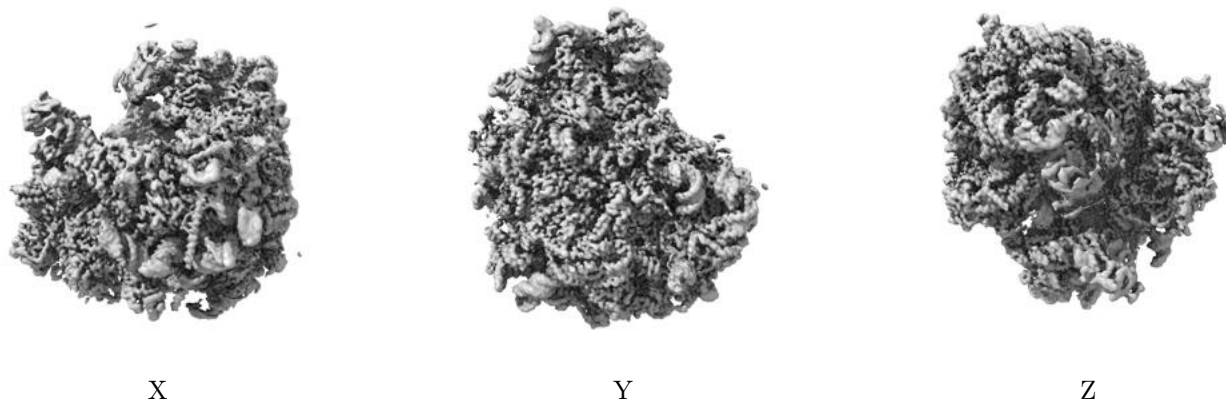


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

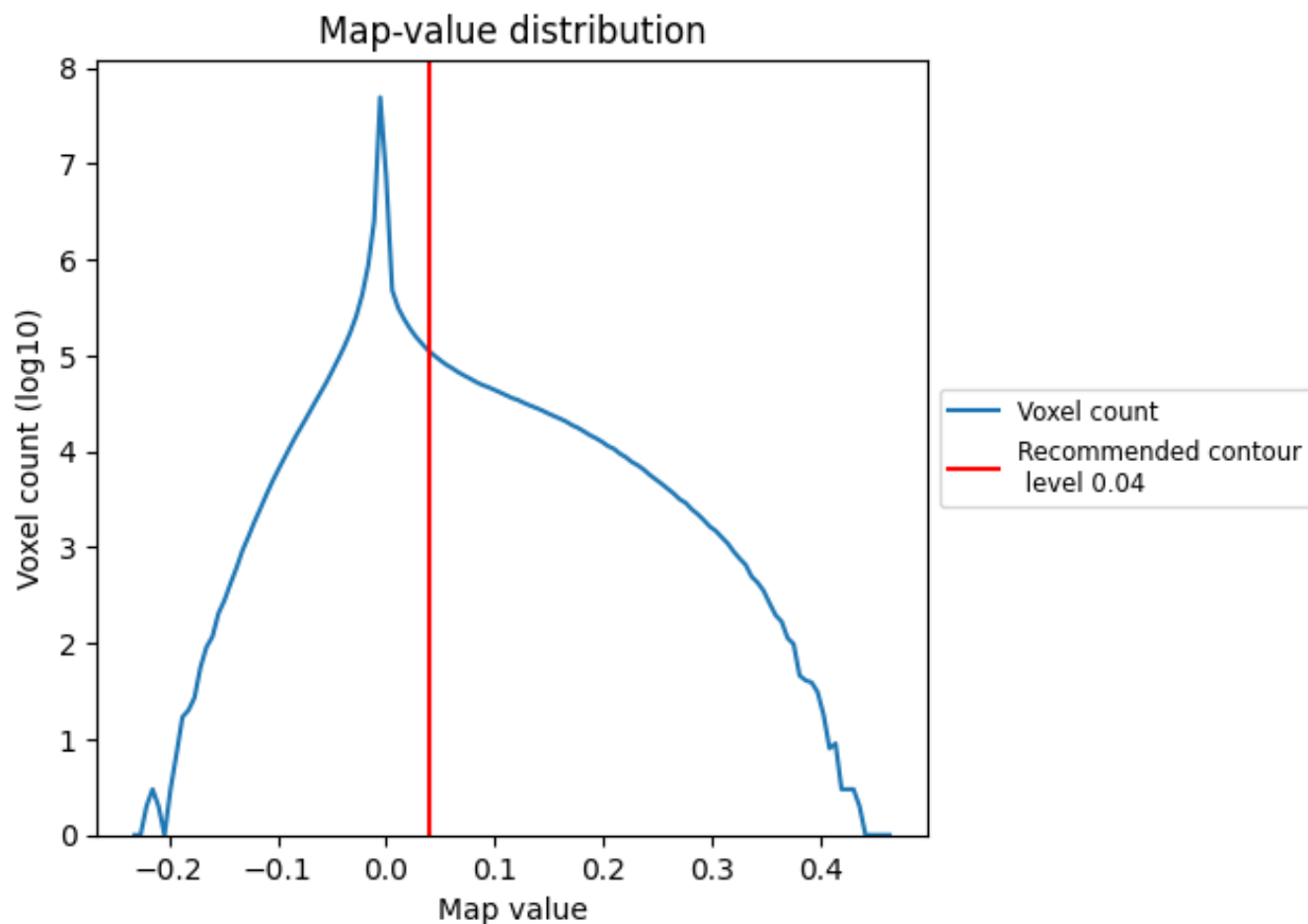
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

