



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:43 PM UTC

PDB ID : 7ZUX / pdb_00007zux
EMDB ID : EMD-14979
Title : Collided ribosome in a disome unit from *S. cerevisiae*
Authors : Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.
Deposited on : 2022-05-13
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

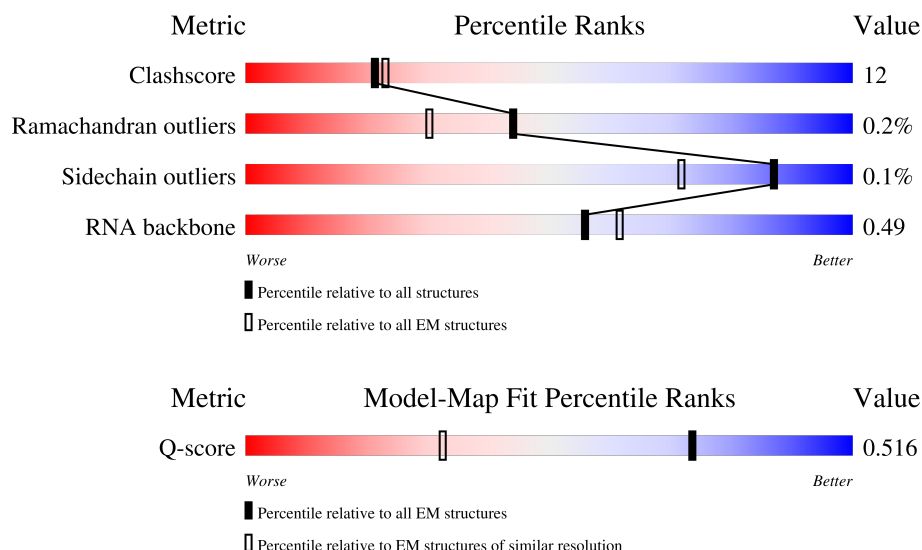
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.50 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.



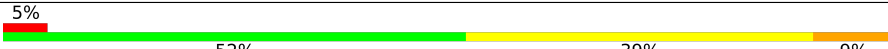
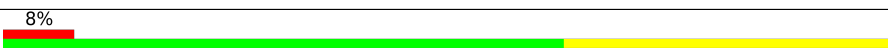
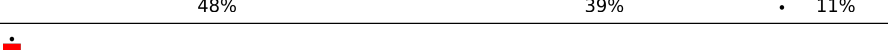
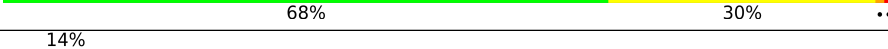
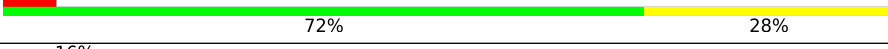
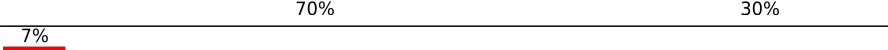
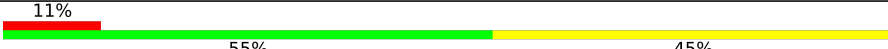
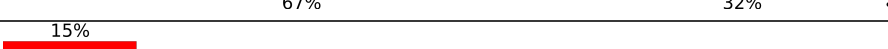
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7115 (2.00 - 3.00)

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	1800	
2	3	158	
3	4	121	

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Mol	Chain	Length	Quality of chain
4	5	3396	
5	6	76	
6	7	77	
7	DA	206	
8	DB	255	
9	DC	216	
10	DD	222	
11	DE	258	
12	DF	206	
13	DG	228	
14	DH	184	
15	DI	200	
16	DJ	184	
17	DK	92	
18	DL	144	
19	DM	121	
20	DN	150	
21	DO	127	
22	DP	117	
23	DQ	141	
24	DR	136	
25	DS	145	
26	DT	143	
27	DU	100	
28	DV	87	

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Mol	Chain	Length	Quality of chain
29	DW	129	
30	DX	144	
31	DY	134	
32	DZ	82	
33	Da	97	
34	Db	81	
35	Dc	63	
36	Dd	53	
37	De	60	
38	Df	73	
39	Dg	312	
40	EA	251	
41	EB	386	
42	EC	361	
43	ED	294	
44	EE	176	
45	EF	222	
46	EG	233	
47	EH	191	
48	EI	218	
49	EJ	169	
50	EK	193	
51	EL	136	
52	EM	203	
53	EN	197	

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Mol	Chain	Length	Quality of chain
54	EO	183	
55	EP	185	
56	EQ	188	
57	ER	171	
58	ES	159	
59	ET	100	
60	EU	136	
61	EV	126	
62	EW	121	
63	EX	125	
64	EY	135	
65	EZ	148	
66	Ea	58	
67	Eb	96	
68	Ec	109	
69	Ed	127	
70	Ee	106	
71	Ef	112	
72	Eg	119	
73	Eh	99	
74	Ei	85	
75	Ej	77	
76	Ek	50	
77	El	52	
78	Em	25	

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Mol	Chain	Length	Quality of chain
79	En	103	 7% 67% 33%
80	Eo	91	 70% 30%

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 202365 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	1769	Total	C	N	O	P	0	0
			37699	16854	6679	12397	1769		

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	3163	Total	C	N	O	P	0	0
			67650	30218	12191	22078	3163		

- Molecule 5 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	76	Total	C	N	O	P	0	0
			1620	723	290	532	75		

- Molecule 6 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	7	77	Total	C	N	O	P	0	0
			1644	732	297	538	77		

- Molecule 7 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	DA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 8 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	DB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 9 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	DC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 10 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	DD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 11 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	DE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 12 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	DF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 13 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	DG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 14 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	DH	184	Total	C	N	O		
			1473	946	263	264	0	0

- Molecule 15 is a protein called 40S ribosomal protein S8-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	DI	187	Total	C	N	O	S		
			1476	916	295	263	2	0	0

- Molecule 16 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	DJ	184	Total	C	N	O	S		
			1479	935	285	258	1	0	0

- Molecule 17 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	DK	92	Total	C	N	O	S		
			752	487	122	141	2	0	0

- Molecule 18 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	DL	144	Total	C	N	O	S		
			1159	742	219	195	3	0	0

- Molecule 19 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	DM	121	Total	C	N	O	S		
			875	551	153	169	2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S13.

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

- Molecule 21 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	DO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 22 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	DP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	DQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	DR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	DS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	DT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 27 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	DU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 28 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	DV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 29 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	DY	134	Total	C	N	O		0	0
			1073	676	208	189			

- Molecule 32 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	DZ	82	Total	C	N	O		0	0
			651	416	123	112			

- Molecule 33 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 34 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 35 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Dc	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 36 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 37 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	De	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 38 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Df	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 39 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Dg	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 40 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	EA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 41 is a protein called 60S ribosomal protein L3.

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

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

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

- Molecule 43 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	ED	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 44 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	EE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EE	146	ILE	LEU	conflict	UNP P05739
EE	173	MET	LEU	conflict	UNP P05739

- Molecule 45 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	EH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 48 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	EI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 49 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	EJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 50 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	EK	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 51 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	EO	183	Total	C	N	O	S	0	0
			1416	879	284	253			

- Molecule 55 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	EQ	188	Total	C	N	O	S	0	0
			1515	932	323	260			

- Molecule 57 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ER	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 58 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L22-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	EV	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
EV	104	GLN	ASN	conflict	UNP P04449
EV	109	GLN	LEU	conflict	UNP P04449
EV	112	ASP	ASN	conflict	UNP P04449
EV	119	ALA	GLU	conflict	UNP P04449

- Molecule 62 is a protein called 60S ribosomal protein L25.

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

- Molecule 63 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	EX	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 64 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	EY	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 65 is a protein called 60S ribosomal protein L28.

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

- Molecule 66 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Ea	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 67 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Eb	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 68 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Ed	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 70 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Eh	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 74 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Ei	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 75 is a protein called 60S ribosomal protein L38.

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

- Molecule 76 is a protein called 60S ribosomal protein L39.

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

- Molecule 77 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Em	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 79 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	En	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 80 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	2	84	Total	Mg	0
			84	84	
81	DF	1	Total	Mg	0
			1	1	
81	DN	1	Total	Mg	0
			1	1	

- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

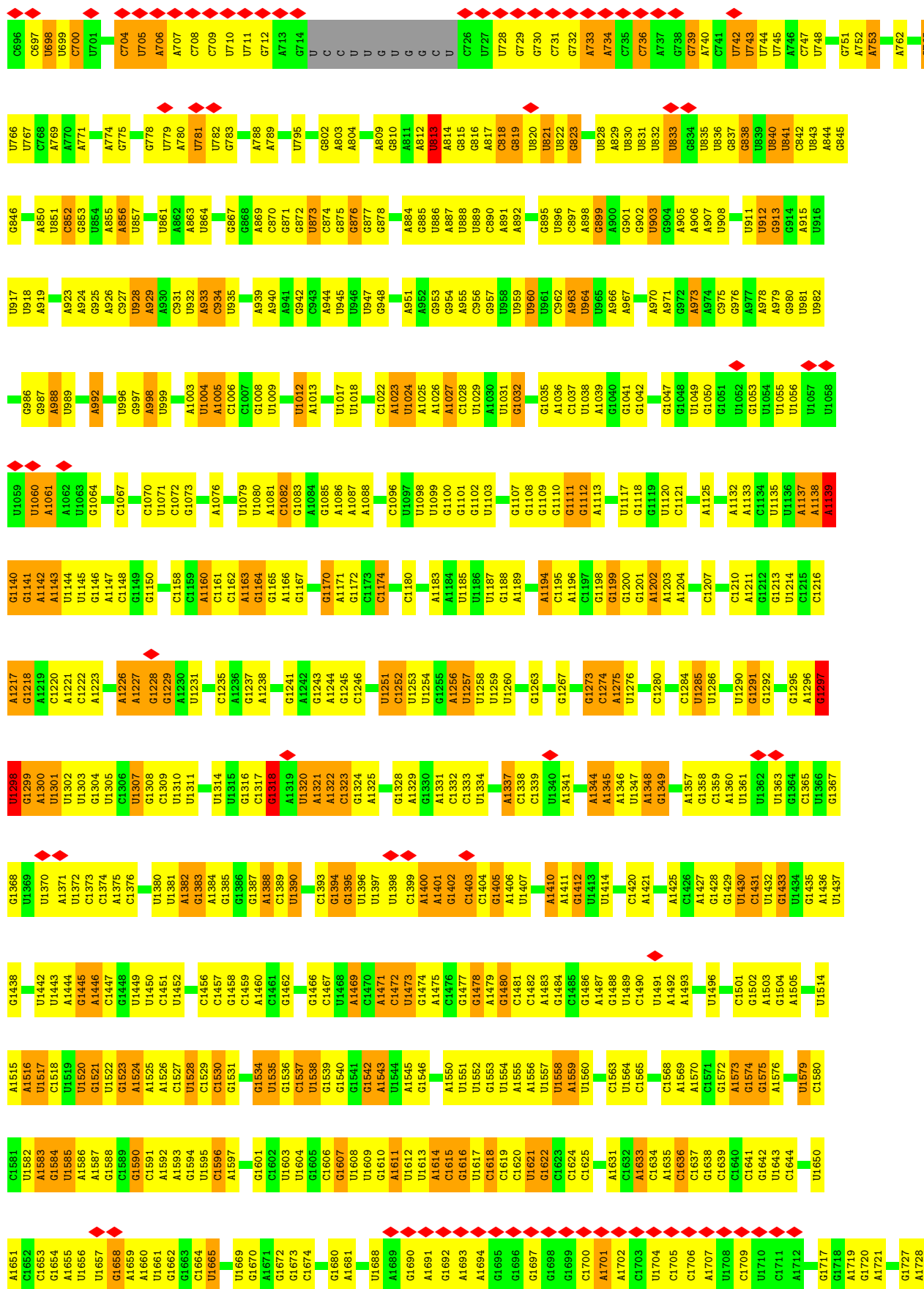
Mol	Chain	Residues	Atoms		AltConf
82	Dd	1	Total 1	Zn 1	0
82	Df	1	Total 1	Zn 1	0
82	Ef	1	Total 1	Zn 1	0
82	Ei	1	Total 1	Zn 1	0
82	El	1	Total 1	Zn 1	0
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82	Eo	1	Total 1	Zn 1	0

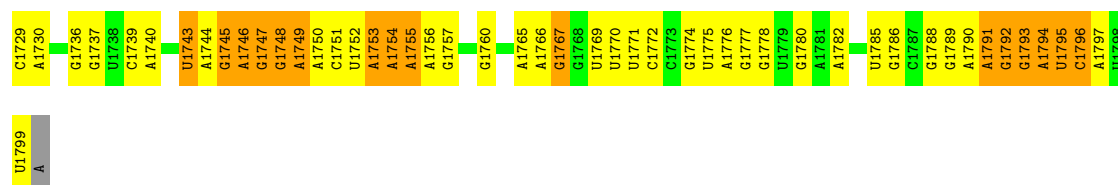
3 Residue-property plots

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.

