wwPDB EM Validation Summary Report

Oct 28, 2024 – 09:30 am GMT

PDB ID	:	4UG0
EMDB ID	:	EMD-2938
Title	:	STRUCTURE OF THE HUMAN 80S RIBOSOME
Authors	:	Khatter, H.; Myasnikov, A.G.; Natchiar, S.K.; Klaholz, B.P.
Deposited on	:	2015-03-20
Resolution	:	3.60 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:

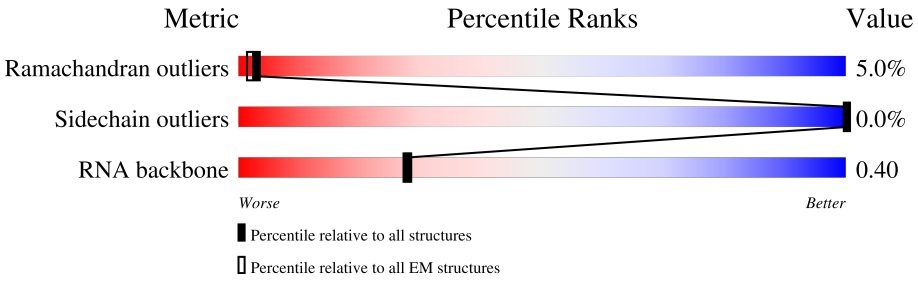
EMDB validation analysis	:	0.0.1.dev113
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 3.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	L5	5070	48% 26% 26%
2	L7	121	82% 17%
3	L8	157	71% 29%
4	LA	257	90% 6%
5	LB	403	96%
6	LC	427	80% 6% 14%
7	LD	297	95%
8	LE	288	77% 7% 16%

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Mol	Chain	Length	Quality of chain
9	LF	248	89% 9%
10	LG	266	85% 6% 9%
11	LH	192	95%
12	LI	214	96%
13	LJ	178	94%
14	LL	211	94% 5%
15	LM	215	62% 35%
16	LN	204	98%
17	LO	203	97%
18	LP	184	80% 17%
19	LQ	188	97%
20	LR	196	95% 5%
21	LS	176	93% 6%
22	LT	160	96%
23	LU	128	78% 21%
24	LV	140	89% 6%
25	LW	157	76% 21%
26	LX	156	76% 23%
27	LY	145	90% 8%
28	LZ	136	97%
29	La	148	96%
30	Lb	159	46% 53%
31	Lc	115	80% 5% 15%
32	Ld	125	82% 14%
33	Le	135	91% 5%

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Mol	Chain	Length	Quality of chain
34	Lf	110	95% 5%
35	Lg	117	97%
36	Lh	123	98%
37	Li	105	93%
38	Lj	97	81% 7% 11%
39	Lk	70	91% 7%
40	Ll	51	96%
41	Lm	128	39% 59%
42	Ln	25	96%
43	Lo	106	96%
44	Lp	92	93% 5%
45	Lr	137	87% 9%
46	Lz	217	12% 93% 7%
47	S2	1869	56% 37% 7%
48	S6	75	63% 36%
49	SA	295	73% 25%
50	SB	264	78% 19%
51	SD	243	86% 7% 7%
52	SE	263	94% 5%
53	SF	204	87% 7% 6%
54	SH	194	90% 8%
55	SI	208	93% 6%
56	SK	165	57% 41%
57	SL	158	91% 6%
58	SP	145	57% 10% 33%

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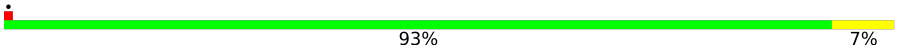
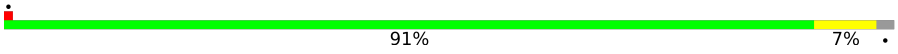
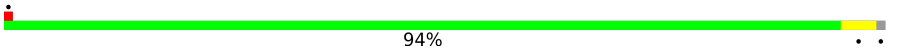
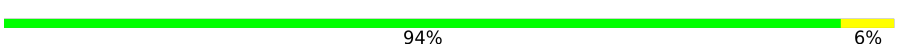
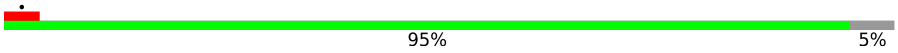
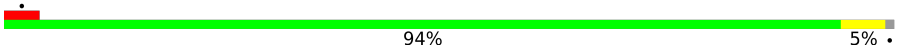
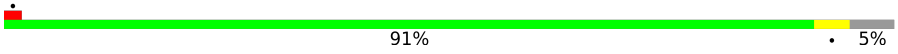
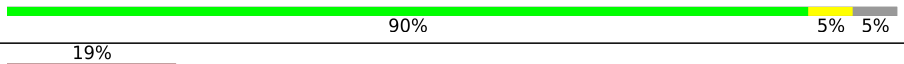
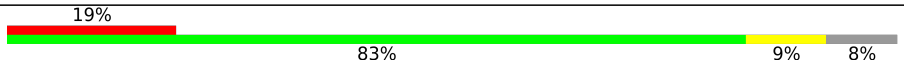
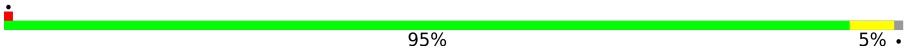
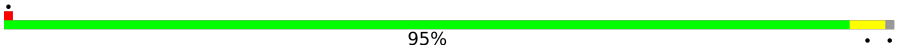
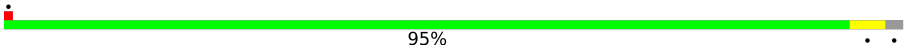
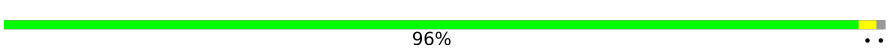
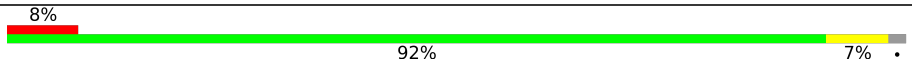
Mol	Chain	Length	Quality of chain
59	SQ	146	
60	SR	135	
61	SS	152	
62	ST	145	
63	SU	119	
64	SV	83	
65	SX	143	
66	Sa	115	
67	Sc	69	
68	Sd	56	
69	Sf	156	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	
79	SZ	125	
80	Sb	84	
81	Se	59	

2 Entry composition (i)

There are 83 unique types of molecules in this entry. The entry contains 218776 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 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	L5	3776	80184	35672	14597	26140	3775	0	0

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	L7	120	2558	1141	456	842	119	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	L8	156	3314	1480	585	1094	155	0	0

- Molecule 4 is a protein called 60S RIBOSOMAL PROTEIN L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	LA	248	1898	1189	389	314	6	0	0

- Molecule 5 is a protein called 60S RIBOSOMAL PROTEIN L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	LB	402	3238	2060	608	556	14	0	0

- Molecule 6 is a protein called 60S RIBOSOMAL PROTEIN L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	LC	367	2919	1835	582	488	14	0	0

- Molecule 7 is a protein called 60S RIBOSOMAL PROTEIN L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 8 is a protein called 60S RIBOSOMAL PROTEIN L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 9 is a protein called 60S RIBOSOMAL PROTEIN L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 10 is a protein called 60S RIBOSOMAL PROTEIN L7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 11 is a protein called 60S RIBOSOMAL PROTEIN L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 12 is a protein called 60S RIBOSOMAL PROTEIN L10-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

- Molecule 13 is a protein called 60S RIBOSOMAL PROTEIN L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 14 is a protein called 60S RIBOSOMAL PROTEIN L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 15 is a protein called 60S RIBOSOMAL PROTEIN L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 16 is a protein called 60S RIBOSOMAL PROTEIN L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 17 is a protein called 60S RIBOSOMAL PROTEIN L13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 18 is a protein called 60S RIBOSOMAL PROTEIN L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 19 is a protein called 60S RIBOSOMAL PROTEIN L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S RIBOSOMAL PROTEIN L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 21 is a protein called 60S RIBOSOMAL PROTEIN L18A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S RIBOSOMAL PROTEIN L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called 60S RIBOSOMAL PROTEIN L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 24 is a protein called 60S RIBOSOMAL PROTEIN L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called 60S RIBOSOMAL PROTEIN L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 26 is a protein called 60S RIBOSOMAL PROTEIN L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 27 is a protein called 60S RIBOSOMAL PROTEIN L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called 60S RIBOSOMAL PROTEIN L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called 60S RIBOSOMAL PROTEIN L27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S RIBOSOMAL PROTEIN L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Lb	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 31 is a protein called 60S RIBOSOMAL PROTEIN L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 32 is a protein called 60S RIBOSOMAL PROTEIN L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called 60S RIBOSOMAL PROTEIN L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called 60S RIBOSOMAL PROTEIN L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 35 is a protein called 60S RIBOSOMAL PROTEIN L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S RIBOSOMAL PROTEIN L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 37 is a protein called 60S RIBOSOMAL PROTEIN L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 38 is a protein called 60S RIBOSOMAL PROTEIN L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called 60S RIBOSOMAL PROTEIN L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called 60S RIBOSOMAL PROTEIN L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 41 is a protein called UBIQUITIN-60S RIBOSOMAL PROTEIN L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 42 is a protein called 60S RIBOSOMAL PROTEIN L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 43 is a protein called 60S RIBOSOMAL PROTEIN L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 44 is a protein called 60S RIBOSOMAL PROTEIN L37A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 45 is a protein called 60S RIBOSOMAL PROTEIN L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 46 is a protein called 60S RIBOSOMAL PROTEIN L10A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

- Molecule 48 is a RNA chain called HUMAN INITIATOR MET-TRNA-I.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 49 is a protein called 40S RIBOSOMAL PROTEIN SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 50 is a protein called 40S RIBOSOMAL PROTEIN S3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 51 is a protein called 40S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 52 is a protein called 40S RIBOSOMAL PROTEIN S4, X ISOFORM.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 53 is a protein called 40S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 54 is a protein called 40S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 55 is a protein called 40S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 56 is a protein called 40S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 57 is a protein called 40S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 58 is a protein called 40S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SP	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 59 is a protein called 40S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 60 is a protein called 40S RIBOSOMAL PROTEIN S17-LIKE.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 61 is a protein called 40S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SS	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 62 is a protein called 40S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 63 is a protein called 40S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 64 is a protein called 40S RIBOSOMAL PROTEIN S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 65 is a protein called 40S RIBOSOMAL PROTEIN S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 66 is a protein called 40S RIBOSOMAL PROTEIN S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Sa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 67 is a protein called 40S RIBOSOMAL PROTEIN S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 68 is a protein called 40S RIBOSOMAL PROTEIN S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 69 is a protein called UBIQUITIN-40S RIBOSOMAL PROTEIN S27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 70 is a protein called GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 71 is a protein called 40S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 72 is a protein called 40S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 73 is a protein called 40S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 74 is a protein called 40S RIBOSOMAL PROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

- Molecule 75 is a protein called 40S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 76 is a protein called 40S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 77 is a protein called 40S RIBOSOMAL PROTEIN S15A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 78 is a protein called 40S RIBOSOMAL PROTEIN S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 79 is a protein called 40S RIBOSOMAL PROTEIN S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 80 is a protein called 40S RIBOSOMAL PROTEIN S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 81 is a protein called 40S RIBOSOMAL PROTEIN S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 82 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
82	L5	149	Total	Mg	0
			149	149	
82	L7	5	Total	Mg	0
			5	5	
82	L8	2	Total	Mg	0
			2	2	
82	LA	1	Total	Mg	0
			1	1	
82	LB	1	Total	Mg	0
			1	1	
82	LH	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
82	LJ	1	Total Mg 1 1	0
82	LN	1	Total Mg 1 1	0
82	LP	1	Total Mg 1 1	0
82	LQ	1	Total Mg 1 1	0
82	La	1	Total Mg 1 1	0
82	Le	1	Total Mg 1 1	0
82	Ll	1	Total Mg 1 1	0
82	S2	66	Total Mg 66 66	0
82	S6	7	Total Mg 7 7	0

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

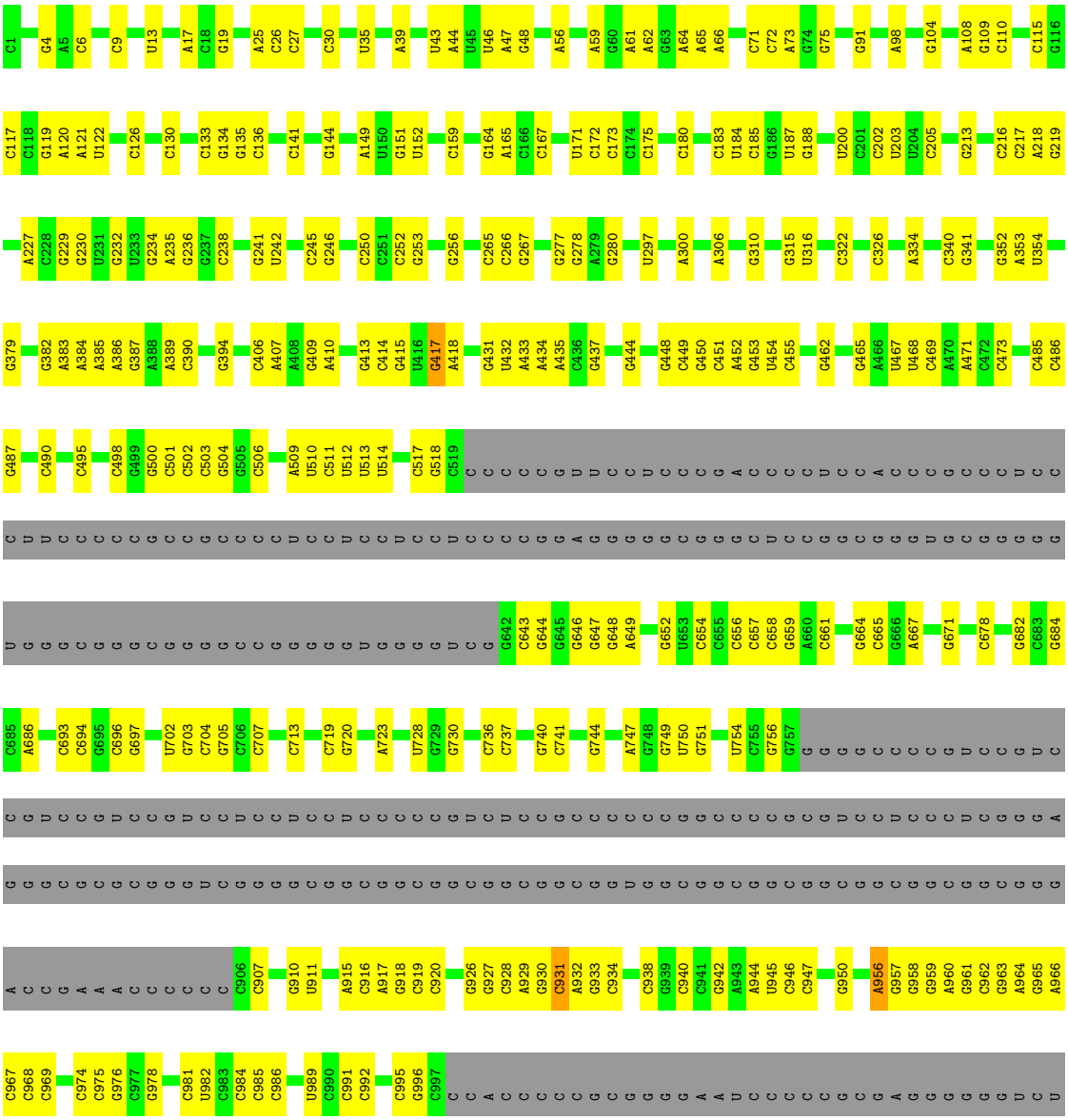
Mol	Chain	Residues	Atoms	AltConf
83	Lg	1	Total Zn 1 1	0
83	Lj	1	Total Zn 1 1	0
83	Lm	1	Total Zn 1 1	0
83	Lo	1	Total Zn 1 1	0
83	Lp	1	Total Zn 1 1	0
83	Sa	1	Total Zn 1 1	0