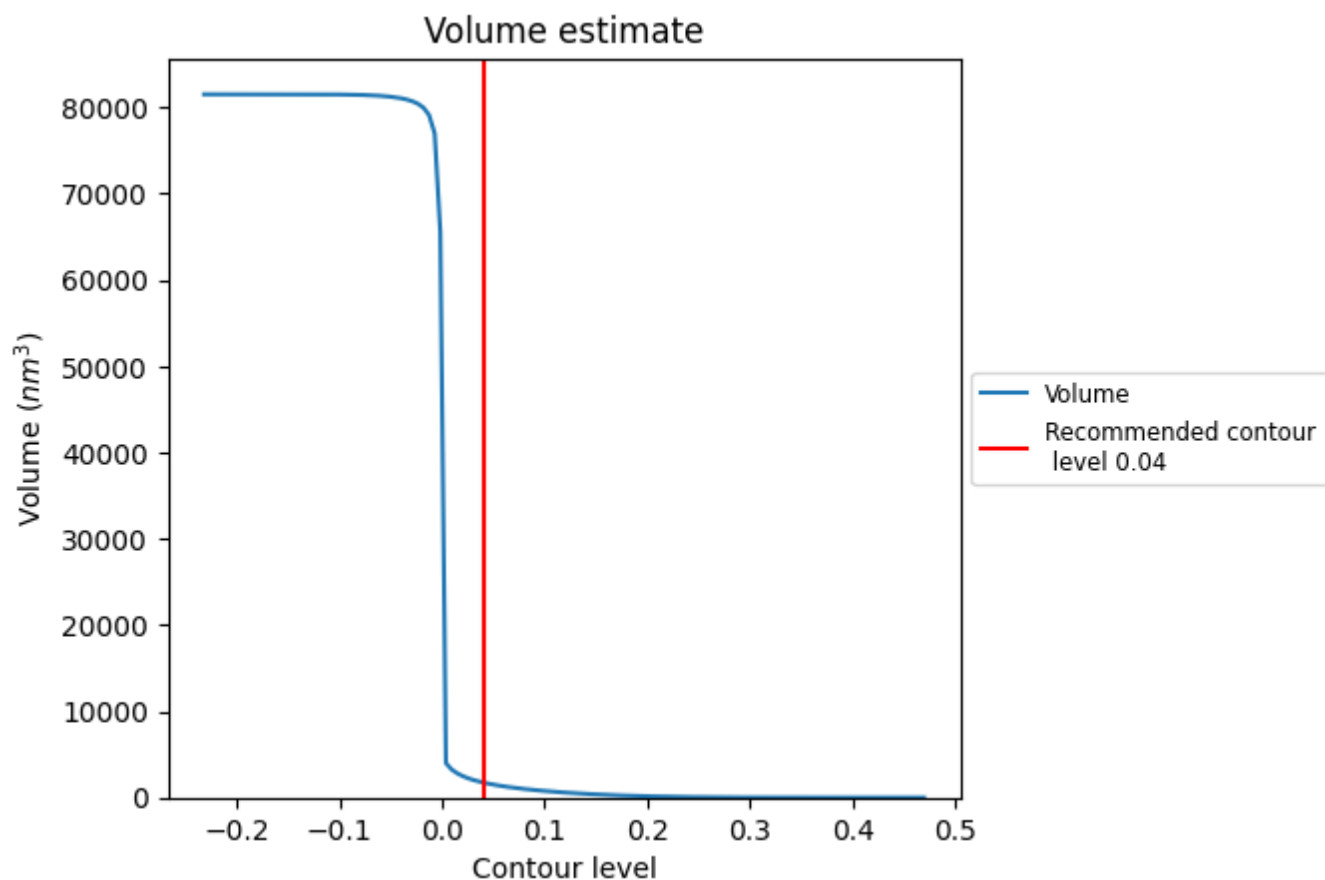
This section contains the results of statistical analysis of the map.

