wwPDB EM Validation Summary Report (i)

Apr 21, 2025 – 03:04 PM EDT

PDB ID	:	9B0J / pdb_00009b0j
EMDB ID	:	EMD-44043
Title	:	In situ human unrotated hibernating with CCDC124 state 80S ribosome
Authors	:	Wei, Z.; Yong, X.
Deposited on	:	2024-03-12
Resolution	:	2.84 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

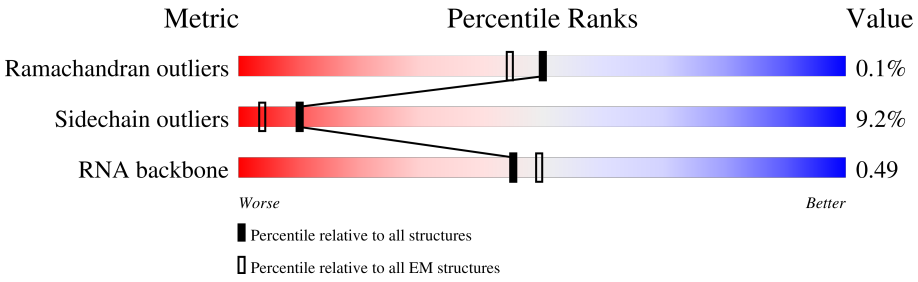
EMDB validation analysis	:	0.0.1.dev117
MolProbity	:	4.02b-467
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.42

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 2.84 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	SE	262	92% 8%
2	SI	206	7% 89% 11%
3	SL	153	12% 85% 15%
4	SX	282	46% 50%
5	SG	237	15% 93% 7%
6	SJ	185	6% 92% 8%
7	SY	131	12% 82% 18%
8	Se	58	19% 95% 5%

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Mol	Chain	Length	Quality of chain
9	SA	221	9% 93% 7%
10	SB	214	94% 6%
11	SH	186	17% 89% 11%
12	SV	83	83% 17%
13	Sa	102	6% 88% 12%
14	SC	222	90% 10%
15	SN	150	90% 10%
16	SO	140	7% 88% 11%
17	SW	129	94% 6%
18	Sb	83	6% 92% 8%
19	L5	3740	5% 75% 24%
20	L7	120	88% 12%
21	L8	156	80% 20%
22	LA	248	92% 8%
23	LB	402	94% 6%
24	LC	368	95% 5%
25	LD	293	92% 8%
26	LE	236	9% 93% 7%
27	LF	225	96%
28	LG	241	12% 94% 6%
29	LH	190	93% 7%
30	LI	202	93% 7%
31	LJ	176	9% 90% 10%
32	LL	210	92% 8%
33	LM	139	88% 12%

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Mol	Chain	Length	Quality of chain
34	LN	203	96%
35	LO	201	96%
36	LP	153	90% 10%
37	LQ	187	96%
38	LR	187	7% 92% 8%
39	LS	175	94% 6%
40	LT	159	91% 9%
41	LU	101	8% 90% 10%
42	LV	131	95% 5%
43	LX	120	93% 7%
44	LY	134	94% 6%
45	LZ	135	92% 8%
46	La	147	97%
47	Lb	109	8% 95% 5%
48	Lc	98	90% 9%
49	Ld	107	96%
50	Le	128	95% 5%
51	Lf	109	91% 9%
52	Lg	114	94% 6%
53	Lh	122	89% 11%
54	Li	102	97%
55	Lj	86	86% 13%
56	Lk	69	6% 96%
57	Ll	50	88% 12%
58	Lm	52	98%

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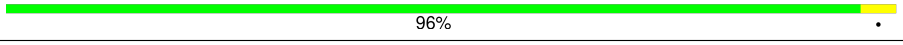
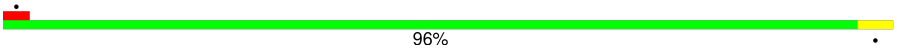
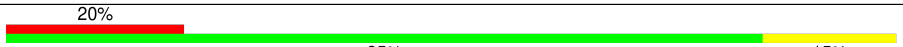
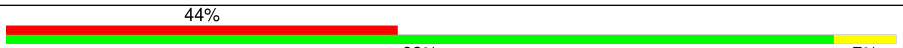
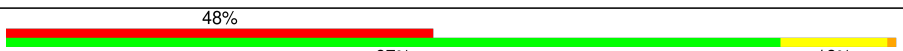
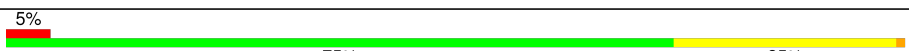
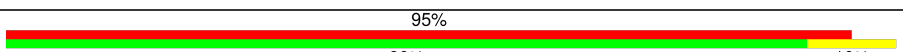
Mol	Chain	Length	Quality of chain
59	Ln	24	
60	Lo	105	
61	Lp	91	
62	Lr	125	
63	SR	135	
64	SD	227	
65	SF	189	
66	SK	98	
67	SP	121	
68	SQ	144	
69	SS	145	
70	ST	143	
71	SU	104	
72	Sc	64	
73	Sd	55	
74	Sg	313	
75	SM	122	
76	SZ	75	
77	Sf	67	
78	S2	1740	
79	Et	75	
80	Lt	141	
81	Lz	217	
82	Ls	196	
83	CB	846	

