



wwPDB EM Validation Summary Report ⓘ

Dec 17, 2022 – 10:15 pm GMT

PDB ID : 6ZME
EMDB ID : EMD-11289
Title : SARS-CoV-2 Nsp1 bound to the human CCDC124-80S-eERF1 ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-02
Resolution : 3.00 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.dev43
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

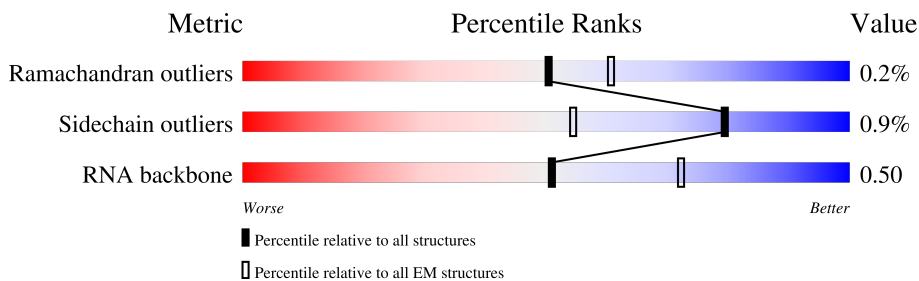
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 Å.

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





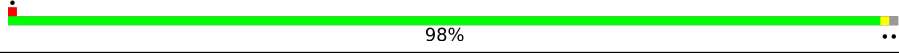
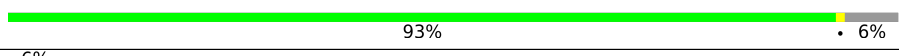
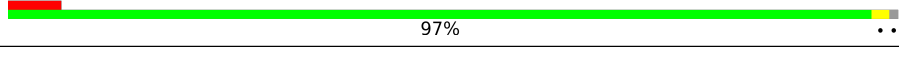
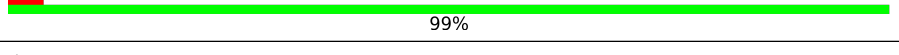

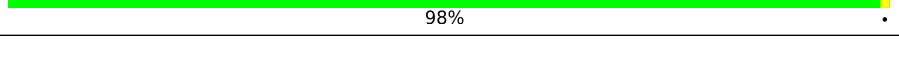
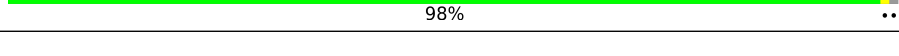
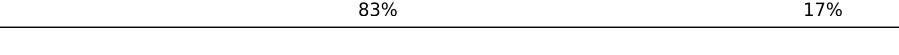
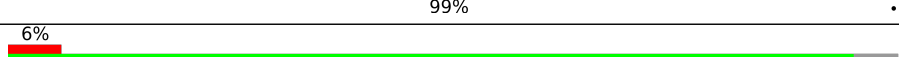
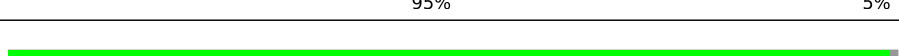
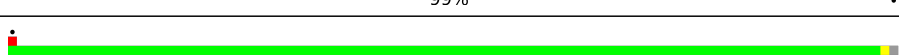
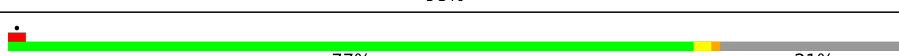
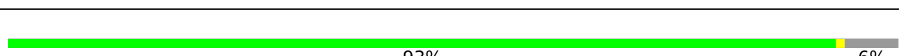
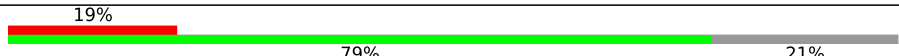

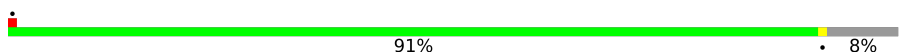
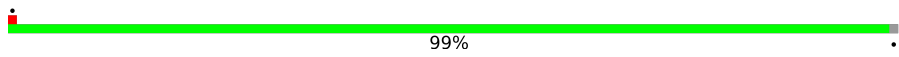
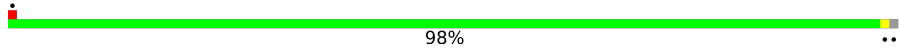

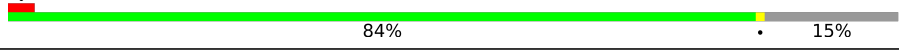

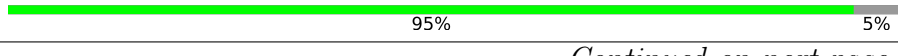

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	L5	5066	
2	L7	121	
3	L8	157	
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	

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Mol	Chain	Length	Quality of chain
9	LF	248	 90% 9%
10	LG	266	 10% 89% 9%
11	LH	192	 98% ..
12	LI	214	 93% 6%
13	LJ	178	 6% 97% ..
14	LL	211	 99%
15	LM	215	 63% .. 35%
16	LN	204	 98% .
17	LO	203	 98% ..
18	LP	184	 83% 17%
19	LQ	188	 99% .
20	LR	196	 6% 95% 5%
21	LS	176	 99% .
22	LT	160	 98% ..
23	LU	128	 77% .. 21%
24	LV	140	 93% 6%
25	LW	157	 19% 79% 21%
26	LX	156	 76% . 23%
27	LY	145	 91% . 8%
28	LZ	136	 99% .
29	La	148	 98% ..
30	Lb	159	 7% 68% 31%
31	Lc	115	 84% . 15%
32	Ld	125	 85% . 14%
33	Le	135	 95% 5%

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Mol	Chain	Length	Quality of chain
34	Lf	110	95%
35	Lg	117	96%
36	Lh	123	98%
37	Li	105	97%
38	Lj	97	87% 11%
39	Lk	70	99%
40	Ll	51	96%
41	Lm	128	41% 59%
42	Ln	25	96%
43	Lo	106	99%
44	Lp	92	99%
45	Lr	137	91% 9%
46	Ls	317	36% 60% 38%
47	Lt	165	29% 79% 5% 15%
48	Lz	217	88% 99%
49	S2	1869	67% 23% 7%
50	SA	295	74% 25%
51	SB	264	80% 19%
52	SD	243	7% 92% 7%
53	SE	263	99%
54	SF	204	89% 10%
55	SH	194	14% 94%
56	SI	208	99%
57	SK	165	58% 41%
58	SL	158	7% 96%

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Mol	Chain	Length	Quality of chain
59	SP	145	8% 85% 11%
60	SQ	146	5% 95%
61	SR	135	5% 99%
62	SS	152	93% 5%
63	ST	145	97% ...
64	SU	119	12% 84% 13%
65	SV	83	98% ..
66	SX	143	94% ...
67	Sa	115	88% 11%
68	Sc	69	91% 7%
69	Sd	56	98% .
70	Sg	317	19% 97% ..
71	SC	293	75% 24%
72	SG	249	8% 94% 5%
73	SJ	194	5% 94% 5%
74	SM	132	63% 89% 8%
75	SN	151	99% .
76	SO	151	5% 91% 7%
77	SW	130	99% .
78	SY	133	5% 97% ..
79	SZ	125	6% 57% 40%
80	Sb	84	6% 96% ..
81	Se	59	17% 98% .
82	Sf	156	17% 42% 57%
83	CA	394	86% 88% 10%

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Mol	Chain	Length	Quality of chain
84	CC	75	<p>63% 35% 5%</p>
85	CE	223	<p>51% 48% 5%</p>
86	CF	180	<p>16% 84% 5%</p>
87	CI	599	<p>15% 96% 5%</p>
88	CH	437	<p>29% 93% 5%</p>

2 Entry composition

There are 92 unique types of molecules in this entry. The entry contains 233375 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	3773	80138	35655	14589	26122	3772	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	2561	1141	456	844	120	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	368	2927	1840	583	489	15	0	0

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

- Molecule 8 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	LE	236	1904	1222	361	317	4	0	0

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

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

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	LI	202	1634	1037	314	269	14	0	0

- Molecule 13 is a protein called 60S ribosomal protein L11.

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

- 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
			Total	C	N	O	S		
21	LS	175	1453	925	283	235	10	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

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

- Molecule 25 is a protein called 60S ribosomal protein L24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

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

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- 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	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- 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 acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 47 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 48 is a protein called 60S ribosomal protein L10a.

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

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	S2	1740	36899	16459	6598	12103	1739	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	SA	221	1741	1106	305	322	8	0	0

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S3.

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

- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	SF	184	1461	914	276	264	7	0	0

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	SH	186	1497	956	274	266	1	0	0

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

- Molecule 57 is a protein called 40S ribosomal protein S10.

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

- Molecule 58 is a protein called 40S ribosomal protein S11.

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

- Molecule 59 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	SP	129	1061	672	202	180	7	0	0

- Molecule 60 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	SQ	144	1142	726	216	197	3	0	0

- Molecule 61 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	SR	135	1090	685	202	198	5	0	0

- Molecule 62 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	SS	145	1198	751	242	203	2	0	0

- Molecule 63 is a protein called 40S ribosomal protein S19.

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

- Molecule 64 is a protein called 40S ribosomal protein S20.

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

- Molecule 65 is a protein called 40S ribosomal protein S21.

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

- Molecule 66 is a protein called 40S ribosomal protein S23.

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

- Molecule 67 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Sa	102	821	512	171	133	5	0	0

- Molecule 68 is a protein called 40S ribosomal protein S28.

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

- Molecule 69 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Sd	55	459	286	94	74	5	0	0

- Molecule 70 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 71 is a protein called 40S ribosomal protein S2.

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

- Molecule 72 is a protein called 40S ribosomal protein S6.

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

- Molecule 73 is a protein called 40S ribosomal protein S9.

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

- Molecule 74 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
74	SM	122	940	590	164	177	9	0	0

- Molecule 75 is a protein called 40S ribosomal protein S13.

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

- Molecule 76 is a protein called 40S ribosomal protein S14.

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

- Molecule 77 is a protein called 40S ribosomal protein S15a.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

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

- Molecule 79 is a protein called 40S ribosomal protein S25.

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

- Molecule 80 is a protein called 40S ribosomal protein S27.

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

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
81	Se	58	439	268	97	73	1	0	0

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
82	Sf	67	548	346	102	93	7	0	0

- Molecule 83 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
83	CA	354	2764	1744	475	528	17	4	0

- Molecule 84 is a RNA chain called tRNA.

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

- Molecule 85 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
85	CE	117	998	611	199	184	4	0	0

- Molecule 86 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
86	CF	29	239	145	43	50	1	0	0

- Molecule 87 is a protein called ATP-binding cassette sub-family E member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
87	CI	582	4586	2931	785	839	31	0	0

- Molecule 88 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
88	CH	415	3257	2073	556	617	11	0	0

- Molecule 89 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	L5	210	Total	Mg	0
			210	210	
89	L7	3	Total	Mg	0
			3	3	
89	L8	4	Total	Mg	0
			4	4	
89	LA	1	Total	Mg	0
			1	1	
89	LB	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	LX	1	Total 1	Mg 1	0
89	Le	2	Total 2	Mg 2	0
89	Lg	1	Total 1	Mg 1	0
89	S2	29	Total 29	Mg 29	0
89	SG	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

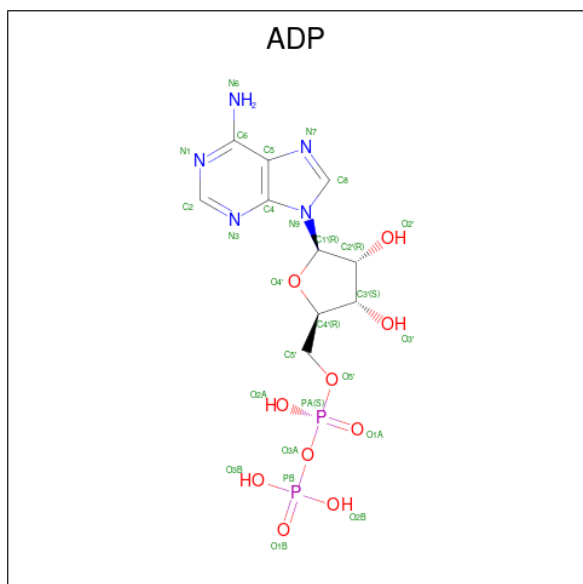
Mol	Chain	Residues	Atoms		AltConf
90	Lg	1	Total 1	Zn 1	0
90	Lj	1	Total 1	Zn 1	0
90	Lm	1	Total 1	Zn 1	0
90	Lo	1	Total 1	Zn 1	0
90	Lp	1	Total 1	Zn 1	0
90	Sa	1	Total 1	Zn 1	0
90	Sd	1	Total 1	Zn 1	0
90	Sf	1	Total 1	Zn 1	0

- Molecule 91 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			AltConf
91	CI	1	Total	Fe	S	0
			16	8	8	
91	CI	1	Total	Fe	S	0
			16	8	8	