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.

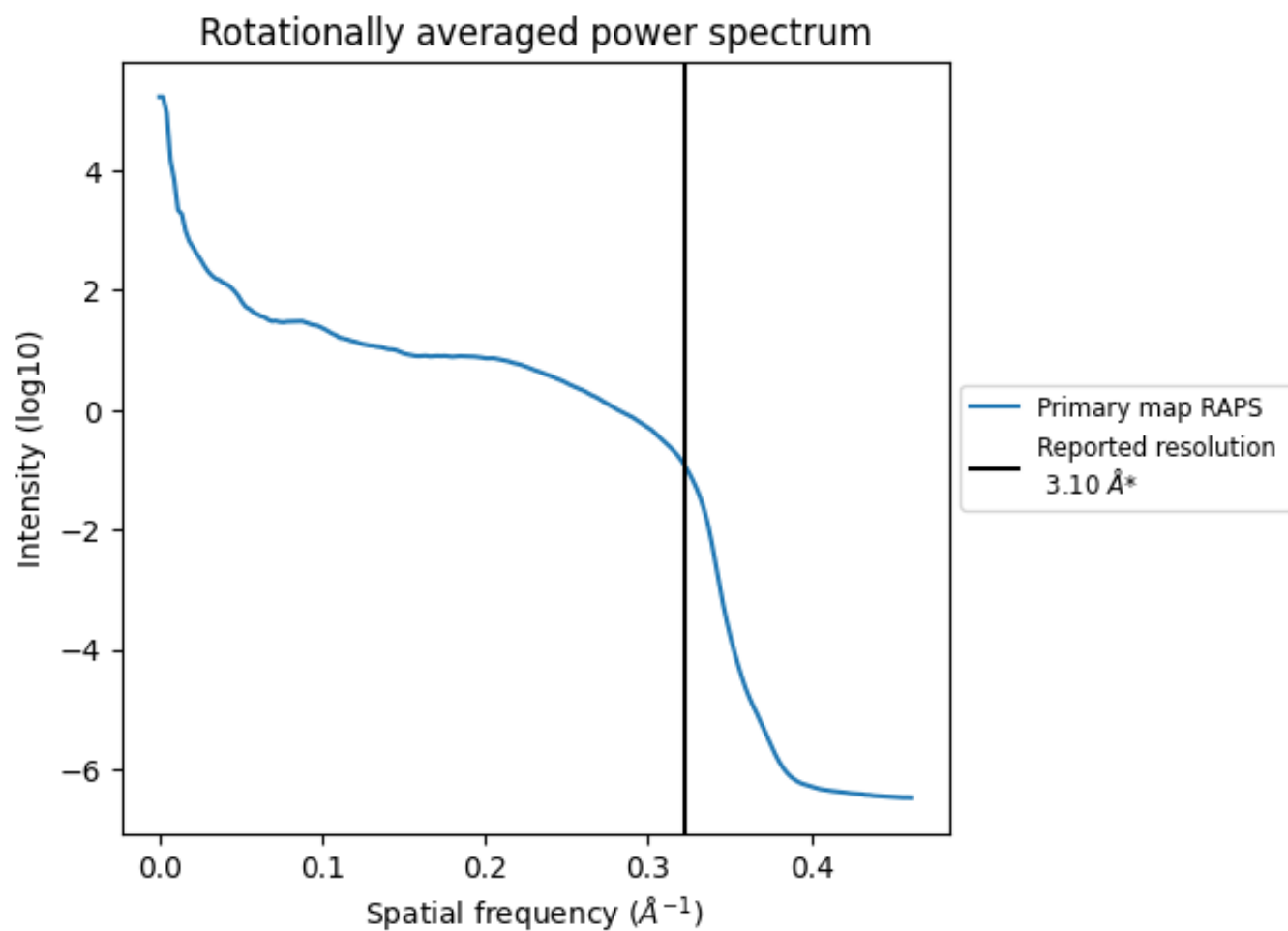
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1744 nm^3 ; this corresponds to an approximate mass of 1575 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 ⓘ