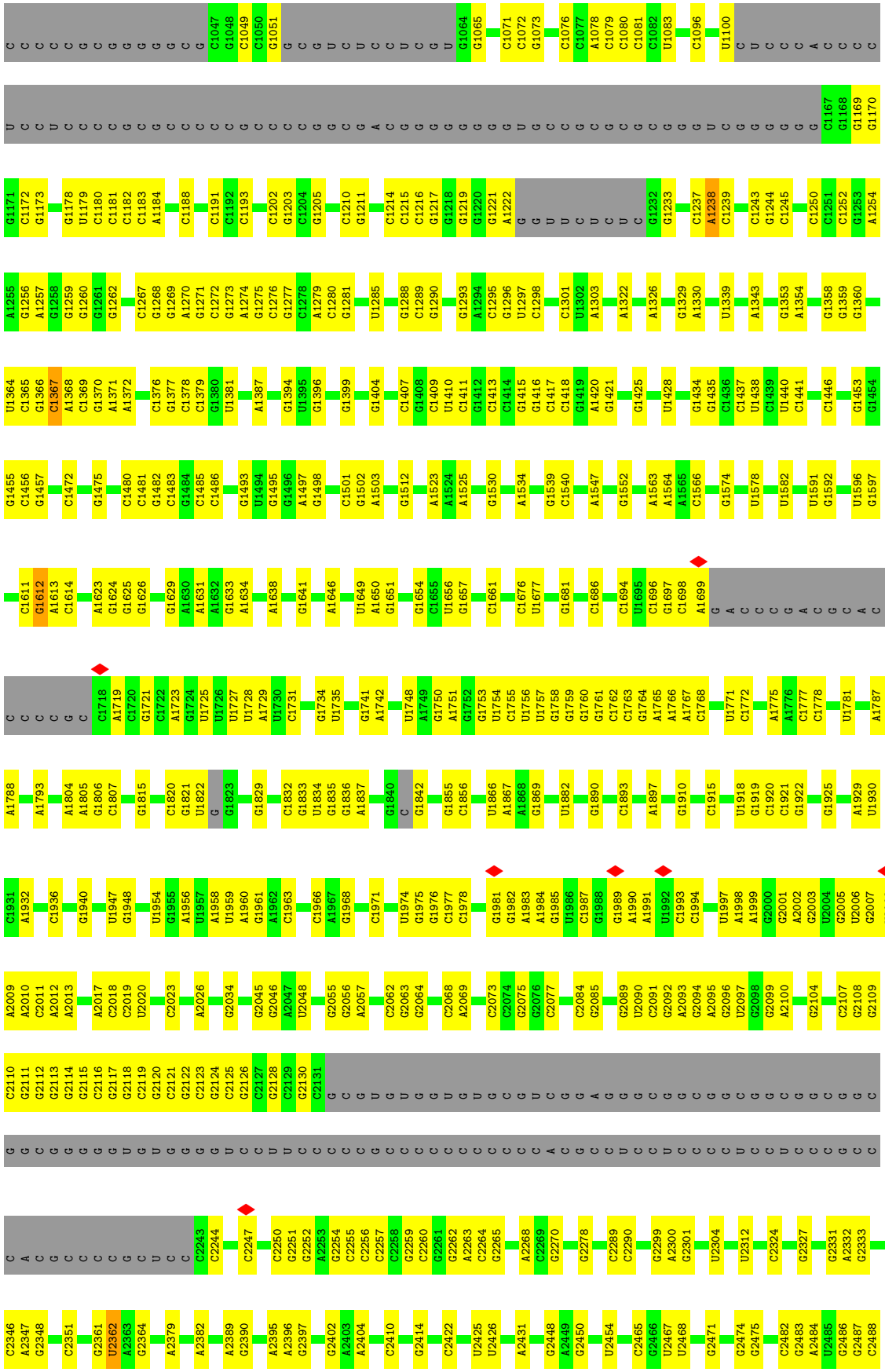
3 Residue-property plots (i)

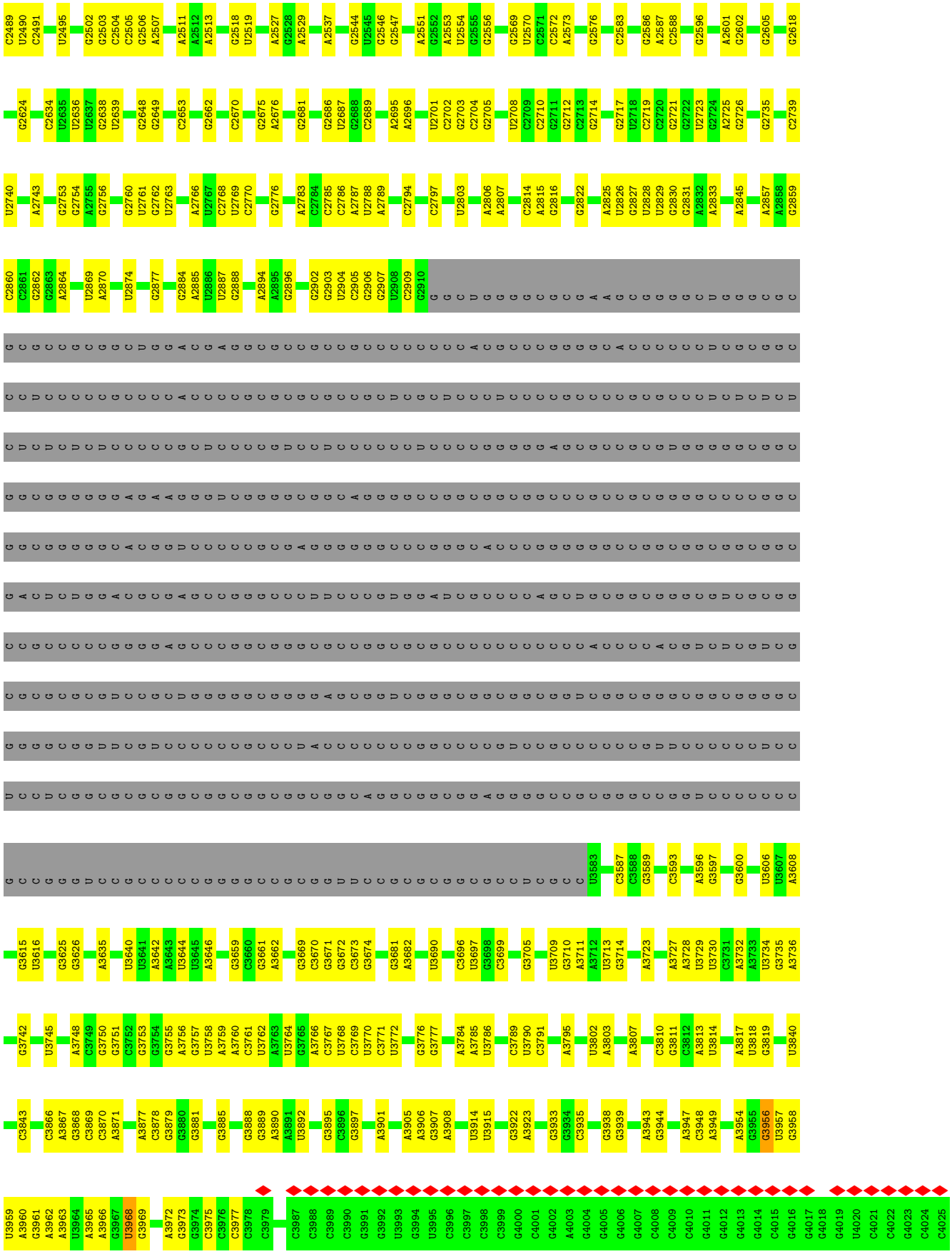
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

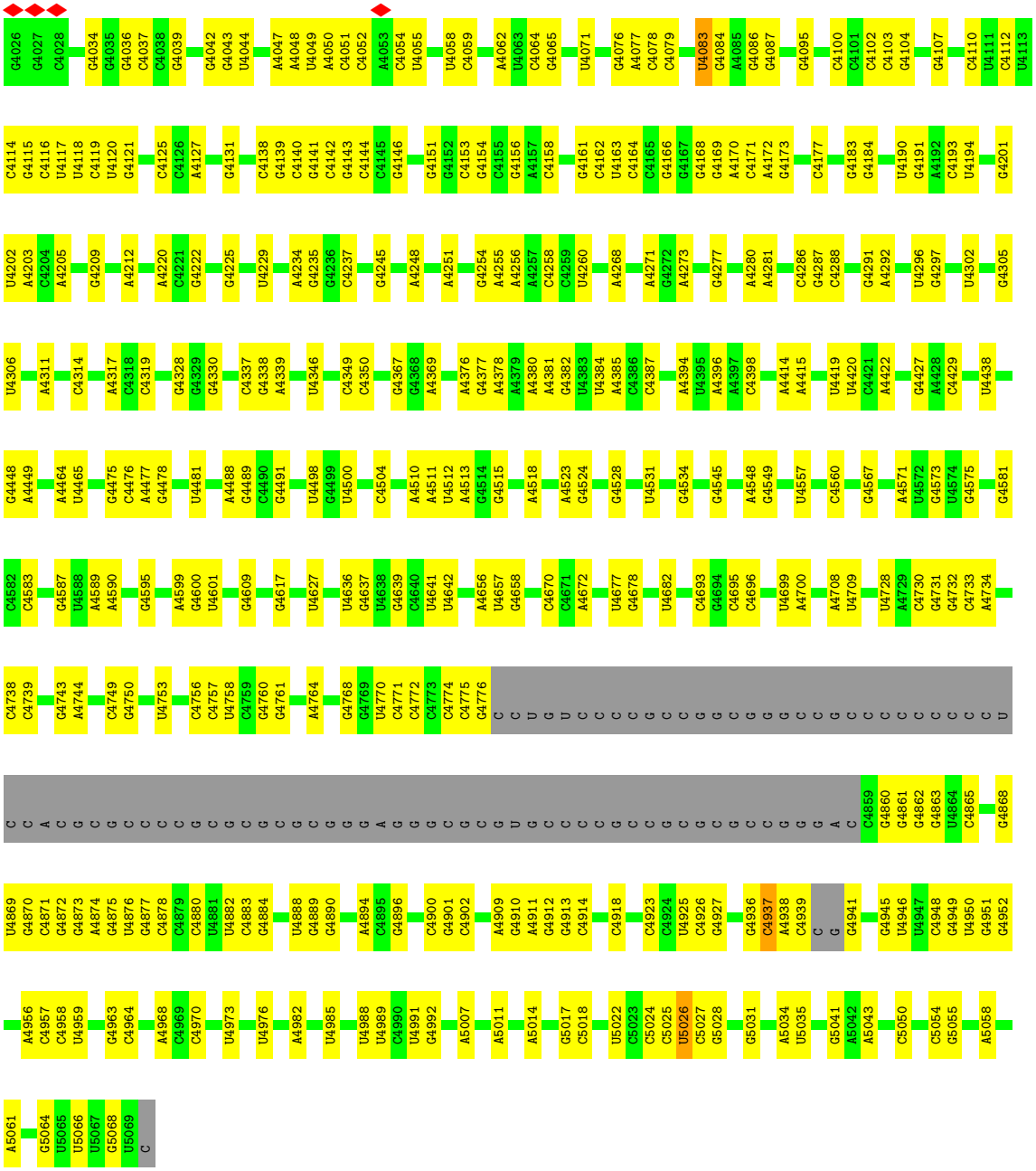
- Molecule 1: 28S ribosomal RNA

Chain L5:






C2489 U2490 C2491 U2495 G2502 G2503 C2504 C2505 G2506 A2507 A2511 A2512 A2513 G2518 U2519 A2527 G2528 A2529 A2537 G2544 U2545 G2546 G2547 A2551 G2552 A2553 U2554 G2555 G2556 G2569 U2570 C2571 C2572 A2573 G2576 C2583 G2586 A2587 C2588 G2596 A2601 G2602 G2605 G2618
G2624 C2634 U2635 U2636 U2637 G2638 U2639 G2648 G2649 C2653 G2662 C2670 G2675 A2676 G2681 G2686 U2687 G2688 C2689 A2695 A2696 U2701 C2702 G2703 C2704 G2705 U2708 C2709 C2710 G2711 G2712 C2713 G2714 G2717 U2718 C2719 C2720 G2721 G2722 U2723 G2724 A2725 G2726 G2735 C2739
U2740 A2743 G2753 G2754 A2755 G2756 G2760 U2761 G2762 U2763 A2766 U2767 C2768 U2769 C2770 G2776 A2783 G2784 C2785 C2786 A2787 U2788 A2789 C2794 C2797 U2803 A2806 A2807 C2814 A2815 G2816 G2822 A2825 U2826 G2827 U2828 U2829 G2830 G2831 A2832 A2833 A2845 A2857 A2888 G2859
C2860 C2861 G2862 G2863 A2864 U2869 A2870 U2874 G2877 G2884 A2885 U2886 U2887 G2888 A2894 A2895 G2896 G2902 G2903 U2904 C2905 G2906 G2907 U2908 C2909 G2910
G C C G C C C

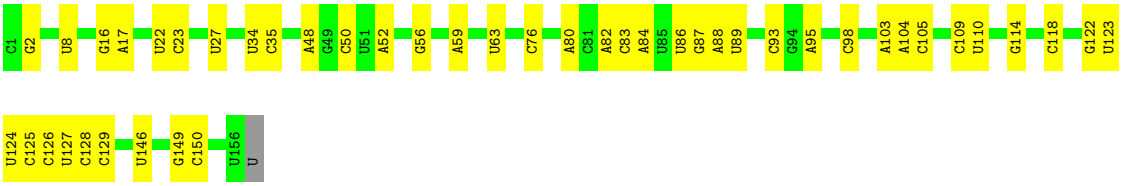


• Molecule 2: 5S ribosomal RNA

Chain L7:

• Molecule 3: 5.8S ribosomal RNA

Chain L8:



• Molecule 4: 60S RIBOSOMAL PROTEIN L8

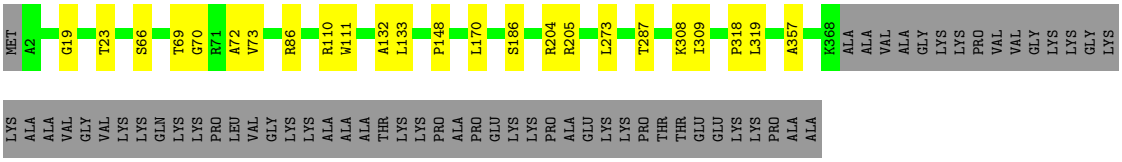
Chain LA:

• Molecule 5: 60S RIBOSOMAL PROTEIN L3

Chain LB:

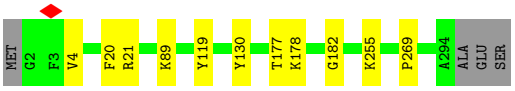
• Molecule 6: 60S RIBOSOMAL PROTEIN L4

Chain LC:



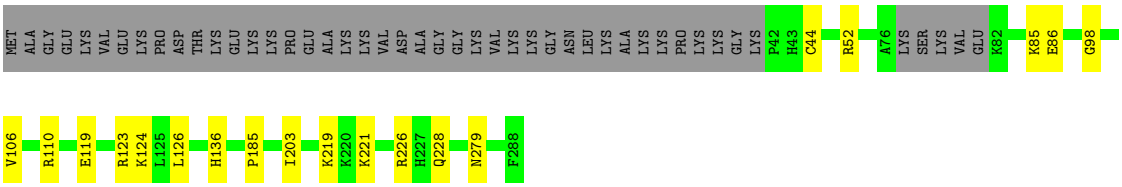
• Molecule 7: 60S RIBOSOMAL PROTEIN L5

Chain LD:



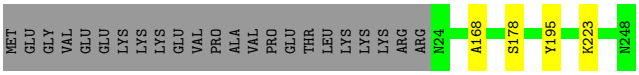
• Molecule 8: 60S RIBOSOMAL PROTEIN L6

Chain LE:



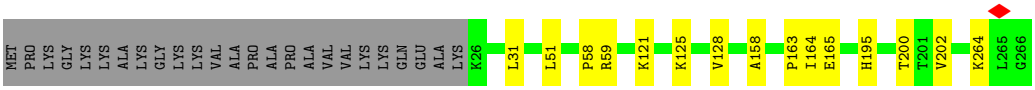
• Molecule 9: 60S RIBOSOMAL PROTEIN L7

Chain LF:



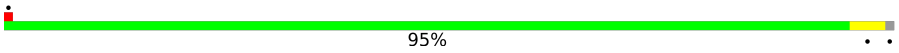
• Molecule 10: 60S RIBOSOMAL PROTEIN L7A

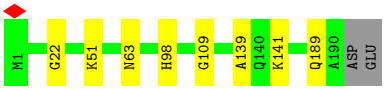
Chain LG:



• Molecule 11: 60S RIBOSOMAL PROTEIN L9

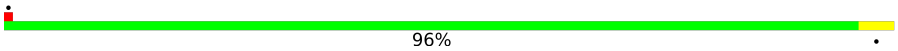
Chain LH:

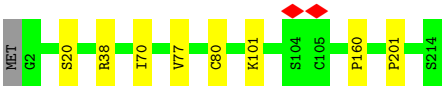




• Molecule 12: 60S RIBOSOMAL PROTEIN L10-LIKE

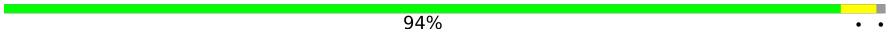
Chain LI:





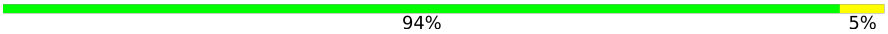
• Molecule 13: 60S RIBOSOMAL PROTEIN L11

Chain LJ:



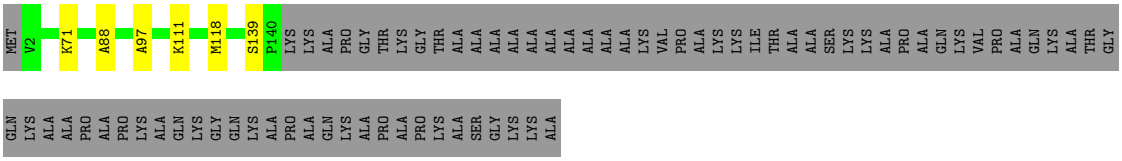
• Molecule 14: 60S RIBOSOMAL PROTEIN L13

Chain LL:



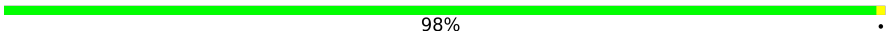
• Molecule 15: 60S RIBOSOMAL PROTEIN L14

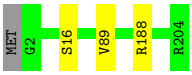
Chain LM:



• Molecule 16: 60S RIBOSOMAL PROTEIN L15

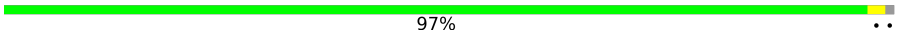
Chain LN:





• Molecule 17: 60S RIBOSOMAL PROTEIN L13A

Chain LO:

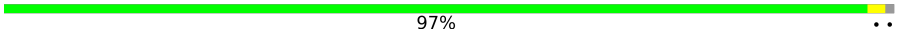


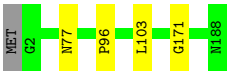
• Molecule 18: 60S RIBOSOMAL PROTEIN L17

Chain LP:

• Molecule 19: 60S RIBOSOMAL PROTEIN L18

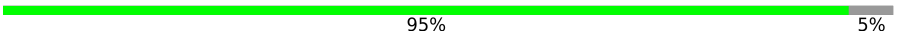
Chain LQ:





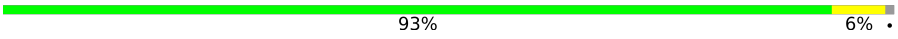
• Molecule 20: 60S RIBOSOMAL PROTEIN L19

Chain LR:



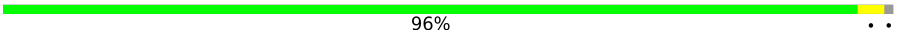
• Molecule 21: 60S RIBOSOMAL PROTEIN L18A

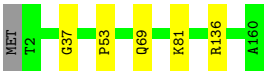
Chain LS:



• Molecule 22: 60S RIBOSOMAL PROTEIN L21

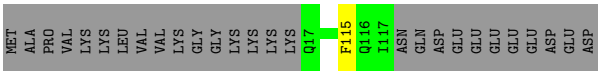
Chain LT:





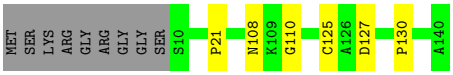
• Molecule 23: 60S RIBOSOMAL PROTEIN L22

Chain LU:



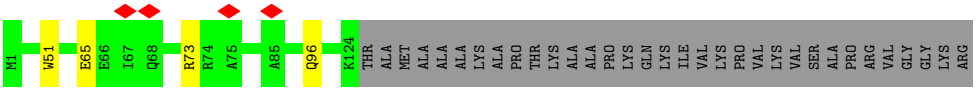
• Molecule 24: 60S RIBOSOMAL PROTEIN L23

Chain LV:



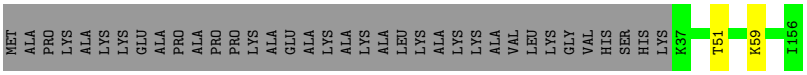
• Molecule 25: 60S RIBOSOMAL PROTEIN L24

Chain LW:



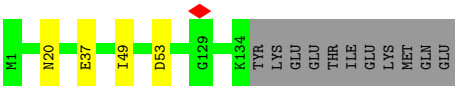
• Molecule 26: 60S RIBOSOMAL PROTEIN L23A

Chain LX:



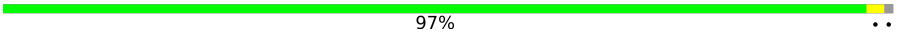
• Molecule 27: 60S RIBOSOMAL PROTEIN L26

Chain LY:



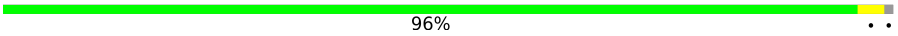
• Molecule 28: 60S RIBOSOMAL PROTEIN L27

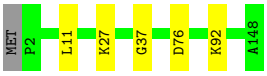
Chain LZ:



• Molecule 29: 60S RIBOSOMAL PROTEIN L27A

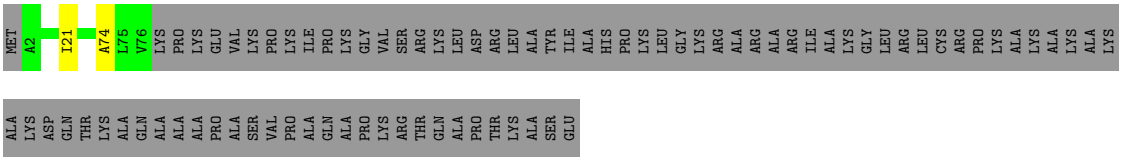
Chain La:





• Molecule 30: 60S RIBOSOMAL PROTEIN L29

Chain Lb:

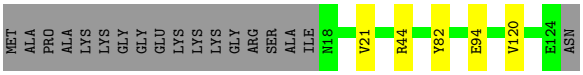


• Molecule 31: 60S RIBOSOMAL PROTEIN L30

Chain Lc:

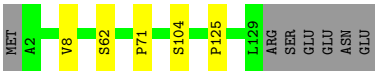
• Molecule 32: 60S RIBOSOMAL PROTEIN L31

Chain Ld:



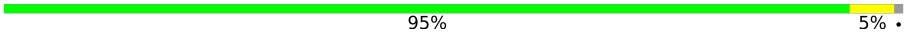
• Molecule 33: 60S RIBOSOMAL PROTEIN L32

Chain Le:



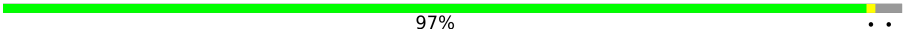
• Molecule 34: 60S RIBOSOMAL PROTEIN L35A

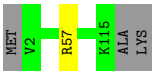
Chain Lf:



• Molecule 35: 60S RIBOSOMAL PROTEIN L34

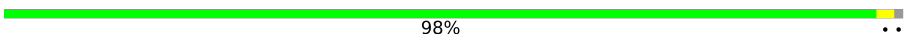
Chain Lg:

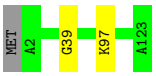




• Molecule 36: 60S RIBOSOMAL PROTEIN L35

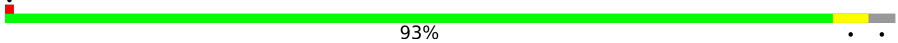
Chain Lh:

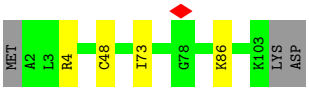




• Molecule 37: 60S RIBOSOMAL PROTEIN L36

Chain Li:





• Molecule 38: 60S RIBOSOMAL PROTEIN L37

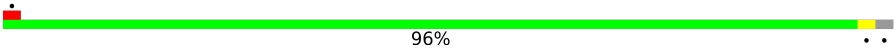
Chain Lj:

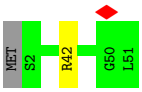
• Molecule 39: 60S RIBOSOMAL PROTEIN L38

Chain Lk:

• Molecule 40: 60S RIBOSOMAL PROTEIN L39

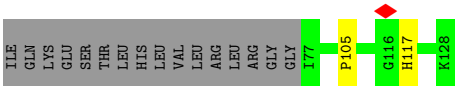
Chain Ll:





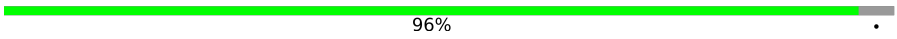
• Molecule 41: UBIQUITIN-60S RIBOSOMAL PROTEIN L40

Chain Lm:



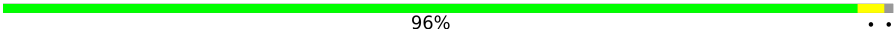
• Molecule 42: 60S RIBOSOMAL PROTEIN L41

Chain Ln:



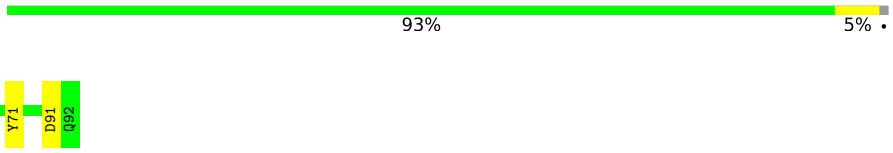
• Molecule 43: 60S RIBOSOMAL PROTEIN L36A

Chain Lo:



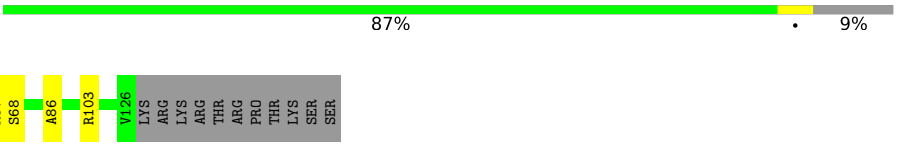
• Molecule 44: 60S RIBOSOMAL PROTEIN L37A

Chain Lp:



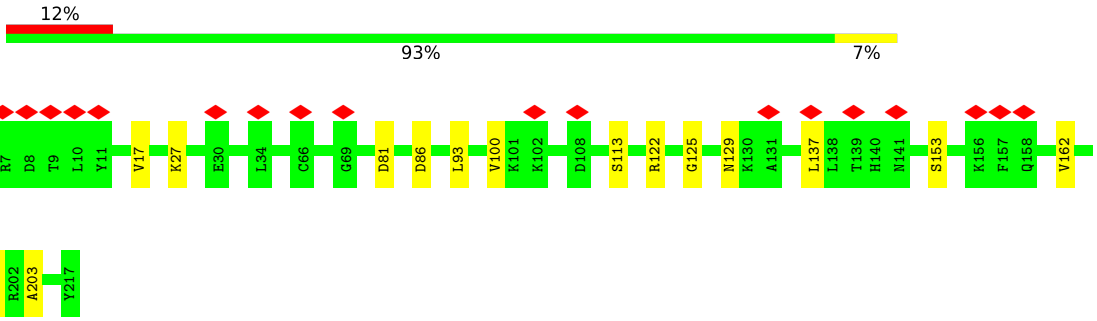
• Molecule 45: 60S RIBOSOMAL PROTEIN L28