- Molecule 92 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

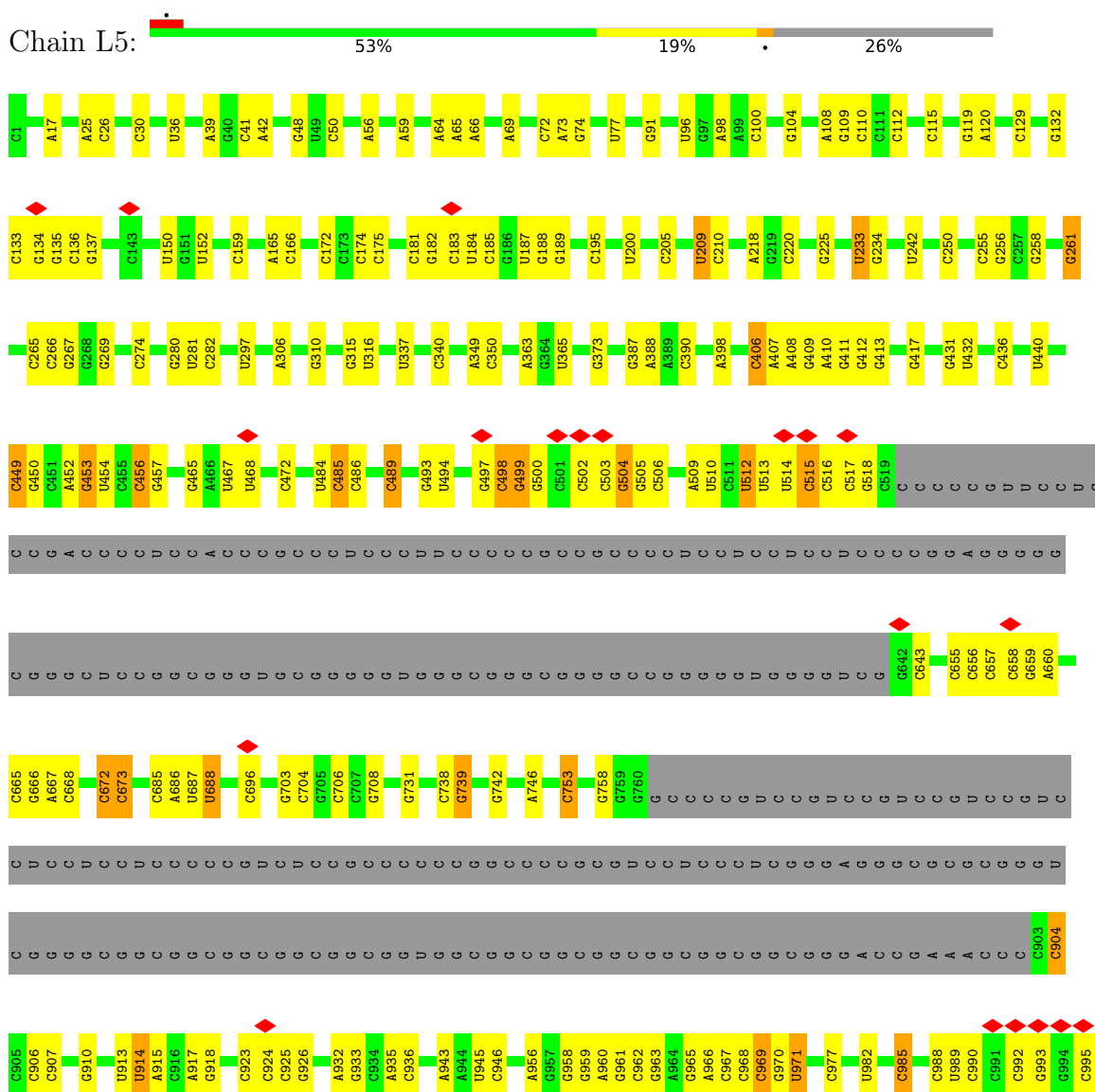


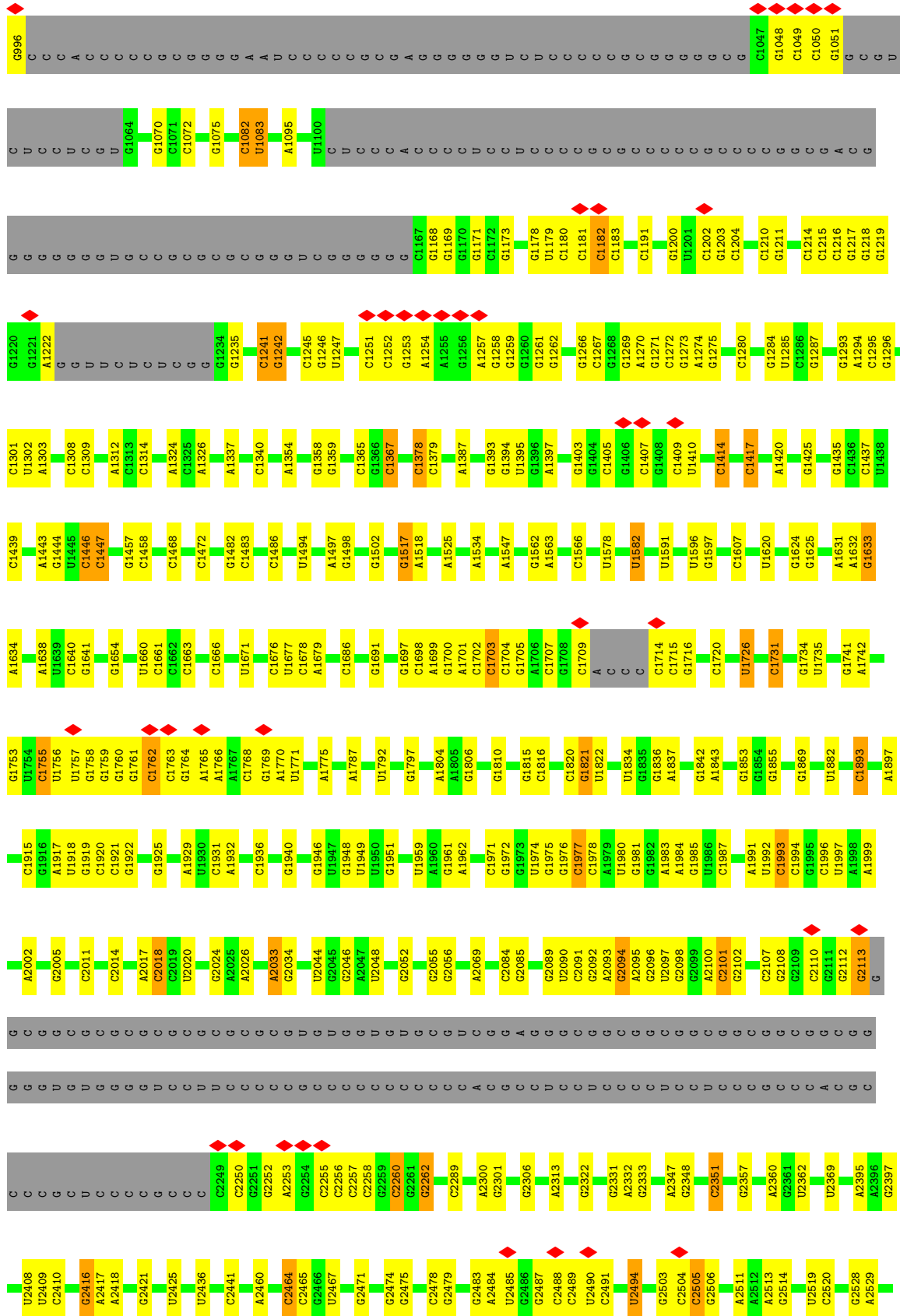
Mol	Chain	Residues	Atoms					AltConf
92	CI	1	Total	C	N	O	P	0
			27	10	5	10	2	

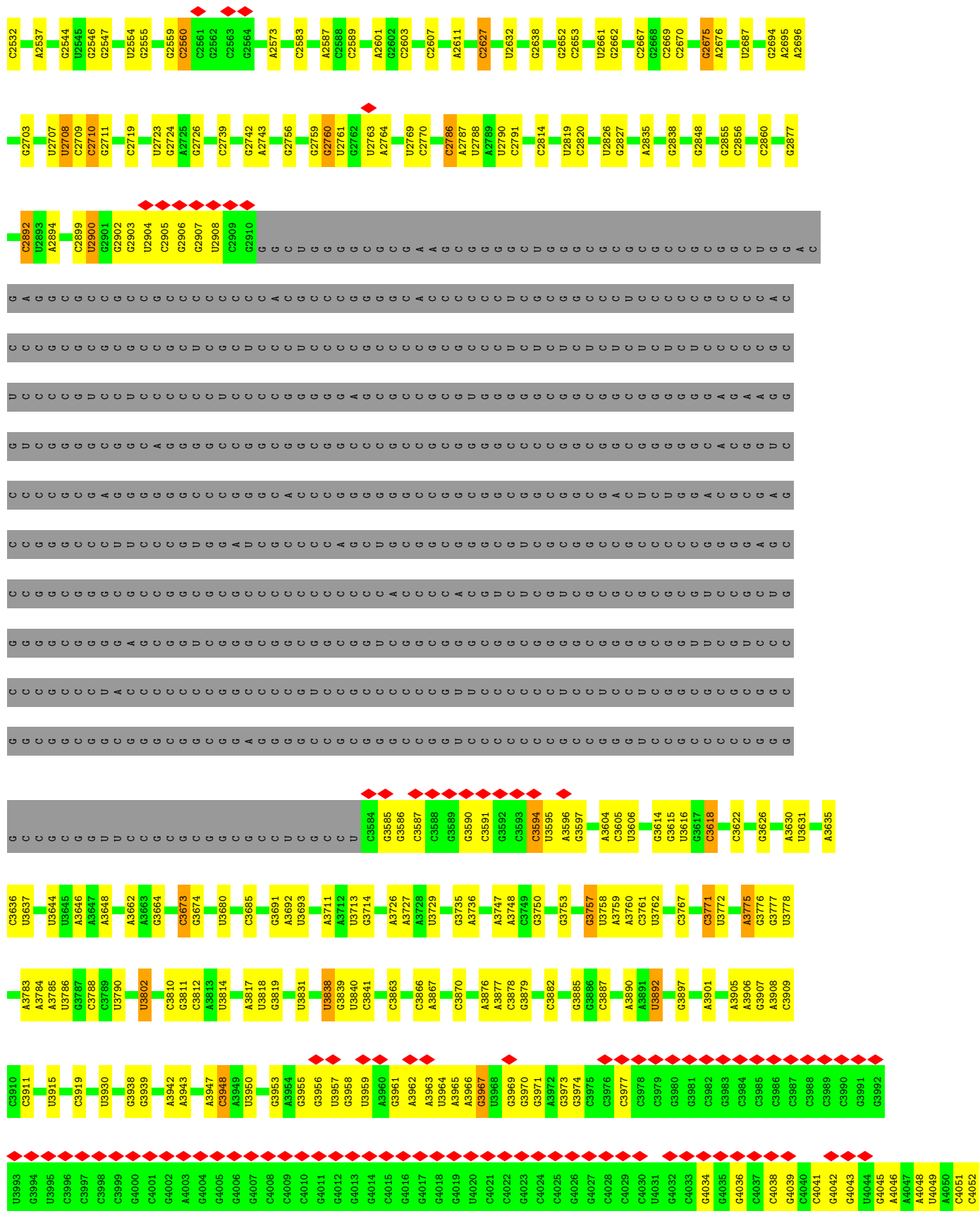
3 Residue-property plots

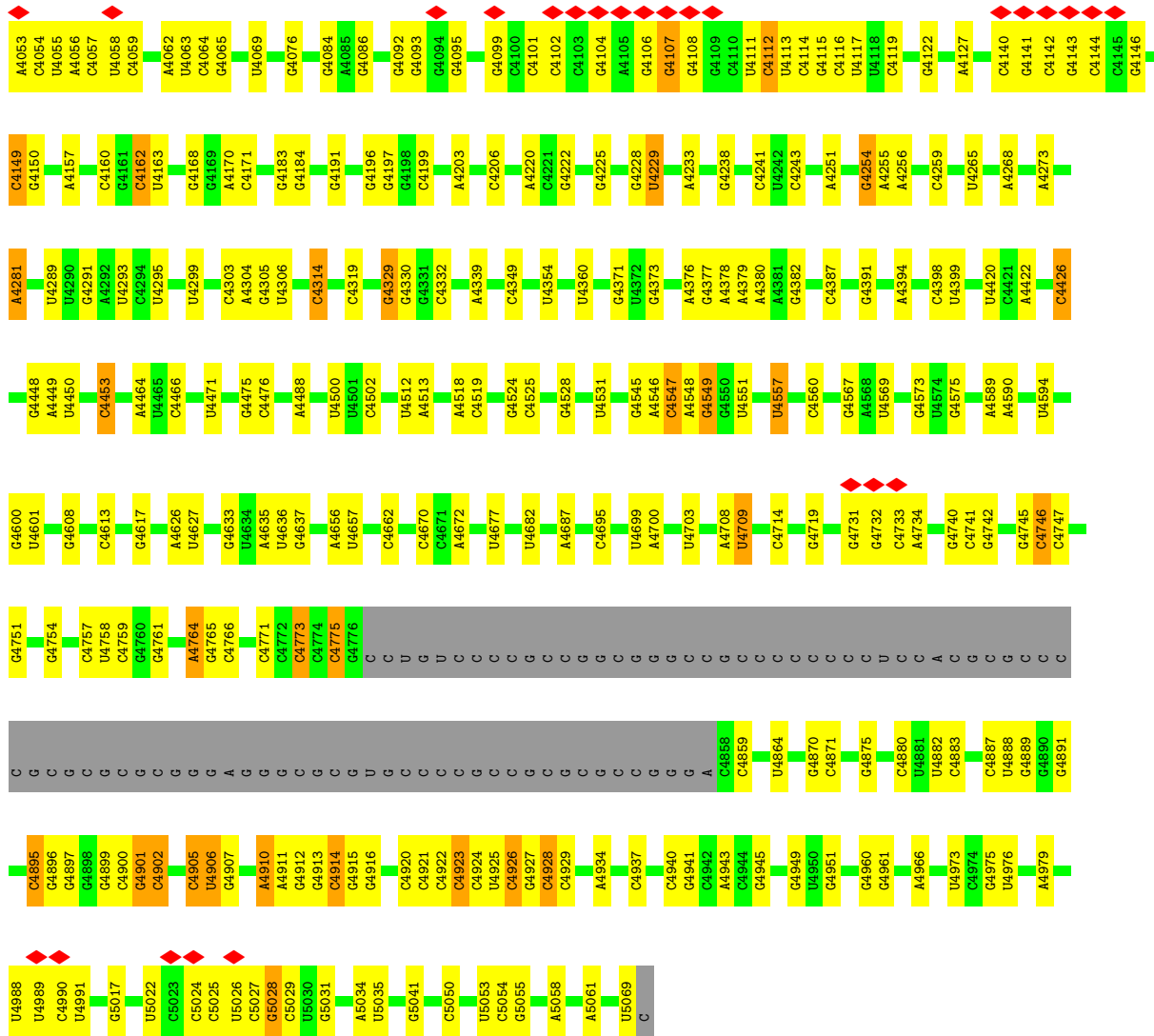
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S ribosomal RNA

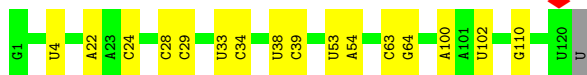
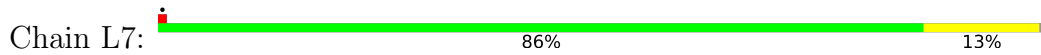




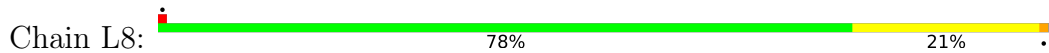




• Molecule 2: 5S ribosomal RNA

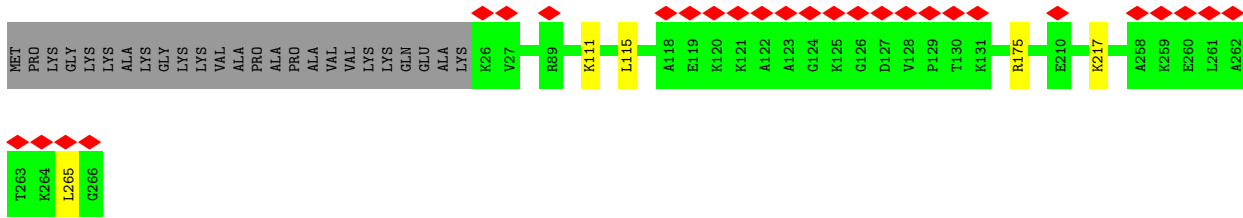


• Molecule 3: 5.8S ribosomal RNA

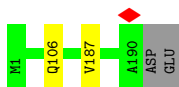


• Molecule 4: 60S ribosomal protein L8

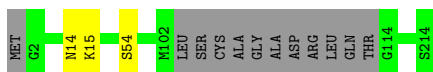




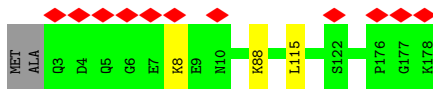
- Molecule 11: 60S ribosomal protein L9



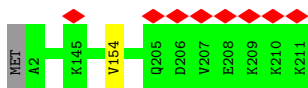
- Molecule 12: 60S ribosomal protein L10-like



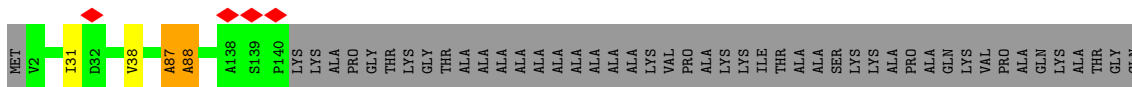
- Molecule 13: 60S ribosomal protein L11



- Molecule 14: 60S ribosomal protein L13



- Molecule 15: 60S ribosomal protein L14



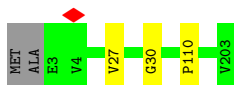
- Molecule 16: 60S ribosomal protein L15





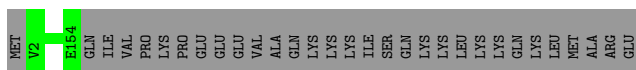
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 98%



- Molecule 18: 60S ribosomal protein L17

Chain LP: 83%



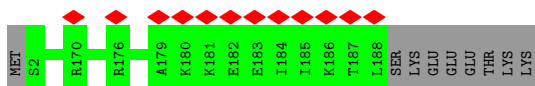
- Molecule 19: 60S ribosomal protein L18

Chain LQ: 99%



- Molecule 20: 60S ribosomal protein L19

Chain LR: 6%



- Molecule 21: 60S ribosomal protein L18a

Chain LS: 99%



- Molecule 22: 60S ribosomal protein L21

Chain LT: 98%

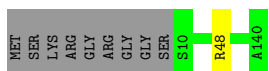


- Molecule 23: 60S ribosomal protein L22

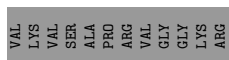
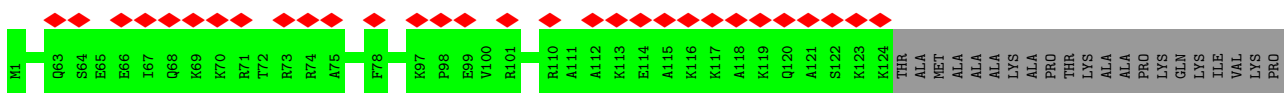
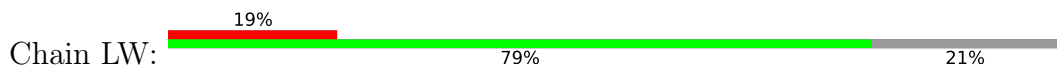
Chain LU: 77%