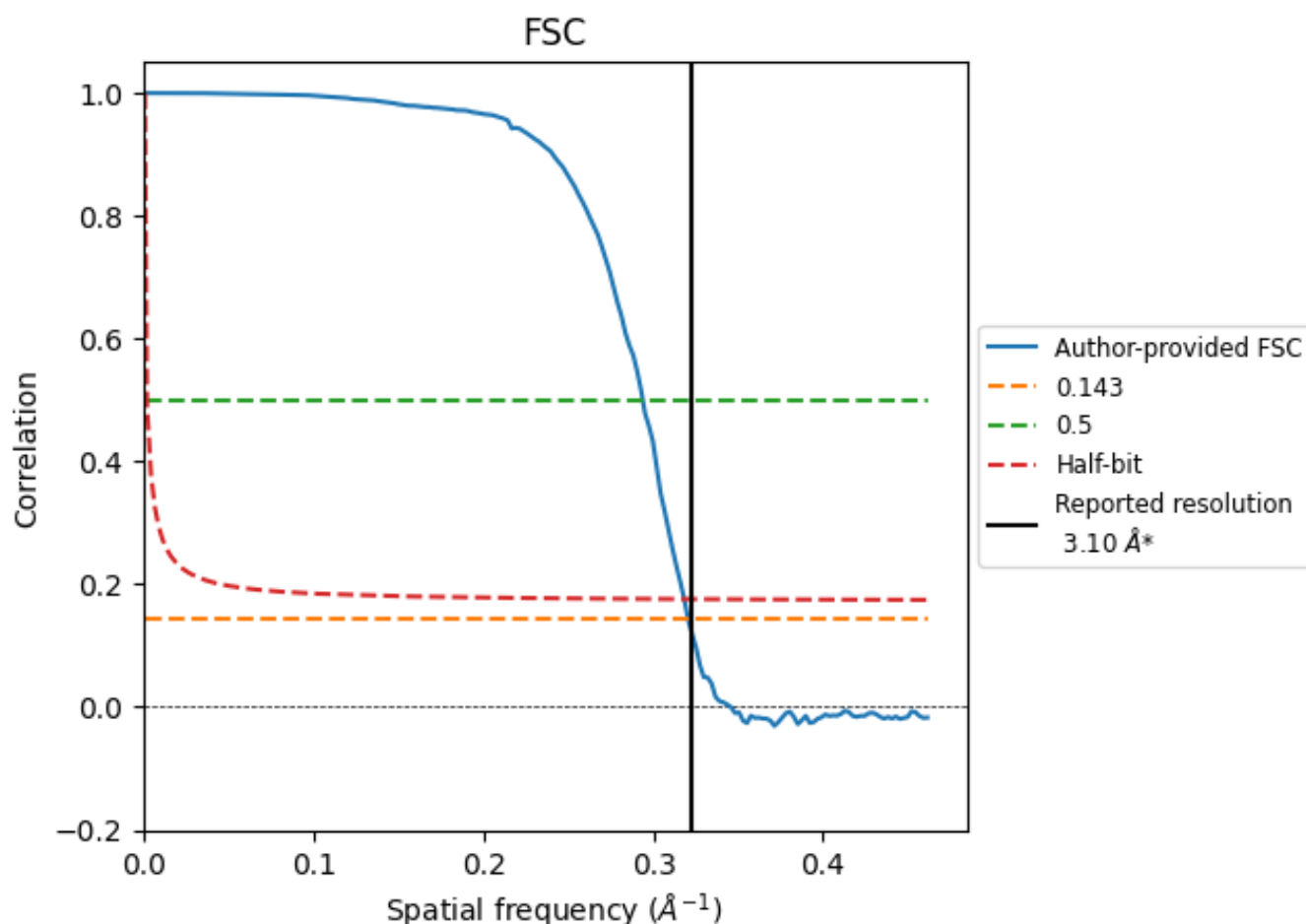


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

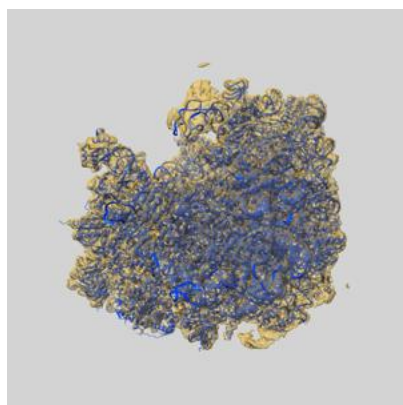
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.40	3.14
Unmasked-calculated*	-	-	-

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

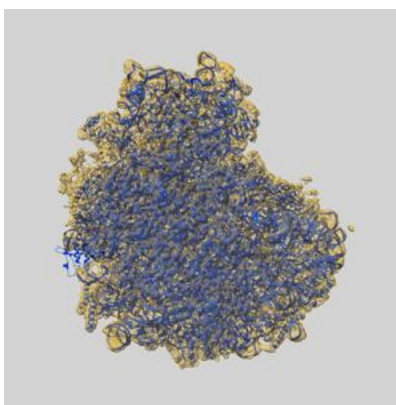
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4474 and PDB model 6Q8Y. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

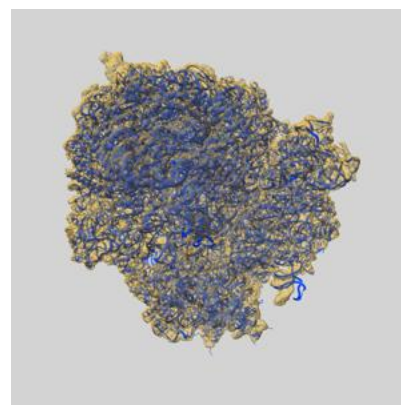
9.1 Map-model overlay [i](#)