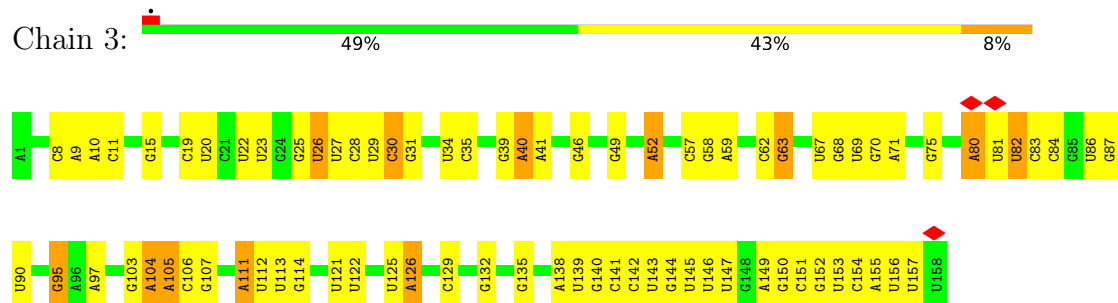
• Molecule 1: 18S ribosomal RNA



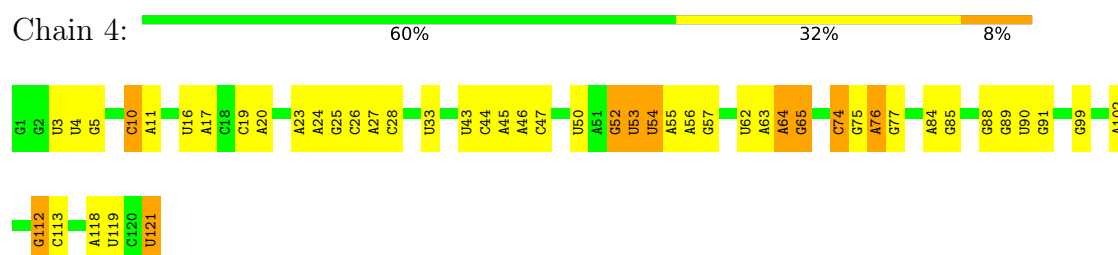




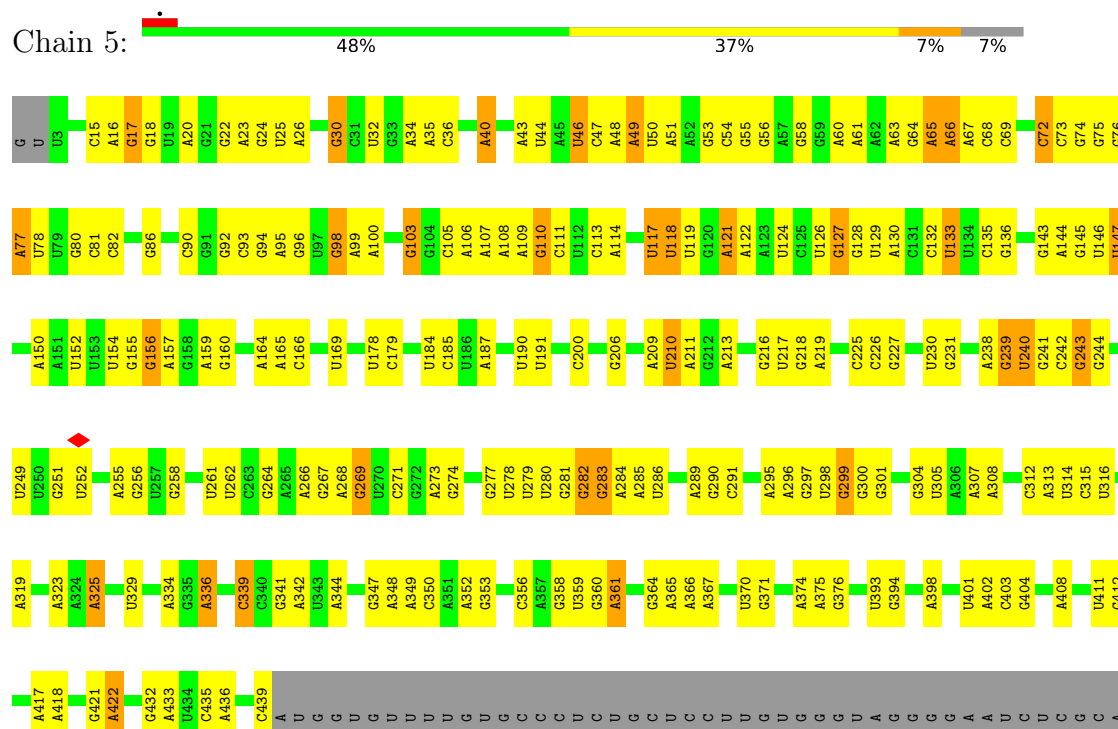
- Molecule 2: 5.8S ribosomal RNA

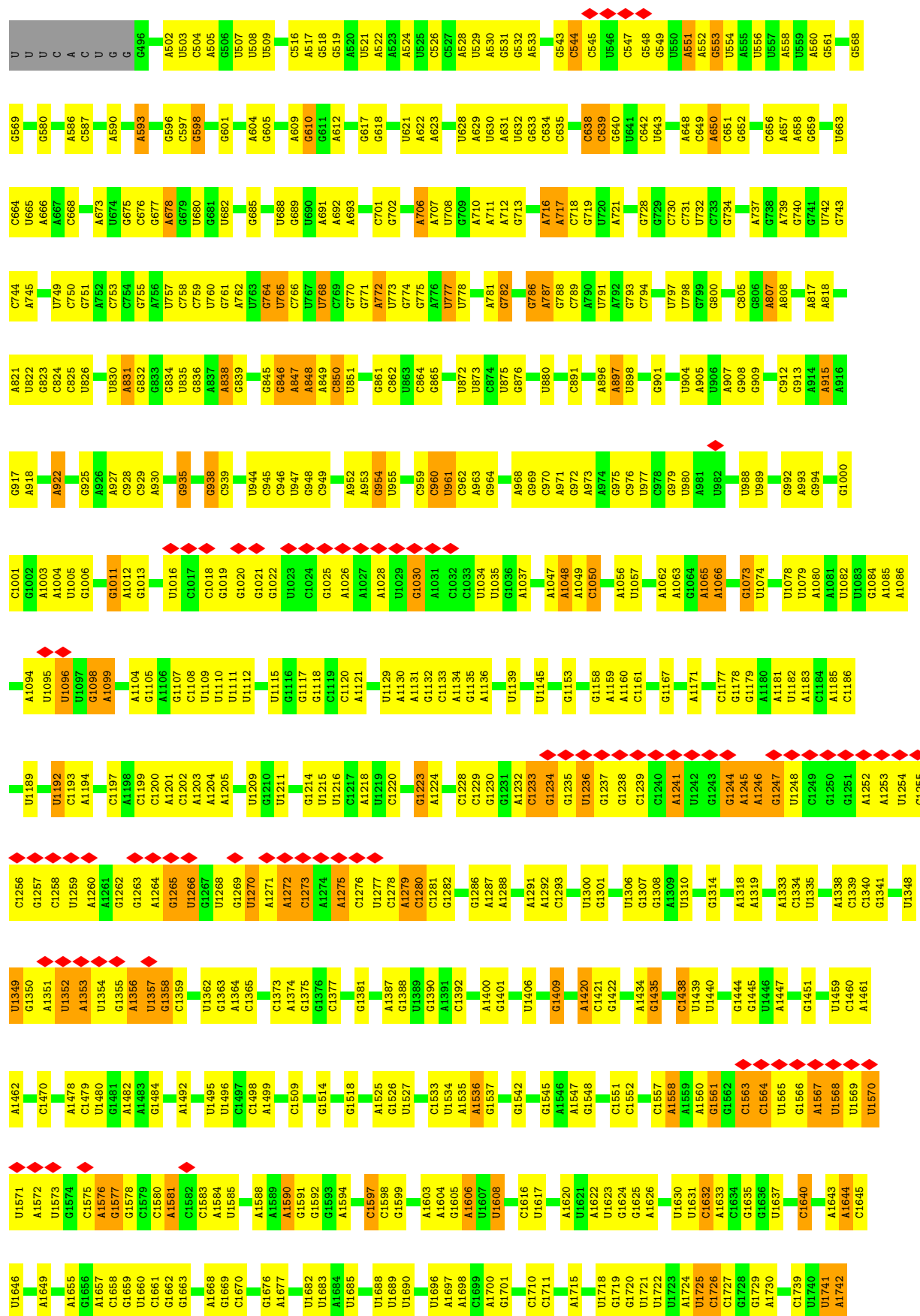


- Molecule 3: 5S ribosomal RNA

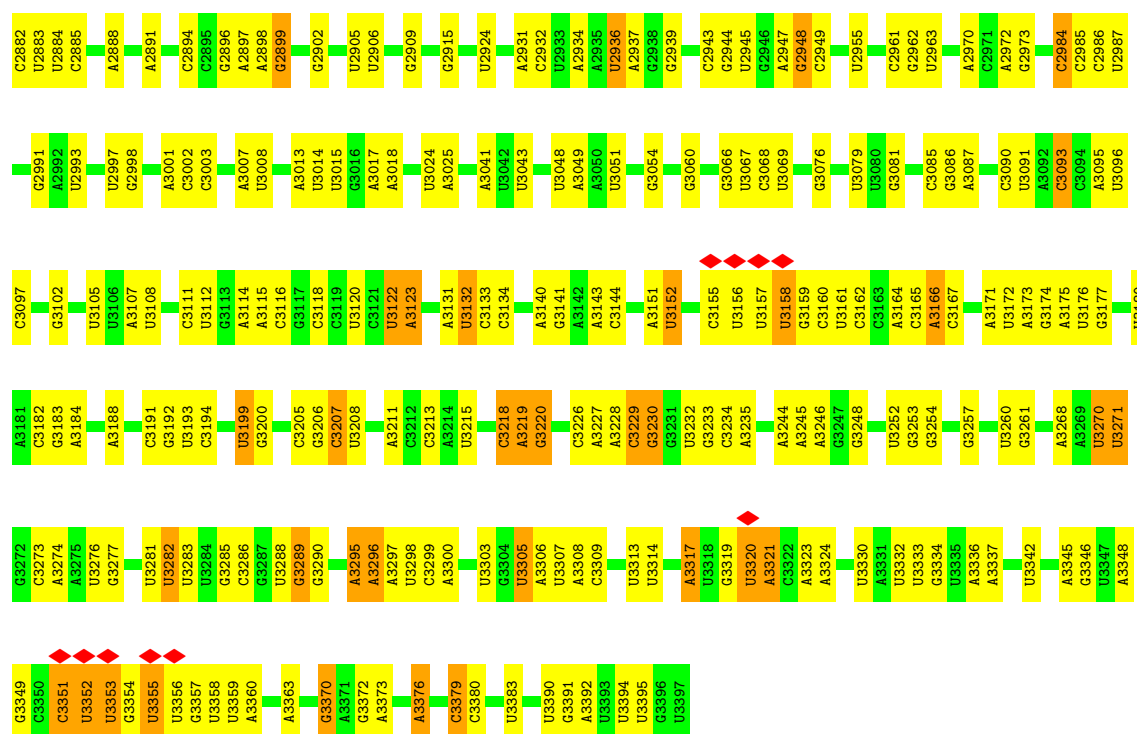


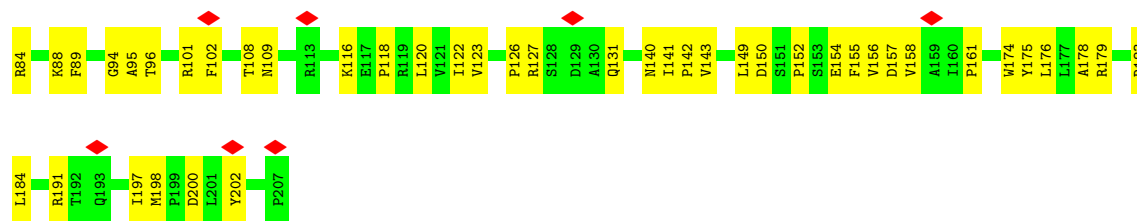
- Molecule 4: 25S ribosomal RNA



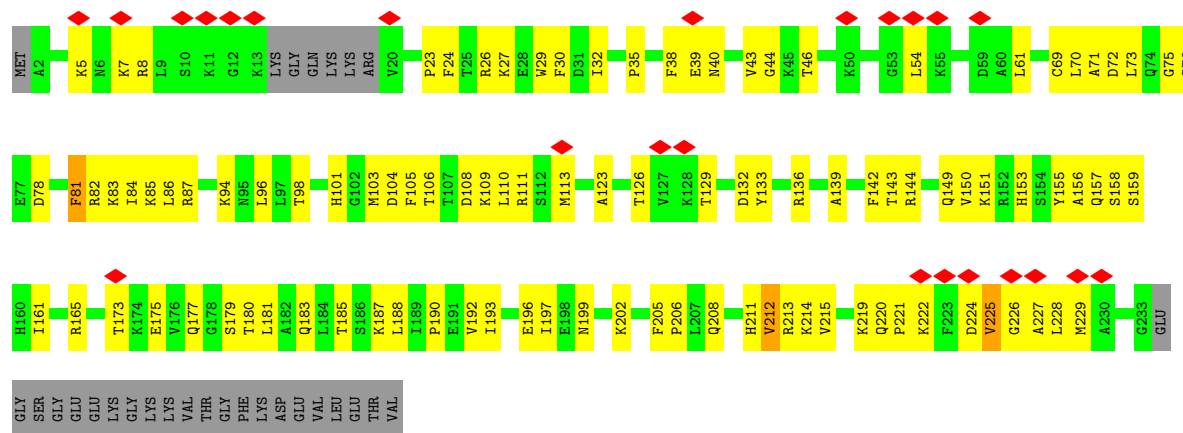




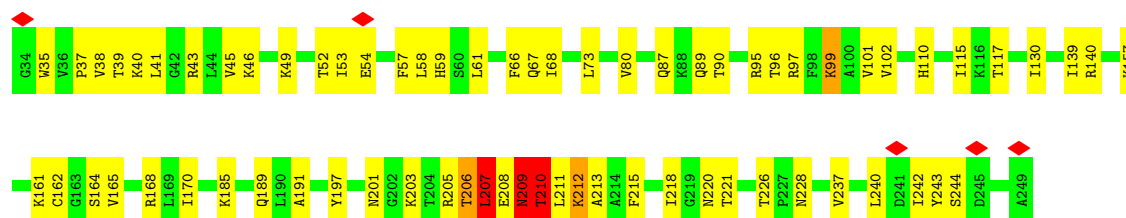




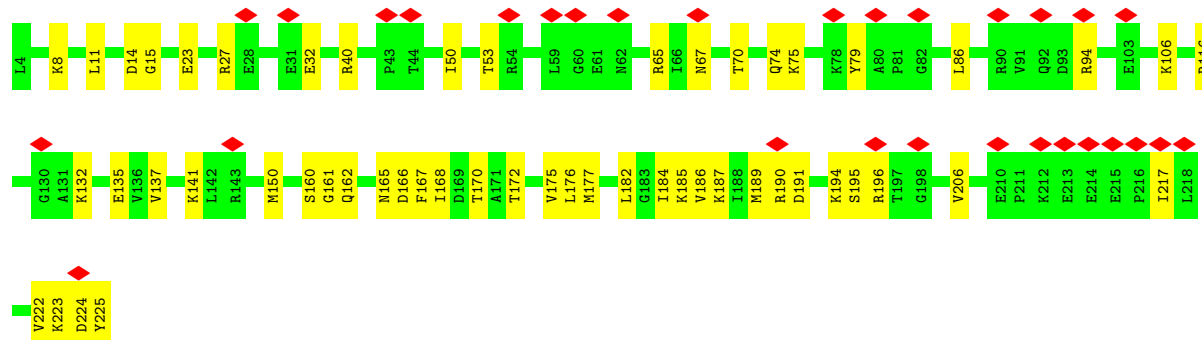
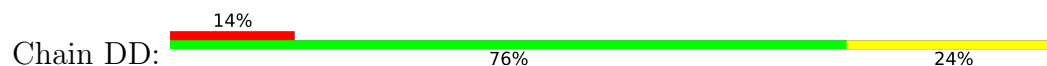
• Molecule 8: 40S ribosomal protein S1-A



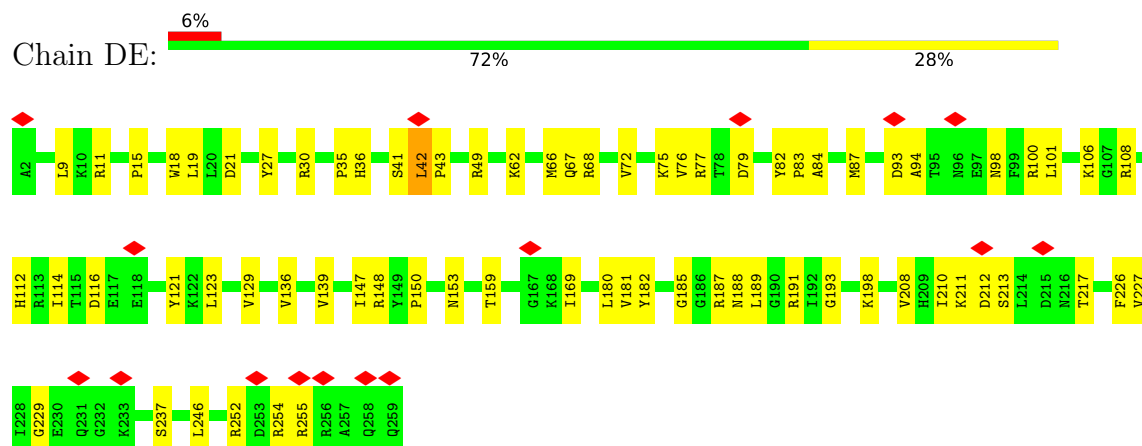
• Molecule 9: 40S ribosomal protein S2



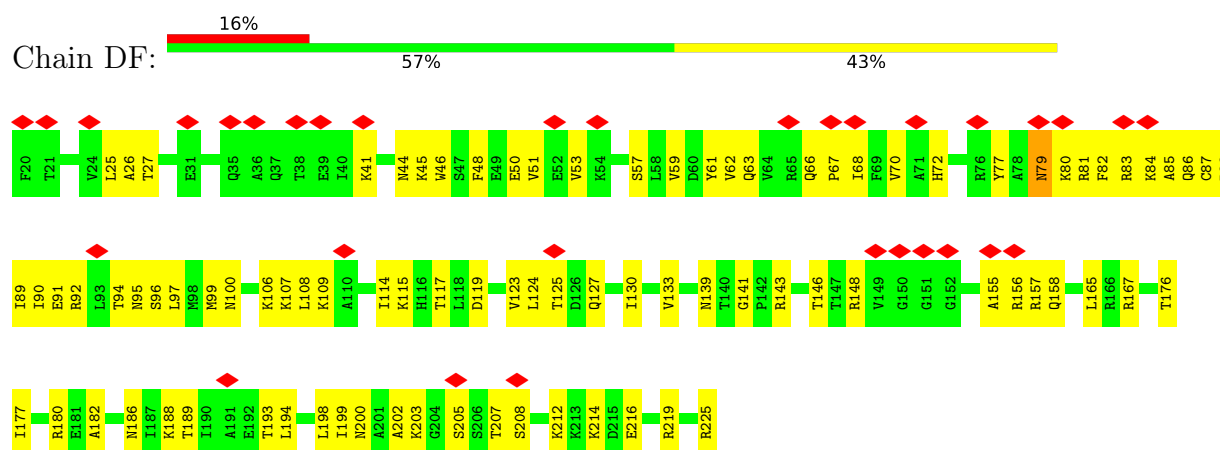
• Molecule 10: 40S ribosomal protein S3



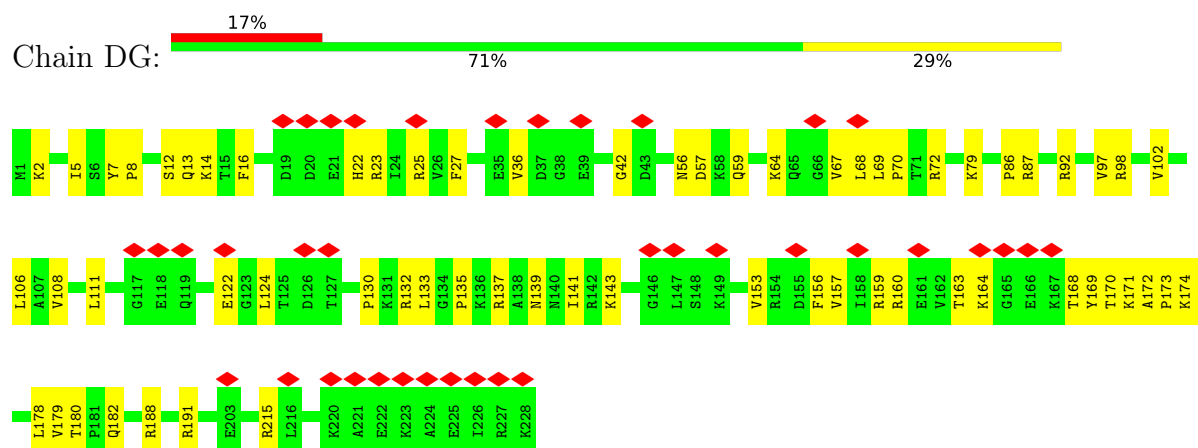
- Molecule 11: 40S ribosomal protein S4-A



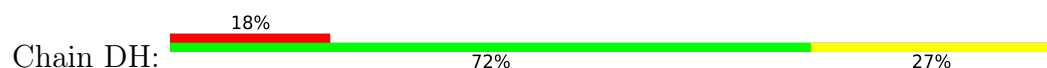
- Molecule 12: 40S ribosomal protein S5

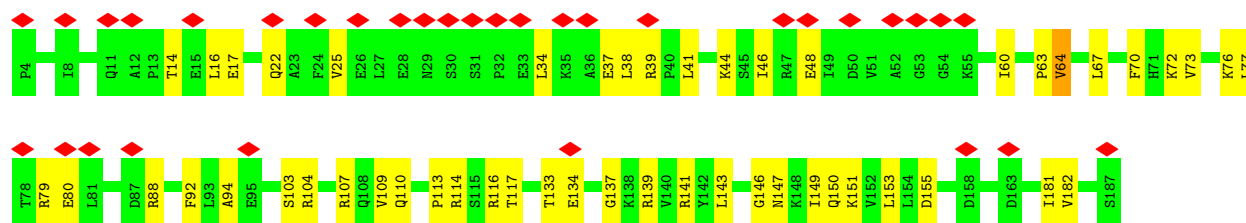


- Molecule 13: 40S ribosomal protein S6-A

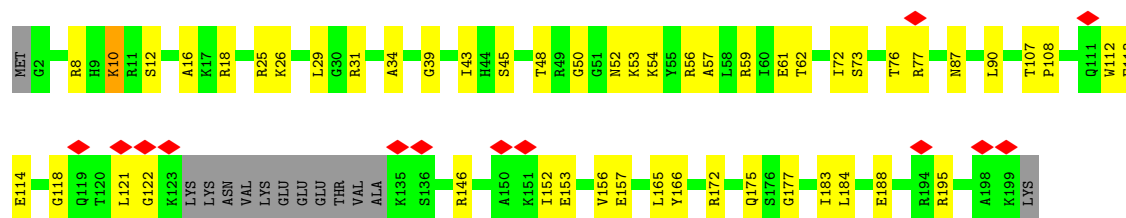


- Molecule 14: 40S ribosomal protein S7-A

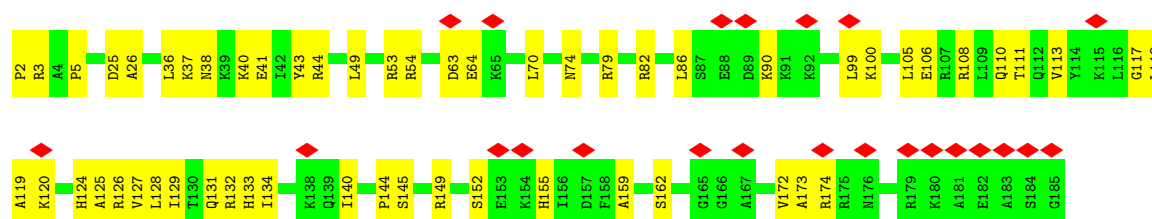
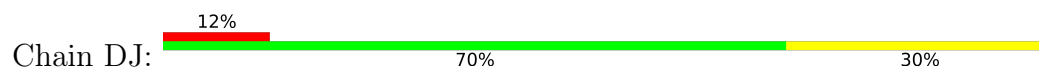