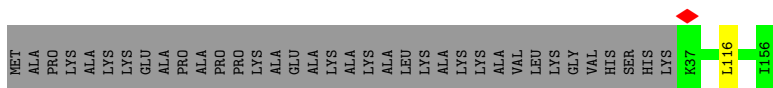
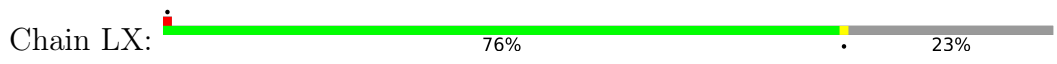
• Molecule 24: 60S ribosomal protein L23



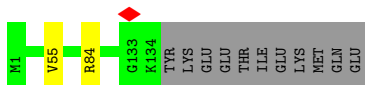
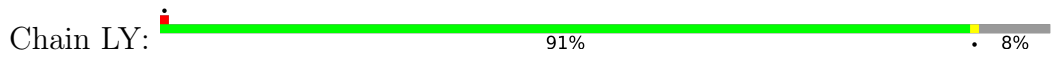
• Molecule 25: 60S ribosomal protein L24



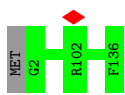
• Molecule 26: 60S ribosomal protein L23a



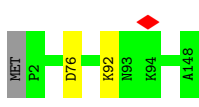
• Molecule 27: 60S ribosomal protein L26



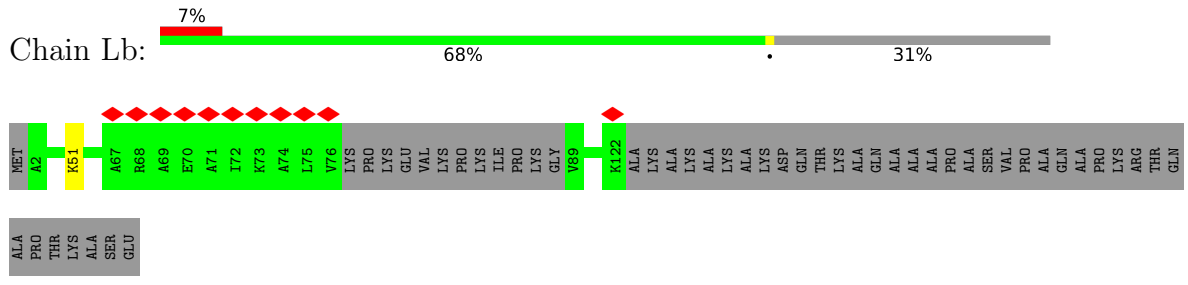
• Molecule 28: 60S ribosomal protein L27



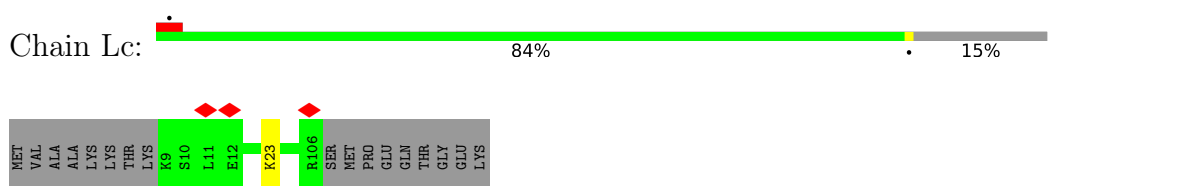
• Molecule 29: 60S ribosomal protein L27a



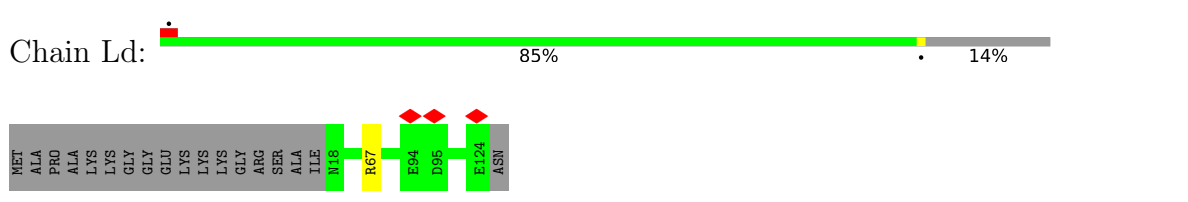
• Molecule 30: 60S ribosomal protein L29



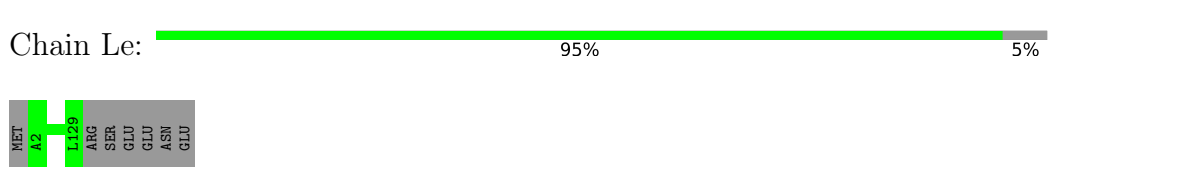
• Molecule 31: 60S ribosomal protein L30



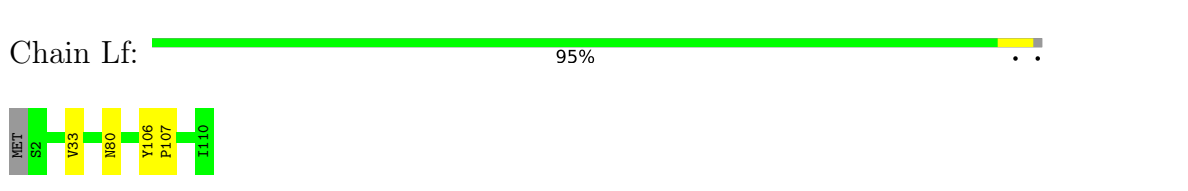
• Molecule 32: 60S ribosomal protein L31



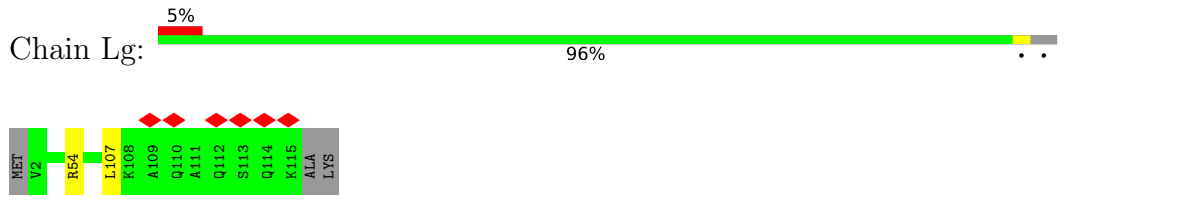
• Molecule 33: 60S ribosomal protein L32



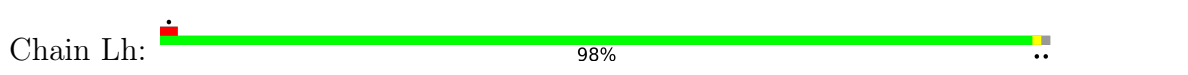
• Molecule 34: 60S ribosomal protein L35a

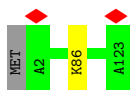


• Molecule 35: 60S ribosomal protein L34

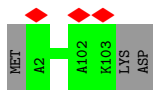


• Molecule 36: 60S ribosomal protein L35

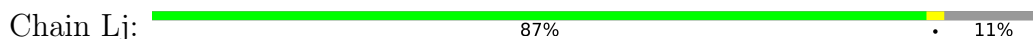




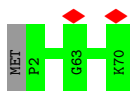
- Molecule 37: 60S ribosomal protein L36



- Molecule 38: 60S ribosomal protein L37



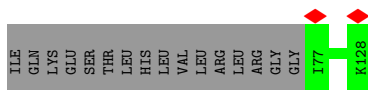
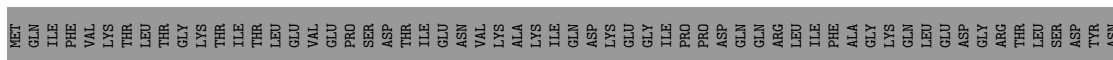
- Molecule 39: 60S ribosomal protein L38



- Molecule 40: 60S ribosomal protein L39



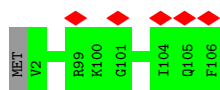
- Molecule 41: Ubiquitin-60S ribosomal protein L40



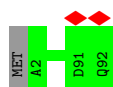
- Molecule 42: 60S ribosomal protein L41



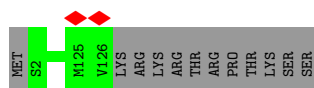
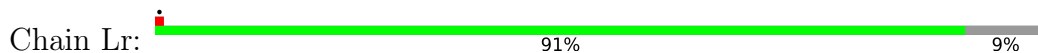
• Molecule 43: 60S ribosomal protein L36a



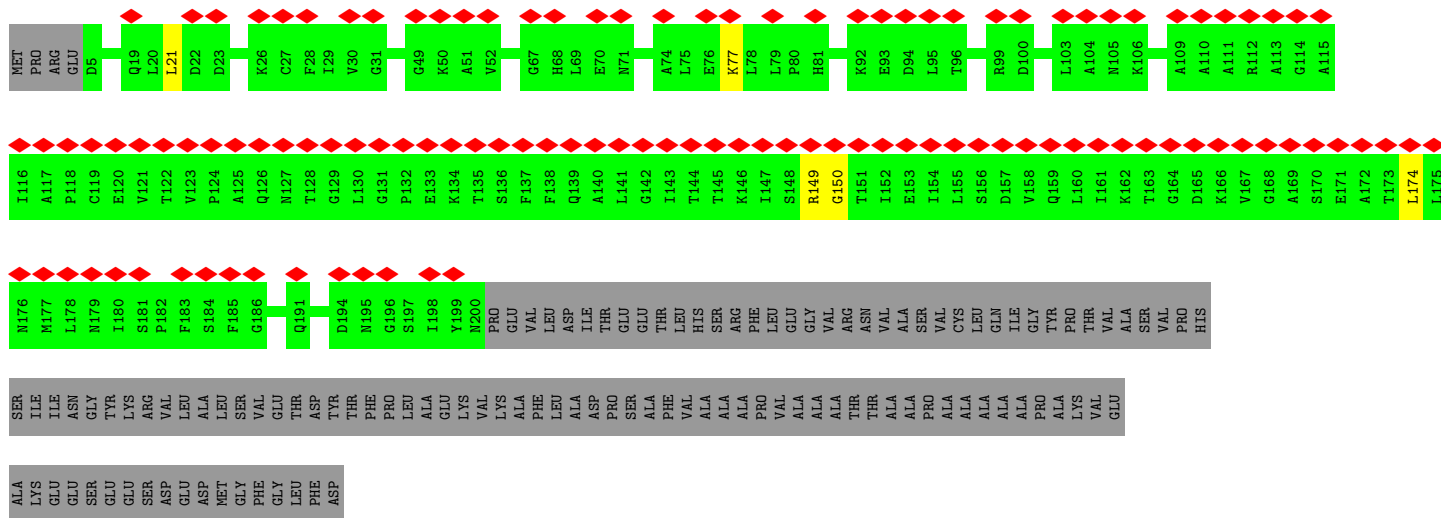
• Molecule 44: 60S ribosomal protein L37a



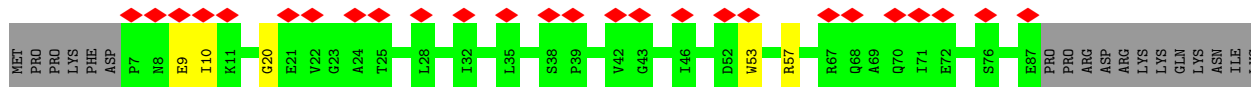
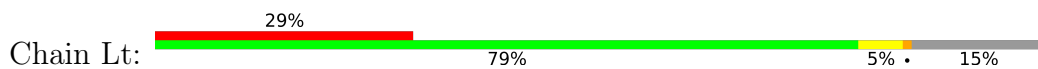
• Molecule 45: 60S ribosomal protein L28