X



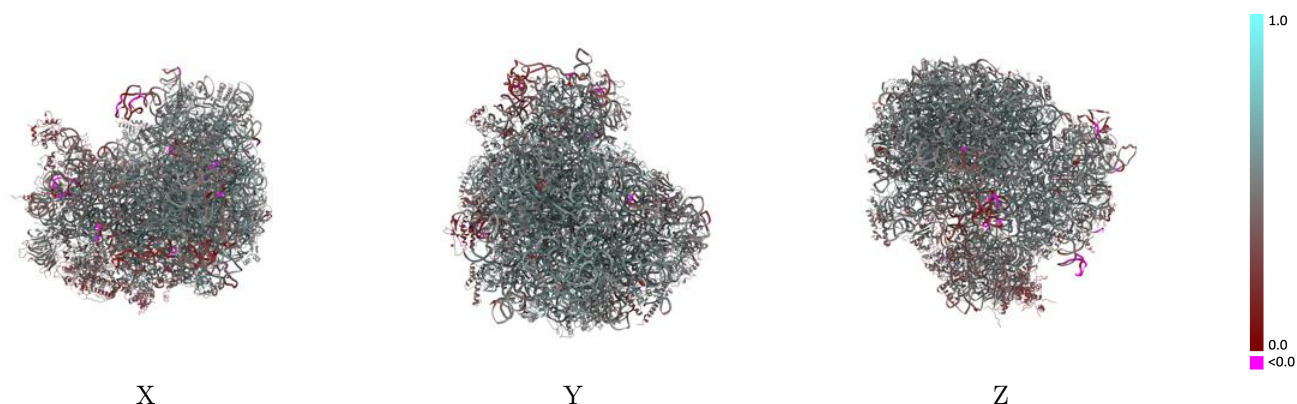
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