Chain Lr:



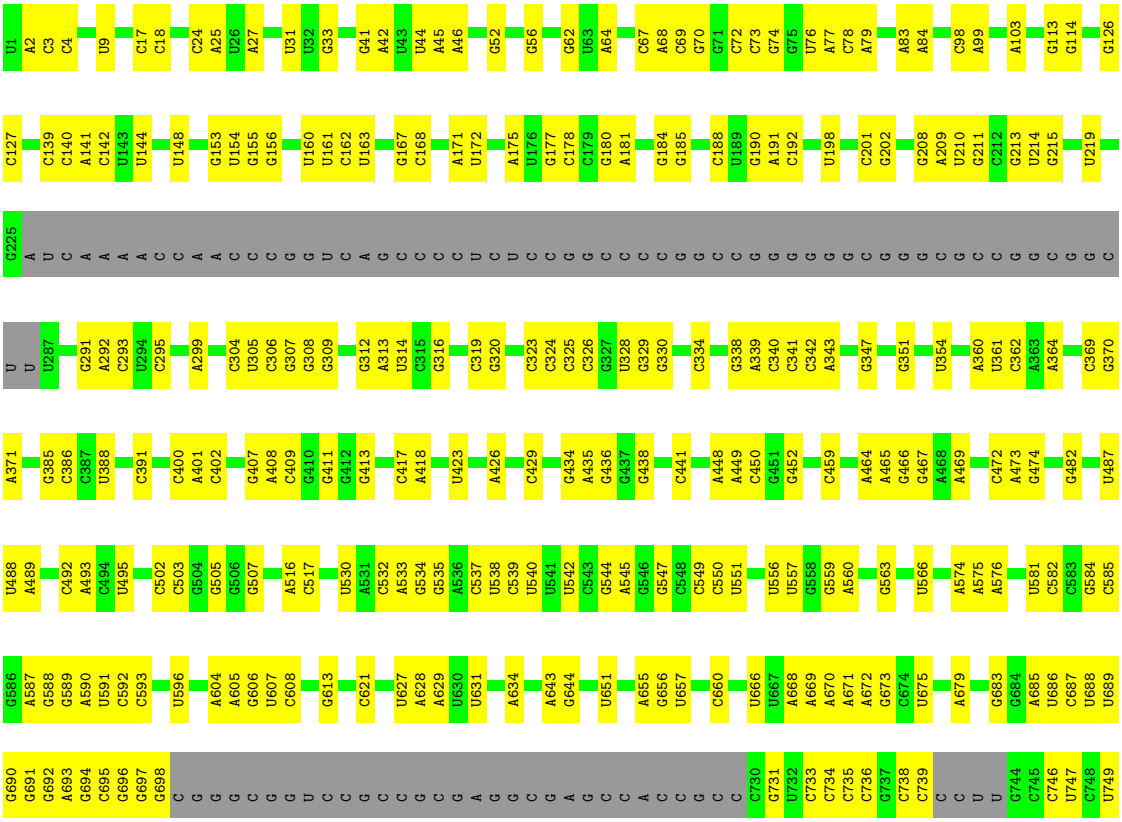
• Molecule 46: 60S RIBOSOMAL PROTEIN L10A

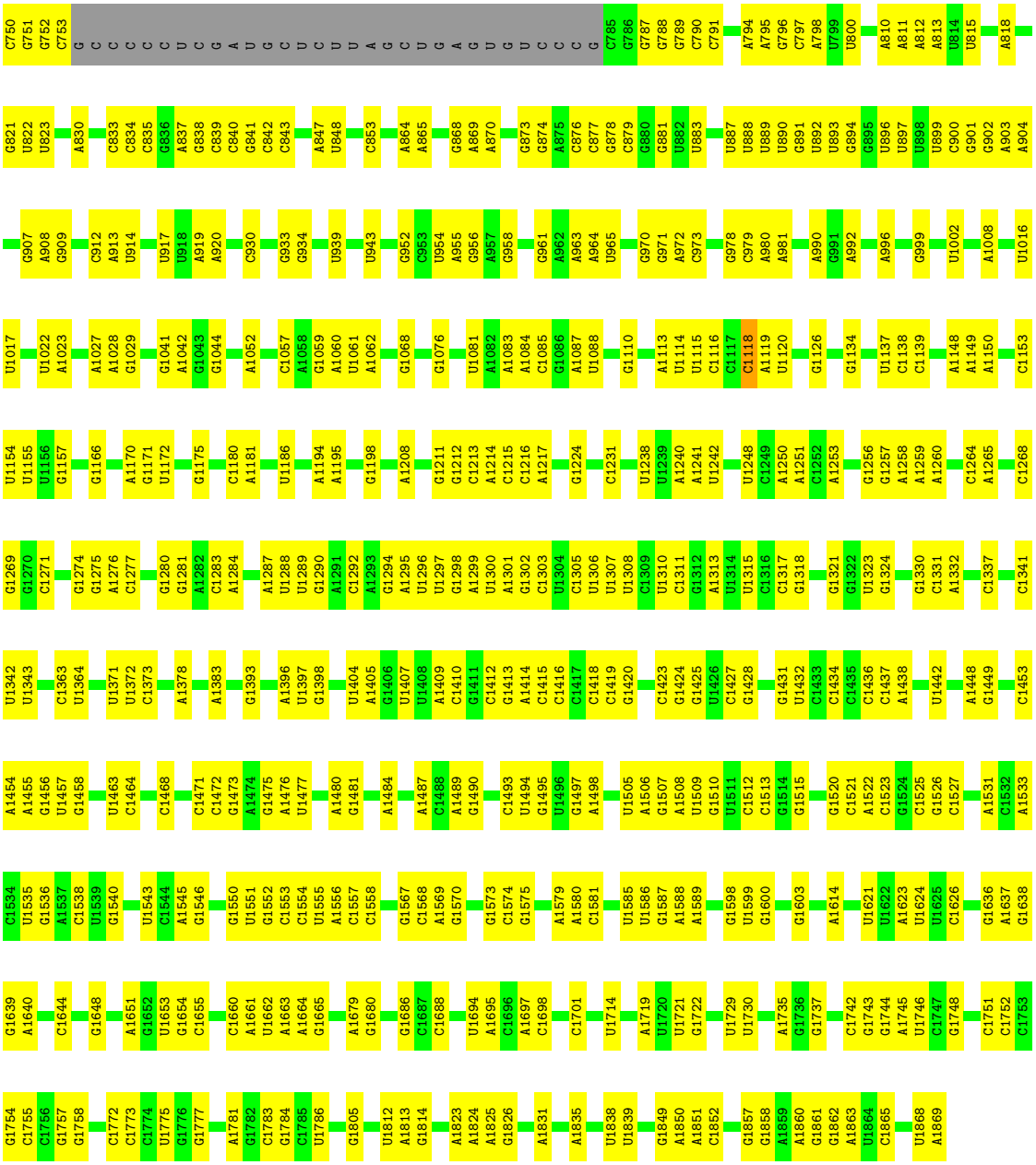
Chain Lz:



• Molecule 47: 18S ribosomal RNA

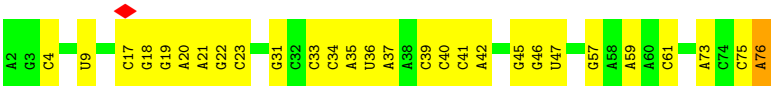
Chain S2:





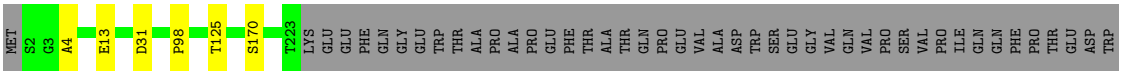
• Molecule 48: HUMAN INITIATOR MET-TRNA-I

Chain S6:



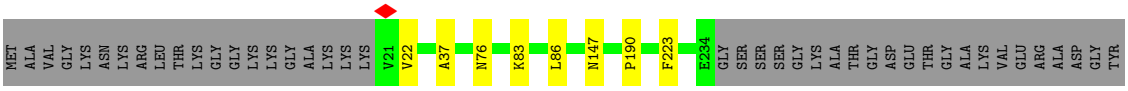
• Molecule 49: 40S RIBOSOMAL PROTEIN SA

Chain SA:



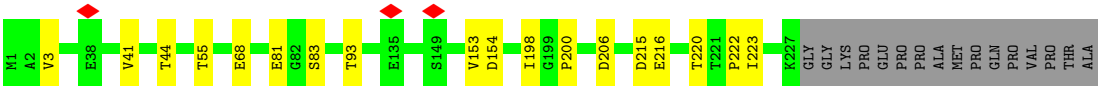
• Molecule 50: 40S RIBOSOMAL PROTEIN S3A

Chain SB:



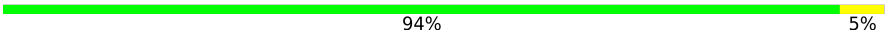
• Molecule 51: 40S RIBOSOMAL PROTEIN S3

Chain SD:



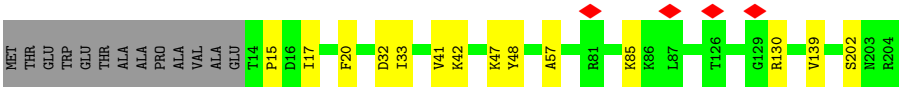
• Molecule 52: 40S RIBOSOMAL PROTEIN S4, X ISOFORM

Chain SE:



• Molecule 53: 40S RIBOSOMAL PROTEIN S5

Chain SF:

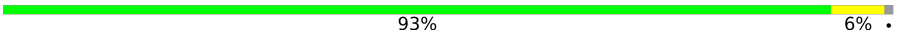


• Molecule 54: 40S RIBOSOMAL PROTEIN S7

Chain SH:

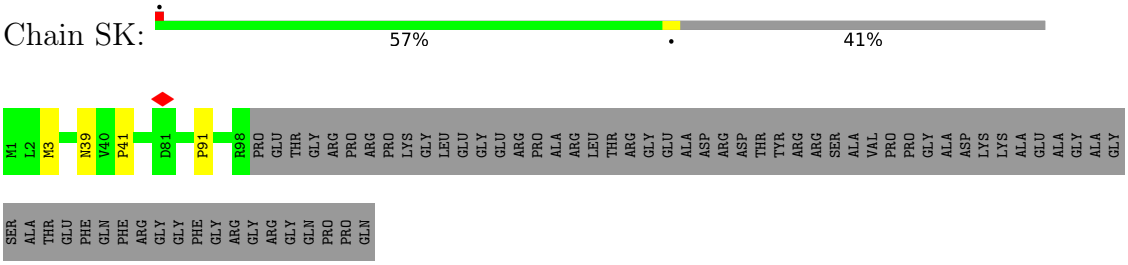
• Molecule 55: 40S RIBOSOMAL PROTEIN S8

Chain SI:



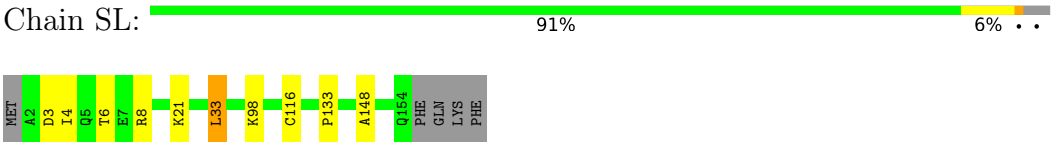
• Molecule 56: 40S RIBOSOMAL PROTEIN S10

Chain SK:



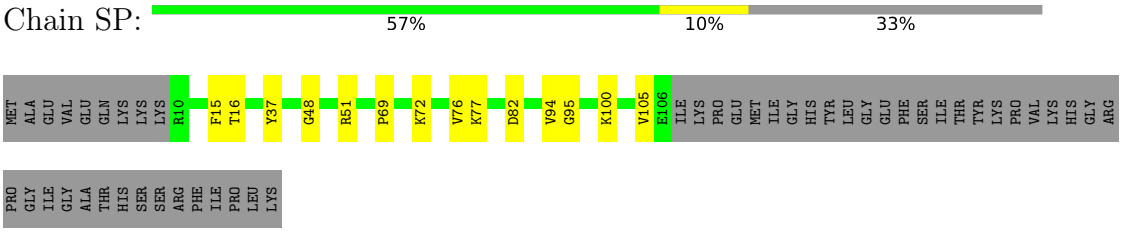
• Molecule 57: 40S RIBOSOMAL PROTEIN S11

Chain SL:



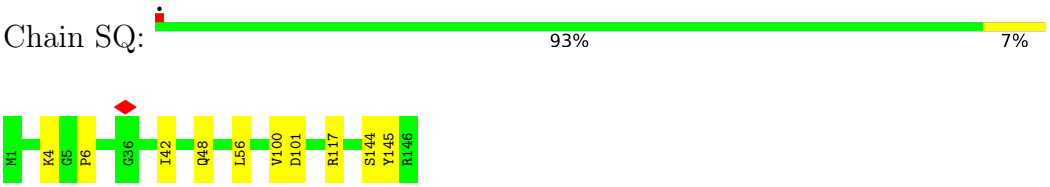
• Molecule 58: 40S RIBOSOMAL PROTEIN S15

Chain SP:



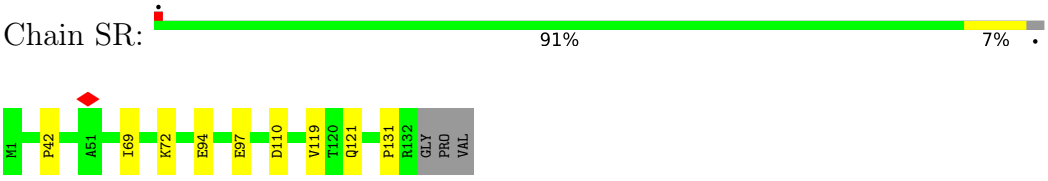
• Molecule 59: 40S RIBOSOMAL PROTEIN S16

Chain SQ:



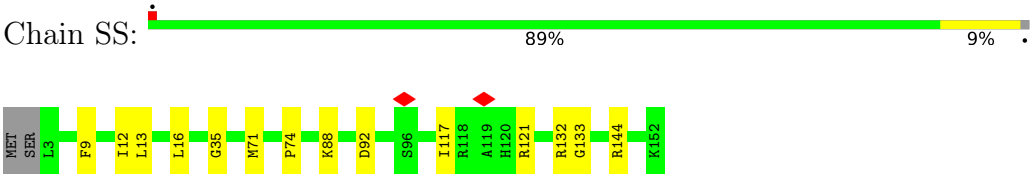
• Molecule 60: 40S RIBOSOMAL PROTEIN S17-LIKE