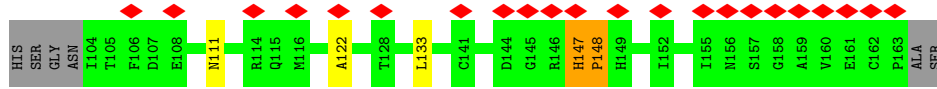


• Molecule 46: 60S acidic ribosomal protein P0

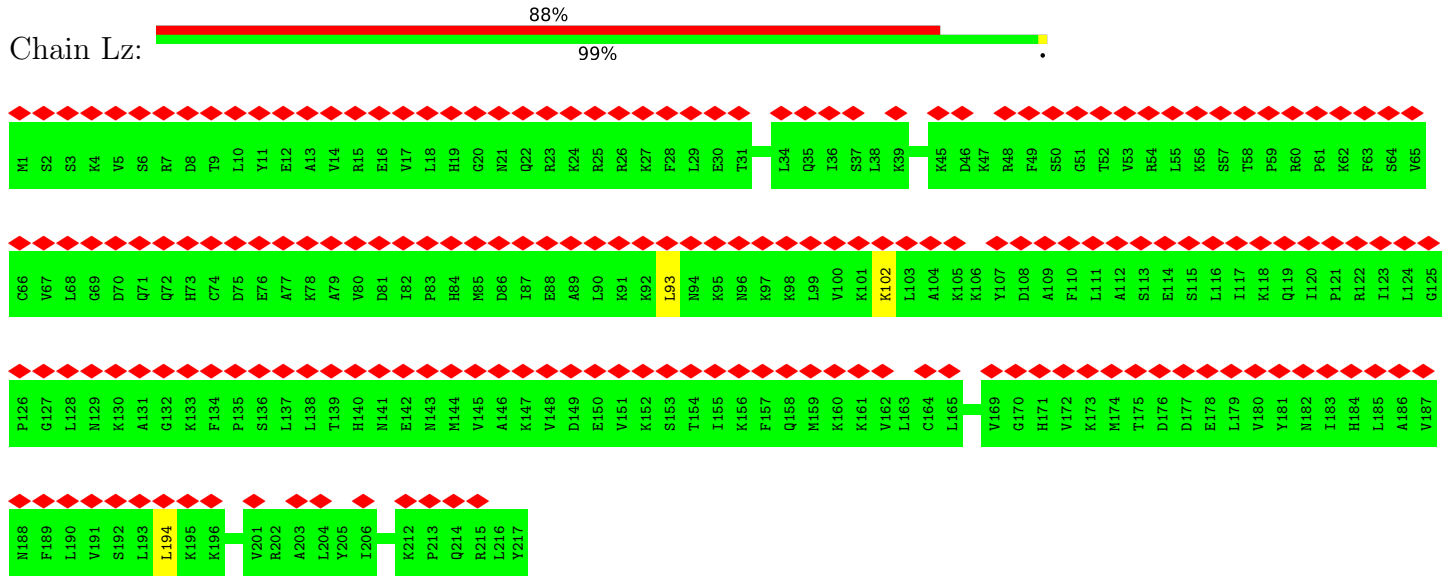


• Molecule 47: 60S ribosomal protein L12

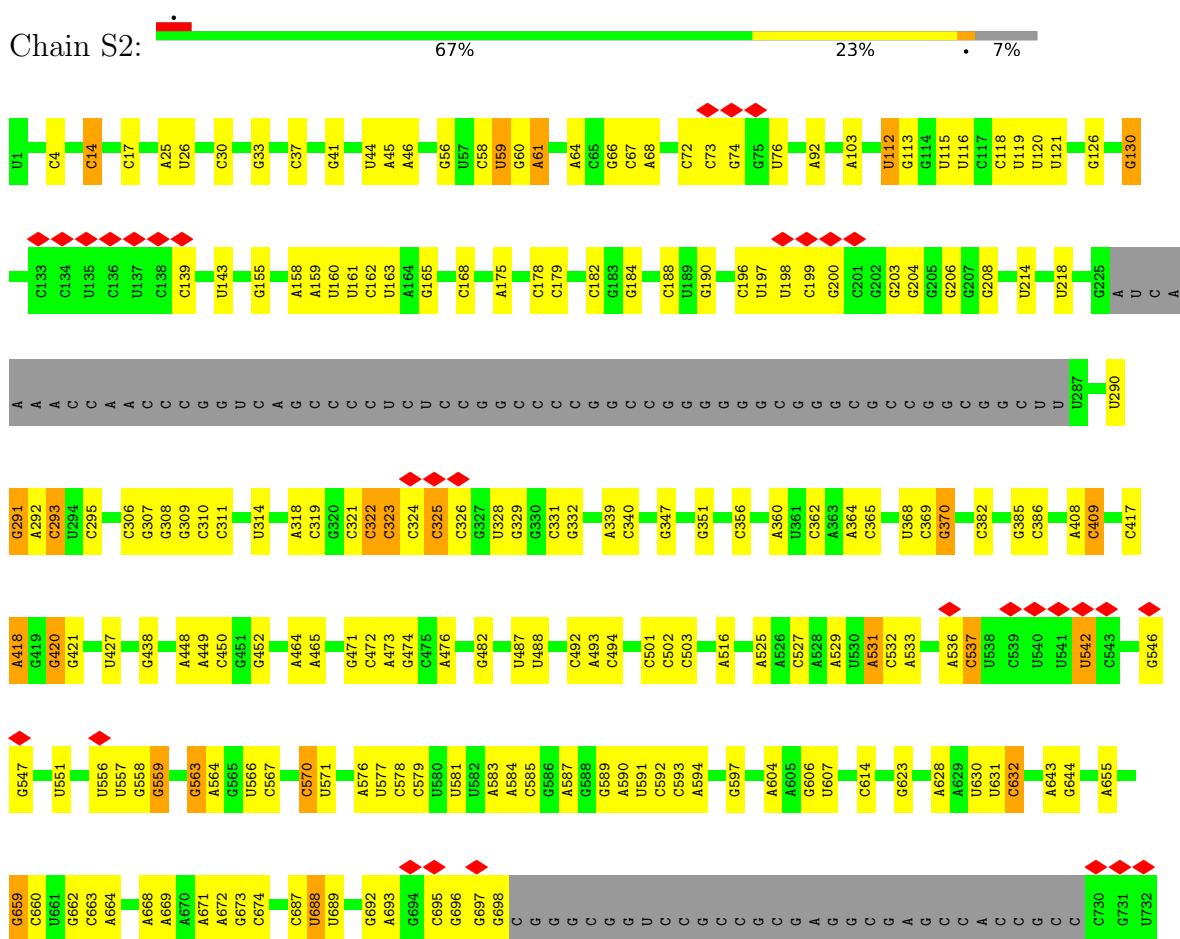


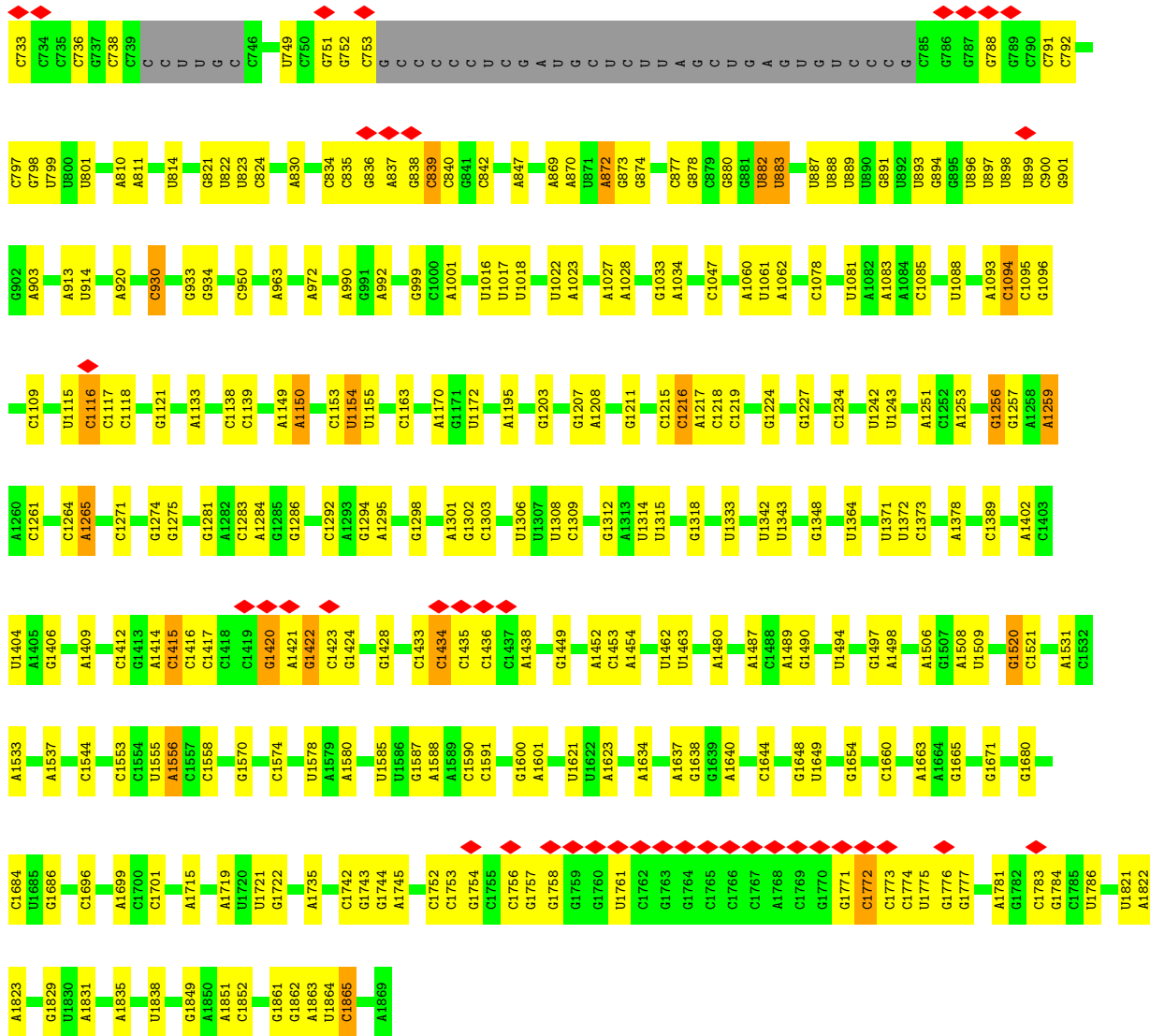


• Molecule 48: 60S ribosomal protein L10a

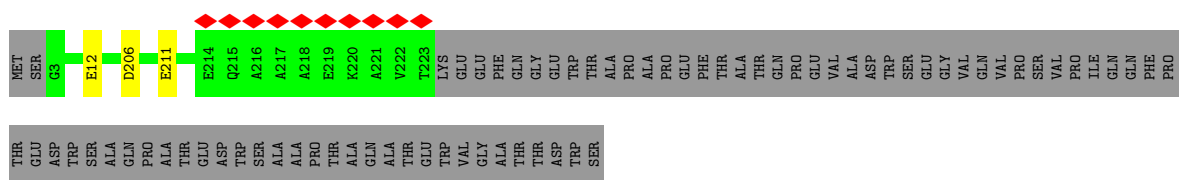
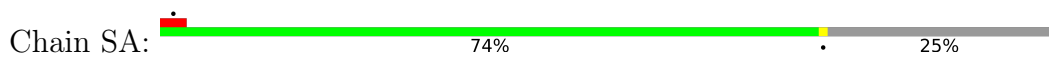


• Molecule 49: 18S ribosomal RNA

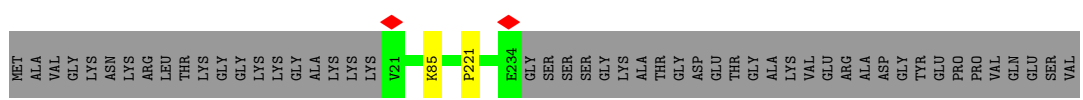
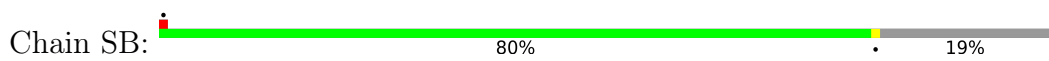




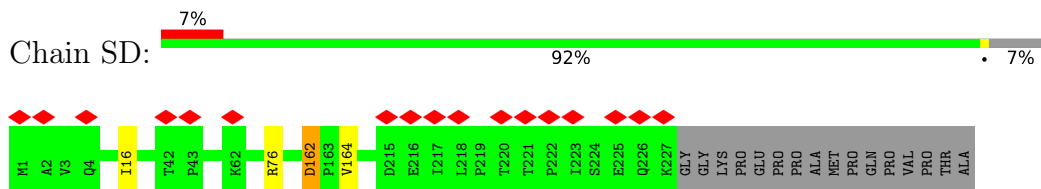
- Molecule 50: 40S ribosomal protein SA



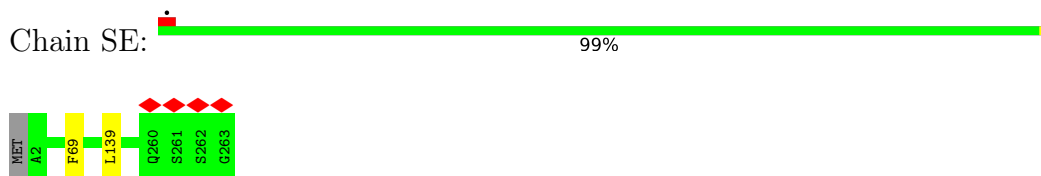
- Molecule 51: 40S ribosomal protein S3a



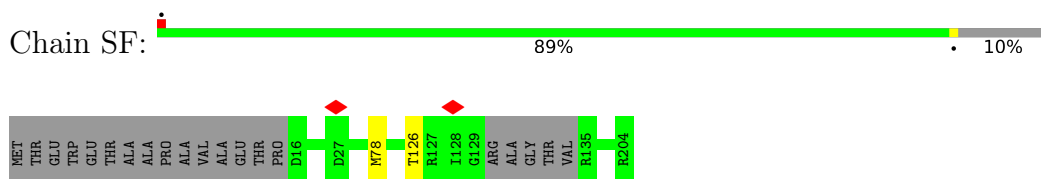
• Molecule 52: 40S ribosomal protein S3



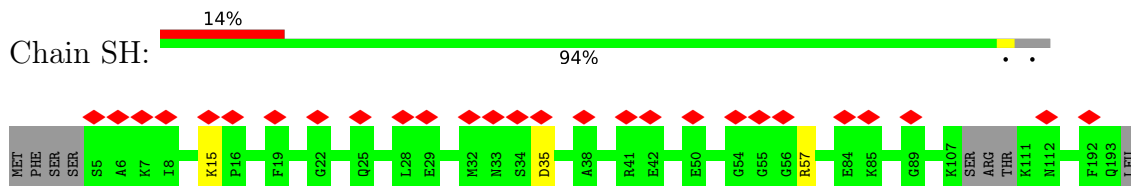
• Molecule 53: 40S ribosomal protein S4, X isoform



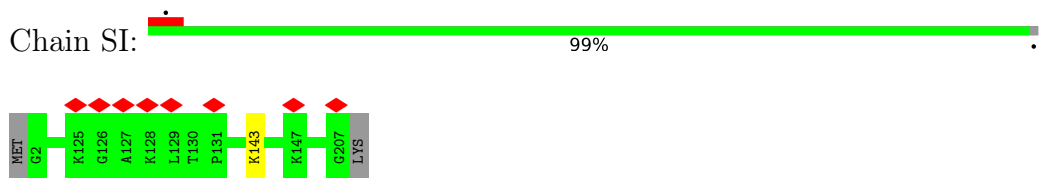
• Molecule 54: 40S ribosomal protein S5



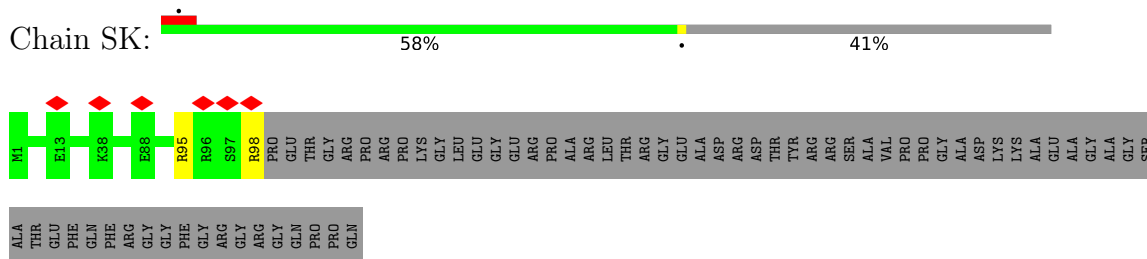
• Molecule 55: 40S ribosomal protein S7



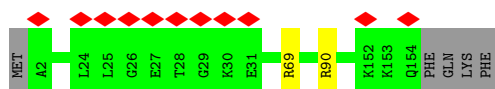
• Molecule 56: 40S ribosomal protein S8



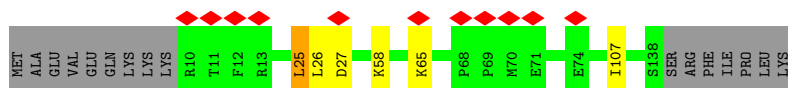
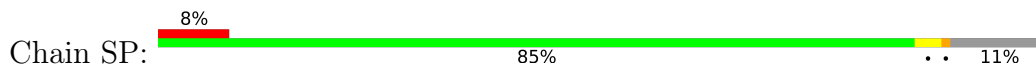
• Molecule 57: 40S ribosomal protein S10



• Molecule 58: 40S ribosomal protein S11



- Molecule 59: 40S ribosomal protein S15



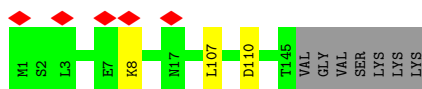
- Molecule 60: 40S ribosomal protein S16



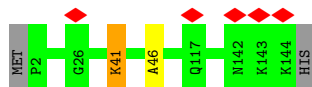
- Molecule 61: 40S ribosomal protein S17



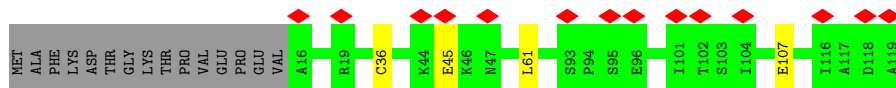
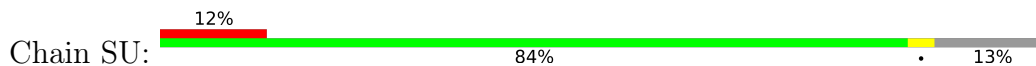
- Molecule 62: 40S ribosomal protein S18



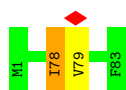
- Molecule 63: 40S ribosomal protein S19



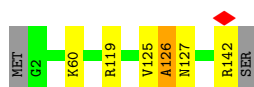
- Molecule 64: 40S ribosomal protein S20



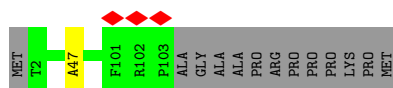
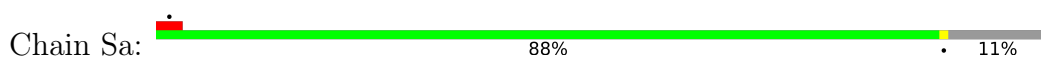
- Molecule 65: 40S ribosomal protein S21