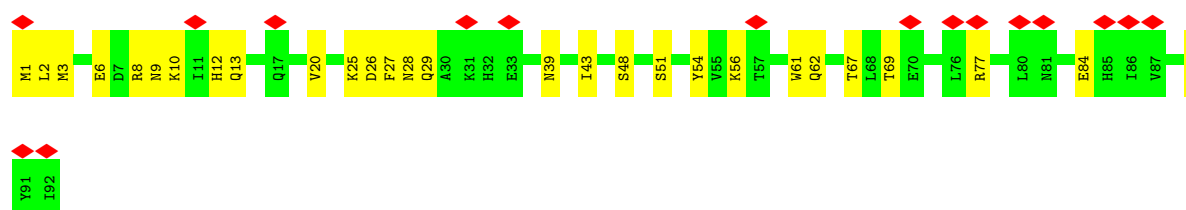
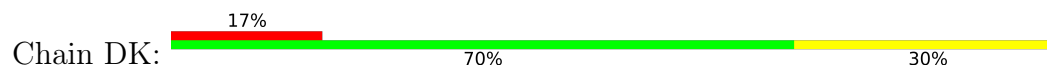
• Molecule 15: 40S ribosomal protein S8-B



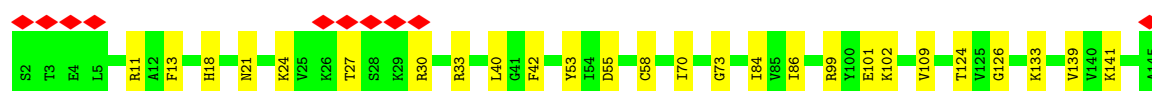
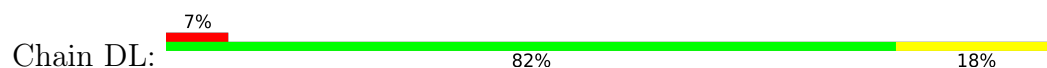
• Molecule 16: 40S ribosomal protein S9-A



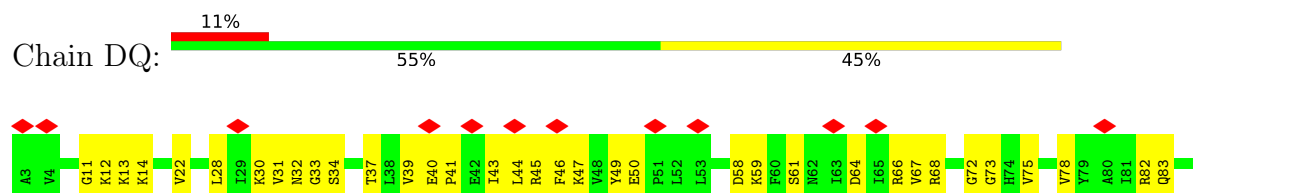
• Molecule 17: 40S ribosomal protein S10-A



• Molecule 18: 40S ribosomal protein S11-A



• Molecule 19: 40S ribosomal protein S12

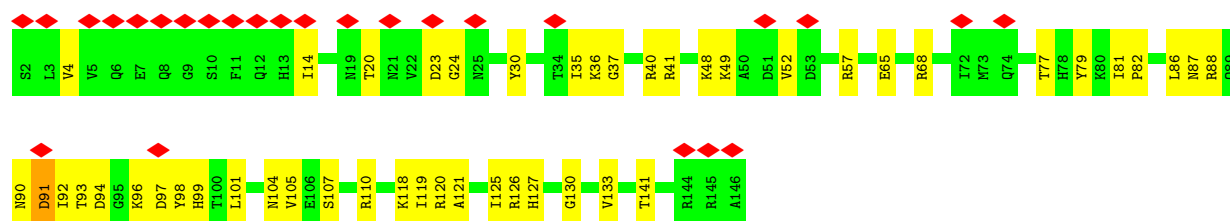




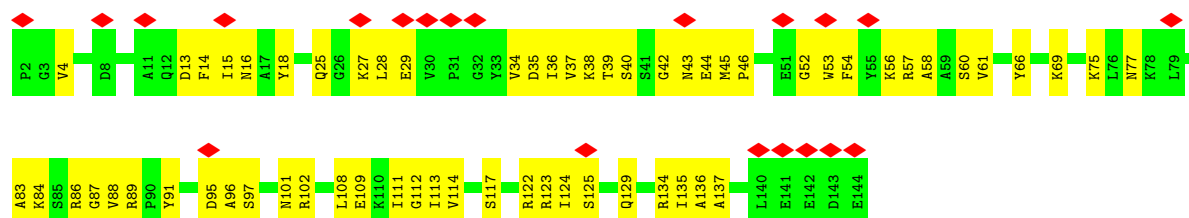
• Molecule 24: 40S ribosomal protein S17-A



• Molecule 25: 40S ribosomal protein S18-A



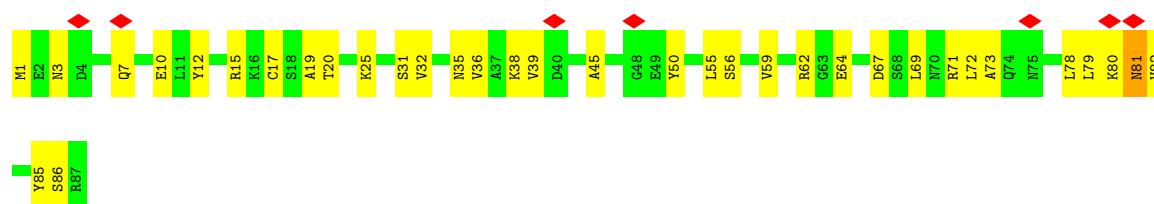
• Molecule 26: 40S ribosomal protein S19-A



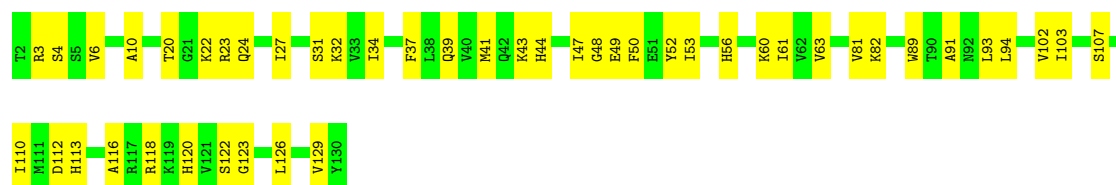
• Molecule 27: 40S ribosomal protein S20



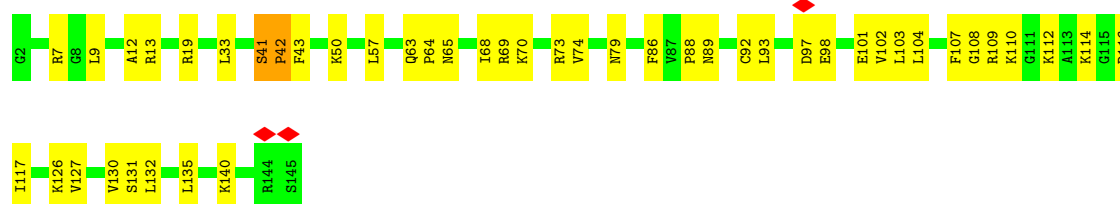
• Molecule 28: 40S ribosomal protein S21-A



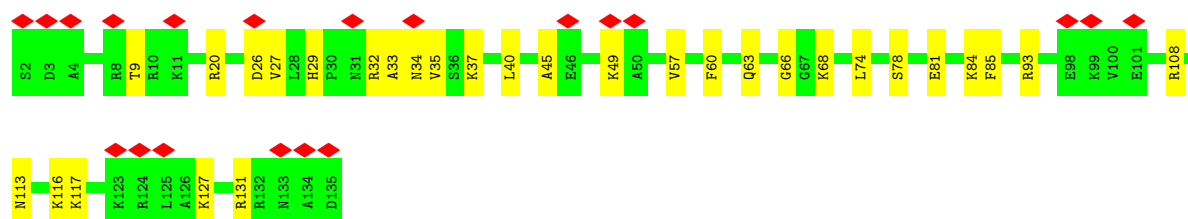
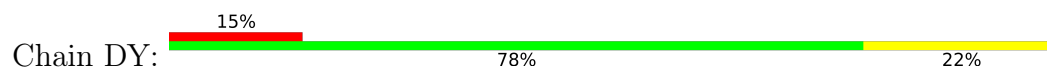
- Molecule 29: 40S ribosomal protein S22-A



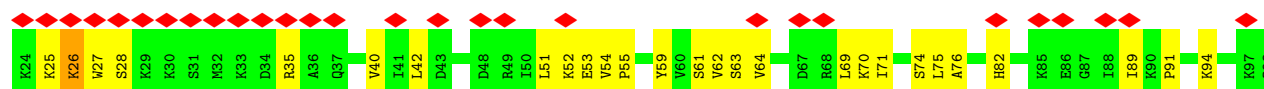
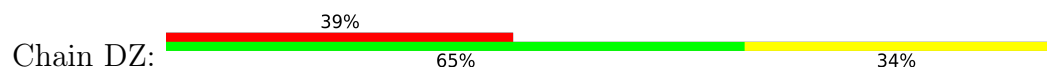
- Molecule 30: 40S ribosomal protein S23-A

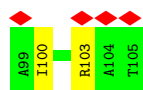


- Molecule 31: 40S ribosomal protein S24-A

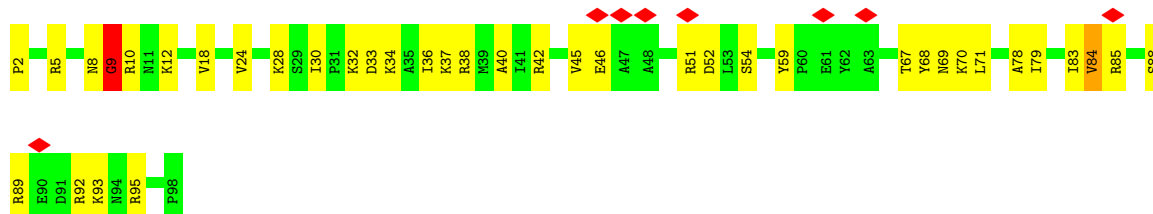


- Molecule 32: 40S ribosomal protein S25-A

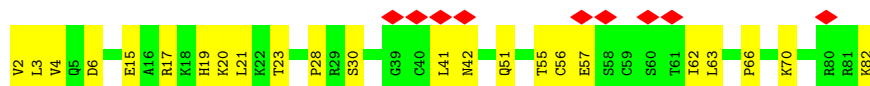
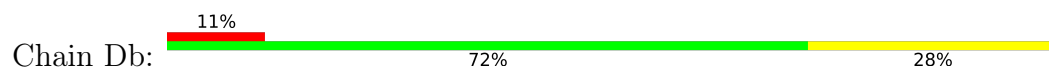




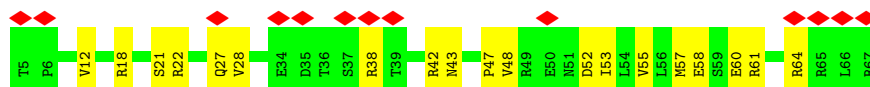
- Molecule 33: 40S ribosomal protein S26-B



- Molecule 34: 40S ribosomal protein S27-A



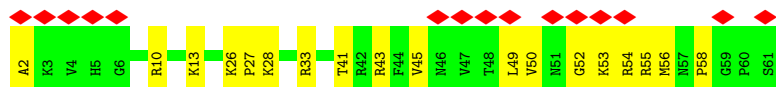
- Molecule 35: 40S ribosomal protein S28-A



- Molecule 36: 40S ribosomal protein S29-A

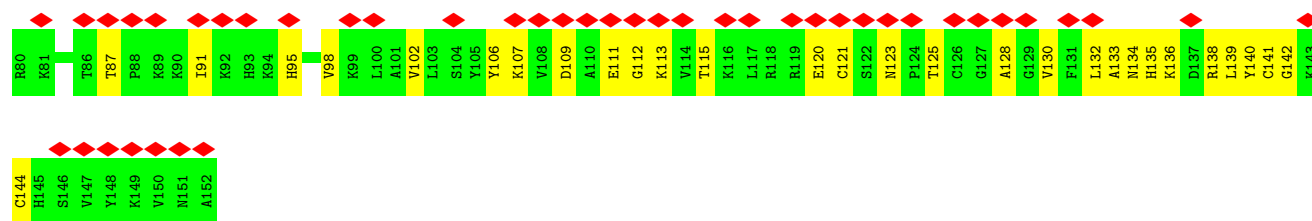


- Molecule 37: 40S ribosomal protein S30-A

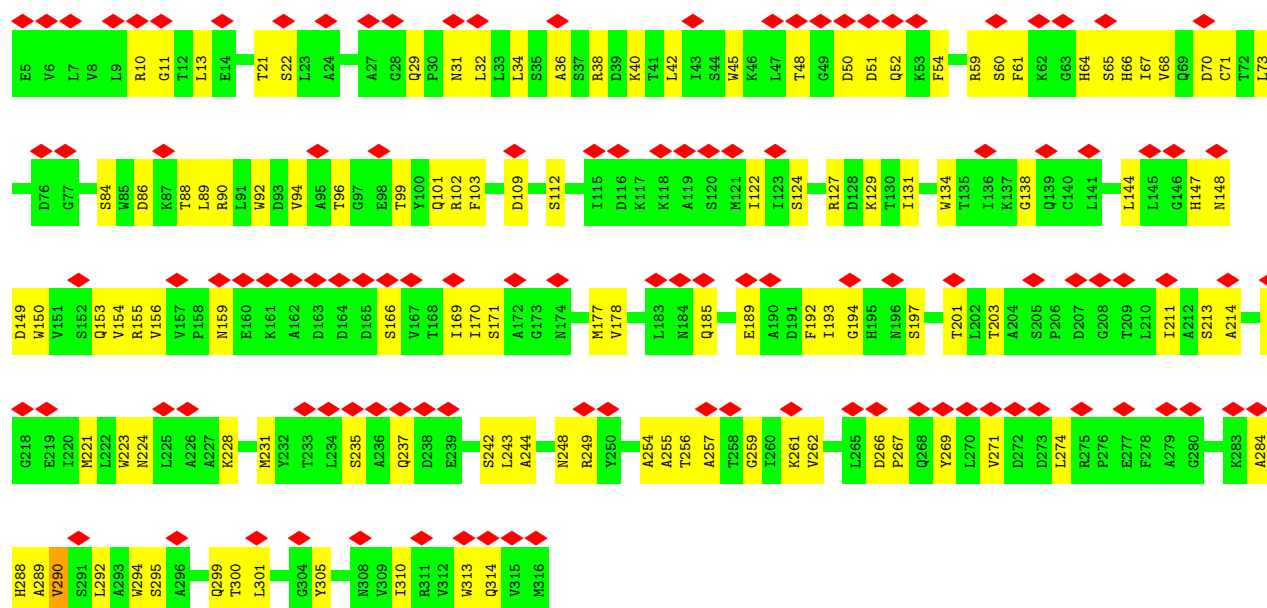
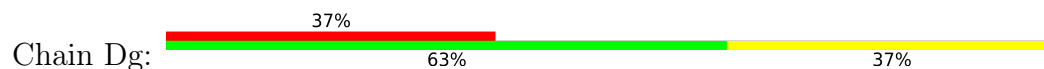


- Molecule 38: Ubiquitin

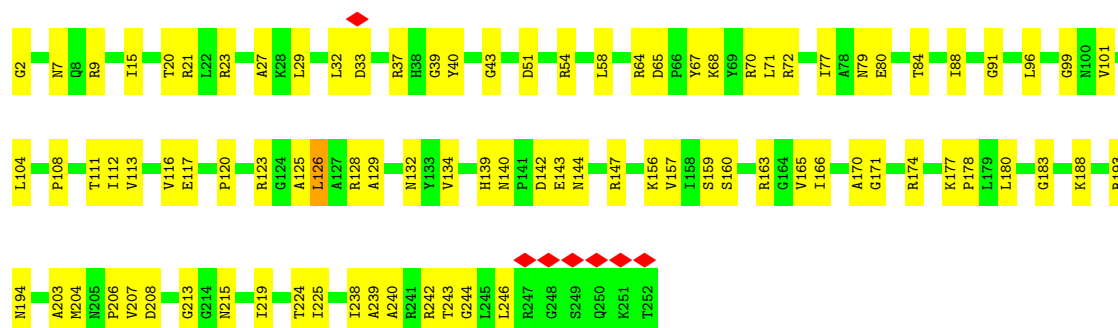




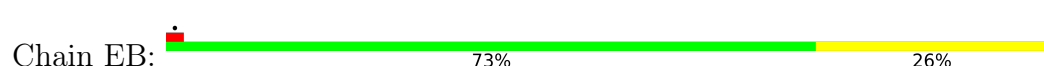
• Molecule 39: Guanine nucleotide-binding protein subunit beta-like protein