Chain SR:



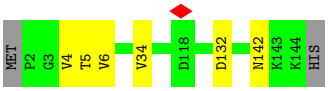
• Molecule 61: 40S RIBOSOMAL PROTEIN S18

Chain SS:



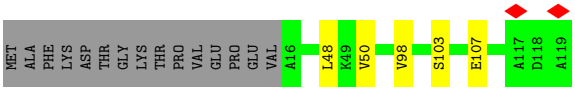
• Molecule 62: 40S RIBOSOMAL PROTEIN S19

Chain ST:



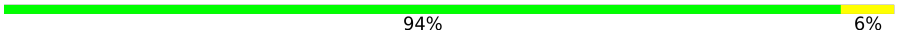
• Molecule 63: 40S RIBOSOMAL PROTEIN S20

Chain SU:



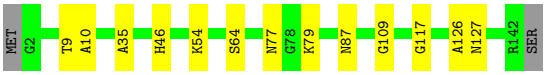
• Molecule 64: 40S RIBOSOMAL PROTEIN S21

Chain SV:



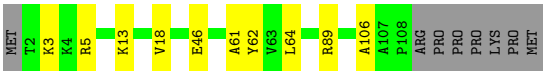
• Molecule 65: 40S RIBOSOMAL PROTEIN S23

Chain SX:



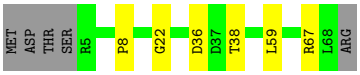
• Molecule 66: 40S RIBOSOMAL PROTEIN S26

Chain Sa:



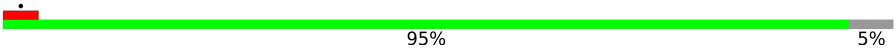
• Molecule 67: 40S RIBOSOMAL PROTEIN S28

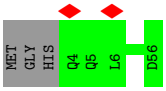
Chain Sc:



• Molecule 68: 40S RIBOSOMAL PROTEIN S29

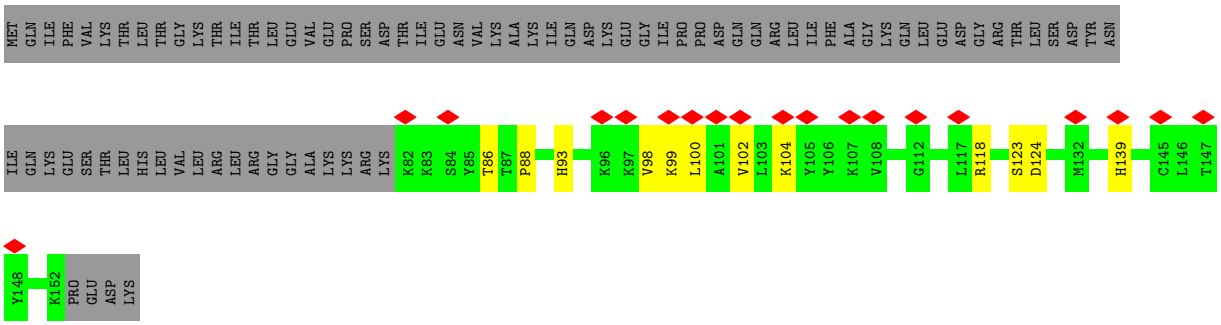
Chain Sd:





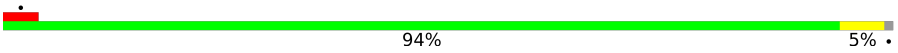
• Molecule 69: UBIQUITIN-40S RIBOSOMAL PROTEIN S27A

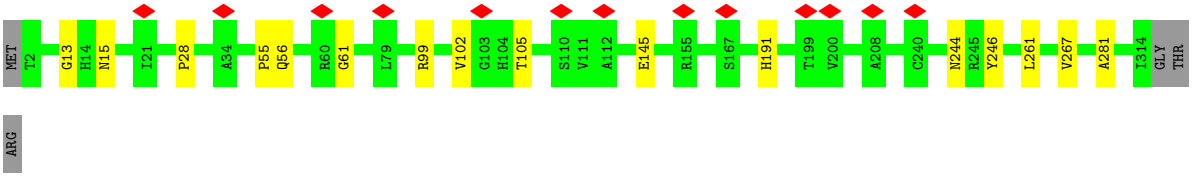
Chain Sf:



• Molecule 70: GUANINE NUCLEOTIDE-BINDING PROTEIN SUBUNIT BETA-2-LIKE 1

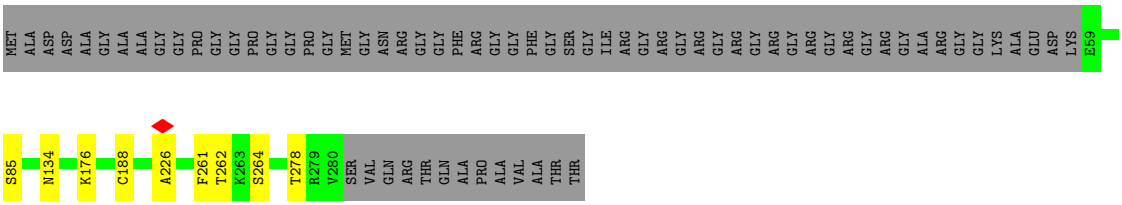
Chain Sg:





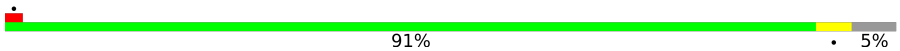
• Molecule 71: 40S RIBOSOMAL PROTEIN S2

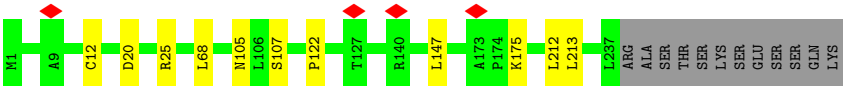
Chain SC:



• Molecule 72: 40S RIBOSOMAL PROTEIN S6

Chain SG:



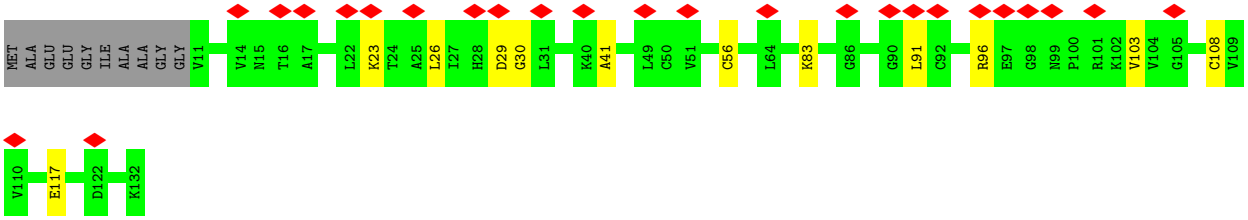


• Molecule 73: 40S RIBOSOMAL PROTEIN S9

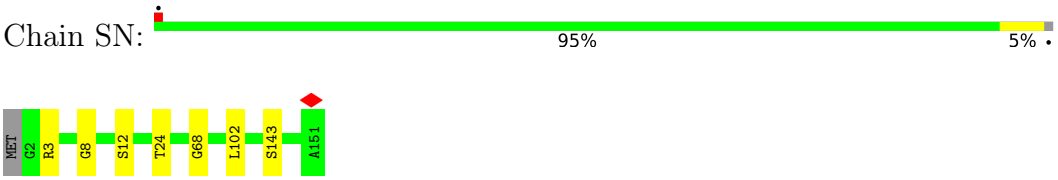
Chain SJ:

• Molecule 74: 40S RIBOSOMAL PROTEIN

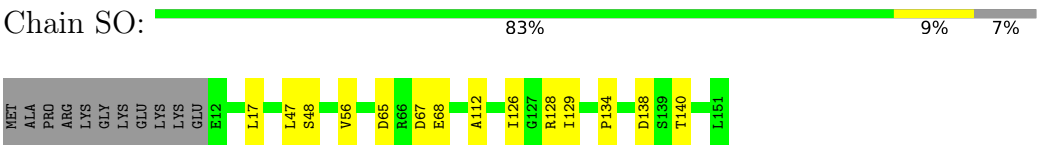
Chain SM:



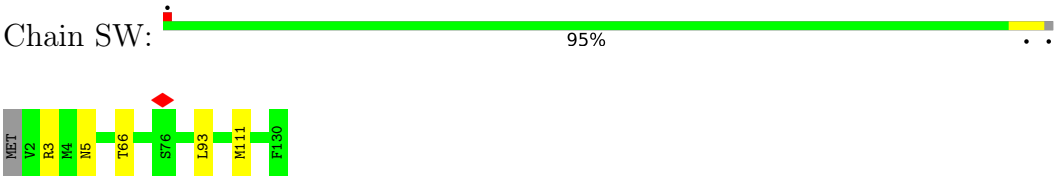
• Molecule 75: 40S RIBOSOMAL PROTEIN S13



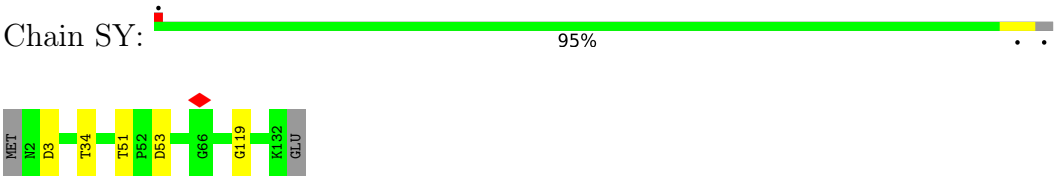
• Molecule 76: 40S RIBOSOMAL PROTEIN S14



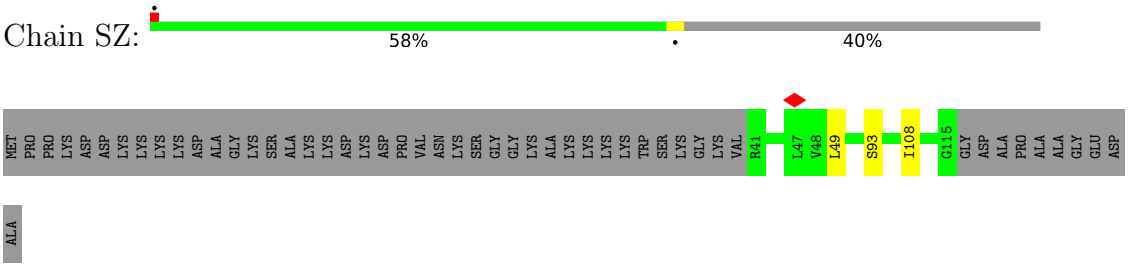
• Molecule 77: 40S RIBOSOMAL PROTEIN S15A



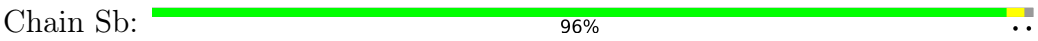
• Molecule 78: 40S RIBOSOMAL PROTEIN S24

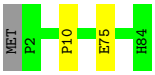


• Molecule 79: 40S RIBOSOMAL PROTEIN S25



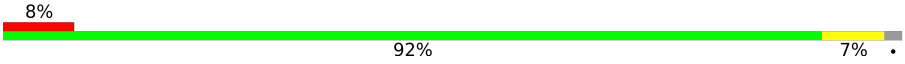
• Molecule 80: 40S RIBOSOMAL PROTEIN S27

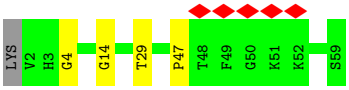




• Molecule 81: 40S RIBOSOMAL PROTEIN S30

Chain Se:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	24000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.362	Depositor
Minimum map value	-0.237	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	330.0, 330.0, 330.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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	L5	0.42	0/89645	0.79	26/139764 (0.0%)
2	L7	0.37	0/2858	0.73	0/4455
3	L8	0.40	0/3701	0.76	0/5766
4	LA	0.34	0/1936	0.56	1/2596 (0.0%)
5	LB	0.30	0/3306	0.52	1/4424 (0.0%)
6	LC	0.29	0/2973	0.50	0/3992
7	LD	0.29	0/2428	0.47	0/3252
8	LE	0.27	0/1996	0.59	0/2673
9	LF	0.31	0/1905	0.49	0/2539
10	LG	0.27	0/1960	0.50	0/2637
11	LH	0.26	0/1537	0.48	0/2066
12	LI	0.30	0/1751	0.50	0/2340
13	LJ	0.26	0/1433	0.49	0/1915
14	LL	0.30	0/1732	0.53	0/2315
15	LM	0.28	0/1161	0.46	0/1554
16	LN	0.33	0/1746	0.51	0/2338
17	LO	0.31	0/1682	0.47	0/2250
18	LP	0.31	0/1268	0.49	0/1701
19	LQ	0.30	0/1537	0.49	0/2052
20	LR	0.28	0/1582	0.49	0/2091
21	LS	0.31	0/1493	0.48	0/2003
22	LT	0.32	0/1326	0.52	0/1770
23	LU	0.27	0/839	0.47	0/1126
24	LV	0.31	0/993	0.49	0/1332
25	LW	0.29	0/1030	0.57	0/1364
26	LX	0.29	0/1002	0.49	0/1345
27	LY	0.28	0/1132	0.47	0/1504
28	LZ	0.29	0/1130	0.47	0/1507
29	La	0.31	0/1191	0.50	0/1591
30	Lb	0.26	0/620	0.44	0/819
31	Lc	0.29	0/774	0.48	0/1038
32	Ld	0.29	0/903	0.50	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Le	0.33	0/1071	0.53	0/1429
34	Lf	0.30	0/895	0.51	0/1198
35	Lg	0.28	0/916	0.49	0/1220
36	Lh	0.28	0/1023	0.46	0/1351
37	Li	0.28	0/843	0.47	0/1115
38	Lj	0.35	0/720	0.55	0/952
39	Lk	0.28	0/575	0.54	0/761
40	Ll	0.28	0/454	0.48	0/599
41	Lm	0.29	0/435	0.47	0/575
42	Ln	0.29	0/231	0.53	0/294
43	Lo	0.31	0/875	0.49	0/1153
44	Lp	0.36	0/718	0.51	0/953
45	Lr	0.27	0/1017	0.50	0/1364
46	Lz	0.24	0/1769	0.49	0/2371
47	S2	0.35	0/41243	0.77	11/64257 (0.0%)
48	S6	0.32	1/1795 (0.1%)	0.80	1/2798 (0.0%)
49	SA	0.26	0/1784	0.49	0/2424
50	SB	0.28	0/1765	0.52	0/2362
51	SD	0.26	0/1793	0.49	0/2414
52	SE	0.26	0/2118	0.53	1/2849 (0.0%)
53	SF	0.27	0/1531	0.52	0/2059
54	SH	0.26	0/1544	0.50	0/2068
55	SI	0.27	0/1715	0.48	0/2287
56	SK	0.27	0/851	0.50	0/1147
57	SL	0.29	0/1268	0.51	1/1696 (0.1%)
58	SP	0.26	0/815	0.56	0/1087
59	SQ	0.26	0/1177	0.48	0/1575
60	SR	0.27	0/1086	0.57	0/1457
61	SS	0.25	0/1253	0.52	0/1676
62	ST	0.25	0/1131	0.48	0/1515
63	SU	0.26	0/831	0.56	0/1115
64	SV	0.26	0/643	0.44	0/860
65	SX	0.29	0/1116	0.47	0/1490
66	Sa	0.31	0/862	0.52	0/1156
67	Sc	0.25	0/508	0.51	0/680
68	Sd	0.26	0/455	0.42	0/603
69	Sf	0.25	0/593	0.47	0/786
70	Sg	0.24	0/2493	0.50	0/3394
71	SC	0.29	0/1762	0.49	0/2381
72	SG	0.25	0/1946	0.52	0/2590
73	SJ	0.26	0/1550	0.47	0/2069
74	SM	0.23	0/962	0.53	0/1290
75	SN	0.28	0/1232	0.48	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	SO	0.29	0/1062	0.57	1/1425 (0.1%)
77	SW	0.30	0/1051	0.52	0/1406
78	SY	0.26	0/1083	0.47	0/1438
79	SZ	0.26	0/604	0.57	0/810
80	Sb	0.27	0/665	0.51	0/891
81	Se	0.24	0/465	0.43	0/612
All	All	0.36	1/234864 (0.0%)	0.69	43/344993 (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
34	Lf	0	1
58	SP	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	S6	76	A	C4'-O4'	-5.87	1.38	1.45