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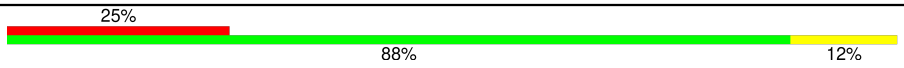
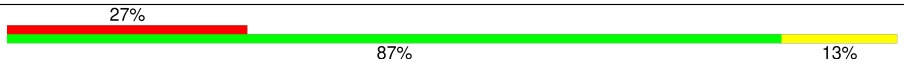
Mol	Chain	Length	Quality of chain
84	CE	73	
85	LW	118	

2 Entry composition (i)

There are 87 unique types of molecules in this entry. The entry contains 228356 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 2 is a protein called 40S ribosomal protein S8.

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

- Molecule 3 is a protein called 40S ribosomal protein S11.

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

- Molecule 4 is a protein called 40S ribosomal protein S23.

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

- Molecule 5 is a protein called 40S ribosomal protein S6.

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

- Molecule 6 is a protein called 40S ribosomal protein S9.

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

- Molecule 7 is a protein called 40S ribosomal protein S24.

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

- Molecule 8 is a protein called Small ribosomal subunit protein eS30.

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

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

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

- Molecule 10 is a protein called 40S ribosomal protein S3a.

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

- Molecule 11 is a protein called 40S ribosomal protein S7 [Homo sapiens].

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

- Molecule 12 is a protein called 40S ribosomal protein S21.

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

- Molecule 13 is a protein called 40S ribosomal protein S26.

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

- Molecule 14 is a protein called 40S ribosomal protein S2.

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

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called Small ribosomal subunit protein uS11.

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

- Molecule 17 is a protein called 40S ribosomal protein S15a.

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

- Molecule 18 is a protein called Small ribosomal subunit protein eS27.

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

- Molecule 19 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L5	3740	Total	C	N	O	P	0	0
			79860	35549	14585	25987	3739		

- Molecule 20 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 21 is a RNA chain called 5.8S rRNA.

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

- Molecule 22 is a protein called 60S ribosomal protein L8.

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

- Molecule 23 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 24 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 25 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 26 is a protein called 60S ribosomal protein L6.

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

- Molecule 27 is a protein called 60S ribosomal protein L7.

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

- Molecule 28 is a protein called 60S ribosomal protein L7a.

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

- Molecule 29 is a protein called 60S ribosomal protein L9.

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

- Molecule 30 is a protein called 60S ribosomal protein L10-like.

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

- Molecule 31 is a protein called 60S ribosomal protein L11.

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

- Molecule 32 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 33 is a protein called 60S ribosomal protein L14.

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

- Molecule 34 is a protein called 60S ribosomal protein L15.

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

- Molecule 35 is a protein called 60S ribosomal protein L13a.

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

- Molecule 36 is a protein called 60S ribosomal protein L17.

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

- Molecule 37 is a protein called 60S ribosomal protein L18.

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

- Molecule 38 is a protein called 60S ribosomal protein L19.

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

- Molecule 39 is a protein called 60S ribosomal protein L18a.

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

- Molecule 40 is a protein called 60S ribosomal protein L21.

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

- Molecule 41 is a protein called Heparin-binding protein HBp15.

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

- Molecule 42 is a protein called 60S ribosomal protein L23.

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

- Molecule 43 is a protein called 60S ribosomal protein L23a.

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

- Molecule 44 is a protein called 60S ribosomal protein L26.

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

- Molecule 45 is a protein called 60S ribosomal protein L27.

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

- Molecule 46 is a protein called 60S ribosomal protein L27a.