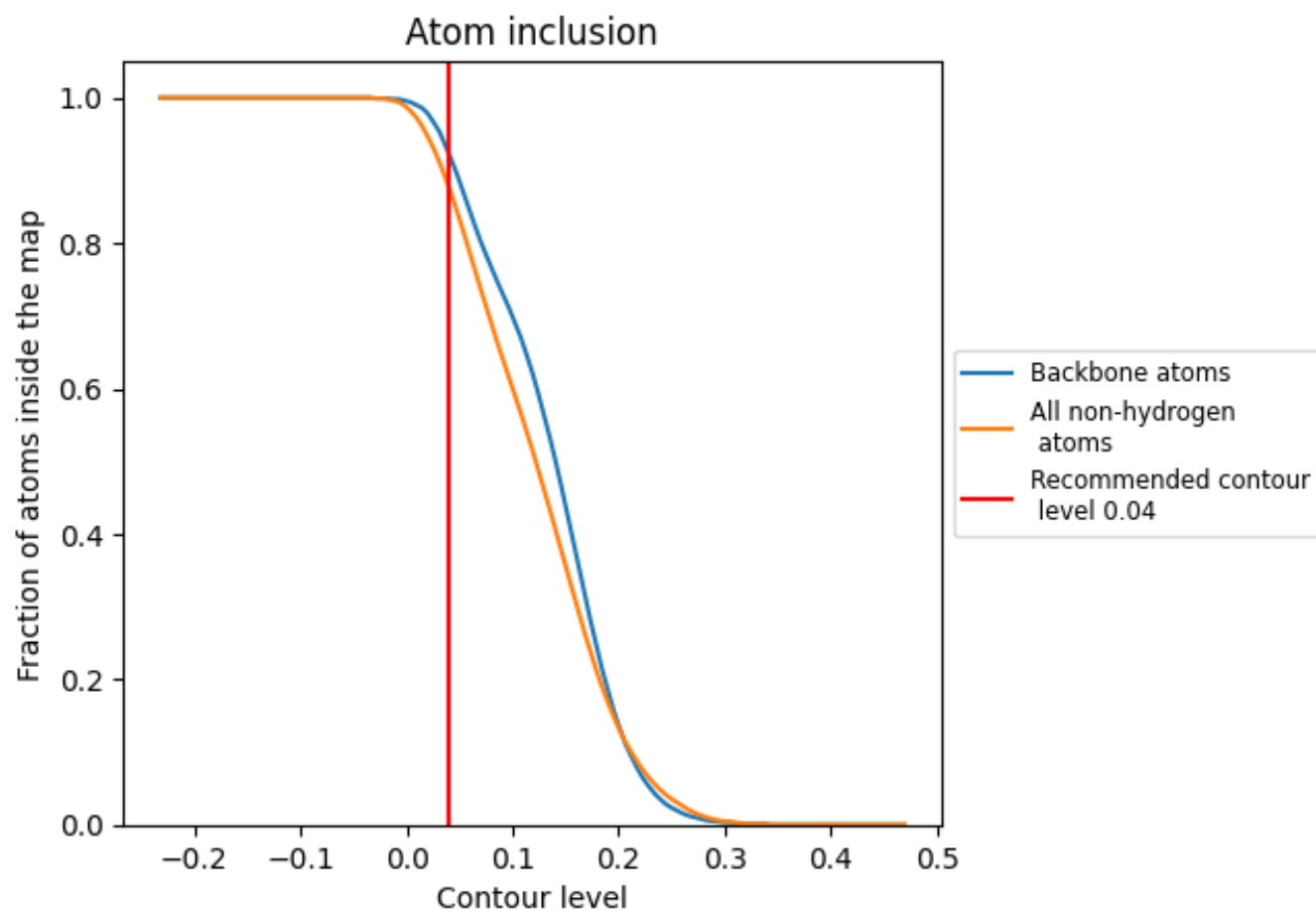


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.4840
2	 0.9310	 0.4700
A	 0.8000	 0.4360
AA	 0.8540	 0.4920
AB	 0.8430	 0.5260
AC	 0.8460	 0.4920
AD	 0.8400	 0.4890
AE	 0.8330	 0.5120
AF	 0.8980	 0.5580
AG	 0.8160	 0.4490
AH	 0.8720	 0.5240
AI	 0.8100	 0.4740
AJ	 0.8720	 0.5100
AK	 0.8760	 0.5100
AL	 0.8720	 0.5360
AM	 0.8700	 0.4830
AN	 0.8760	 0.5090
AO	 0.8490	 0.5030
AP	 0.8340	 0.5250
AQ	 0.8770	 0.5510
AR	 0.8810	 0.5320
AS	 0.7920	 0.5220
AT	 0.8390	 0.5320
AU	 0.8670	 0.5120
AV	 0.8030	 0.4750
AW	 0.8750	 0.5530
AX	 0.8690	 0.5180
AY	 0.8640	 0.5170
B	 0.7710	 0.4210
BA	 0.8840	 0.5280
BB	 0.8820	 0.5210
BC	 0.8530	 0.5110
BD	 0.8040	 0.4710
BE	 0.8830	 0.5210
BF	 0.8230	 0.4880



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Chain	Atom inclusion	Q-score
BG	 0.8650	 0.5330
BH	 0.8520	 0.5090
BI	 0.8420	 0.4480