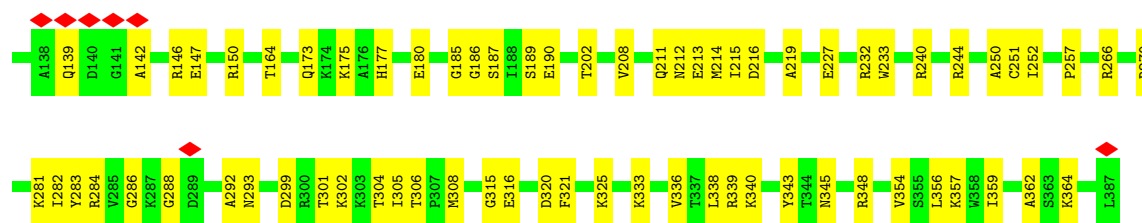


• Molecule 40: 60S ribosomal protein L2-A

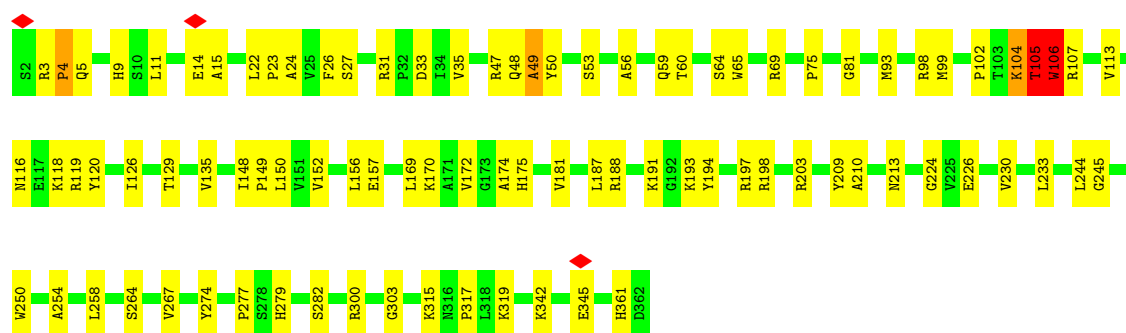
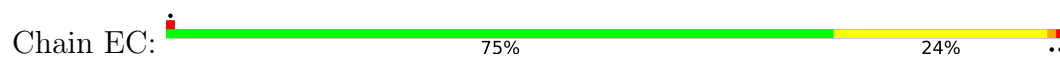


• Molecule 41: 60S ribosomal protein L3

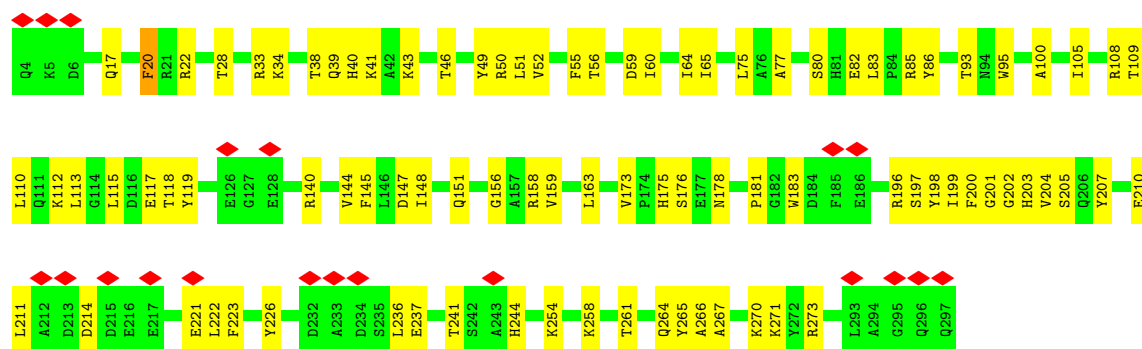
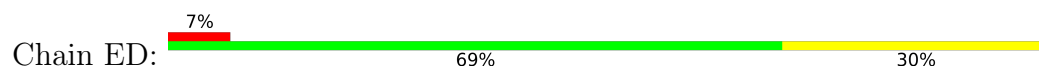




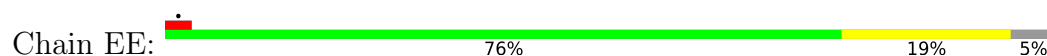
• Molecule 42: 60S ribosomal protein L4-A



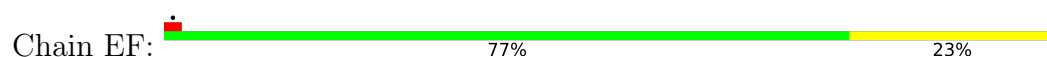
• Molecule 43: 60S ribosomal protein L5



• Molecule 44: 60S ribosomal protein L6-B

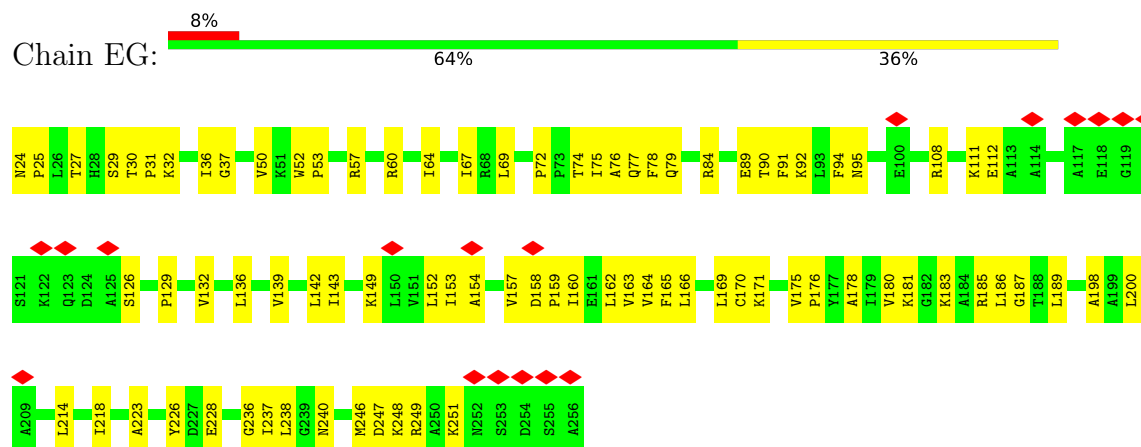


• Molecule 45: 60S ribosomal protein L7-A

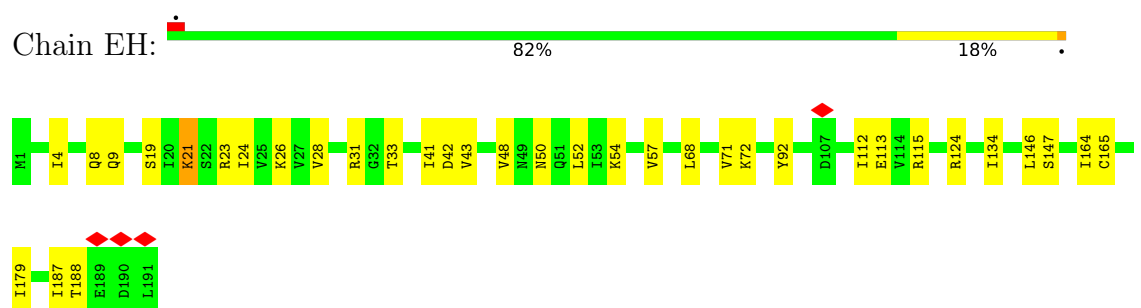




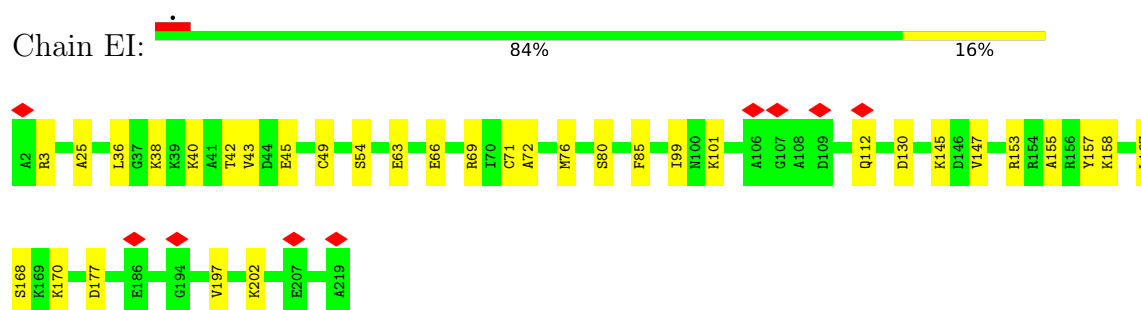
- Molecule 46: 60S ribosomal protein L8-A



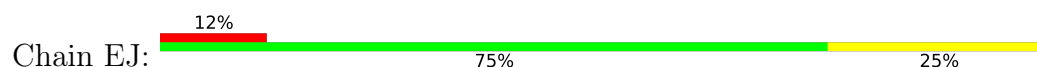
- Molecule 47: 60S ribosomal protein L9-A

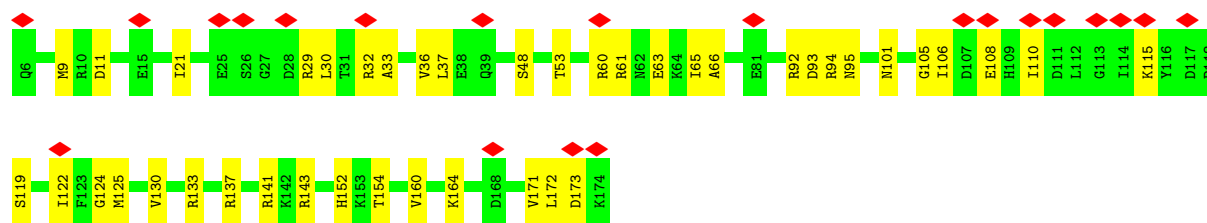


- Molecule 48: 60S ribosomal protein L10

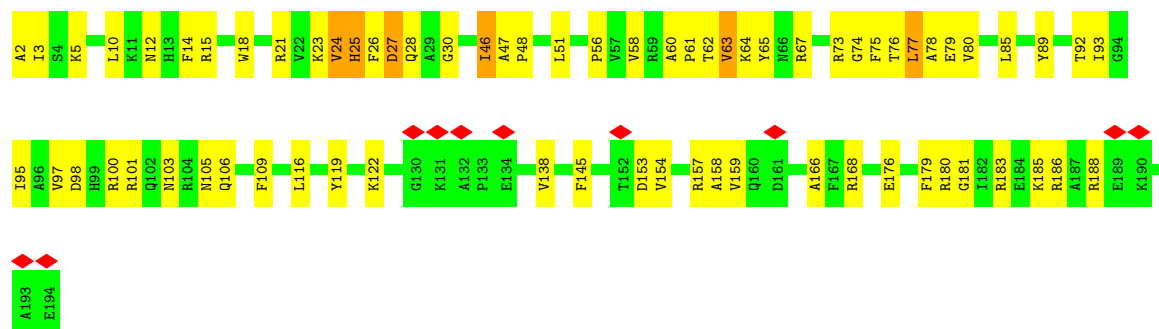


- Molecule 49: 60S ribosomal protein L11-B

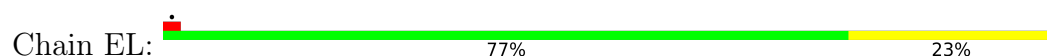




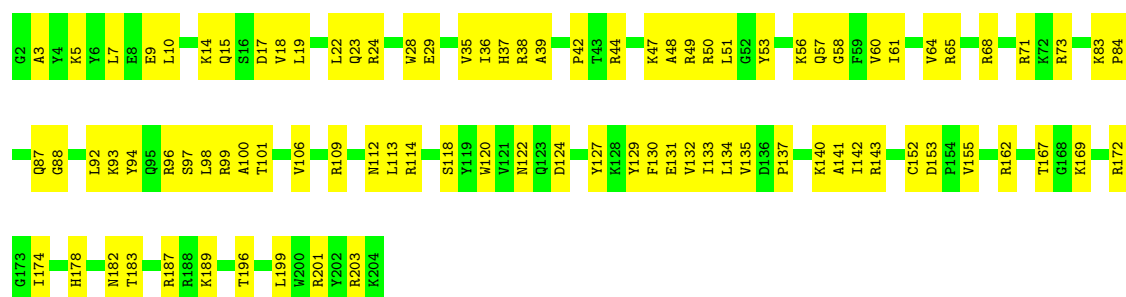
- Molecule 50: 60S ribosomal protein L13-A



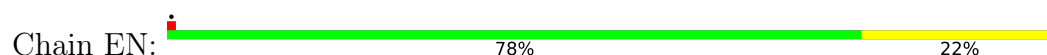
- Molecule 51: 60S ribosomal protein L14-A

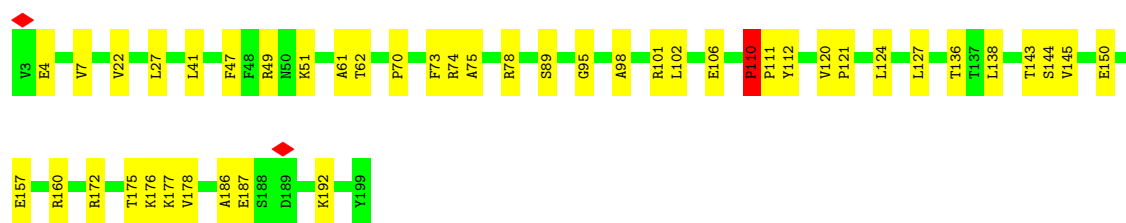


- Molecule 52: 60S ribosomal protein L15-A

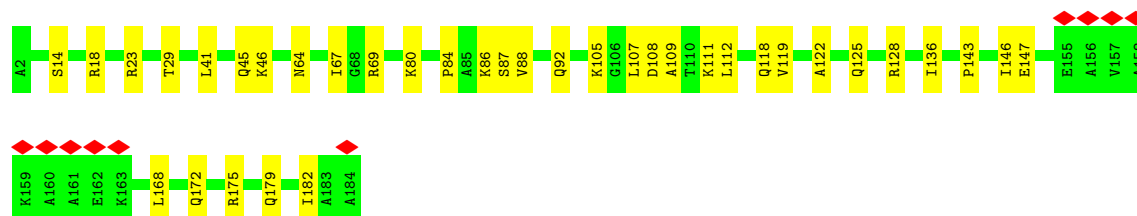
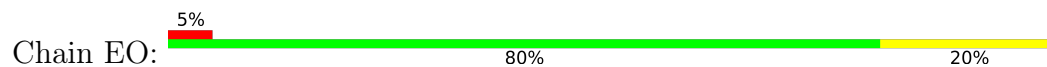


- Molecule 53: 60S ribosomal protein L16-A

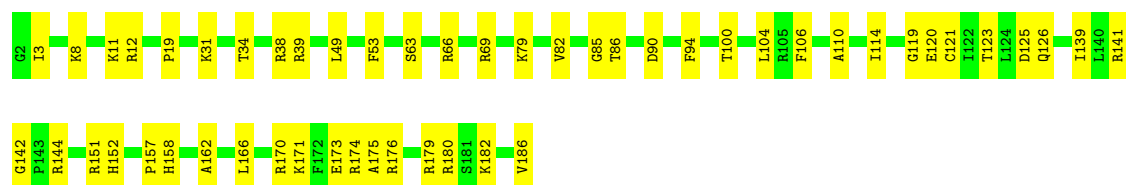




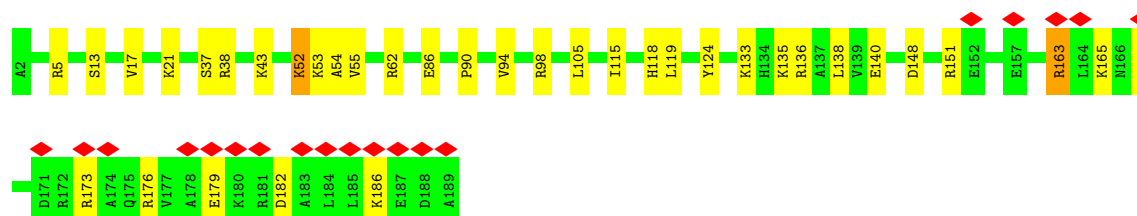
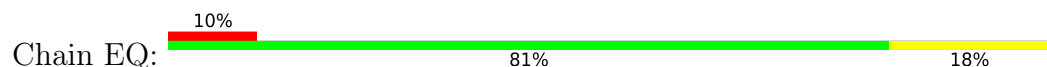
- Molecule 54: 60S ribosomal protein L17-A



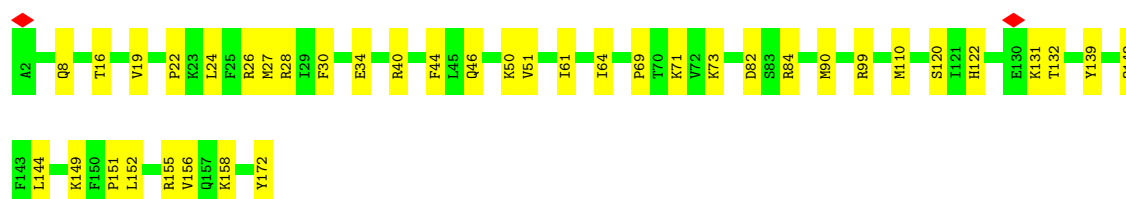
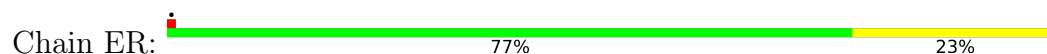
- Molecule 55: 60S ribosomal protein L18-A