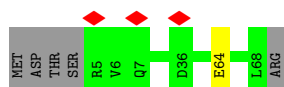
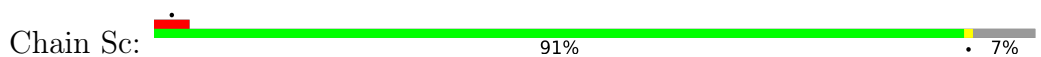
- Molecule 66: 40S ribosomal protein S23



- Molecule 67: 40S ribosomal protein S26



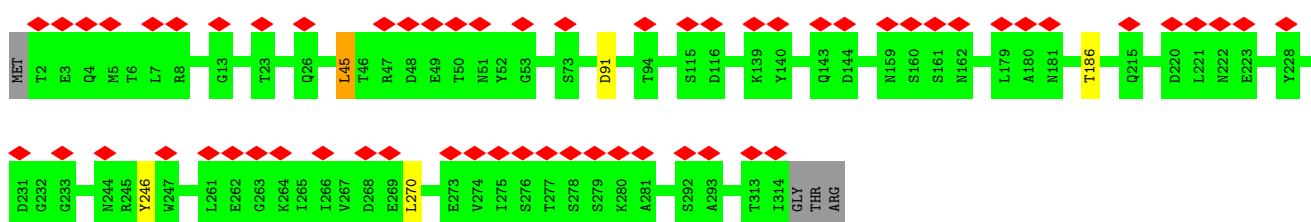
- Molecule 68: 40S ribosomal protein S28



- Molecule 69: 40S ribosomal protein S29



- Molecule 70: Receptor of activated protein C kinase 1

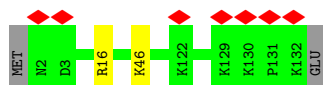


- Molecule 71: 40S ribosomal protein S2

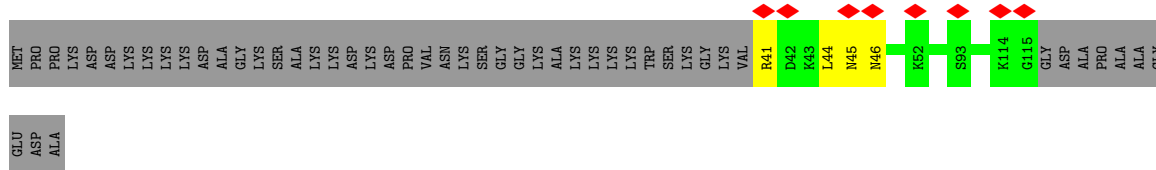
- Molecule 77: 40S ribosomal protein S15a



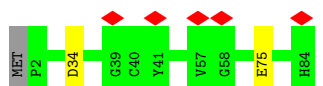
- Molecule 78: 40S ribosomal protein S24



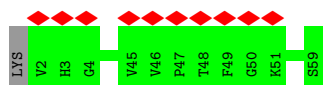
- Molecule 79: 40S ribosomal protein S25



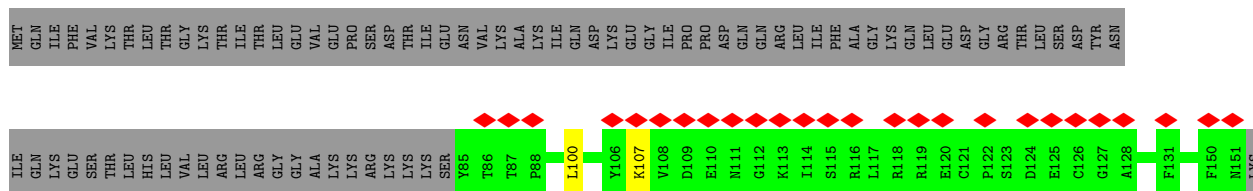
- Molecule 80: 40S ribosomal protein S27



- Molecule 81: 40S ribosomal protein S30

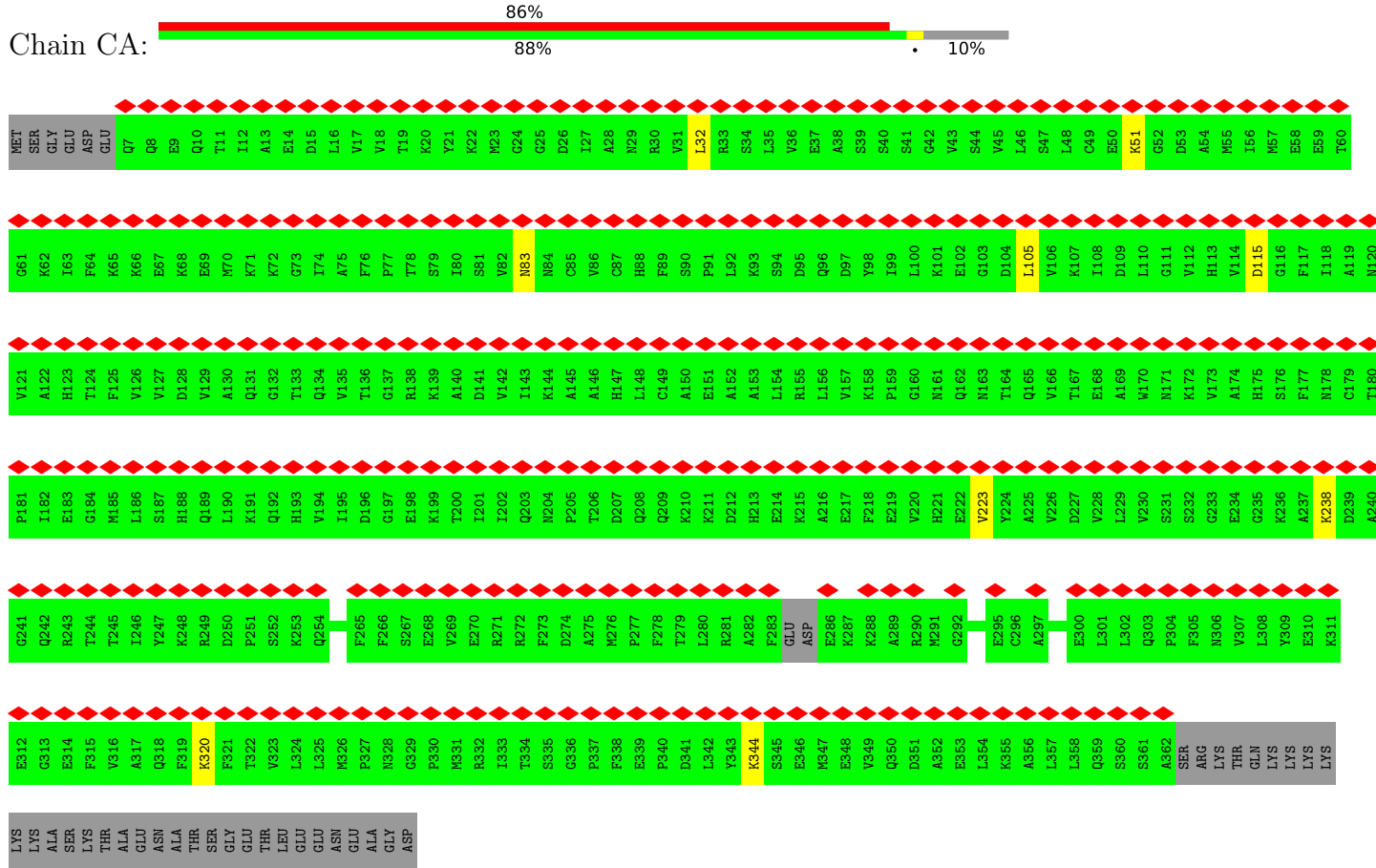


- Molecule 82: Ubiquitin-40S ribosomal protein S27a

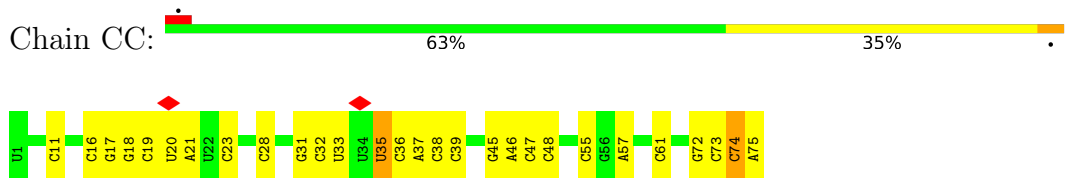


PRO
GLU
ASP
LYS

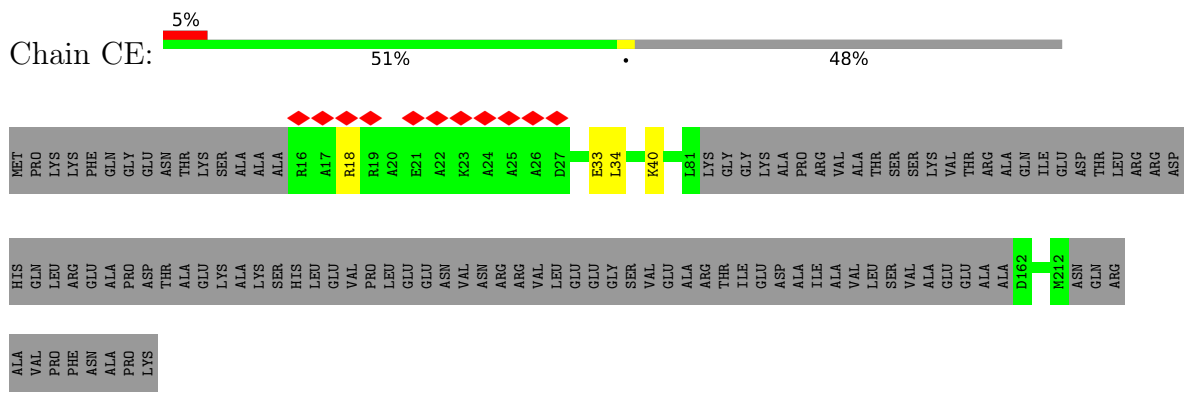
Molecule 83: Proliferation-associated protein 2G4



Molecule 84: tRNA



Molecule 85: Coiled-coil domain-containing protein 124



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13337	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 ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.457	Depositor
Minimum map value	-0.148	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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, ADP, MG, SF4

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	0.68	3/89595 (0.0%)	1.12	547/139686 (0.4%)
2	L7	0.61	0/2861	1.06	13/4459 (0.3%)
3	L8	0.66	0/3701	1.02	13/5766 (0.2%)
4	LA	0.43	0/1936	0.63	0/2596
5	LB	0.38	0/3306	0.60	2/4424 (0.0%)
6	LC	0.38	0/2981	0.59	2/4002 (0.0%)
7	LD	0.34	0/2428	0.54	1/3252 (0.0%)
8	LE	0.32	0/1942	0.57	1/2606 (0.0%)
9	LF	0.40	0/1905	0.55	0/2539
10	LG	0.34	0/1960	0.56	1/2637 (0.0%)
11	LH	0.35	0/1537	0.55	0/2066
12	LI	0.36	0/1673	0.54	0/2233
13	LJ	0.32	0/1433	0.61	1/1915 (0.1%)
14	LL	0.35	0/1732	0.54	0/2315
15	LM	0.36	0/1161	0.55	1/1554 (0.1%)
16	LN	0.41	0/1746	0.57	1/2338 (0.0%)
17	LO	0.38	0/1682	0.50	0/2250
18	LP	0.39	0/1268	0.50	0/1701
19	LQ	0.39	0/1537	0.51	0/2052
20	LR	0.34	0/1582	0.53	0/2091
21	LS	0.38	0/1493	0.50	0/2003
22	LT	0.39	0/1326	0.57	0/1770
23	LU	0.35	0/839	0.64	0/1126
24	LV	0.37	0/993	0.57	0/1332
25	LW	0.36	0/1030	0.55	0/1364
26	LX	0.34	0/1002	0.53	1/1345 (0.1%)
27	LY	0.35	0/1132	0.53	0/1504
28	LZ	0.37	0/1130	0.50	0/1507
29	La	0.38	0/1191	0.52	0/1591
30	Lb	0.30	0/889	0.52	0/1175
31	Lc	0.38	0/774	0.54	0/1038
32	Ld	0.36	0/903	0.55	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.40	0/1071	0.55	0/1429
34	Lf	0.41	0/895	0.57	0/1198
35	Lg	0.38	0/916	0.56	1/1220 (0.1%)
36	Lh	0.31	0/1023	0.49	0/1351
37	Li	0.31	0/843	0.49	0/1115
38	Lj	0.41	0/720	0.59	0/952
39	Lk	0.33	0/575	0.52	0/761
40	Ll	0.34	0/454	0.54	0/599
41	Lm	0.36	0/435	0.51	0/575
42	Ln	0.36	0/231	0.44	0/294
43	Lo	0.35	0/876	0.49	0/1156
44	Lp	0.40	0/718	0.56	0/953
45	Lr	0.35	0/1017	0.51	0/1364
46	Ls	0.32	0/1519	0.65	0/2052
47	Lt	0.34	0/1058	0.79	1/1430 (0.1%)
48	Lz	0.31	0/1769	0.69	2/2371 (0.1%)
49	S2	0.62	6/41245 (0.0%)	1.12	272/64265 (0.4%)
50	SA	0.34	0/1778	0.57	0/2416
51	SB	0.32	0/1765	0.55	0/2362
52	SD	0.32	0/1793	0.59	0/2414
53	SE	0.34	0/2118	0.56	1/2849 (0.0%)
54	SF	0.30	0/1481	0.54	0/1988
55	SH	0.32	0/1519	0.62	1/2033 (0.0%)
56	SI	0.34	0/1715	0.56	0/2287
57	SK	0.31	0/851	0.57	0/1147
58	SL	0.39	0/1268	0.55	0/1696
59	SP	0.29	0/1082	0.66	4/1446 (0.3%)
60	SQ	0.32	0/1160	0.62	0/1553
61	SR	0.30	0/1105	0.60	1/1484 (0.1%)
62	SS	0.31	0/1216	0.62	2/1628 (0.1%)
63	ST	0.32	0/1131	0.51	0/1515
64	SU	0.32	0/831	0.60	0/1115
65	SV	0.33	0/643	0.62	1/860 (0.1%)
66	SX	0.39	0/1116	0.58	0/1490
67	Sa	0.38	0/836	0.61	0/1121
68	Sc	0.31	0/508	0.61	0/680
69	Sd	0.35	0/470	0.55	0/623
70	Sg	0.32	0/2493	0.71	2/3394 (0.1%)
71	SC	0.38	0/1762	0.60	0/2381
72	SG	0.30	0/1946	0.57	1/2590 (0.0%)
73	SJ	0.34	0/1550	0.53	0/2069
74	SM	0.32	0/950	0.64	0/1275
75	SN	0.33	0/1232	0.50	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.34	0/1062	0.61	0/1425
77	SW	0.38	0/1051	0.54	0/1406
78	SY	0.33	0/1083	0.51	0/1438
79	SZ	0.30	0/604	0.73	1/810 (0.1%)
80	Sb	0.32	0/665	0.55	0/891
81	Se	0.30	0/444	0.58	0/588
82	Sf	0.29	0/560	0.63	1/745 (0.1%)
83	CA	0.34	0/2810	0.75	4/3780 (0.1%)
84	CC	0.33	0/1773	1.00	4/2759 (0.1%)
85	CE	0.28	0/1010	0.54	1/1339 (0.1%)
86	CF	0.31	0/244	0.44	0/328
87	CI	0.31	0/4672	0.57	1/6308 (0.0%)
88	CH	0.34	0/3309	0.62	3/4450 (0.1%)
All	All	0.54	9/249639 (0.0%)	0.93	888/364877 (0.2%)

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
4	LA	0	1
5	LB	0	3
8	LE	0	1
11	LH	0	1
12	LI	0	3
14	LL	0	1
15	LM	0	3
17	LO	0	2
22	LT	0	1
34	Lf	0	1
36	Lh	0	1
38	Lj	0	1
46	Ls	0	1
47	Lt	0	6
51	SB	0	1
52	SD	0	2
54	SF	0	2
55	SH	0	1
60	SQ	0	1
63	ST	0	1
64	SU	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
65	SV	0	1
66	SX	0	3
73	SJ	0	1
74	SM	0	1
76	SO	0	1
79	SZ	0	1
80	Sb	0	1
87	CI	0	5
88	CH	0	1
All	All	0	51

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
49	S2	61	A	O3'-P	-8.05	1.51	1.61
1	L5	4546	A	O3'-P	-6.98	1.52	1.61
1	L5	2113	G	C1'-N9	-6.71	1.37	1.46
49	S2	59	U	O3'-P	-6.53	1.53	1.61
49	S2	1093	A	O3'-P	-6.38	1.53	1.61

The worst 5 of 888 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	S2	1417	C	N3-C4-N4	-25.06	100.46	118.00
49	S2	1422	G	N1-C6-O6	-23.97	105.52	119.90
49	S2	1422	G	C5-C6-O6	21.36	141.42	128.60
49	S2	1417	C	C5-C4-N4	19.22	133.65	120.20
49	S2	1772	C	N1-C2-O2	15.49	128.19	118.90

There are no chirality outliers.