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
48	S6	76	A	C5'-C4'-O4'	13.26	125.02	109.10
1	L5	4083	U	N1-C2-O2	8.35	128.64	122.80
1	L5	4083	U	C2-N1-C1'	8.04	127.35	117.70
1	L5	4937	C	C2-N1-C1'	7.68	127.25	118.80
1	L5	1367	C	N1-C2-O2	7.38	123.33	118.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
34	Lf	105	LEU	Peptide
58	SP	72	LYS	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	LA	246/257 (96%)	207 (84%)	25 (10%)	14 (6%)	1 14
5	LB	400/403 (99%)	344 (86%)	42 (10%)	14 (4%)	3 24
6	LC	365/427 (86%)	311 (85%)	30 (8%)	24 (7%)	1 12
7	LD	291/297 (98%)	258 (89%)	22 (8%)	11 (4%)	2 22
8	LE	238/288 (83%)	182 (76%)	37 (16%)	19 (8%)	1 8
9	LF	223/248 (90%)	201 (90%)	18 (8%)	4 (2%)	7 35
10	LG	239/266 (90%)	205 (86%)	19 (8%)	15 (6%)	1 13
11	LH	188/192 (98%)	162 (86%)	18 (10%)	8 (4%)	2 19
12	LI	211/214 (99%)	177 (84%)	26 (12%)	8 (4%)	2 22
13	LJ	174/178 (98%)	147 (84%)	19 (11%)	8 (5%)	2 18
14	LL	208/211 (99%)	179 (86%)	18 (9%)	11 (5%)	1 15
15	LM	137/215 (64%)	115 (84%)	16 (12%)	6 (4%)	2 19
16	LN	201/204 (98%)	180 (90%)	18 (9%)	3 (2%)	8 39
17	LO	199/203 (98%)	180 (90%)	15 (8%)	4 (2%)	6 34
18	LP	151/184 (82%)	130 (86%)	16 (11%)	5 (3%)	3 25
19	LQ	185/188 (98%)	159 (86%)	22 (12%)	4 (2%)	5 32
20	LR	185/196 (94%)	168 (91%)	17 (9%)	0	100 100
21	LS	173/176 (98%)	141 (82%)	21 (12%)	11 (6%)	1 13
22	LT	157/160 (98%)	134 (85%)	18 (12%)	5 (3%)	3 25
23	LU	99/128 (77%)	81 (82%)	17 (17%)	1 (1%)	13 46
24	LV	129/140 (92%)	105 (81%)	18 (14%)	6 (5%)	2 18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
25	LW	122/157 (78%)	96 (79%)	22 (18%)	4 (3%)	3 25
26	LX	118/156 (76%)	103 (87%)	13 (11%)	2 (2%)	7 37
27	LY	132/145 (91%)	118 (89%)	10 (8%)	4 (3%)	3 26
28	LZ	133/136 (98%)	118 (89%)	12 (9%)	3 (2%)	5 31
29	La	145/148 (98%)	122 (84%)	18 (12%)	5 (3%)	3 25
30	Lb	73/159 (46%)	62 (85%)	9 (12%)	2 (3%)	4 28
31	Lc	96/115 (84%)	81 (84%)	9 (9%)	6 (6%)	1 13
32	Ld	105/125 (84%)	85 (81%)	15 (14%)	5 (5%)	2 17
33	Le	126/135 (93%)	107 (85%)	14 (11%)	5 (4%)	2 21
34	Lf	107/110 (97%)	87 (81%)	16 (15%)	4 (4%)	2 22
35	Lg	112/117 (96%)	103 (92%)	8 (7%)	1 (1%)	14 48
36	Lh	120/123 (98%)	110 (92%)	8 (7%)	2 (2%)	7 37
37	Li	100/105 (95%)	92 (92%)	4 (4%)	4 (4%)	2 21
38	Lj	84/97 (87%)	67 (80%)	10 (12%)	7 (8%)	0 8
39	Lk	67/70 (96%)	50 (75%)	12 (18%)	5 (8%)	1 9
40	Ll	48/51 (94%)	44 (92%)	3 (6%)	1 (2%)	5 33
41	Lm	50/128 (39%)	43 (86%)	5 (10%)	2 (4%)	2 21
42	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100 100
43	Lo	102/106 (96%)	85 (83%)	15 (15%)	2 (2%)	6 34
44	Lp	89/92 (97%)	71 (80%)	13 (15%)	5 (6%)	1 15
45	Lr	123/137 (90%)	102 (83%)	15 (12%)	6 (5%)	2 17
46	Lz	215/217 (99%)	168 (78%)	31 (14%)	16 (7%)	1 10
49	SA	220/295 (75%)	187 (85%)	27 (12%)	6 (3%)	4 28
50	SB	212/264 (80%)	174 (82%)	30 (14%)	8 (4%)	2 22
51	SD	225/243 (93%)	183 (81%)	24 (11%)	18 (8%)	1 8
52	SE	260/263 (99%)	215 (83%)	30 (12%)	15 (6%)	1 14
53	SF	189/204 (93%)	144 (76%)	31 (16%)	14 (7%)	1 10
54	SH	187/194 (96%)	145 (78%)	27 (14%)	15 (8%)	1 8
55	SI	204/208 (98%)	168 (82%)	24 (12%)	12 (6%)	1 14
56	SK	96/165 (58%)	76 (79%)	16 (17%)	4 (4%)	2 20
57	SL	151/158 (96%)	130 (86%)	11 (7%)	10 (7%)	1 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
58	SP	95/145 (66%)	61 (64%)	21 (22%)	13 (14%)	0 3
59	SQ	144/146 (99%)	114 (79%)	20 (14%)	10 (7%)	1 11
60	SR	130/135 (96%)	104 (80%)	17 (13%)	9 (7%)	1 11
61	SS	148/152 (97%)	121 (82%)	13 (9%)	14 (10%)	0 6
62	ST	141/145 (97%)	119 (84%)	16 (11%)	6 (4%)	2 19
63	SU	102/119 (86%)	86 (84%)	11 (11%)	5 (5%)	2 17
64	SV	81/83 (98%)	65 (80%)	11 (14%)	5 (6%)	1 13
65	SX	139/143 (97%)	114 (82%)	12 (9%)	13 (9%)	0 6
66	Sa	103/115 (90%)	77 (75%)	16 (16%)	10 (10%)	0 6
67	Sc	62/69 (90%)	47 (76%)	9 (14%)	6 (10%)	0 6
68	Sd	51/56 (91%)	44 (86%)	7 (14%)	0	100 100
69	Sf	69/156 (44%)	47 (68%)	10 (14%)	12 (17%)	0 2
70	Sg	311/317 (98%)	237 (76%)	58 (19%)	16 (5%)	1 16
71	SC	220/293 (75%)	188 (86%)	23 (10%)	9 (4%)	2 20
72	SG	235/249 (94%)	198 (84%)	26 (11%)	11 (5%)	2 18
73	SJ	183/194 (94%)	157 (86%)	16 (9%)	10 (6%)	1 15
74	SM	120/132 (91%)	79 (66%)	29 (24%)	12 (10%)	0 6
75	SN	148/151 (98%)	133 (90%)	8 (5%)	7 (5%)	2 18
76	SO	138/151 (91%)	101 (73%)	24 (17%)	13 (9%)	0 6
77	SW	127/130 (98%)	109 (86%)	13 (10%)	5 (4%)	2 21
78	SY	129/133 (97%)	108 (84%)	16 (12%)	5 (4%)	2 21
79	SZ	73/125 (58%)	59 (81%)	11 (15%)	3 (4%)	2 20
80	Sb	81/84 (96%)	67 (83%)	12 (15%)	2 (2%)	4 29
81	Se	56/59 (95%)	41 (73%)	11 (20%)	4 (7%)	1 11
All	All	11518/12905 (89%)	9598 (83%)	1346 (12%)	574 (5%)	3 17

5 of 574 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	LA	118	GLU
5	LB	360	LEU
6	LC	23	THR
6	LC	148	PRO
6	LC	186	SER

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	LA	190/199 (96%)	189 (100%)	1 (0%)	86	93
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	305/348 (88%)	305 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	215/252 (85%)	215 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	180/181 (99%)	180 (100%)	0	100	100
13	LJ	148/149 (99%)	148 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	Lb	63/126 (50%)	63 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	92 (99%)	1 (1%)	70	83
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Lz	195/196 (100%)	195 (100%)	0	100	100
49	SA	184/243 (76%)	184 (100%)	0	100	100
50	SB	195/231 (84%)	195 (100%)	0	100	100
51	SD	190/202 (94%)	190 (100%)	0	100	100
52	SE	224/225 (100%)	224 (100%)	0	100	100
53	SF	161/170 (95%)	161 (100%)	0	100	100
54	SH	169/174 (97%)	169 (100%)	0	100	100
55	SI	178/180 (99%)	178 (100%)	0	100	100
56	SK	89/136 (65%)	89 (100%)	0	100	100
57	SL	137/142 (96%)	137 (100%)	0	100	100
58	SP	87/130 (67%)	87 (100%)	0	100	100
59	SQ	121/121 (100%)	121 (100%)	0	100	100
60	SR	120/122 (98%)	120 (100%)	0	100	100
61	SS	130/132 (98%)	130 (100%)	0	100	100
62	ST	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	SU	94/107 (88%)	94 (100%)	0	100	100
64	SV	67/67 (100%)	67 (100%)	0	100	100
65	SX	113/115 (98%)	113 (100%)	0	100	100
66	Sa	90/98 (92%)	90 (100%)	0	100	100
67	Sc	57/62 (92%)	57 (100%)	0	100	100
68	Sd	47/49 (96%)	47 (100%)	0	100	100
69	Sf	64/140 (46%)	64 (100%)	0	100	100
70	Sg	272/275 (99%)	272 (100%)	0	100	100
71	SC	188/225 (84%)	188 (100%)	0	100	100
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	161 (100%)	0	100	100
74	SM	104/108 (96%)	104 (100%)	0	100	100
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	110 (100%)	0	100	100
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	113 (100%)	0	100	100
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	75 (100%)	0	100	100
81	Se	47/48 (98%)	47 (100%)	0	100	100
All	All	10039/10997 (91%)	10037 (100%)	2 (0%)	100	100

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	LA	215	ASN
43	Lo	31	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 95 such sidechains are listed below:

Mol	Chain	Res	Type
46	Lz	143	ASN
57	SL	13	GLN
50	SB	202	GLN
54	SH	33	ASN

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Mol	Chain	Res	Type
63	SU	81	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3707/5070 (73%)	1303 (35%)	56 (1%)
2	L7	119/121 (98%)	21 (17%)	0
3	L8	155/157 (98%)	44 (28%)	2 (1%)
47	S2	1716/1869 (91%)	677 (39%)	22 (1%)
48	S6	74/75 (98%)	28 (37%)	2 (2%)
All	All	5771/7292 (79%)	2073 (35%)	82 (1%)

5 of 2073 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	4	G
1	L5	6	C
1	L5	9	C
1	L5	13	U
1	L5	17	A

5 of 82 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L8	87	G
47	S2	912	C
47	S2	213	G
47	S2	606	G
47	S2	1404	U

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 245 ligands modelled in this entry, 245 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
43	Lo	1
66	Sa	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lo	105:GLN	C	106:PHE	N	3.21
1	Sa	99:PRO	C	100:ARG	N	3.14

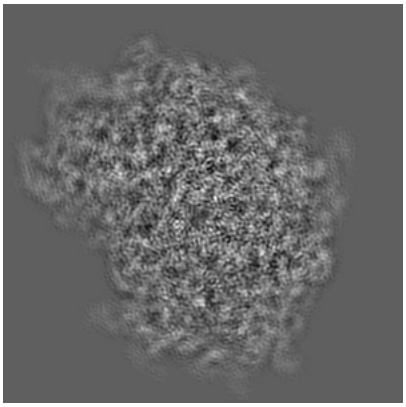
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-2938. These allow visual inspection of the internal detail of the map and identification of artifacts.