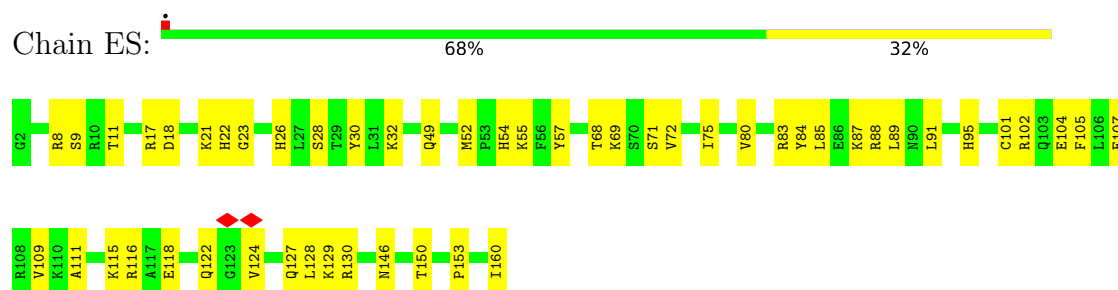
- Molecule 56: 60S ribosomal protein L19-A



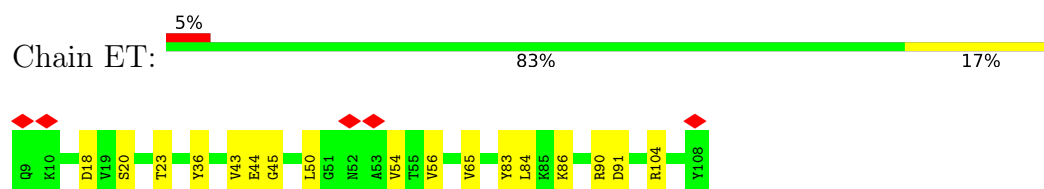
- Molecule 57: 60S ribosomal protein L20-A



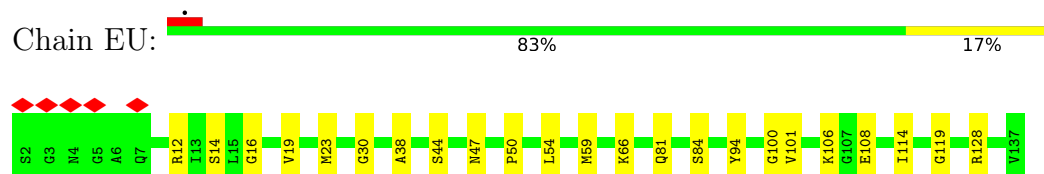
- Molecule 58: 60S ribosomal protein L21-A



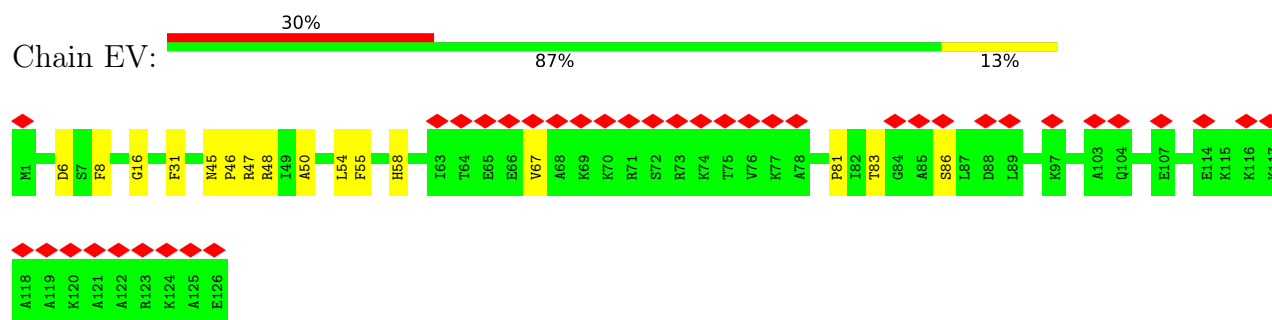
- Molecule 59: 60S ribosomal protein L22-A



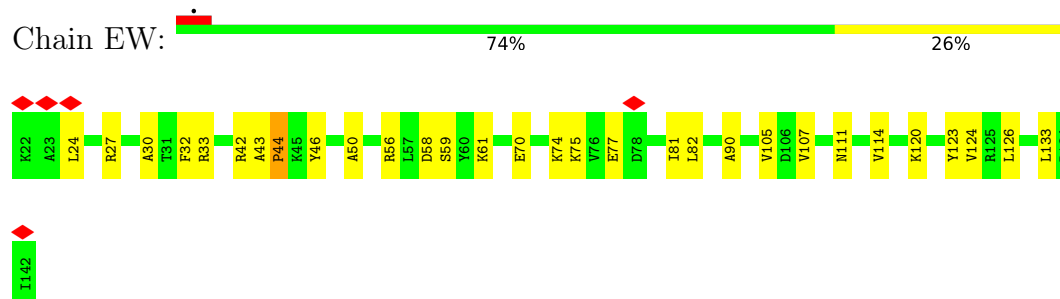
- Molecule 60: 60S ribosomal protein L23-A



- Molecule 61: 60S ribosomal protein L24-A



- Molecule 62: 60S ribosomal protein L25



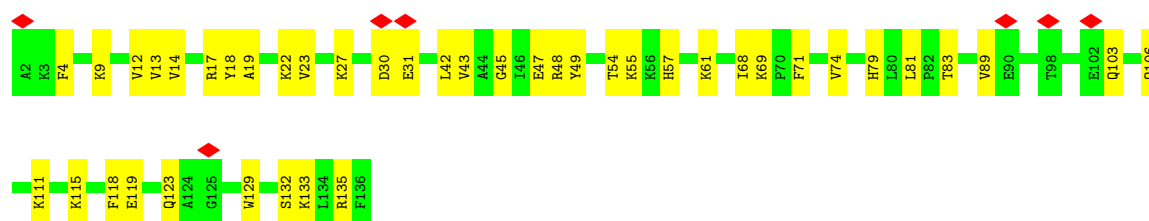
- Molecule 63: 60S ribosomal protein L26-A

Chain EX:  77% 23%



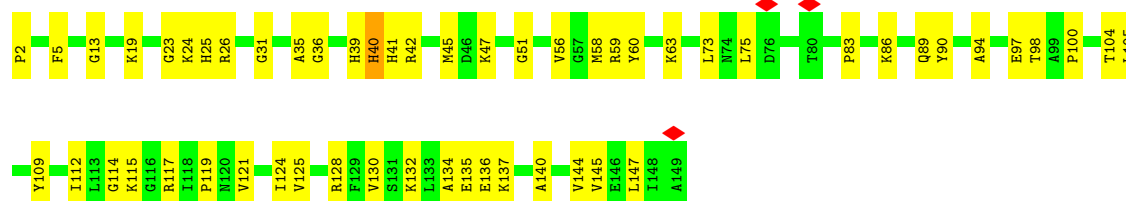
- Molecule 64: 60S ribosomal protein L27-A

Chain EY:  5% 69% 31%



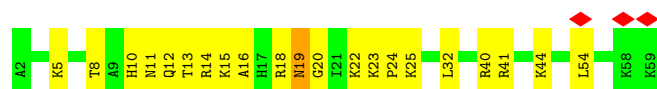
- Molecule 65: 60S ribosomal protein L28

Chain EZ:  63% 36%



- Molecule 66: 60S ribosomal protein L29

Chain Ea:  5% 64% 34%



- Molecule 67: 60S ribosomal protein L30

Chain Eb:  72% 28%



- Molecule 68: 60S ribosomal protein L31-A

Chain Ec:  10% 80% 20%



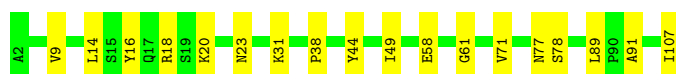
- Molecule 69: 60S ribosomal protein L32

Chain Ed:  86% 14%



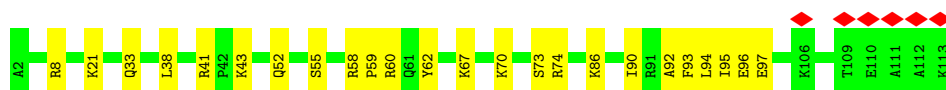
- Molecule 70: 60S ribosomal protein L33-A

Chain Ee:  83% 17%



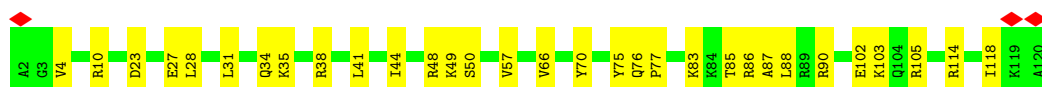
- Molecule 71: 60S ribosomal protein L34-A

Chain Ef:  5% 79% 21%



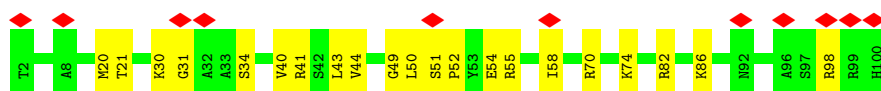
- Molecule 72: 60S ribosomal protein L35-A

Chain Eg:  74% 26%



- Molecule 73: 60S ribosomal protein L36-A

Chain Eh:  11% 79% 21%



- Molecule 74: 60S ribosomal protein L37-A

Chain Ei:  76% 24%

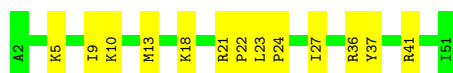
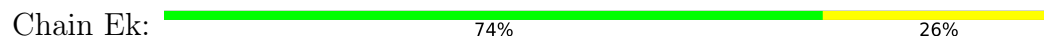


- Molecule 75: 60S ribosomal protein L38

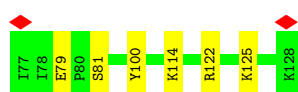
Chain Ej:  71% 29%



- Molecule 76: 60S ribosomal protein L39



- Molecule 77: 60S ribosomal protein L40-A



- Molecule 78: 60S ribosomal protein L41-A



- Molecule 79: 60S ribosomal protein L42-A



- Molecule 80: 60S ribosomal protein L43-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95228	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 ($e^-/\text{\AA}^2$)	44	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	7.114	Depositor
Minimum map value	-3.966	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.134	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.57	27/42166 (0.1%)	0.36	3/65701 (0.0%)
2	3	0.26	0/3746	0.33	0/5832
3	4	0.17	0/2883	0.28	0/4491
4	5	0.23	6/75723 (0.0%)	0.32	0/118057
5	6	0.14	0/1810	0.30	0/2821
6	7	0.13	0/1836	0.25	0/2859
7	DA	0.17	0/1644	0.42	0/2249
8	DB	0.21	0/1823	0.54	1/2447 (0.0%)
9	DC	0.67	8/1656 (0.5%)	0.73	7/2251 (0.3%)
10	DD	0.14	0/1754	0.39	0/2361
11	DE	0.14	0/2097	0.37	0/2823
12	DF	0.18	0/1625	0.46	0/2197
13	DG	0.13	0/1839	0.36	0/2460
14	DH	0.17	0/1498	0.48	0/2019
15	DI	0.13	0/1501	0.38	0/2006
16	DJ	0.15	0/1504	0.43	0/2016
17	DK	0.14	0/769	0.40	0/1039
18	DL	0.16	0/1185	0.35	0/1598
19	DM	0.15	0/883	0.56	0/1199
20	DN	0.17	0/1215	0.42	0/1638
21	DO	0.20	0/937	0.44	0/1261
22	DP	0.15	0/936	0.40	0/1259
23	DQ	0.16	0/1125	0.48	0/1510
24	DR	0.18	0/957	0.47	0/1283
25	DS	0.14	0/1211	0.43	0/1628
26	DT	0.16	0/1130	0.45	0/1517
27	DU	0.15	0/807	0.38	0/1091
28	DV	0.17	0/682	0.39	0/921
29	DW	0.18	0/1038	0.40	0/1395
30	DX	0.18	0/1139	0.46	0/1518
31	DY	0.13	0/1087	0.32	0/1449
32	DZ	0.17	0/661	0.47	0/888

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Da	0.20	0/782	0.57	0/1047
34	Db	0.14	0/620	0.41	0/838
35	Dc	0.16	0/493	0.37	0/663
36	Dd	0.18	0/452	0.39	0/600
37	De	0.14	0/480	0.38	0/639
38	Df	0.14	0/567	0.49	0/764
39	Dg	0.14	0/2436	0.39	1/3318 (0.0%)
40	EA	0.22	0/1933	0.45	0/2598
41	EB	0.18	0/3146	0.38	0/4228
42	EC	0.52	9/2800 (0.3%)	0.47	1/3790 (0.0%)
43	ED	0.18	0/2400	0.40	0/3239
44	EE	0.17	0/1327	0.40	0/1790
45	EF	0.19	0/1821	0.36	0/2451
46	EG	0.18	0/1836	0.44	0/2481
47	EH	1.56	1/1529 (0.1%)	0.39	1/2060 (0.0%)
48	EI	0.18	0/1801	0.36	0/2416
49	EJ	0.16	0/1371	0.50	2/1838 (0.1%)
50	EK	0.61	8/1568 (0.5%)	0.56	1/2106 (0.0%)
51	EL	0.16	0/1068	0.33	0/1438
52	EM	0.21	0/1757	0.43	0/2354
53	EN	0.19	0/1585	0.33	0/2128
54	EO	0.17	0/1439	0.36	0/1938
55	EP	0.19	0/1465	0.39	0/1965
56	EQ	0.68	2/1532 (0.1%)	0.64	2/2043 (0.1%)
57	ER	0.18	0/1473	0.37	0/1980
58	ES	0.19	0/1300	0.40	0/1743
59	ET	0.17	0/812	0.44	0/1099
60	EU	0.18	0/1018	0.35	0/1369
61	EV	0.16	0/850	0.37	1/1152 (0.1%)
62	EW	0.17	0/979	0.35	0/1321
63	EX	0.20	0/995	0.35	0/1329
64	EY	0.17	0/1118	0.39	0/1497
65	EZ	0.22	0/1204	0.47	0/1612
66	Ea	0.19	0/473	0.50	0/629
67	Eb	0.17	0/745	0.34	0/1001
68	Ec	0.16	0/890	0.33	0/1196
69	Ed	0.17	0/1038	0.37	0/1390
70	Ee	0.18	0/868	0.36	0/1168
71	Ef	0.18	0/890	0.38	0/1189
72	Eg	0.17	0/978	0.35	0/1301
73	Uh	0.18	0/772	0.40	0/1026
74	Ei	0.22	0/685	0.45	0/908
75	Ej	0.15	0/618	0.33	0/826

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Ek	0.18	0/443	0.34	0/588
77	El	0.16	0/423	0.38	0/562
78	Em	0.22	0/230	0.51	0/296
79	En	0.19	0/836	0.40	0/1104
80	Eo	0.19	0/701	0.40	0/934
All	All	0.35	61/217414 (0.0%)	0.37	20/319736 (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
8	DB	0	2
11	DE	0	1
12	DF	0	1
14	DH	0	1
23	DQ	0	1
25	DS	0	1
30	DX	0	2
32	DZ	0	1
33	Da	0	1
41	EB	0	1
46	EG	0	1
50	EK	0	1
53	EN	0	1
62	EW	0	1
66	Ea	0	1
All	All	0	17

The worst 5 of 61 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	EH	21	LYS	CD-CE	60.85	3.35	1.52
1	2	9	U	C5-C6	38.41	2.10	1.34
1	2	9	U	C2-N3	35.97	2.09	1.37
1	2	813	U	N3-C4	24.31	1.87	1.38
1	2	813	U	C2-N3	23.87	1.85	1.37

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	EQ	163	ARG	CD-NE-CZ	22.26	155.56	124.40
9	DC	210	THR	N-CA-C	-13.43	97.36	113.88
56	EQ	163	ARG	CG-CD-NE	10.21	134.46	112.00
9	DC	207	LEU	CB-CA-C	-9.68	96.42	112.00
9	DC	207	LEU	N-CA-C	9.16	123.95	109.39

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	DB	211	HIS	Peptide
8	DB	81	PHE	Peptide
11	DE	42	LEU	Peptide
12	DF	79	ASN	Peptide
14	DH	64	VAL	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	37699	0	18969	959	0
2	3	3353	0	1695	70	0
3	4	2579	0	1304	43	0
4	5	67650	0	33997	1100	0
5	6	1620	0	822	25	0
6	7	1644	0	836	33	0
7	DA	1603	0	1610	58	0
8	DB	1798	0	1890	104	0
9	DC	1626	0	1715	59	0
10	DD	1729	0	1812	45	0
11	DE	2056	0	2140	48	0
12	DF	1605	0	1668	77	0
13	DG	1815	0	1894	54	0
14	DH	1473	0	1555	36	0
15	DI	1476	0	1501	39	0
16	DJ	1479	0	1556	43	0
17	DK	752	0	719	24	0
18	DL	1159	0	1225	20	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	DM	875	0	878	30	0
20	DN	1192	0	1255	28	0
21	DO	926	0	950	59	0
22	DP	916	0	941	21	0
23	DQ	1105	0	1166	53	0
24	DR	948	0	990	44	0
25	DS	1192	0	1222	42	0
26	DT	1112	0	1124	57	0
27	DU	797	0	863	33	0
28	DV	673	0	662	32	0
29	DW	1021	0	1060	38	0
30	DX	1121	0	1195	41	0
31	DY	1073	0	1132	23	0
32	DZ	651	0	682	31	0
33	Da	769	0	818	49	0
34	Db	610	0	633	22	0
35	Dc	491	0	524	20	0
36	Dd	442	0	428	24	0
37	De	472	0	521	14	0
38	Df	556	0	546	22	0
39	Dg	2383	0	2332	89	0
40	EA	1899	0	1957	83	0
41	EB	3075	0	3142	72	0
42	EC	2748	0	2859	64	0
43	ED	2351	0	2294	72	0
44	EE	1305	0	1370	25	0
45	EF	1784	0	1862	35	0
46	EG	1804	0	1877	62	0
47	EH	1508	0	1572	43	0
48	EI	1764	0	1804	23	0
49	EJ	1350	0	1381	37	0
50	EK	1543	0	1608	70	0
51	EL	1053	0	1149	28	0
52	EM	1720	0	1779	88	0
53	EN	1555	0	1659	27	0
54	EO	1416	0	1433	24	0
55	EP	1441	0	1543	52	0
56	EQ	1515	0	1606	58	0
57	ER	1437	0	1475	36	0
58	ES	1276	0	1323	42	0
59	ET	796	0	812	10	0
60	EU	1003	0	1048	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	EV	836	0	709	8	0
62	EW	964	0	1025	28	0
63	EX	984	0	1075	23	0
64	EY	1092	0	1155	39	0
65	EZ	1173	0	1215	59	0
66	Ea	462	0	491	20	0
67	Eb	737	0	792	23	0
68	Ec	876	0	912	13	0
69	Ed	1017	0	1081	13	0
70	Ee	850	0	880	14	0
71	Ef	880	0	942	21	0
72	Eg	969	0	1078	25	0
73	Eh	766	0	844	23	0
74	Ei	670	0	673	20	0
75	Ej	612	0	682	16	0
76	Ek	436	0	475	13	0
77	El	417	0	455	7	0
78	Em	229	0	273	8	0
79	En	824	0	889	29	0
80	Eo	694	0	735	24	0
81	2	84	0	0	0	0
81	DF	1	0	0	0	0
81	DN	1	0	0	0	0
82	Dd	1	0	0	0	0
82	Df	1	0	0	0	0
82	Ef	1	0	0	0	0
82	Ei	1	0	0	0	0
82	El	1	0	0	0	0
82	En	1	0	0	0	0
82	Eo	1	0	0	0	0
All	All	202365	0	148764	4068	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 12.