5 of 51 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide
5	LB	301	ASN	Peptide
8	LE	129	GLY	Peptide

5.2 Too-close contacts [i](#)

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

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	
4	LA	246/257 (96%)	223 (91%)	22 (9%)	1 (0%)	34	72
5	LB	400/403 (99%)	374 (94%)	25 (6%)	1 (0%)	41	76
6	LC	366/427 (86%)	337 (92%)	29 (8%)	0	100	100
7	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
8	LE	232/288 (81%)	212 (91%)	20 (9%)	0	100	100
9	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
10	LG	239/266 (90%)	223 (93%)	16 (7%)	0	100	100
11	LH	188/192 (98%)	172 (92%)	16 (8%)	0	100	100
12	LI	198/214 (92%)	182 (92%)	16 (8%)	0	100	100
13	LJ	174/178 (98%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	LM	137/215 (64%)	125 (91%)	11 (8%)	1 (1%)	22	60
16	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	15	53
17	LO	199/203 (98%)	186 (94%)	13 (6%)	0	100	100
18	LP	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
19	LQ	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
20	LR	185/196 (94%)	176 (95%)	9 (5%)	0	100	100
21	LS	173/176 (98%)	163 (94%)	10 (6%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
23	LU	99/128 (77%)	84 (85%)	13 (13%)	2 (2%)	7	34
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	LW	122/157 (78%)	113 (93%)	9 (7%)	0	100	100
26	LX	118/156 (76%)	113 (96%)	5 (4%)	0	100	100
27	LY	132/145 (91%)	123 (93%)	9 (7%)	0	100	100
28	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	La	145/148 (98%)	135 (93%)	10 (7%)	0	100	100
30	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	117 (93%)	9 (7%)	0	100	100
34	Lf	107/110 (97%)	97 (91%)	8 (8%)	2 (2%)	8	36
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/97 (87%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Ls	194/317 (61%)	173 (89%)	20 (10%)	1 (0%)	29	68
47	Lt	137/165 (83%)	107 (78%)	27 (20%)	3 (2%)	6	31
48	Lz	215/217 (99%)	159 (74%)	56 (26%)	0	100	100
50	SA	219/295 (74%)	194 (89%)	24 (11%)	1 (0%)	29	68
51	SB	212/264 (80%)	199 (94%)	13 (6%)	0	100	100
52	SD	225/243 (93%)	200 (89%)	25 (11%)	0	100	100
53	SE	260/263 (99%)	242 (93%)	18 (7%)	0	100	100
54	SF	180/204 (88%)	163 (91%)	17 (9%)	0	100	100
55	SH	182/194 (94%)	157 (86%)	25 (14%)	0	100	100
56	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	SK	96/165 (58%)	86 (90%)	10 (10%)	0	100	100
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	116 (91%)	11 (9%)	0	100	100
60	SQ	142/146 (97%)	124 (87%)	17 (12%)	1 (1%)	22	60
61	SR	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
62	SS	143/152 (94%)	132 (92%)	11 (8%)	0	100	100
63	ST	141/145 (97%)	129 (92%)	11 (8%)	1 (1%)	22	60
64	SU	102/119 (86%)	89 (87%)	13 (13%)	0	100	100
65	SV	81/83 (98%)	72 (89%)	8 (10%)	1 (1%)	13	48
66	SX	139/143 (97%)	130 (94%)	7 (5%)	2 (1%)	11	43
67	Sa	100/115 (87%)	90 (90%)	9 (9%)	1 (1%)	15	53
68	Sc	62/69 (90%)	49 (79%)	12 (19%)	1 (2%)	9	40
69	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
70	Sg	311/317 (98%)	269 (86%)	41 (13%)	1 (0%)	41	76
71	SC	220/293 (75%)	206 (94%)	14 (6%)	0	100	100
72	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
73	SJ	183/194 (94%)	171 (93%)	12 (7%)	0	100	100
74	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
75	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
76	SO	138/151 (91%)	126 (91%)	11 (8%)	1 (1%)	22	60
77	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
78	SY	129/133 (97%)	122 (95%)	7 (5%)	0	100	100
79	SZ	73/125 (58%)	59 (81%)	13 (18%)	1 (1%)	11	43
80	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
81	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
82	Sf	65/156 (42%)	54 (83%)	11 (17%)	0	100	100
83	CA	350/394 (89%)	331 (95%)	18 (5%)	1 (0%)	41	76
85	CE	113/223 (51%)	109 (96%)	4 (4%)	0	100	100
86	CF	27/180 (15%)	26 (96%)	1 (4%)	0	100	100
87	CI	578/599 (96%)	537 (93%)	39 (7%)	2 (0%)	41	76
88	CH	413/437 (94%)	388 (94%)	24 (6%)	1 (0%)	47	82

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	13353/15220 (88%)	12258 (92%)	1067 (8%)	28 (0%)	50 82

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
66	SX	127	ASN
15	LM	88	ALA
23	LU	59	GLY
47	Lt	10	ILE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
4	LA	190/199 (96%)	188 (99%)	2 (1%)	73 90
5	LB	348/349 (100%)	347 (100%)	1 (0%)	92 97
6	LC	306/348 (88%)	300 (98%)	6 (2%)	55 83
7	LD	246/250 (98%)	245 (100%)	1 (0%)	91 97
8	LE	209/252 (83%)	208 (100%)	1 (0%)	88 96
9	LF	194/215 (90%)	193 (100%)	1 (0%)	88 96
10	LG	203/223 (91%)	199 (98%)	4 (2%)	55 83
11	LH	169/171 (99%)	168 (99%)	1 (1%)	86 95
12	LI	172/181 (95%)	172 (100%)	0	100 100
13	LJ	148/149 (99%)	146 (99%)	2 (1%)	67 88
14	LL	176/177 (99%)	176 (100%)	0	100 100
15	LM	118/161 (73%)	117 (99%)	1 (1%)	81 93
16	LN	171/172 (99%)	171 (100%)	0	100 100
17	LO	173/174 (99%)	172 (99%)	1 (1%)	86 95
18	LP	134/163 (82%)	134 (100%)	0	100 100
19	LQ	164/165 (99%)	164 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	138 (99%)	1 (1%)	84	94
23	LU	91/115 (79%)	89 (98%)	2 (2%)	52	81
24	LV	101/107 (94%)	100 (99%)	1 (1%)	76	91
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%)	122 (98%)	2 (2%)	62	86
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	118 (98%)	2 (2%)	60	85
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	73	90
31	Lc	83/97 (86%)	82 (99%)	1 (1%)	71	90
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	76	91
33	Le	114/121 (94%)	114 (100%)	0	100	100
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	73	90
35	Lg	98/100 (98%)	97 (99%)	1 (1%)	76	91
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%)	72 (99%)	1 (1%)	67	88
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	46 (98%)	1 (2%)	53	82
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%)	93 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
46	Ls	162/258 (63%)	159 (98%)	3 (2%)	57	84
47	Lt	112/137 (82%)	110 (98%)	2 (2%)	59	85
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	88	96
50	SA	183/243 (75%)	181 (99%)	2 (1%)	73	90
51	SB	195/231 (84%)	194 (100%)	1 (0%)	88	96

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
52	SD	190/202 (94%)	187 (98%)	3 (2%)	62	86
53	SE	224/225 (100%)	223 (100%)	1 (0%)	91	97
54	SF	156/170 (92%)	156 (100%)	0	100	100
55	SH	166/174 (95%)	165 (99%)	1 (1%)	86	95
56	SI	178/180 (99%)	177 (99%)	1 (1%)	86	95
57	SK	89/136 (65%)	87 (98%)	2 (2%)	52	81
58	SL	137/142 (96%)	135 (98%)	2 (2%)	65	87
59	SP	115/130 (88%)	112 (97%)	3 (3%)	46	78
60	SQ	119/121 (98%)	116 (98%)	3 (2%)	47	79
61	SR	122/122 (100%)	122 (100%)	0	100	100
62	SS	126/132 (96%)	125 (99%)	1 (1%)	81	93
63	ST	113/115 (98%)	112 (99%)	1 (1%)	78	92
64	SU	94/107 (88%)	92 (98%)	2 (2%)	53	82
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	111 (98%)	2 (2%)	59	85
67	Sa	89/98 (91%)	89 (100%)	0	100	100
68	Sc	57/62 (92%)	57 (100%)	0	100	100
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	269 (99%)	3 (1%)	73	90
71	SC	188/225 (84%)	187 (100%)	1 (0%)	88	96
72	SG	207/218 (95%)	203 (98%)	4 (2%)	57	84
73	SJ	161/168 (96%)	160 (99%)	1 (1%)	86	95
74	SM	102/108 (94%)	98 (96%)	4 (4%)	32	69
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	109 (99%)	1 (1%)	78	92
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	111 (98%)	2 (2%)	59	85
79	SZ	66/103 (64%)	65 (98%)	1 (2%)	65	87
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	69	89
81	Se	42/48 (88%)	42 (100%)	0	100	100
82	Sf	60/140 (43%)	59 (98%)	1 (2%)	60	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
83	CA	303/336 (90%)	299 (99%)	4 (1%)	69	89
85	CE	104/190 (55%)	101 (97%)	3 (3%)	42	76
86	CF	26/151 (17%)	26 (100%)	0	100	100
87	CI	511/526 (97%)	510 (100%)	1 (0%)	93	98
88	CH	353/376 (94%)	348 (99%)	5 (1%)	67	88
All	All	11626/12971 (90%)	11527 (99%)	99 (1%)	79	92

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	SP	65	LYS
72	SG	20	ASP
60	SQ	71	ARG
66	SX	119	ARG
73	SJ	5	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
57	SK	50	GLN
68	Sc	7	GLN
88	CH	380	ASN
58	SL	11	GLN
62	SS	76	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3706/5066 (73%)	904 (24%)	20 (0%)
2	L7	119/121 (98%)	9 (7%)	0
3	L8	155/157 (98%)	27 (17%)	0
49	S2	1717/1869 (91%)	404 (23%)	12 (0%)
84	CC	74/75 (98%)	26 (35%)	2 (2%)
All	All	5771/7288 (79%)	1370 (23%)	34 (0%)

5 of 1370 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A
1	L5	25	A
1	L5	26	C
1	L5	30	C
1	L5	39	A

5 of 34 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S2	567	C
49	S2	688	U
84	CC	35	U
1	L5	3673	C
1	L5	3614	G

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 267 ligands modelled in this entry, 264 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
91	SF4	CI	601	-	0,12,12	-	-	-	-	-
92	ADP	CI	603	-	24,29,29	0.94	1 (4%)	29,45,45	1.35	4 (13%)
91	SF4	CI	602	-	0,12,12	-	-	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
91	SF4	CI	601	-	-	-	0/6/5/5
92	ADP	CI	603	-	-	6/12/32/32	0/3/3/3
91	SF4	CI	602	-	-	-	0/6/5/5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
92	CI	603	ADP	C5-C4	2.41	1.47	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
92	CI	603	ADP	N3-C2-N1	-3.25	123.59	128.68
92	CI	603	ADP	C4-C5-N7	-2.78	106.50	109.40
92	CI	603	ADP	C3'-C2'-C1'	2.72	105.07	100.98
92	CI	603	ADP	PA-O3A-PB	-2.49	124.29	132.83

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

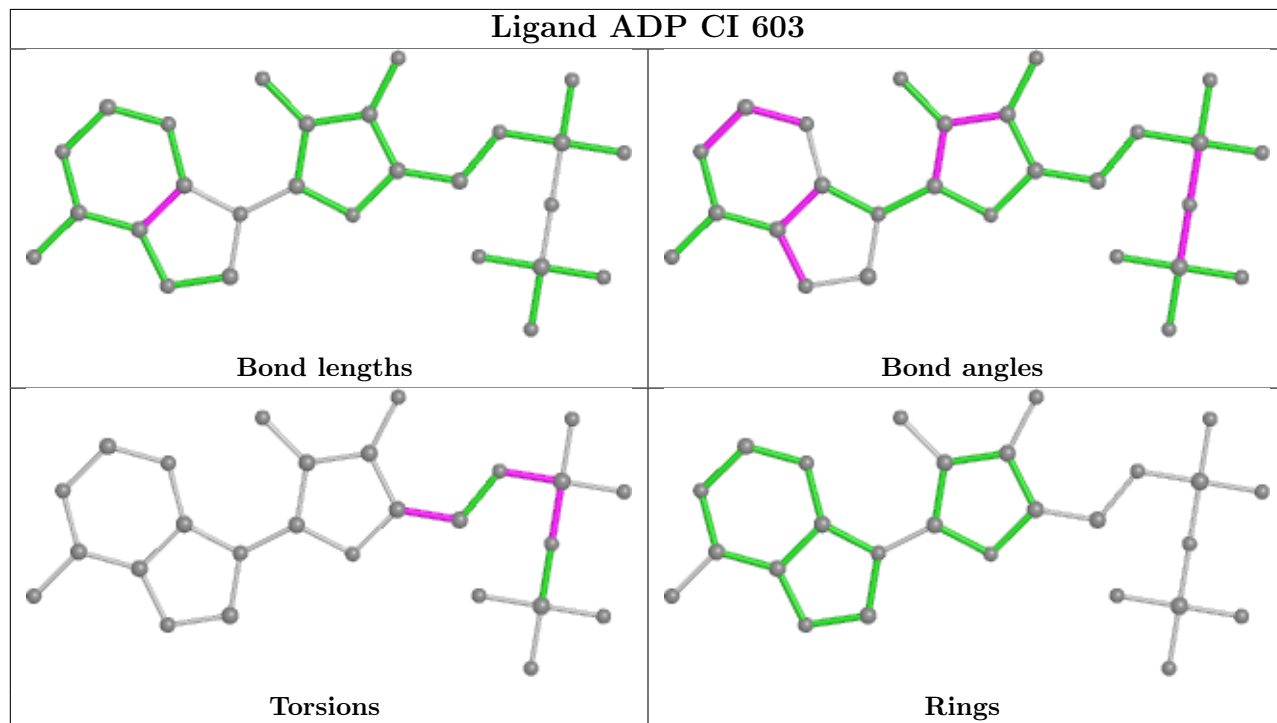
Mol	Chain	Res	Type	Atoms
92	CI	603	ADP	PB-O3A-PA-O5'
92	CI	603	ADP	C5'-O5'-PA-O1A
92	CI	603	ADP	C5'-O5'-PA-O2A
92	CI	603	ADP	O4'-C4'-C5'-O5'
92	CI	603	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

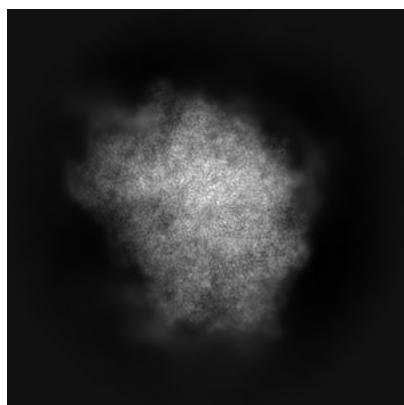
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11289. These allow visual inspection of the internal detail of the map and identification of artifacts.