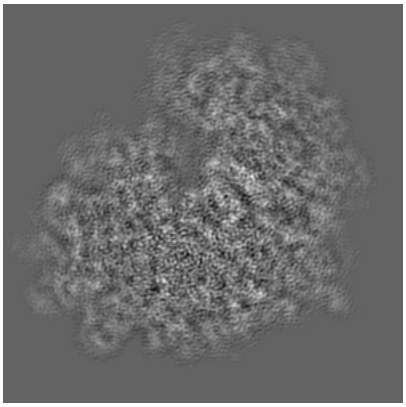
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

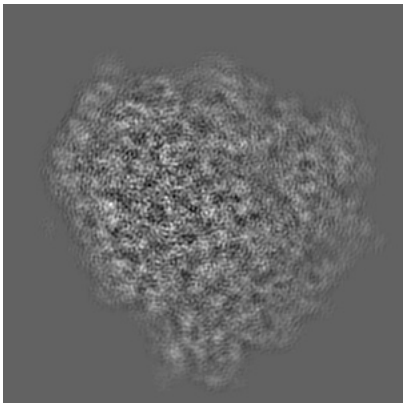
6.1.1 Primary map



X



Y

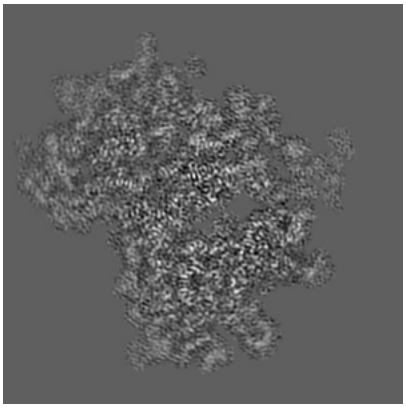


Z

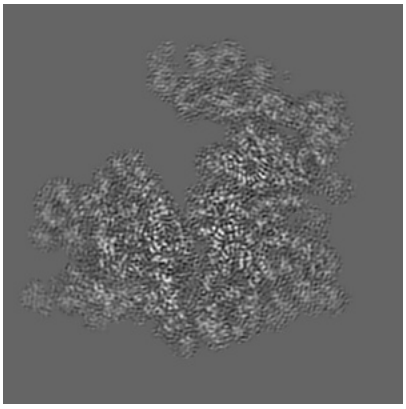
The images above show the map projected in three orthogonal directions.

6.2 Central slices

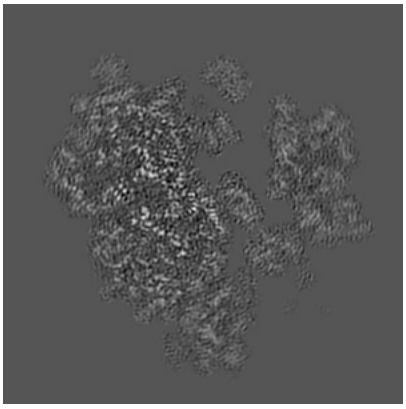
6.2.1 Primary map



X Index: 150



Y Index: 150

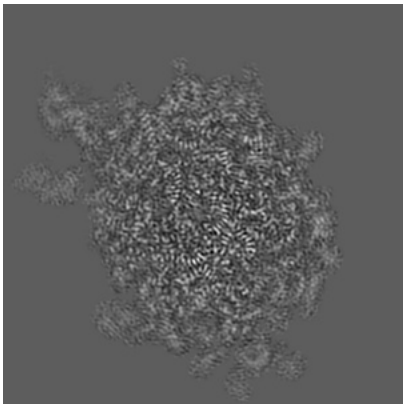


Z Index: 150

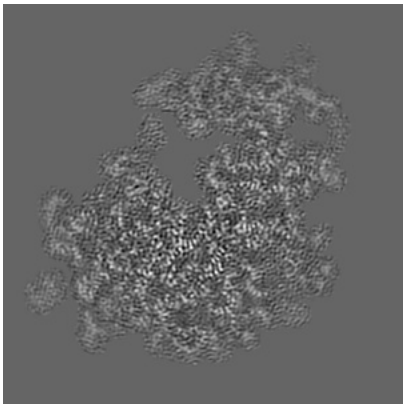
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

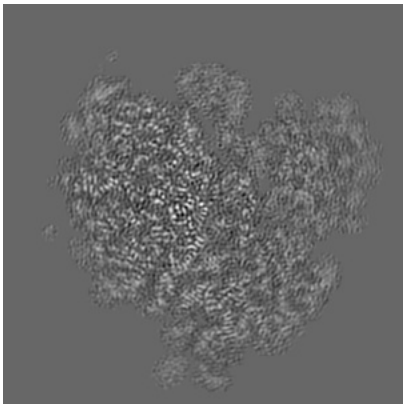
6.3.1 Primary map



X Index: 123



Y Index: 162

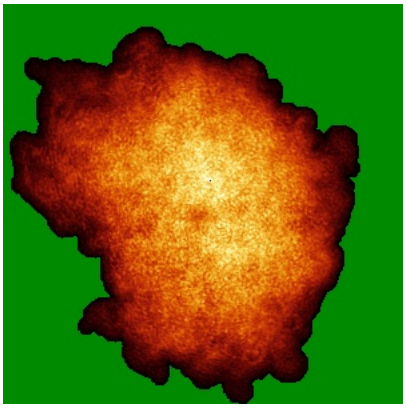


Z Index: 172

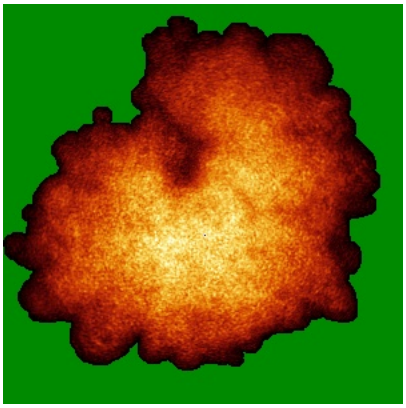
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

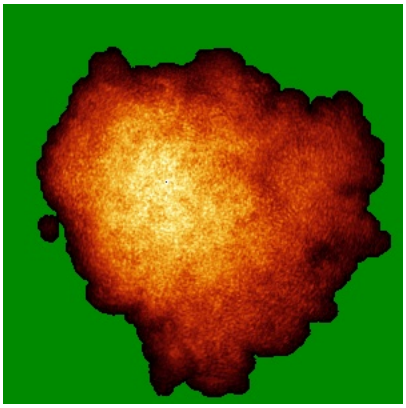
6.4.1 Primary map



X



Y

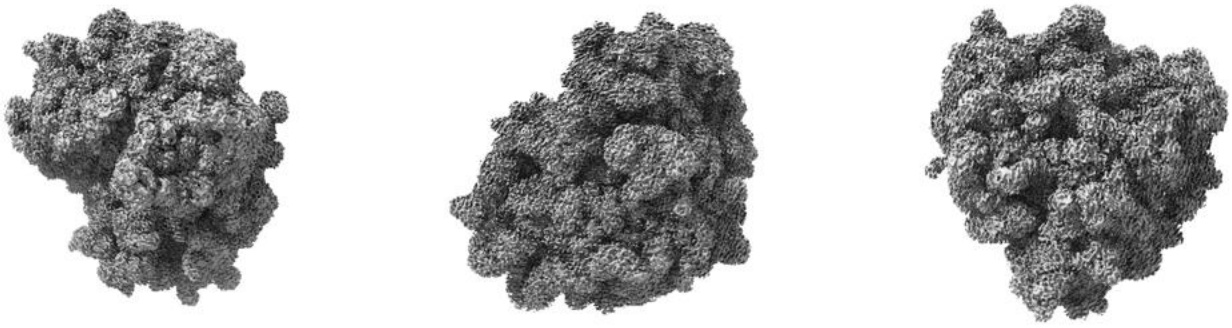


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

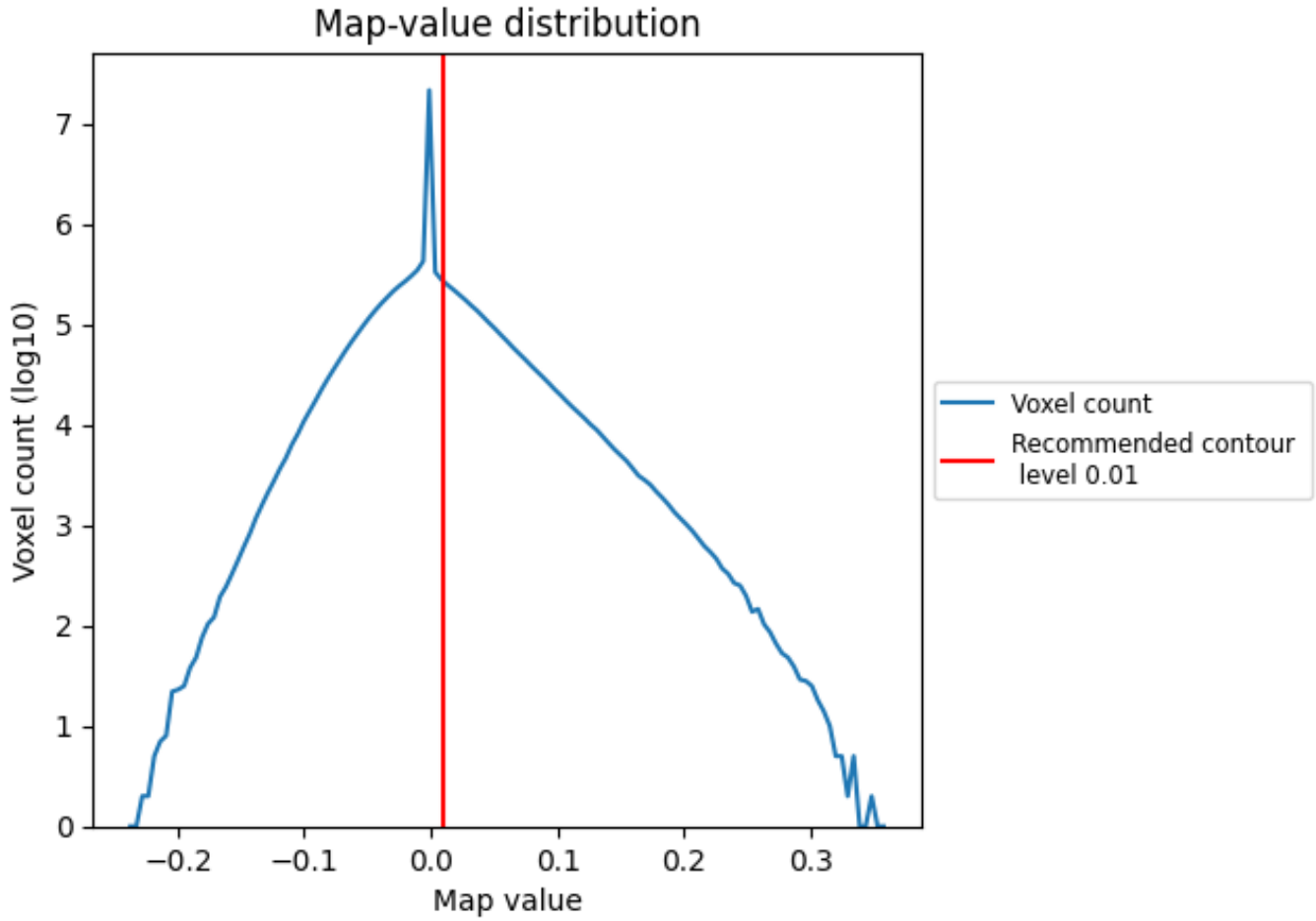
6.6 Mask visualisation (i)

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

7 Map analysis

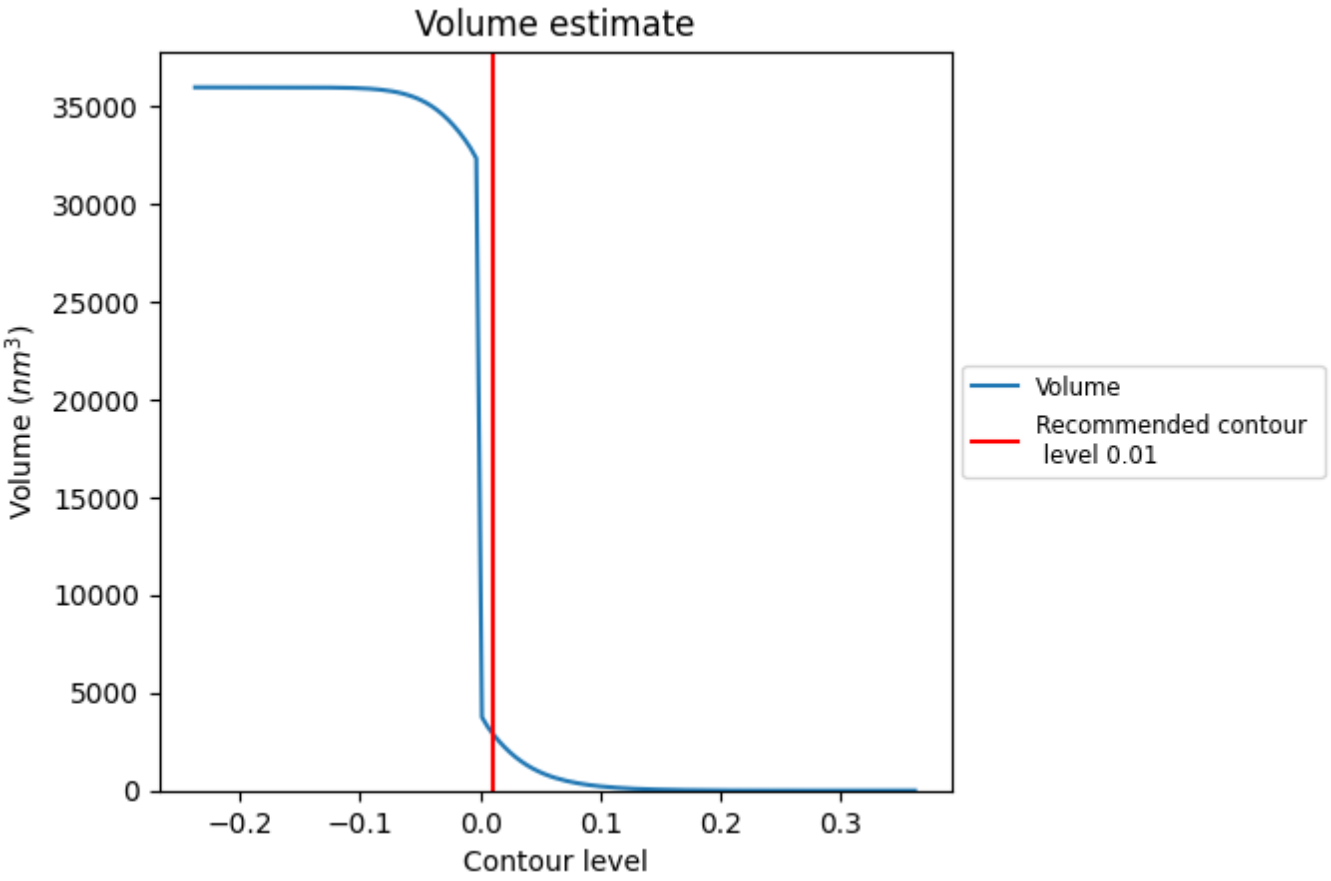
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