The worst 5 of 4068 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)
1:2:813:U:C4	1:2:813:U:C5	1.85	1.65
1:2:1139:A:C5	1:2:1139:A:C6	1.85	1.64
1:2:1318:G:N3	1:2:1318:G:C2	1.68	1.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1139:A:C2	1:2:1139:A:N1	1.72	1.56
1:2:1139:A:C2	1:2:1139:A:N3	1.69	1.56

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	
7	DA	204/206 (99%)	187 (92%)	17 (8%)	0	100	100
8	DB	222/255 (87%)	196 (88%)	25 (11%)	1 (0%)	24	43
9	DC	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
10	DD	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
11	DE	256/258 (99%)	250 (98%)	5 (2%)	1 (0%)	30	49
12	DF	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
13	DG	226/228 (99%)	216 (96%)	9 (4%)	1 (0%)	30	49
14	DH	182/184 (99%)	168 (92%)	14 (8%)	0	100	100
15	DI	183/200 (92%)	174 (95%)	8 (4%)	1 (0%)	24	43
16	DJ	182/184 (99%)	170 (93%)	12 (7%)	0	100	100
17	DK	90/92 (98%)	87 (97%)	3 (3%)	0	100	100
18	DL	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
19	DM	119/121 (98%)	94 (79%)	25 (21%)	0	100	100
20	DN	148/150 (99%)	142 (96%)	6 (4%)	0	100	100
21	DO	125/127 (98%)	117 (94%)	8 (6%)	0	100	100
22	DP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
23	DQ	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	18	34
24	DR	117/136 (86%)	113 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	DS	143/145 (99%)	136 (95%)	6 (4%)	1 (1%)	18	34
26	DT	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
27	DU	98/100 (98%)	98 (100%)	0	0	100	100
28	DV	85/87 (98%)	77 (91%)	7 (8%)	1 (1%)	10	20
29	DW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
30	DX	142/144 (99%)	129 (91%)	12 (8%)	1 (1%)	18	34
31	DY	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
32	DZ	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
33	Da	95/97 (98%)	81 (85%)	12 (13%)	2 (2%)	5	9
34	Db	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
35	Dc	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
36	Dd	51/53 (96%)	51 (100%)	0	0	100	100
37	De	58/60 (97%)	56 (97%)	2 (3%)	0	100	100
38	Df	71/73 (97%)	59 (83%)	12 (17%)	0	100	100
39	Dg	310/312 (99%)	303 (98%)	7 (2%)	0	100	100
40	EA	249/251 (99%)	236 (95%)	12 (5%)	1 (0%)	30	49
41	EB	384/386 (100%)	366 (95%)	17 (4%)	1 (0%)	36	55
42	EC	359/361 (99%)	342 (95%)	16 (4%)	1 (0%)	36	55
43	ED	292/294 (99%)	280 (96%)	11 (4%)	1 (0%)	36	55
44	EE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
45	EF	220/222 (99%)	217 (99%)	3 (1%)	0	100	100
46	EG	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
47	EH	189/191 (99%)	184 (97%)	5 (3%)	0	100	100
48	EI	216/218 (99%)	213 (99%)	3 (1%)	0	100	100
49	EJ	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
50	EK	191/193 (99%)	173 (91%)	16 (8%)	2 (1%)	12	24
51	EL	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
52	EM	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
53	EN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	12	24
54	EO	181/183 (99%)	174 (96%)	7 (4%)	0	100	100
55	EP	183/185 (99%)	178 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	EQ	186/188 (99%)	184 (99%)	1 (0%)	1 (0%)	24	43
57	ER	169/171 (99%)	166 (98%)	3 (2%)	0	100	100
58	ES	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
59	ET	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
60	EU	134/136 (98%)	133 (99%)	1 (1%)	0	100	100
61	EV	124/126 (98%)	119 (96%)	3 (2%)	2 (2%)	7	14
62	EW	119/121 (98%)	115 (97%)	3 (2%)	1 (1%)	16	31
63	EX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
64	EY	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
65	EZ	146/148 (99%)	135 (92%)	10 (7%)	1 (1%)	18	34
66	Ea	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
67	Eb	94/96 (98%)	94 (100%)	0	0	100	100
68	Ec	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
69	Ed	125/127 (98%)	123 (98%)	2 (2%)	0	100	100
70	Ee	104/106 (98%)	104 (100%)	0	0	100	100
71	Ef	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
72	Eg	117/119 (98%)	116 (99%)	1 (1%)	0	100	100
73	Eh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
74	Ei	83/85 (98%)	83 (100%)	0	0	100	100
75	Ej	75/77 (97%)	75 (100%)	0	0	100	100
76	Ek	48/50 (96%)	48 (100%)	0	0	100	100
77	El	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
78	Em	23/25 (92%)	23 (100%)	0	0	100	100
79	En	101/103 (98%)	98 (97%)	3 (3%)	0	100	100
80	Eo	89/91 (98%)	88 (99%)	1 (1%)	0	100	100
All	All	10984/11206 (98%)	10510 (96%)	451 (4%)	23 (0%)	44	63

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	DI	10	LYS
33	Da	84	VAL
41	EB	128	LYS

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Mol	Chain	Res	Type
53	EN	111[A]	PRO
50	EK	63	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	DA	170/173 (98%)	170 (100%)	0	100	100
8	DB	200/224 (89%)	200 (100%)	0	100	100
9	DC	175/175 (100%)	172 (98%)	3 (2%)	53	78
10	DD	182/182 (100%)	182 (100%)	0	100	100
11	DE	220/220 (100%)	220 (100%)	0	100	100
12	DF	172/173 (99%)	172 (100%)	0	100	100
13	DG	189/195 (97%)	189 (100%)	0	100	100
14	DH	163/165 (99%)	163 (100%)	0	100	100
15	DI	148/161 (92%)	148 (100%)	0	100	100
16	DJ	156/157 (99%)	156 (100%)	0	100	100
17	DK	77/85 (91%)	77 (100%)	0	100	100
18	DL	129/129 (100%)	128 (99%)	1 (1%)	73	88
19	DM	88/98 (90%)	88 (100%)	0	100	100
20	DN	127/127 (100%)	127 (100%)	0	100	100
21	DO	91/96 (95%)	91 (100%)	0	100	100
22	DP	95/98 (97%)	95 (100%)	0	100	100
23	DQ	117/117 (100%)	117 (100%)	0	100	100
24	DR	101/124 (82%)	101 (100%)	0	100	100
25	DS	128/128 (100%)	128 (100%)	0	100	100
26	DT	115/115 (100%)	115 (100%)	0	100	100
27	DU	93/93 (100%)	93 (100%)	0	100	100
28	DV	71/74 (96%)	71 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	DW	110/110 (100%)	110 (100%)	0	100	100
30	DX	119/119 (100%)	119 (100%)	0	100	100
31	DY	112/112 (100%)	112 (100%)	0	100	100
32	DZ	67/73 (92%)	67 (100%)	0	100	100
33	Da	83/83 (100%)	83 (100%)	0	100	100
34	Db	70/70 (100%)	70 (100%)	0	100	100
35	Dc	55/56 (98%)	55 (100%)	0	100	100
36	Dd	47/47 (100%)	47 (100%)	0	100	100
37	De	50/51 (98%)	50 (100%)	0	100	100
38	Df	56/64 (88%)	56 (100%)	0	100	100
39	Dg	250/257 (97%)	250 (100%)	0	100	100
40	EA	190/193 (98%)	190 (100%)	0	100	100
41	EB	319/322 (99%)	318 (100%)	1 (0%)	86	94
42	EC	288/288 (100%)	285 (99%)	3 (1%)	68	86
43	ED	241/243 (99%)	241 (100%)	0	100	100
44	EE	138/155 (89%)	138 (100%)	0	100	100
45	EF	186/186 (100%)	186 (100%)	0	100	100
46	EG	187/191 (98%)	187 (100%)	0	100	100
47	EH	168/171 (98%)	168 (100%)	0	100	100
48	EI	185/185 (100%)	185 (100%)	0	100	100
49	EJ	146/147 (99%)	146 (100%)	0	100	100
50	EK	154/154 (100%)	154 (100%)	0	100	100
51	EL	107/107 (100%)	107 (100%)	0	100	100
52	EM	175/175 (100%)	175 (100%)	0	100	100
53	EN	160/160 (100%)	160 (100%)	0	100	100
54	EO	138/145 (95%)	138 (100%)	0	100	100
55	EP	150/150 (100%)	150 (100%)	0	100	100
56	EQ	152/153 (99%)	152 (100%)	0	100	100
57	ER	155/155 (100%)	155 (100%)	0	100	100
58	ES	136/136 (100%)	136 (100%)	0	100	100
59	ET	87/87 (100%)	87 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
60	EU	104/104 (100%)	104 (100%)	0	100	100
61	EV	56/107 (52%)	56 (100%)	0	100	100
62	EW	104/105 (99%)	104 (100%)	0	100	100
63	EX	108/108 (100%)	108 (100%)	0	100	100
64	EY	115/115 (100%)	115 (100%)	0	100	100
65	EZ	118/118 (100%)	118 (100%)	0	100	100
66	Ea	46/46 (100%)	46 (100%)	0	100	100
67	Eb	81/81 (100%)	81 (100%)	0	100	100
68	Ec	92/96 (96%)	92 (100%)	0	100	100
69	Ed	108/109 (99%)	108 (100%)	0	100	100
70	Ee	90/90 (100%)	90 (100%)	0	100	100
71	Ef	95/95 (100%)	95 (100%)	0	100	100
72	Eg	104/104 (100%)	104 (100%)	0	100	100
73	Eh	80/81 (99%)	80 (100%)	0	100	100
74	Ei	69/69 (100%)	69 (100%)	0	100	100
75	Ej	68/68 (100%)	68 (100%)	0	100	100
76	Ek	45/45 (100%)	45 (100%)	0	100	100
77	El	47/47 (100%)	47 (100%)	0	100	100
78	Em	22/23 (96%)	22 (100%)	0	100	100
79	En	87/88 (99%)	87 (100%)	0	100	100
80	Eo	71/71 (100%)	71 (100%)	0	100	100
All	All	9198/9424 (98%)	9190 (100%)	8 (0%)	87	96

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
42	EC	106	TRP
42	EC	105	THR
41	EB	104	THR
18	DL	18	HIS
42	EC	104	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
52	EM	182	ASN
61	EV	59	HIS
54	EO	54	HIS
56	EQ	134	HIS
66	Ea	6	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1765/1800 (98%)	468 (26%)	46 (2%)
2	3	157/158 (99%)	27 (17%)	1 (0%)
3	4	120/121 (99%)	15 (12%)	1 (0%)
4	5	3159/3396 (93%)	581 (18%)	31 (0%)
5	6	75/76 (98%)	34 (45%)	3 (4%)
6	7	76/77 (98%)	13 (17%)	1 (1%)
All	All	5352/5628 (95%)	1138 (21%)	83 (1%)

5 of 1138 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	12	U
1	2	13	C
1	2	14	C

5 of 83 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	1356	A
4	5	3122	U
4	5	1816	U
4	5	2536	A
4	5	3276	U

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 93 ligands modelled in this entry, 93 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 [i](#)

There are no chain breaks in this entry.

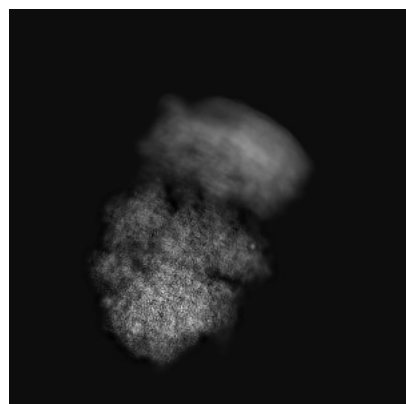
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14979. These allow visual inspection of the internal detail of the map and identification of artifacts.

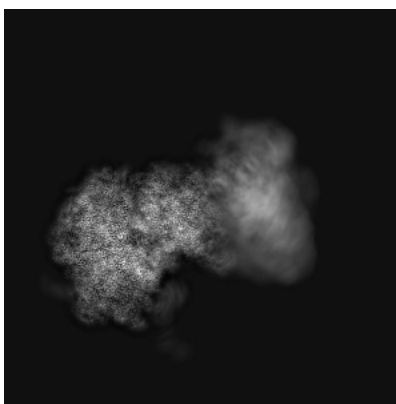
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

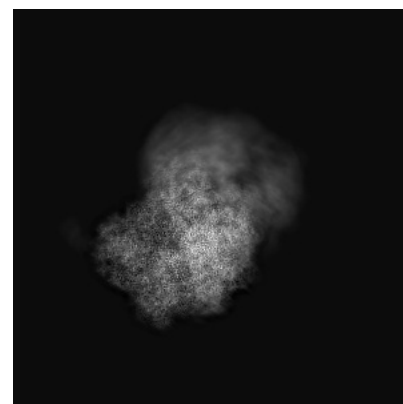
6.1.1 Primary map



X

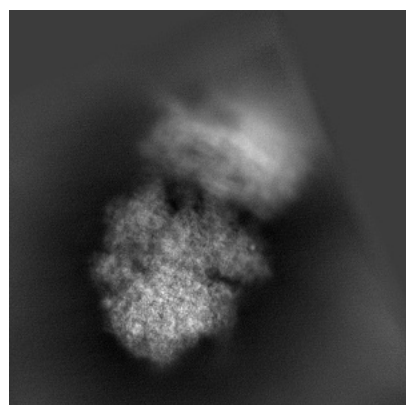


Y

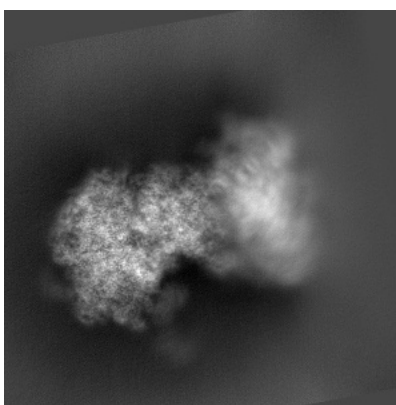


Z

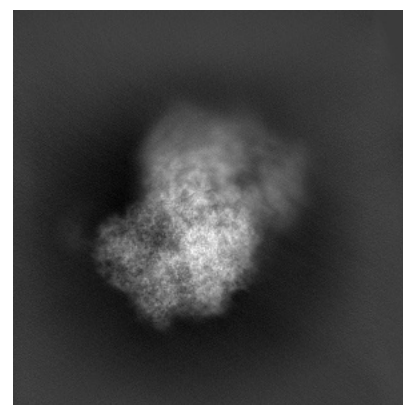
6.1.2 Raw map



X



Y

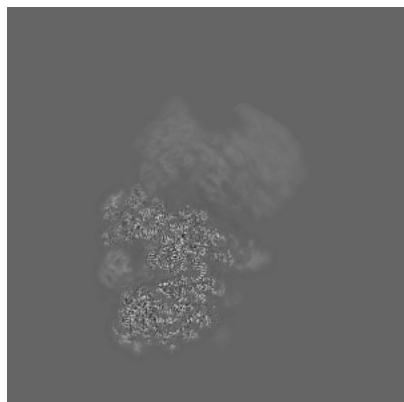


Z

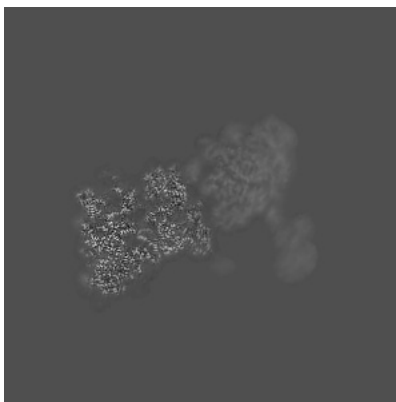
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