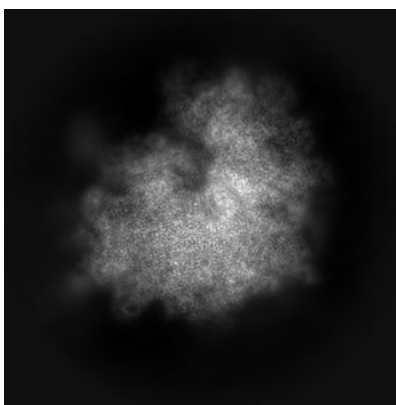
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

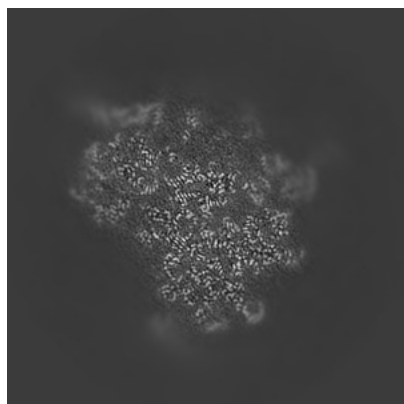


Z

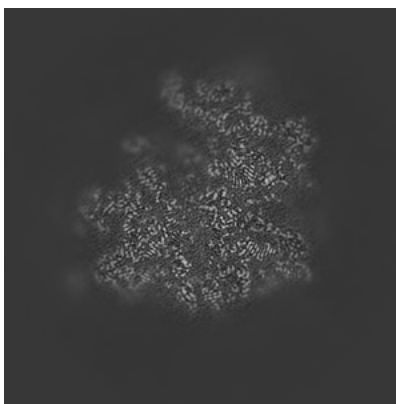
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

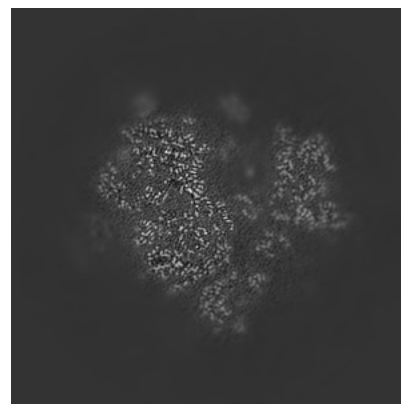
6.2.1 Primary map



X Index: 200



Y Index: 200

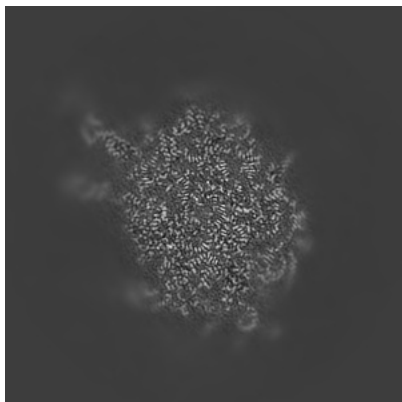


Z Index: 200

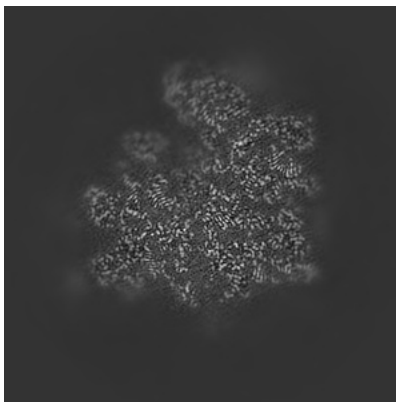
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

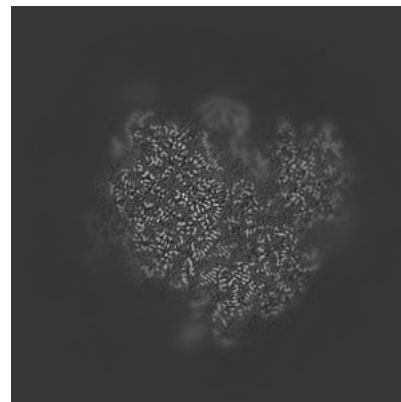
6.3.1 Primary map



X Index: 178



Y Index: 194

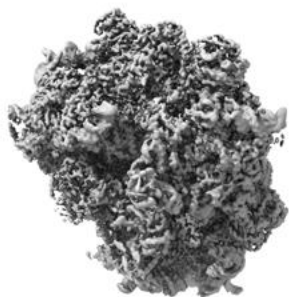


Z Index: 224

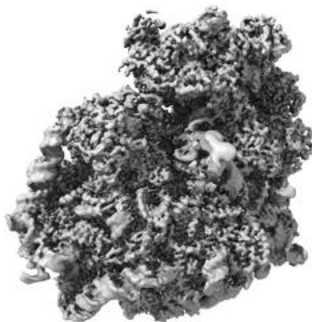
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

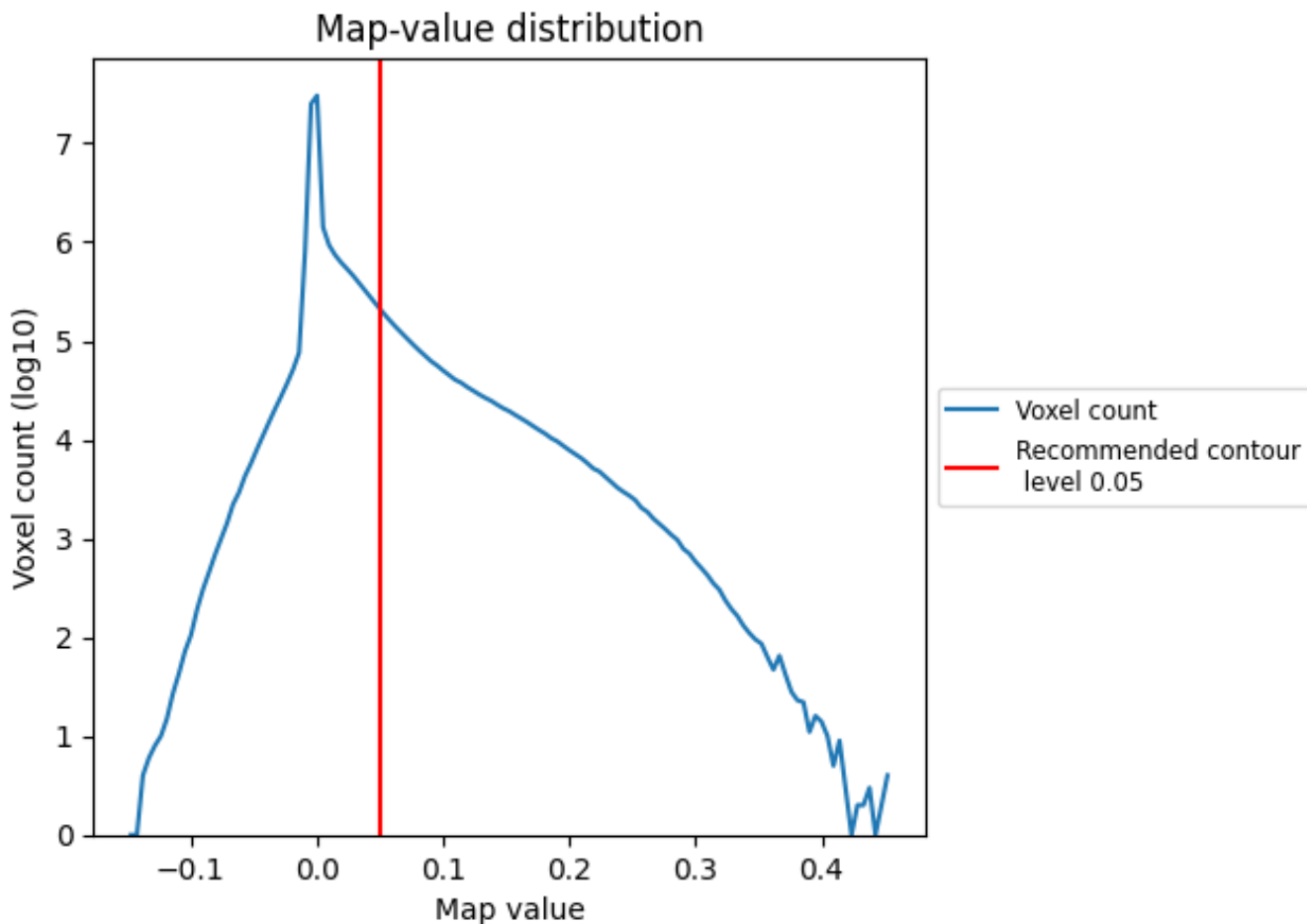
6.5 Mask visualisation

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

7 Map analysis [i](#)

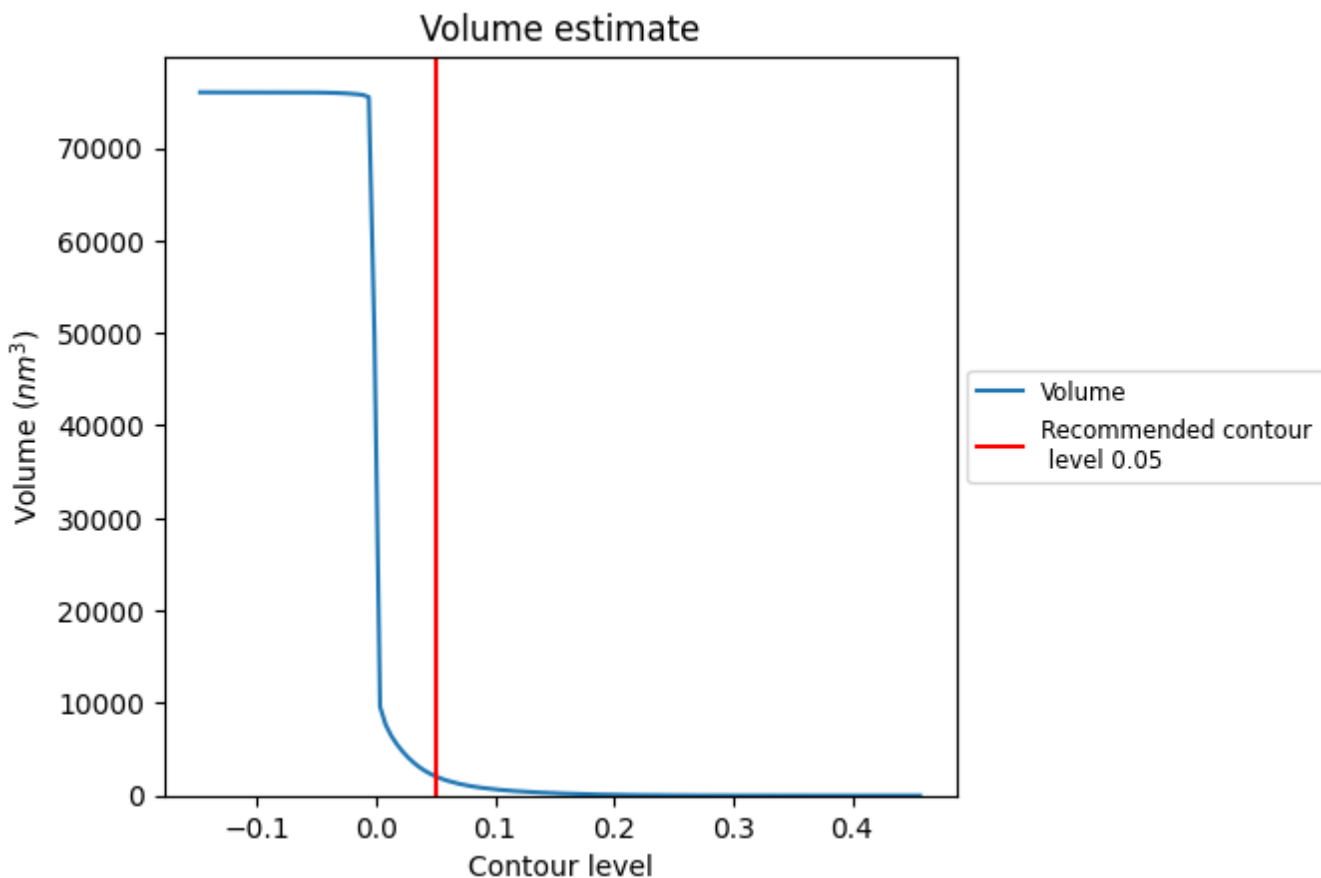
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

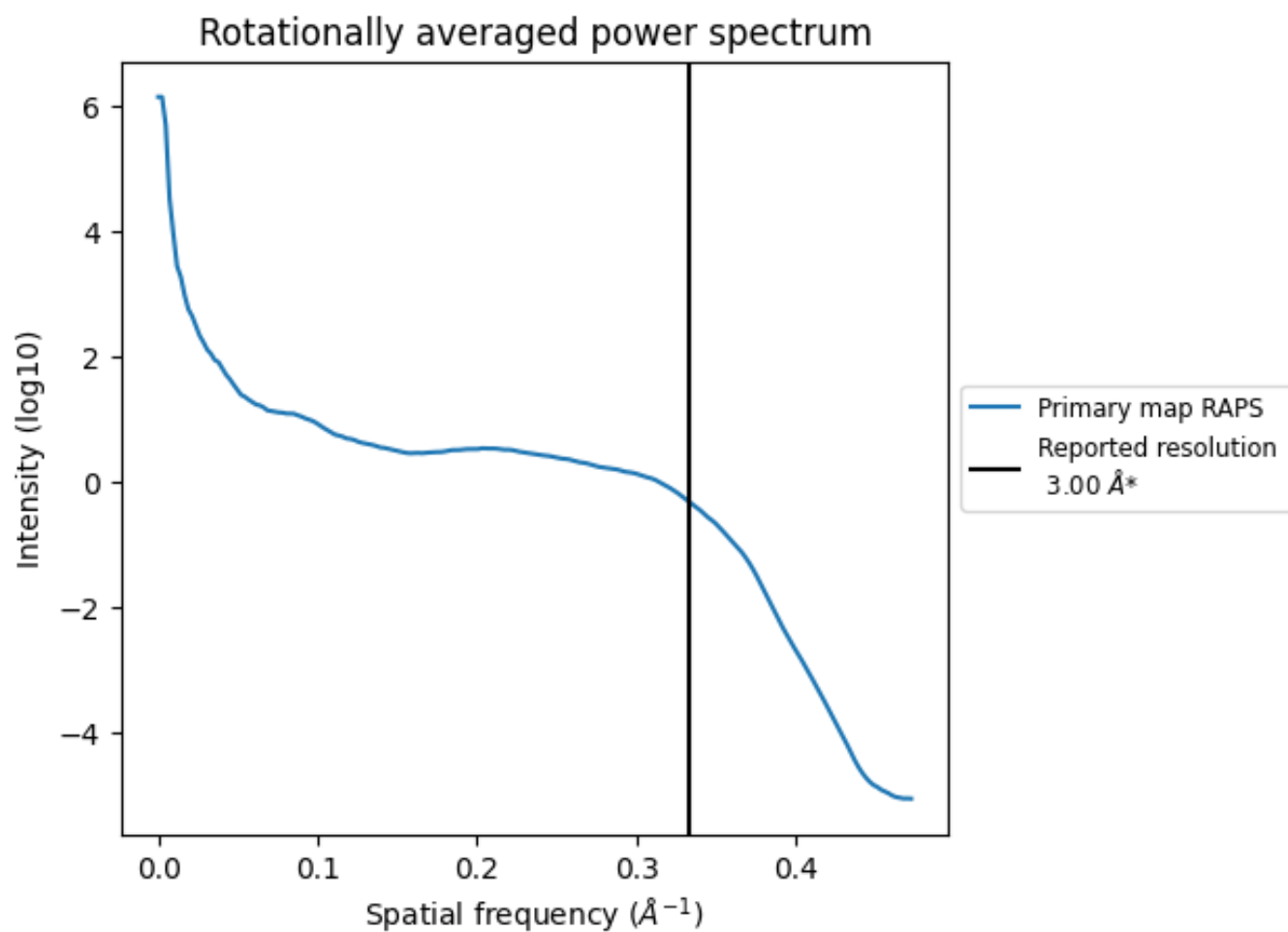
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2092 nm³; this corresponds to an approximate mass of 1890 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](#)