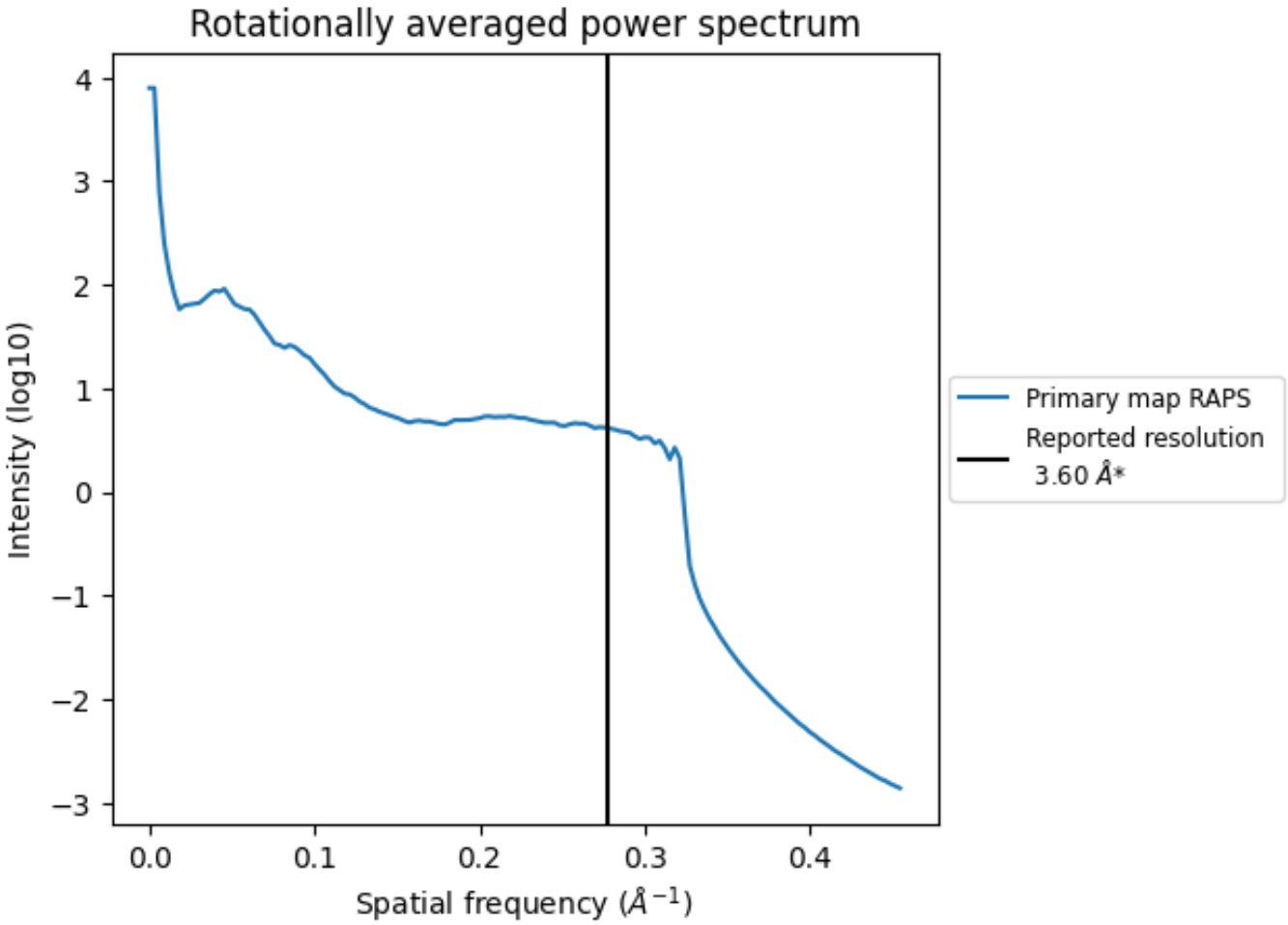
7.2 Volume estimate (i)



The volume at the recommended contour level is 2951 nm^3; this corresponds to an approximate mass of 2666 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.278 Å^{-1}

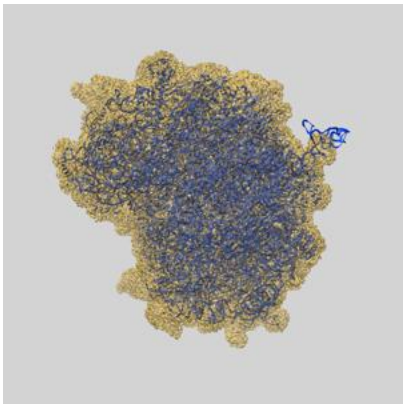
8 Fourier-Shell correlation

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

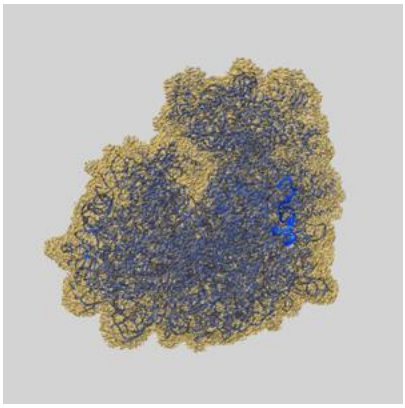
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-2938 and PDB model 4UG0. Per-residue inclusion information can be found in section 3 on page 19.

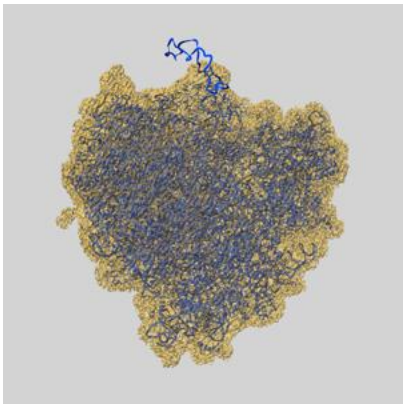
9.1 Map-model overlay



X



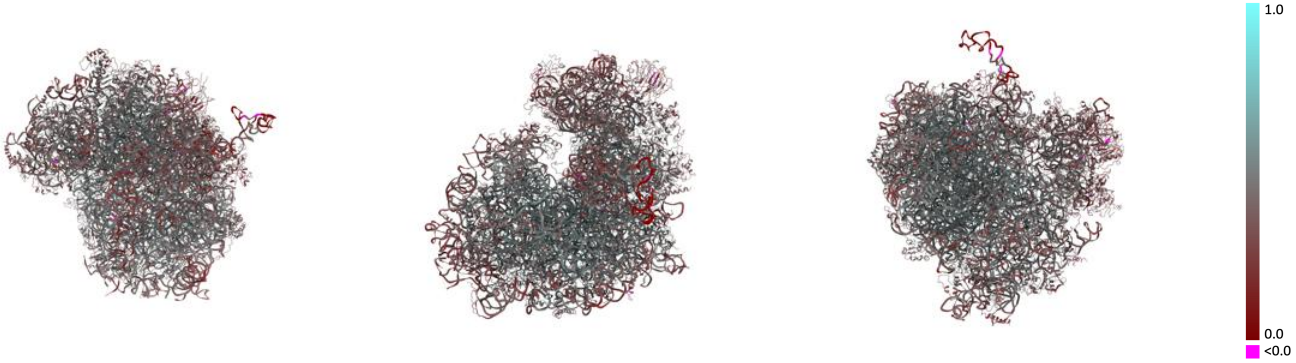
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

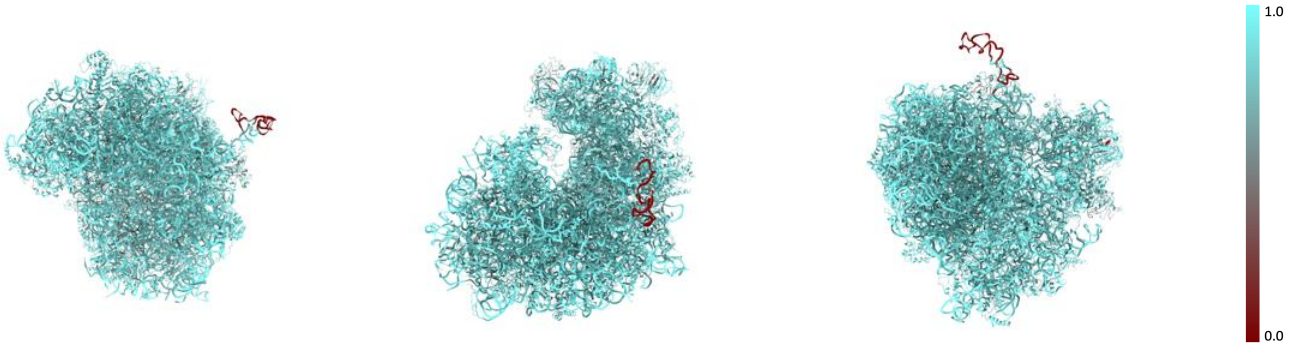
9.2 Q-score mapped to coordinate model



X Y Z

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

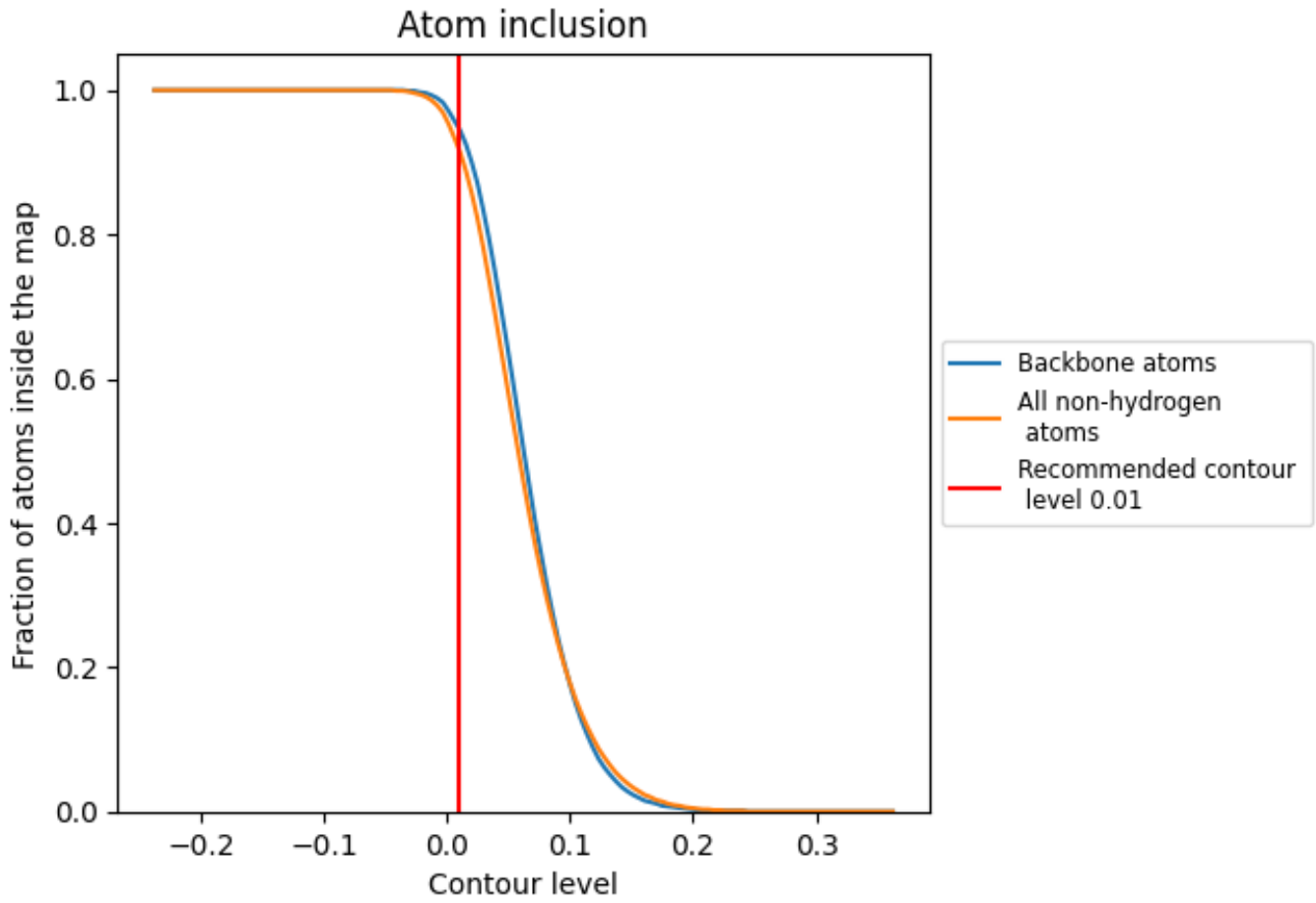
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion (i)



At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9180	0.4400
L5	0.9450	0.4620
L7	0.9730	0.4890
L8	0.9590	0.4900
LA	0.9160	0.5040
LB	0.9120	0.4670
LC	0.9040	0.4700
LD	0.8970	0.4170
LE	0.8790	0.4070
LF	0.8920	0.4770
LG	0.8960	0.4090
LH	0.9030	0.4300
LI	0.8930	0.4370
LJ	0.8880	0.3890
LL	0.9250	0.4550
LM	0.9090	0.4410
LN	0.8950	0.5010
LO	0.9180	0.4750
LP	0.9070	0.4790
LQ	0.9000	0.4750
LR	0.9110	0.4530
LS	0.9130	0.4730
LT	0.9090	0.4680
LU	0.9110	0.4010
LV	0.9250	0.4790
LW	0.8720	0.3930
LX	0.8910	0.4510
LY	0.9130	0.4350
LZ	0.9020	0.4380
La	0.9190	0.4960
Lb	0.8800	0.4310
Lc	0.9140	0.4480
Ld	0.9220	0.4620
Le	0.9050	0.4980
Lf	0.9240	0.5010

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Chain	Atom inclusion	Q-score
Lg	0.9000	0.4660
Lh	0.9030	0.4350
Li	0.9060	0.4380
Lj	0.9150	0.4900
Lk	0.9140	0.4010
Ll	0.9010	0.4850
Lm	0.9090	0.4620
Ln	0.9330	0.5140
Lo	0.9200	0.4800
Lp	0.9240	0.4920
Lr	0.9210	0.4730
Lz	0.7030	0.2650
S2	0.9430	0.4350
S6	0.8860	0.3390
SA	0.8920	0.4110
SB	0.9040	0.4260
SC	0.8890	0.4200
SD	0.8440	0.3480
SE	0.8780	0.4290
SF	0.8400	0.3670
SG	0.8730	0.3710
SH	0.8900	0.3800
SI	0.8870	0.4320
SJ	0.8800	0.4030
SK	0.8210	0.3020
SL	0.8940	0.4650
SM	0.6630	0.2750
SN	0.8920	0.4370
SO	0.8870	0.4430
SP	0.8590	0.3280
SQ	0.8210	0.3530
SR	0.8620	0.3650
SS	0.8560	0.3290
ST	0.8360	0.3470
SU	0.8340	0.3320
SV	0.9020	0.4270
SW	0.8770	0.4560
SX	0.8890	0.4620
SY	0.8820	0.3870
SZ	0.8830	0.3340
Sa	0.9070	0.4620
Sb	0.9220	0.4170

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Chain	Atom inclusion	Q-score
Sc	0.8750	0.3650
Sd	0.7940	0.3770
Se	0.8060	0.3550
Sf	0.5800	0.2200
Sg	0.8160	0.3010