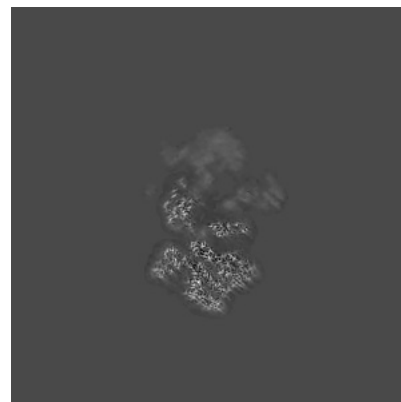
6.2.1 Primary map



X Index: 280

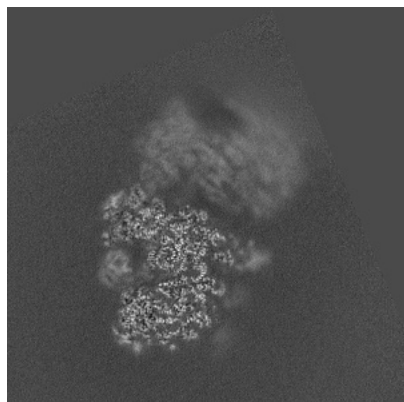


Y Index: 280

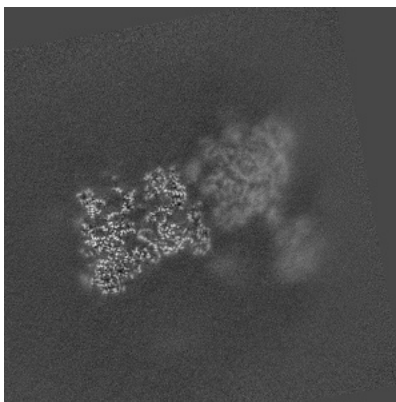


Z Index: 280

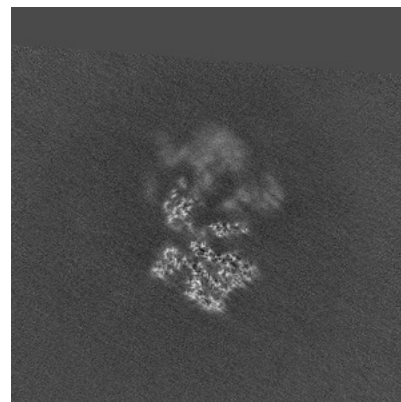
6.2.2 Raw map



X Index: 280



Y Index: 280

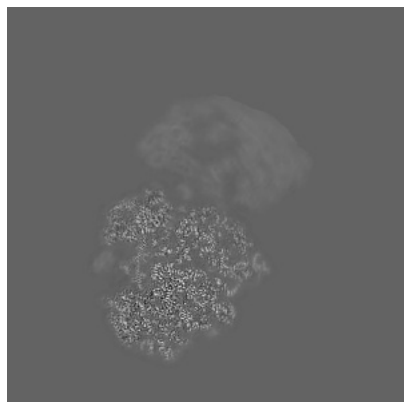


Z Index: 280

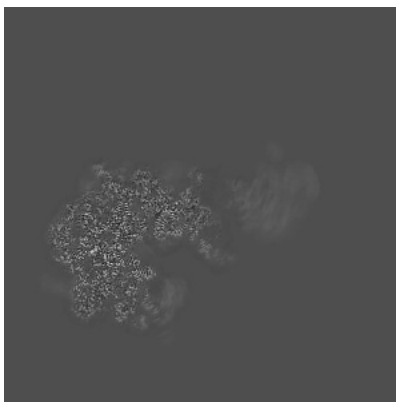
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

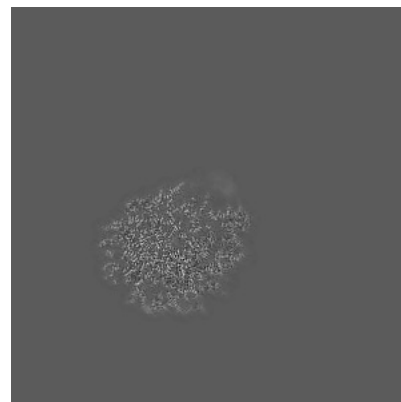
6.3.1 Primary map



X Index: 255

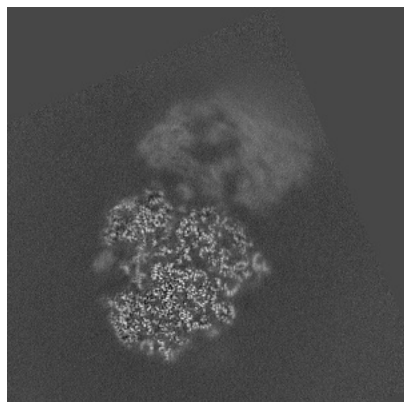


Y Index: 220

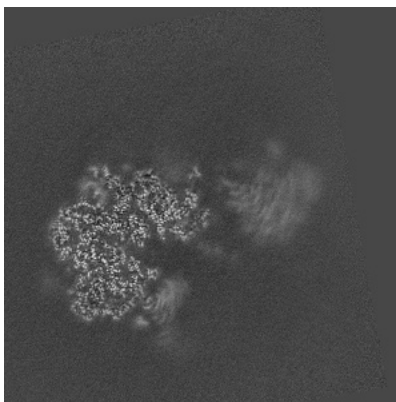


Z Index: 153

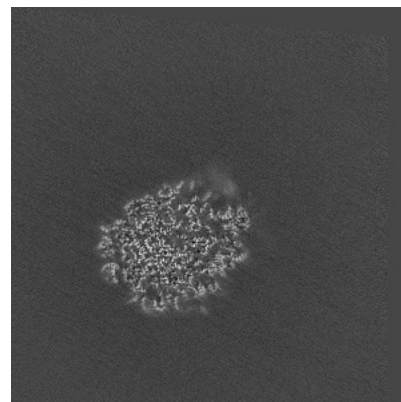
6.3.2 Raw map



X Index: 255



Y Index: 226

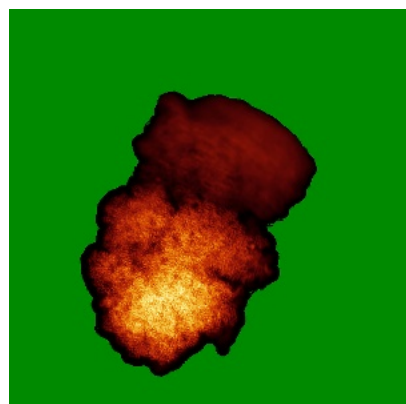


Z Index: 155

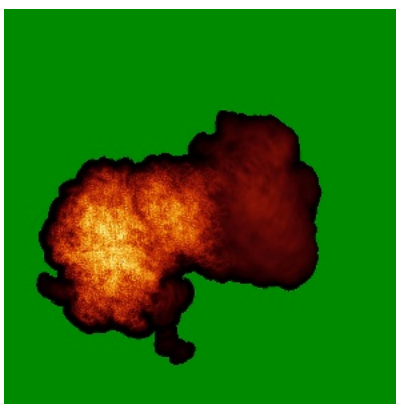
The images above show the largest variance slices of the map in three orthogonal directions.

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

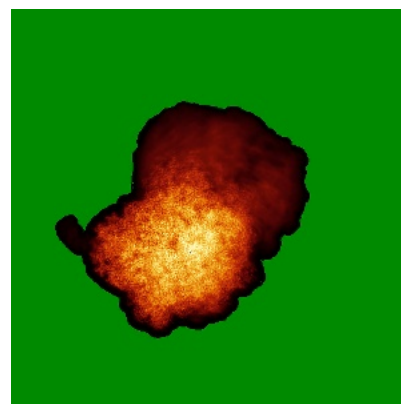
6.4.1 Primary map



X

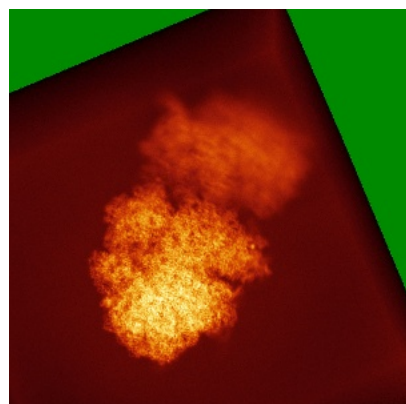


Y

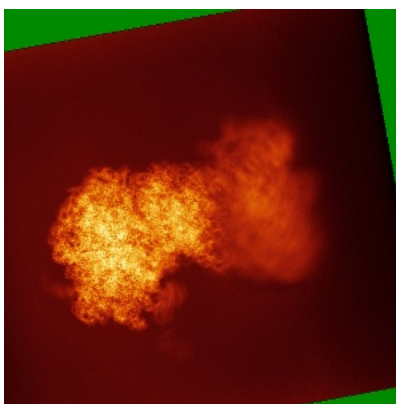


Z

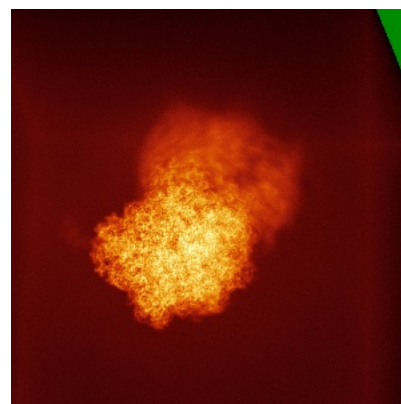
6.4.2 Raw map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

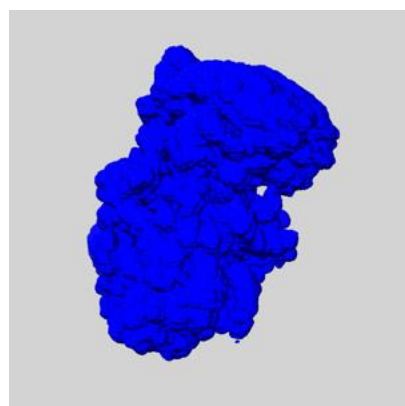
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

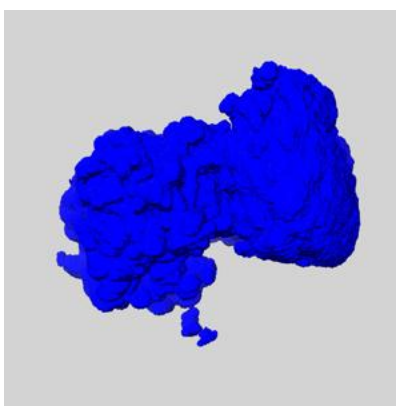
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

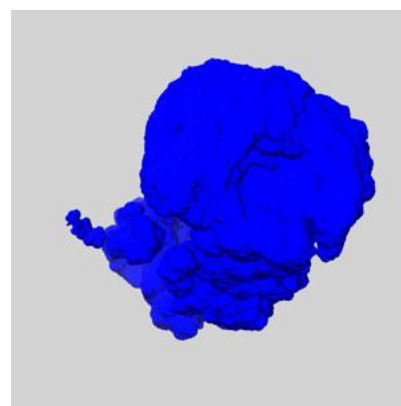
6.6.1 emd_14979_msk_1.map [i](#)



X



Y

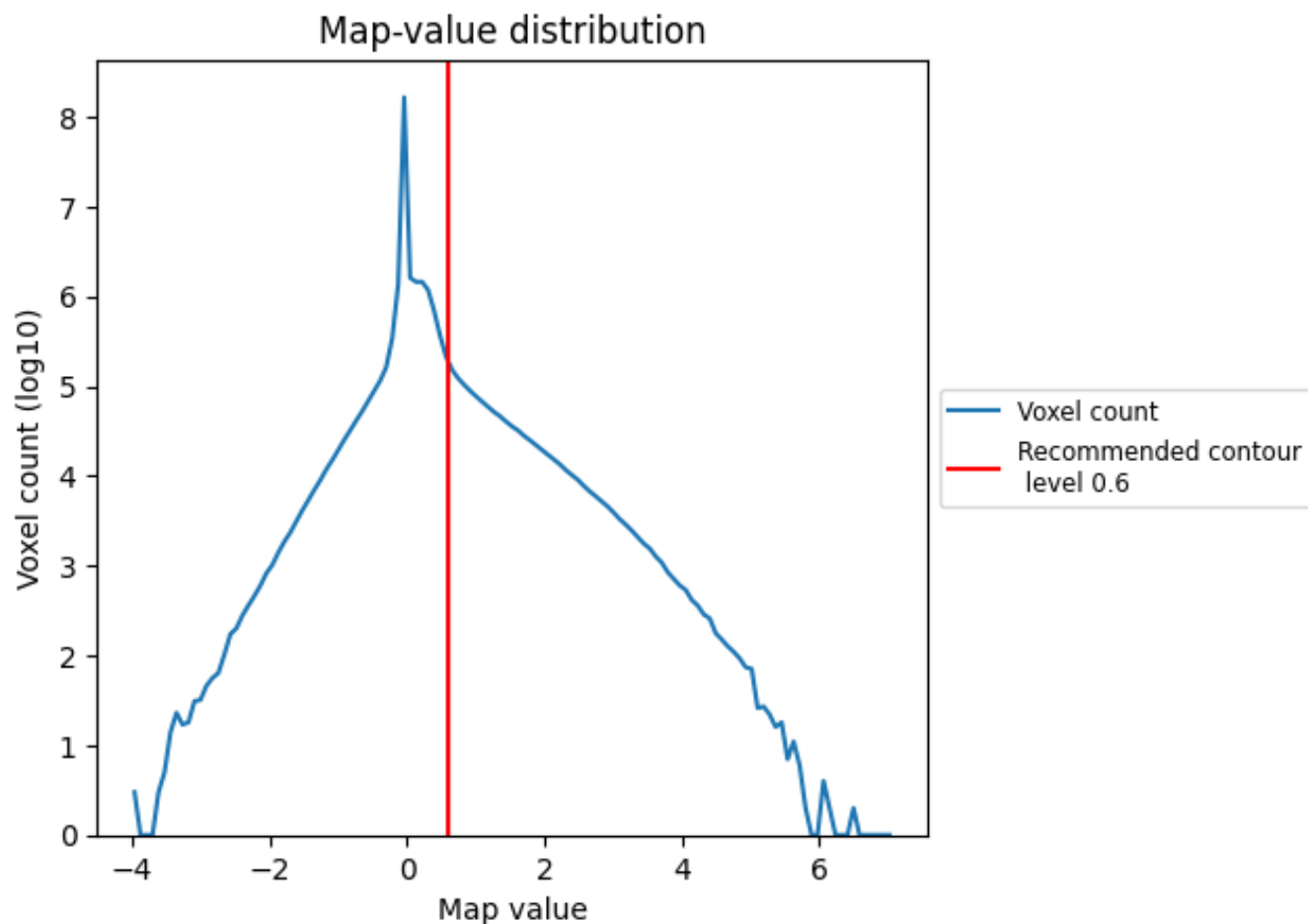


Z

7 Map analysis [i](#)

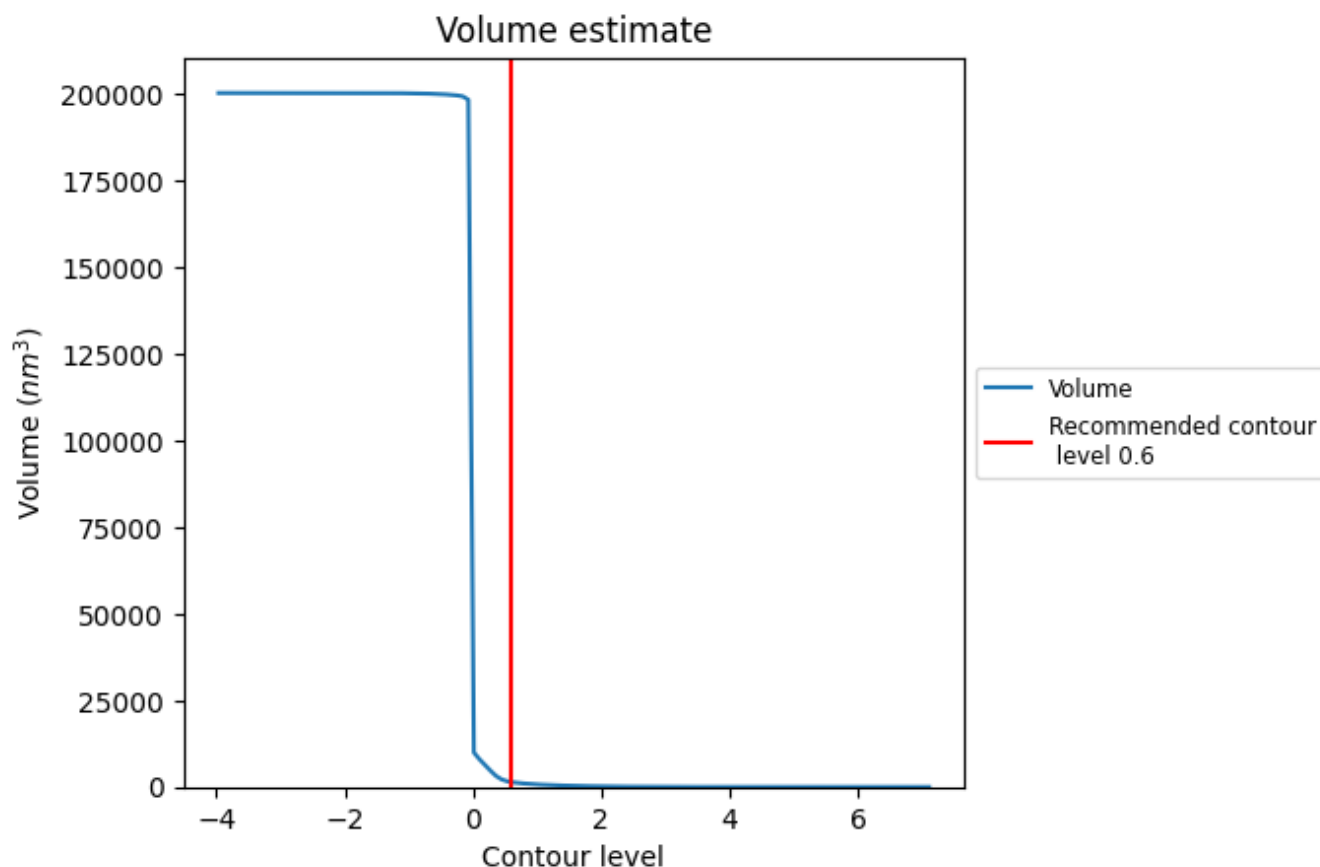
This section contains the results of statistical analysis of the map.

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.