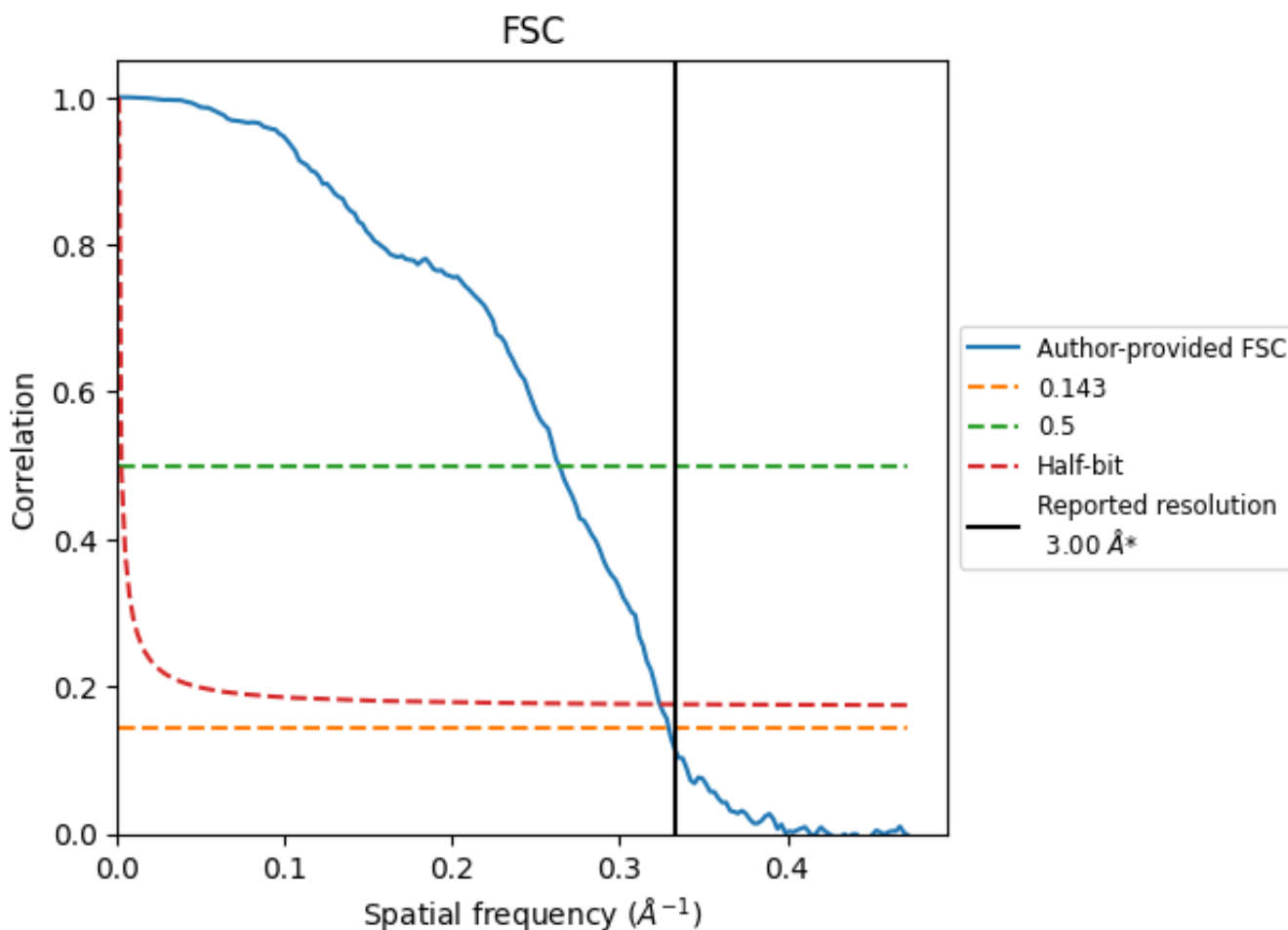


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [\(i\)](#)

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

8.1 FSC [\(i\)](#)



*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

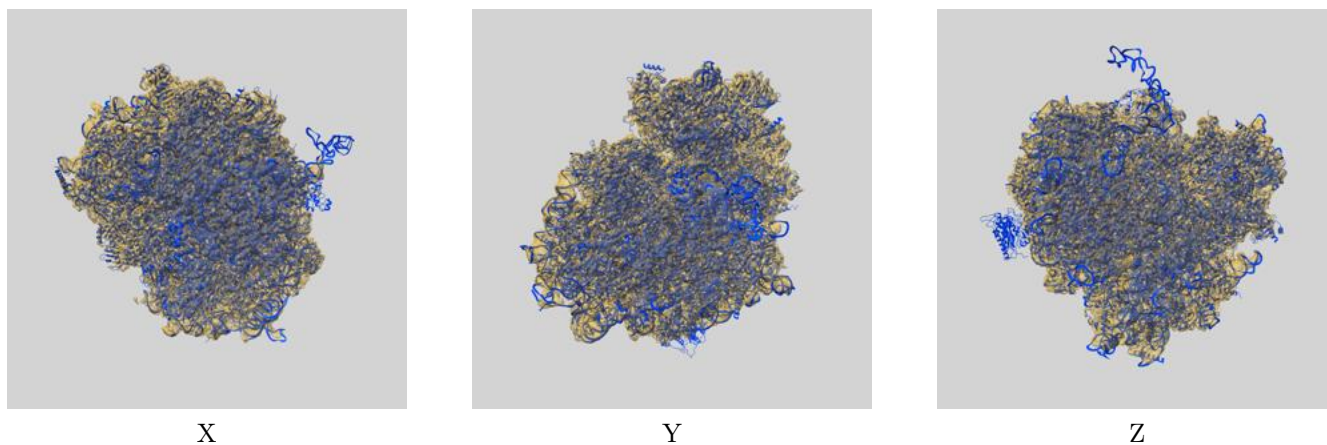
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.04	3.79	3.09
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

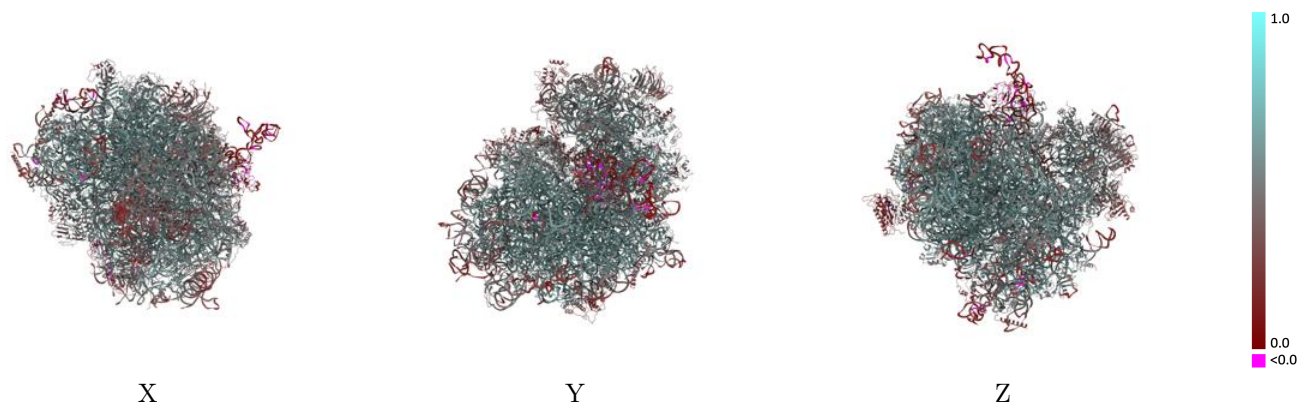
This section contains information regarding the fit between EMDB map EMD-11289 and PDB model 6ZME. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



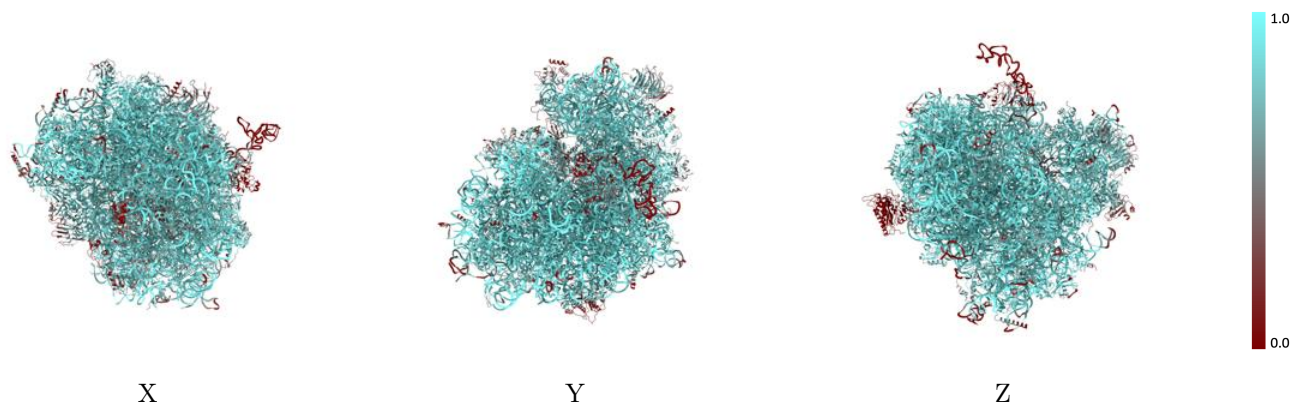
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



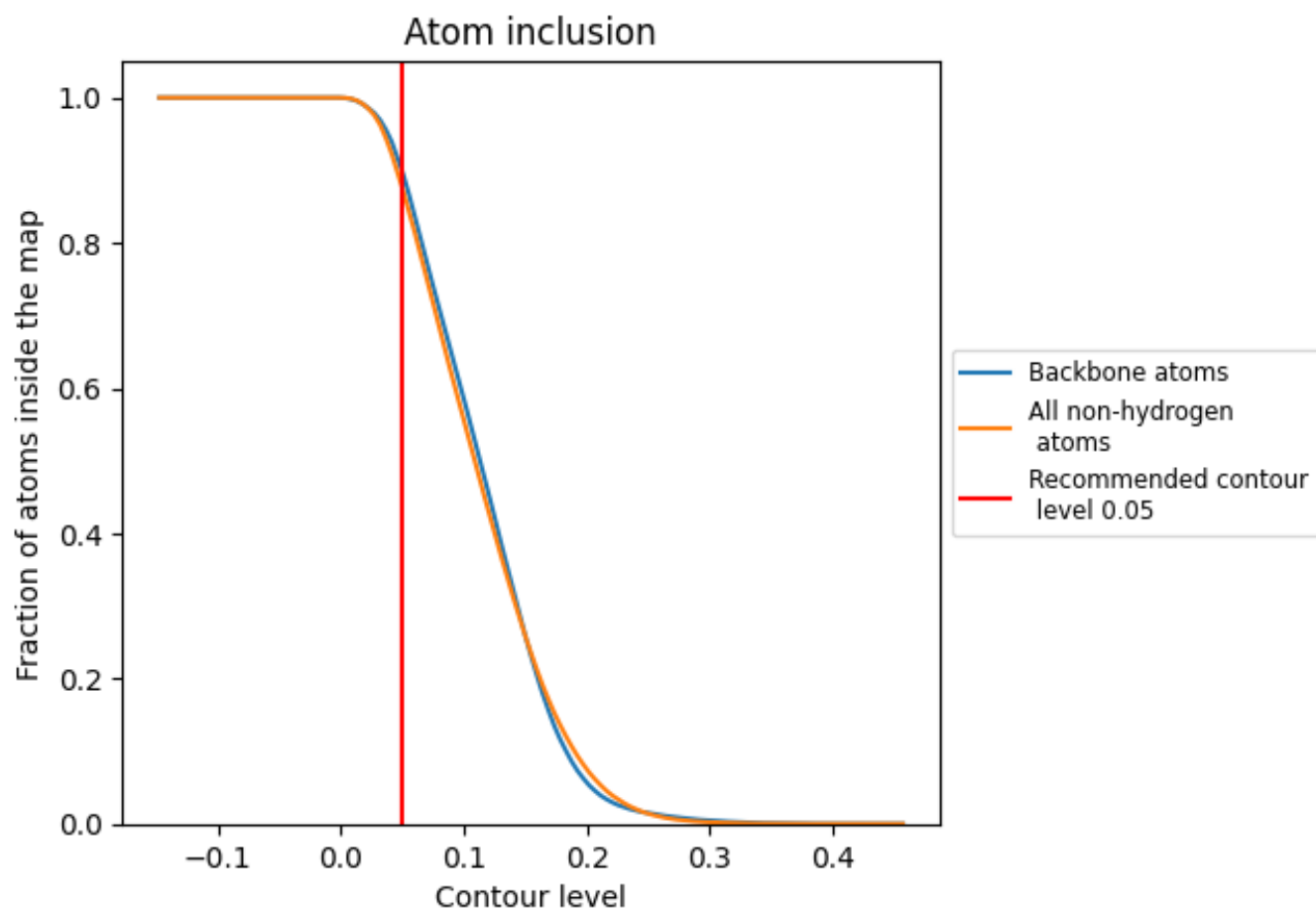
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8752	 0.5200
CA	 0.0418	 0.2520
CC	 0.8735	 0.2970
CE	 0.7321	 0.4260
CF	 0.9227	 0.5470
CH	 0.5680	 0.3700
CI	 0.6837	 0.4610
L5	 0.9331	 0.5400
L7	 0.9860	 0.5750
L8	 0.9656	 0.5680
LA	 0.9809	 0.6180
LB	 0.9339	 0.5870
LC	 0.9283	 0.5780
LD	 0.8681	 0.5220
LE	 0.8254	 0.4970
LF	 0.9629	 0.5860
LG	 0.8067	 0.5060
LH	 0.9054	 0.5490
LI	 0.9364	 0.5660
LJ	 0.7787	 0.4470
LL	 0.8819	 0.5450
LM	 0.9160	 0.5440
LN	 0.9870	 0.6250
LO	 0.9442	 0.5940
LP	 0.9577	 0.6110
LQ	 0.9675	 0.6020
LR	 0.8753	 0.5450
LS	 0.9636	 0.5930
LT	 0.9311	 0.5590
LU	 0.8154	 0.4710
LV	 0.9676	 0.5970
LW	 0.7010	 0.4520
LX	 0.9187	 0.5670
LY	 0.9026	 0.5640
LZ	 0.8993	 0.5590



























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Chain	Atom inclusion	Q-score
La	 0.9540	 0.6050
Lb	 0.8300	 0.5030
Lc	 0.9116	 0.5520
Ld	 0.9125	 0.5680
Le	 0.9676	 0.5970
Lf	 0.9667	 0.6100
Lg	 0.9208	 0.5790
Lh	 0.9001	 0.5490
Li	 0.8972	 0.5450
Lj	 0.9807	 0.6110
Lk	 0.7774	 0.5000
Ll	 0.9811	 0.5910
Lm	 0.9327	 0.5710
Ln	 0.9856	 0.6110
Lo	 0.9104	 0.5780
Lp	 0.9463	 0.6000
Lr	 0.9491	 0.5740
Ls	 0.3313	 0.2650
Lt	 0.4747	 0.2590
Lz	 0.1144	 0.1150
S2	 0.9383	 0.5330
SA	 0.8447	 0.5200
SB	 0.8858	 0.5350
SC	 0.9143	 0.5530
SD	 0.7770	 0.4540
SE	 0.9096	 0.5520
SF	 0.8551	 0.4850
SG	 0.7753	 0.4650
SH	 0.7211	 0.4510
SI	 0.8783	 0.5330
SJ	 0.8805	 0.5310
SK	 0.7441	 0.4100
SL	 0.8977	 0.5670
SM	 0.2511	 0.2210
SN	 0.9300	 0.5670
SO	 0.8784	 0.5390
SP	 0.7342	 0.4250
SQ	 0.8092	 0.4820
SR	 0.7604	 0.4670
SS	 0.7858	 0.4500
ST	 0.8272	 0.4790
SU	 0.7338	 0.4230

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Chain	Atom inclusion	Q-score
SV	 0.8762	 0.5390
SW	 0.9455	 0.5830
SX	 0.9421	 0.5810
SY	 0.8184	 0.5020
SZ	 0.7101	 0.4320
Sa	 0.9202	 0.5630
Sb	 0.8388	 0.5140
Sc	 0.7387	 0.4570
Sd	 0.9525	 0.5380
Se	 0.8184	 0.5030
Sf	 0.4494	 0.2880
Sg	 0.6098	 0.3900