BJ	 0.8500	 0.5060
BK	 0.8870	 0.5440
BL	 0.8630	 0.4760
BM	 0.8620	 0.4890
BN	 0.8700	 0.5320
BO	 0.8740	 0.5020
BP	 0.8670	 0.5070
BQ	 0.9600	 0.5200
BR	 0.9820	 0.4980
BS	 0.9720	 0.5500
C	 0.7510	 0.3850
D	 0.6740	 0.2640
E	 0.7540	 0.3870
F	 0.8240	 0.4640
G	 0.7890	 0.4330
H	 0.7920	 0.4120
I	 0.8080	 0.4130
J	 0.7360	 0.4070
K	 0.8010	 0.3730
L	 0.7500	 0.4470
M	 0.8770	 0.4910
N	 0.7090	 0.2760
O	 0.7880	 0.4260
P	 0.8280	 0.4600
Q	 0.8230	 0.4760
R	 0.8310	 0.4910
S	 0.8350	 0.4980
T	 0.7900	 0.4180
U	 0.8130	 0.4330
V	 0.7850	 0.4590
W	 0.8120	 0.4480
X	 0.8110	 0.5070
Y	 0.8390	 0.5020
Z	 0.8820	 0.5040
a	 0.8360	 0.4730
b	 0.8700	 0.5270
c	 0.8270	 0.5180
d	 0.7740	 0.4190
e	 0.7590	 0.4340

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Chain	Atom inclusion	Q-score
f	 0.8450	 0.4920
g	 0.7830	 0.4470
l	 0.6680	 0.3580
m	 0.8190	 0.3660
n	 0.9080	 0.4430
z	 0.2310	 0.2590