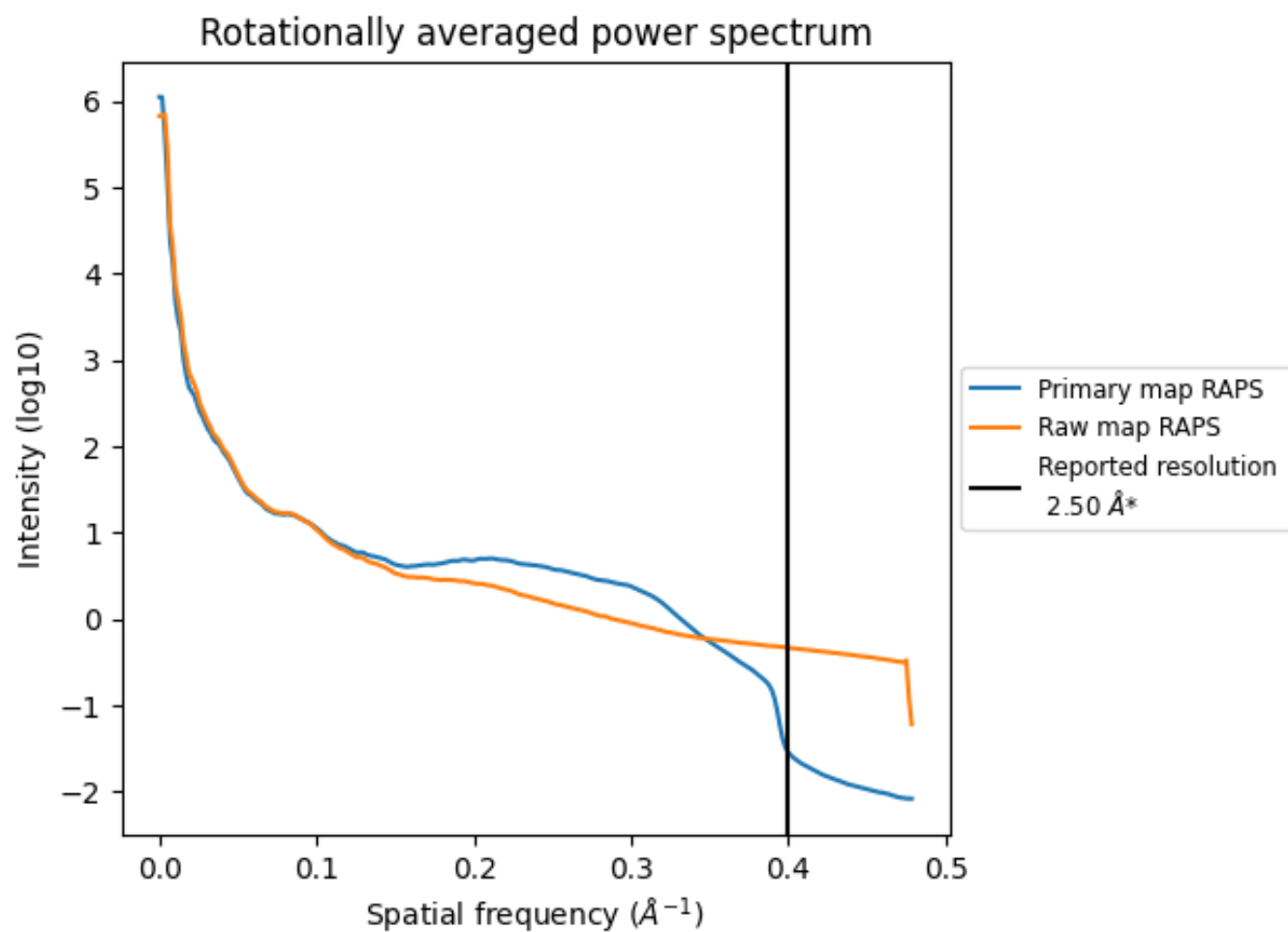
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1420 nm^3 ; this corresponds to an approximate mass of 1283 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 ⓘ

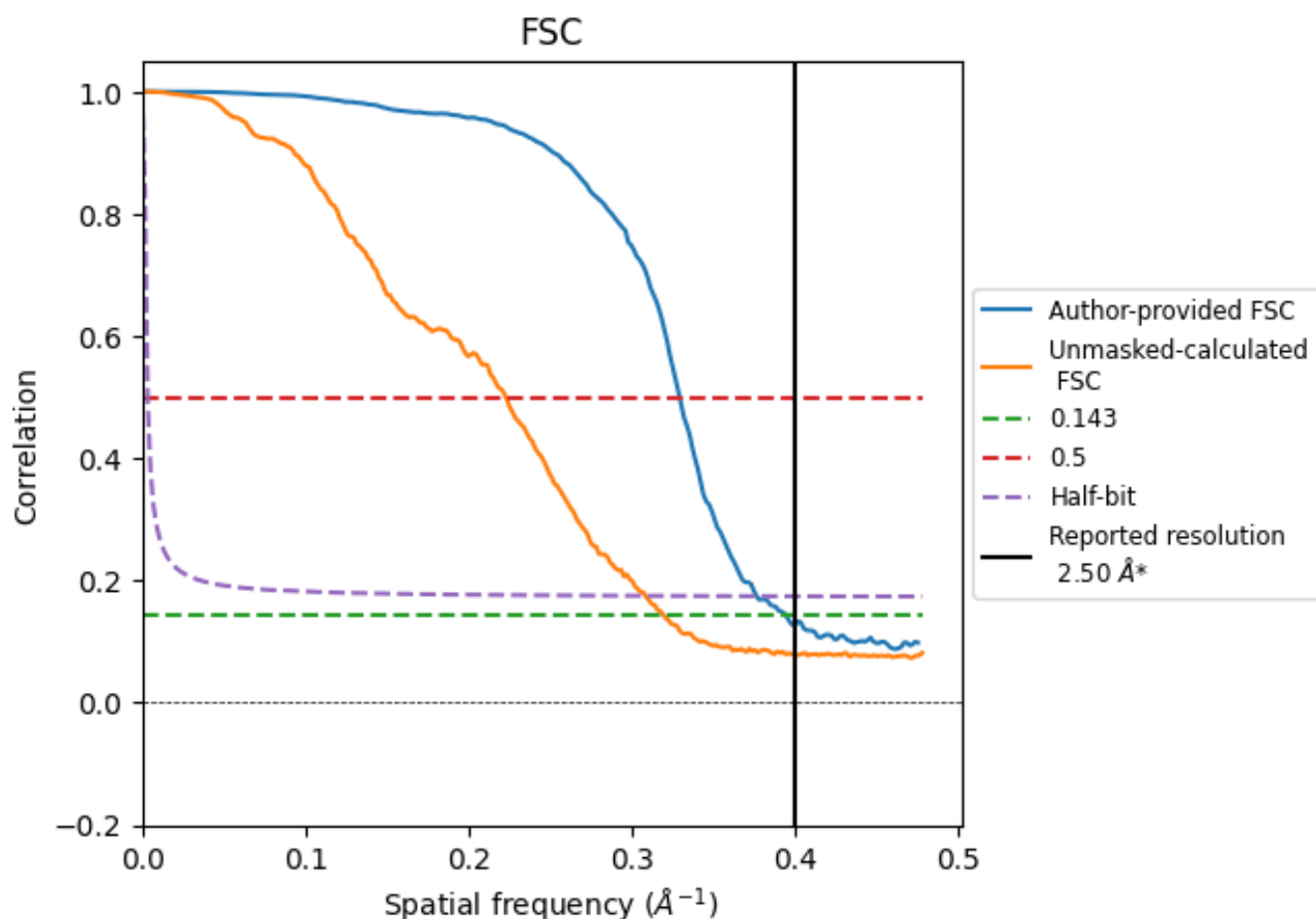


*Reported resolution corresponds to spatial frequency of $0.400 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.400 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

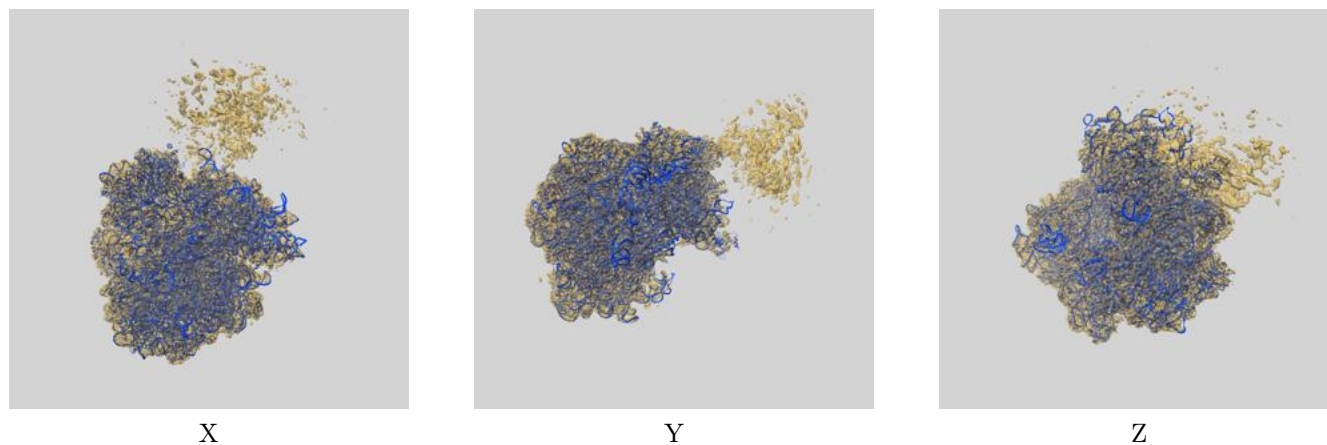
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.50	-	-
Author-provided FSC curve	2.53	3.03	2.65
Unmasked-calculated*	3.13	4.48	3.24

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.13 differs from the reported value 2.5 by more than 10 %

9 Map-model fit [i](#)

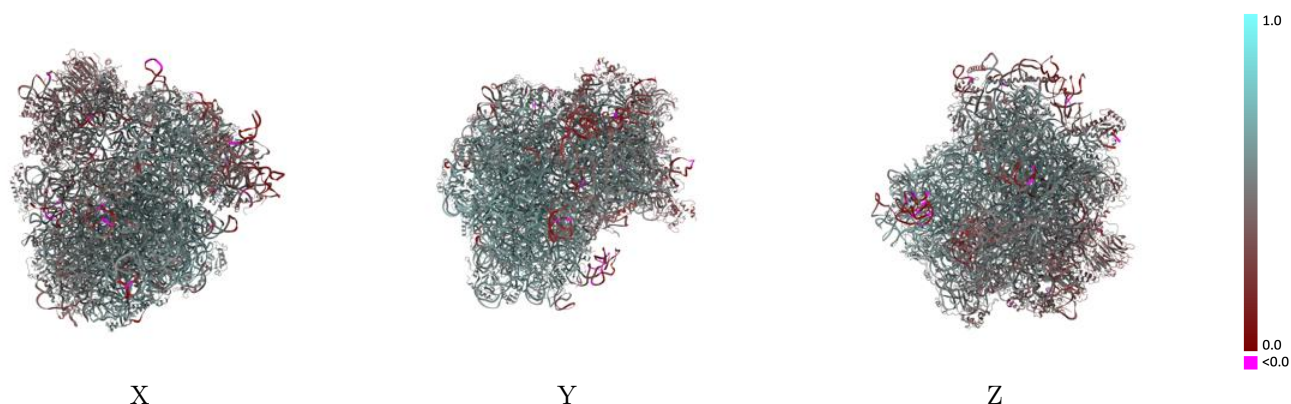
This section contains information regarding the fit between EMDB map EMD-14979 and PDB model 7ZUX. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

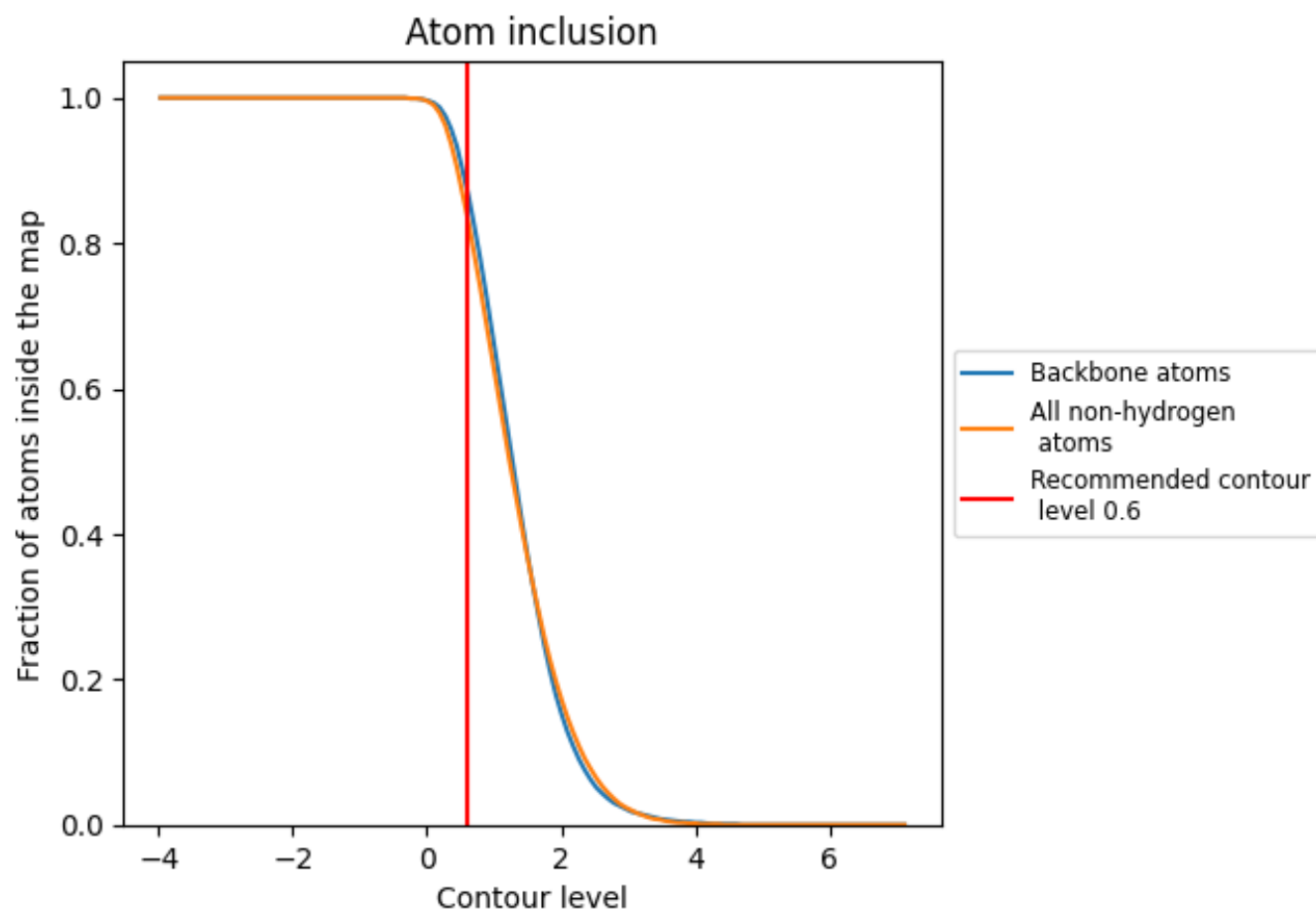


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.5160
2	 0.8300	 0.4760
3	 0.9460	 0.5700
4	 0.9480	 0.5450
5	 0.9190	 0.5550
6	 0.5590	 0.3390
7	 0.7680	 0.4430
DA	 0.7180	 0.4480
DB	 0.6980	 0.4460
DC	 0.7950	 0.5280
DD	 0.6440	 0.4700
DE	 0.7390	 0.5180
DF	 0.6210	 0.3890
DG	 0.6330	 0.4600
DH	 0.6060	 0.4450
DI	 0.7390	 0.5020
DJ	 0.6910	 0.4780
DK	 0.6570	 0.4230
DL	 0.8000	 0.5410
DM	 0.3020	 0.2890
DN	 0.8240	 0.5220
DO	 0.7800	 0.4550
DP	 0.6710	 0.4410
DQ	 0.6670	 0.4050
DR	 0.6670	 0.4240
DS	 0.6400	 0.4100
DT	 0.6690	 0.4000
DU	 0.6350	 0.4250
DV	 0.7530	 0.4890
DW	 0.8660	 0.5520
DX	 0.8390	 0.5530
DY	 0.6510	 0.4720
DZ	 0.4670	 0.3480
Da	 0.7960	 0.4710
Db	 0.7400	 0.4850



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Chain	Atom inclusion	Q-score
Dc	 0.6130	 0.4080
Dd	 0.8470	 0.4890
De	 0.6100	 0.4550
Df	 0.3680	 0.2930
Dg	 0.4940	 0.3630
EA	 0.8780	 0.5490
EB	 0.9060	 0.5940
EC	 0.8930	 0.5710
ED	 0.7700	 0.4640
EE	 0.8520	 0.5570
EF	 0.8970	 0.5830
EG	 0.7230	 0.4440
EH	 0.8430	 0.5530
EI	 0.8640	 0.5680
EJ	 0.7220	 0.4320
EK	 0.8250	 0.5070
EL	 0.8690	 0.5560
EM	 0.9060	 0.5310
EN	 0.9210	 0.6050
EO	 0.9100	 0.6130
EP	 0.9120	 0.5600
EQ	 0.8030	 0.5240
ER	 0.8940	 0.5730
ES	 0.8690	 0.5450
ET	 0.7740	 0.5140
EU	 0.8600	 0.5890
EV	 0.6850	 0.5030
EW	 0.8460	 0.5440
EX	 0.9040	 0.5800
EY	 0.7750	 0.4880
EZ	 0.8770	 0.5250
Ea	 0.8140	 0.5090
Eb	 0.8040	 0.5070
Ec	 0.8410	 0.5810
Ed	 0.9310	 0.6180
Ee	 0.9350	 0.6220
Ef	 0.8600	 0.5480
Eg	 0.8380	 0.5180
Eh	 0.7530	 0.4580
Ei	 0.9610	 0.5980
Ej	 0.7860	 0.5160
Ek	 0.9130	 0.5920

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Chain	Atom inclusion	Q-score
El	 0.8640	 0.5800
Em	 0.7400	 0.4950
En	 0.8310	 0.4960
Eo	 0.8760	 0.5450