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

- Molecule 47 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 48 is a protein called 60S ribosomal protein L30.

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

- Molecule 49 is a protein called 60S ribosomal protein L31.

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

- Molecule 50 is a protein called 60S ribosomal protein L32.

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

- Molecule 51 is a protein called 60S ribosomal protein L35a.

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

- Molecule 52 is a protein called 60S ribosomal protein L34.

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

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

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

- Molecule 54 is a protein called 60S ribosomal protein L36.

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

- Molecule 55 is a protein called 60S ribosomal protein L37.

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

- Molecule 56 is a protein called 60S ribosomal protein L38.

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

- Molecule 57 is a protein called 60S ribosomal protein L39.

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

- Molecule 58 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 59 is a protein called 60S ribosomal protein L41.

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

- Molecule 60 is a protein called 60S ribosomal protein L36a.

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

- Molecule 61 is a protein called 60S ribosomal protein L37a.

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

- Molecule 62 is a protein called 60S ribosomal protein L28.

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

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

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 65 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 66 is a protein called 40S ribosomal protein S10.

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

- Molecule 67 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 68 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 69 is a protein called 40S ribosomal protein S18.

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

- Molecule 70 is a protein called 40S ribosomal protein S19.

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

- Molecule 71 is a protein called 40S ribosomal protein S20.

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

- Molecule 72 is a protein called 40S ribosomal protein S28.

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

- Molecule 73 is a protein called 40S ribosomal protein S29.

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

- Molecule 74 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 75 is a protein called Small ribosomal subunit protein eS12.

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

- Molecule 76 is a protein called Small ribosomal subunit protein eS25.

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

- Molecule 77 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 78 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 79 is a RNA chain called E site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Et	75	Total	C	N	O	P	0	0
			1593	712	281	526	74		

- Molecule 80 is a protein called 60S ribosomal protein L12.

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

- Molecule 81 is a protein called 60S ribosomal protein L10a.

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

- Molecule 82 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 83 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 84 is a protein called Coiled-coil domain-containing protein 124.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CE	73	Total	C	N	O	S	0	0
			613	369	122	121	1		

- Molecule 85 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
87	L5	210	Total	Mg	0
			210	210	
87	L7	3	Total	Mg	0
			3	3	
87	L8	6	Total	Mg	0
			6	6	
87	LA	1	Total	Mg	0
			1	1	
87	LB	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	

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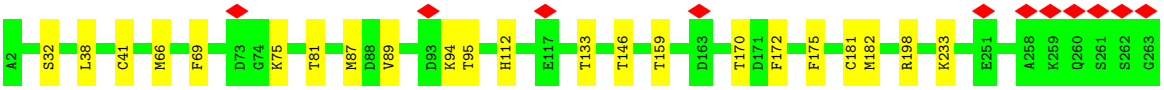
Mol	Chain	Residues	Atoms	AltConf
87	LP	1	Total Mg 1 1	0
87	LV	1	Total Mg 1 1	0
87	Le	1	Total Mg 1 1	0
87	Lg	1	Total Mg 1 1	0
87	S2	29	Total Mg 29 29	0

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.

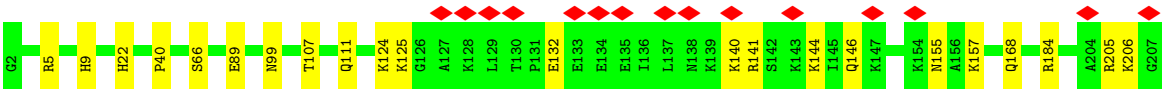
• Molecule 1: Small ribosomal subunit protein eS4, X isoform

Chain SE:



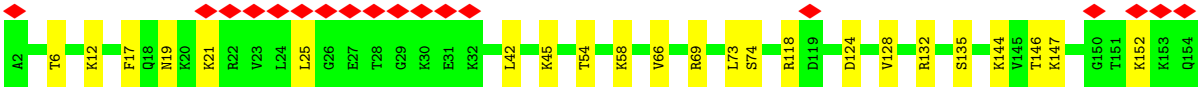
• Molecule 2: 40S ribosomal protein S8

Chain SI:



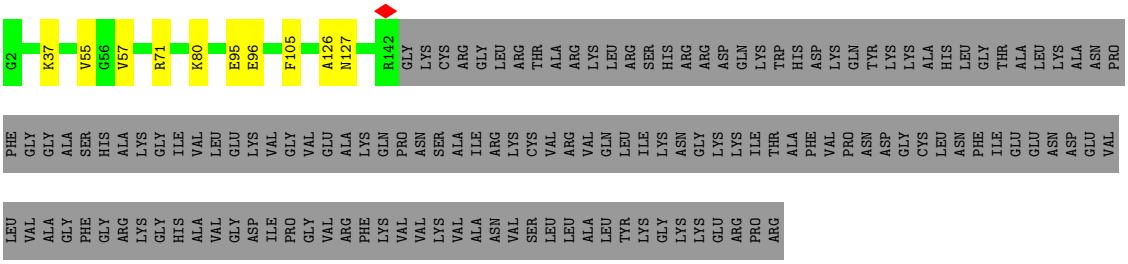
• Molecule 3: 40S ribosomal protein S11

Chain SL:



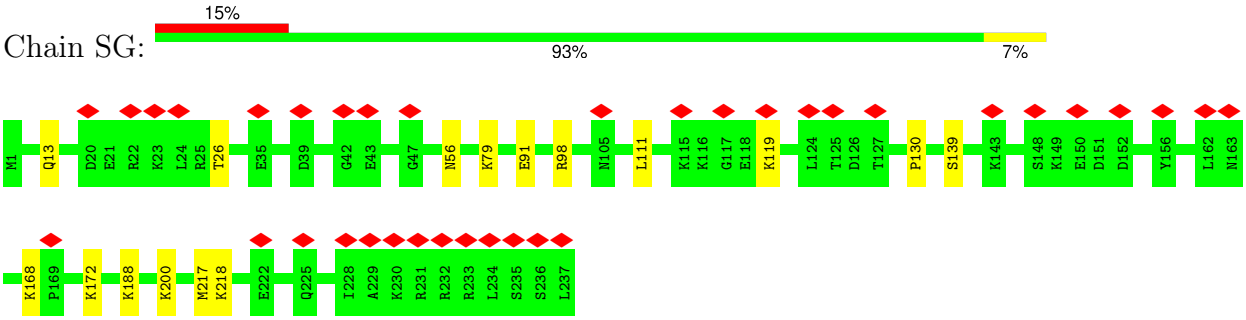
• Molecule 4: 40S ribosomal protein S23

Chain SX:



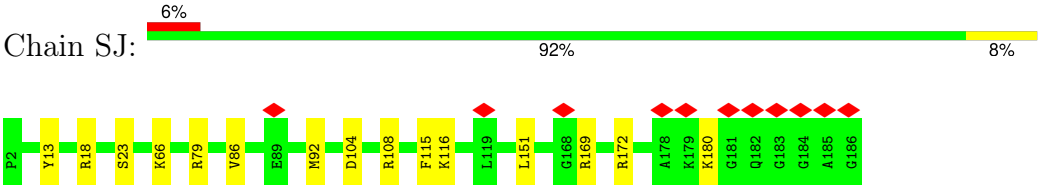
• Molecule 5: 40S ribosomal protein S6

Chain SG:



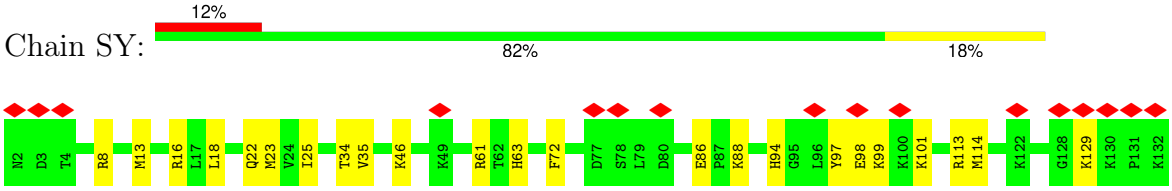
• Molecule 6: 40S ribosomal protein S9

Chain SJ:



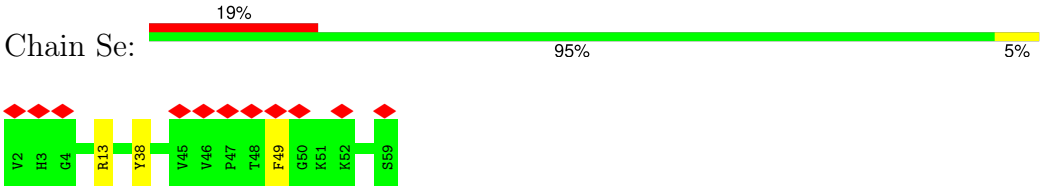
• Molecule 7: 40S ribosomal protein S24

Chain SY:



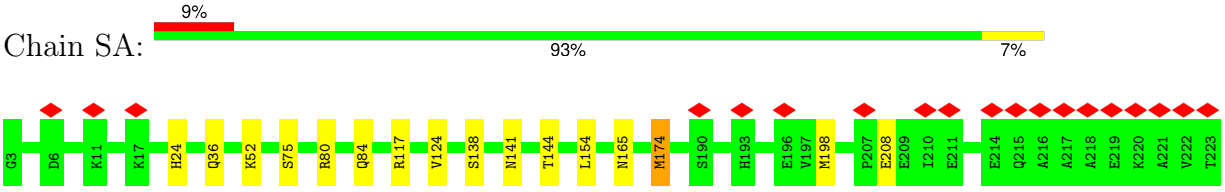
• Molecule 8: Small ribosomal subunit protein eS30

Chain Se:



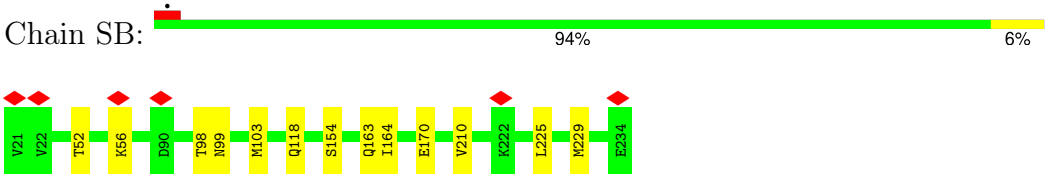
• Molecule 9: 40S ribosomal protein SA

Chain SA:



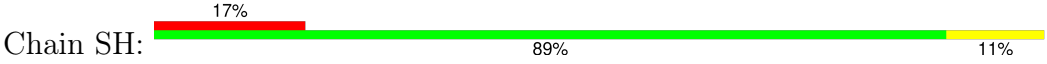
• Molecule 10: 40S ribosomal protein S3a

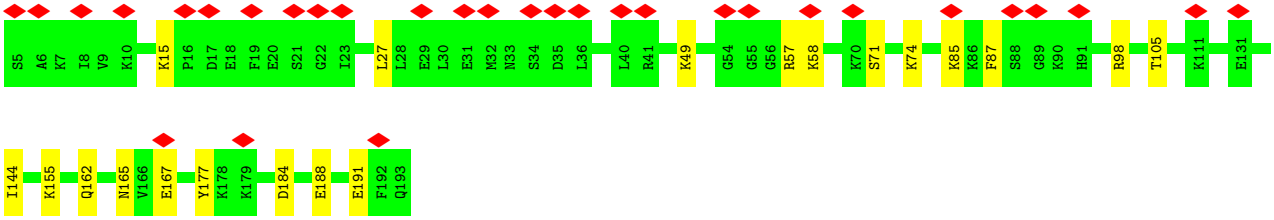
Chain SB:



• Molecule 11: 40S ribosomal protein S7 [Homo sapiens]

Chain SH:



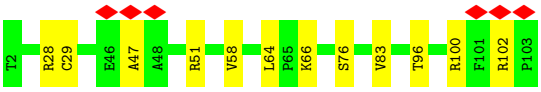


• Molecule 12: 40S ribosomal protein S21

Chain SV:

• Molecule 13: 40S ribosomal protein S26

Chain Sa:

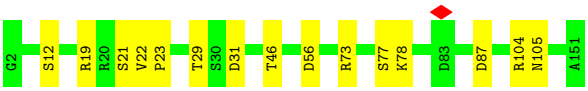


• Molecule 14: 40S ribosomal protein S2

Chain SC:

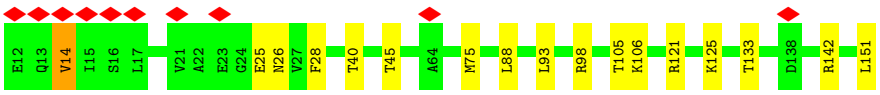
• Molecule 15: 40S ribosomal protein S13

Chain SN:



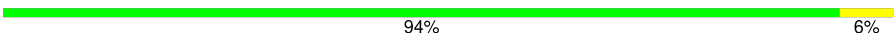
• Molecule 16: Small ribosomal subunit protein uS11

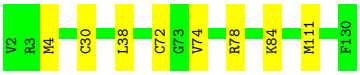
Chain SO:



• Molecule 17: 40S ribosomal protein S15a

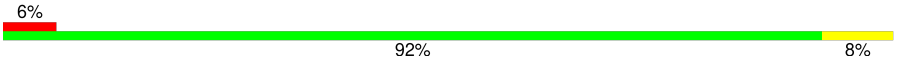
Chain SW:

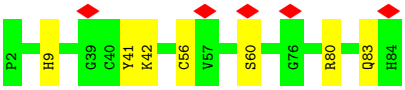




• Molecule 18: Small ribosomal subunit protein eS27

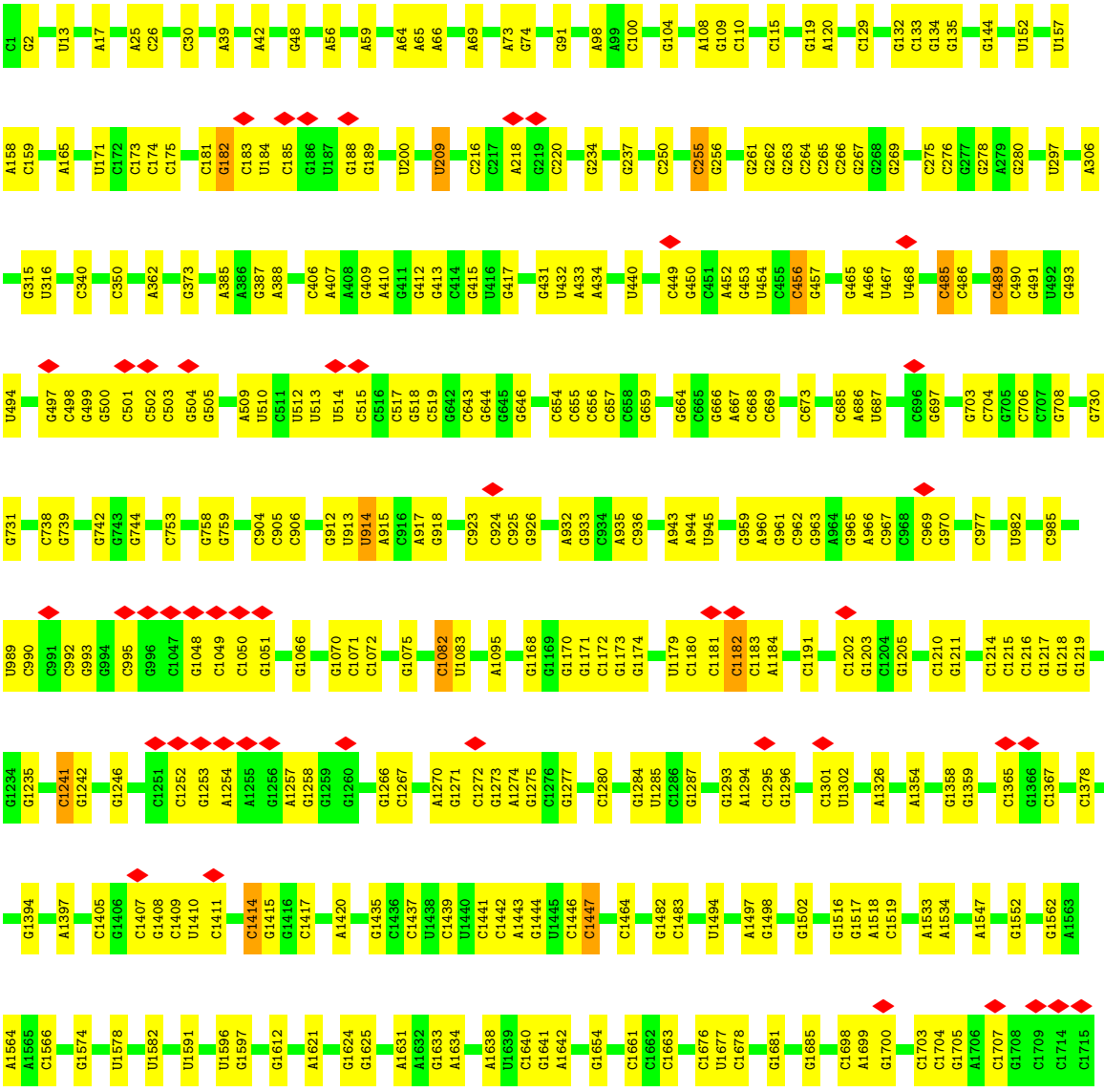
Chain Sb:

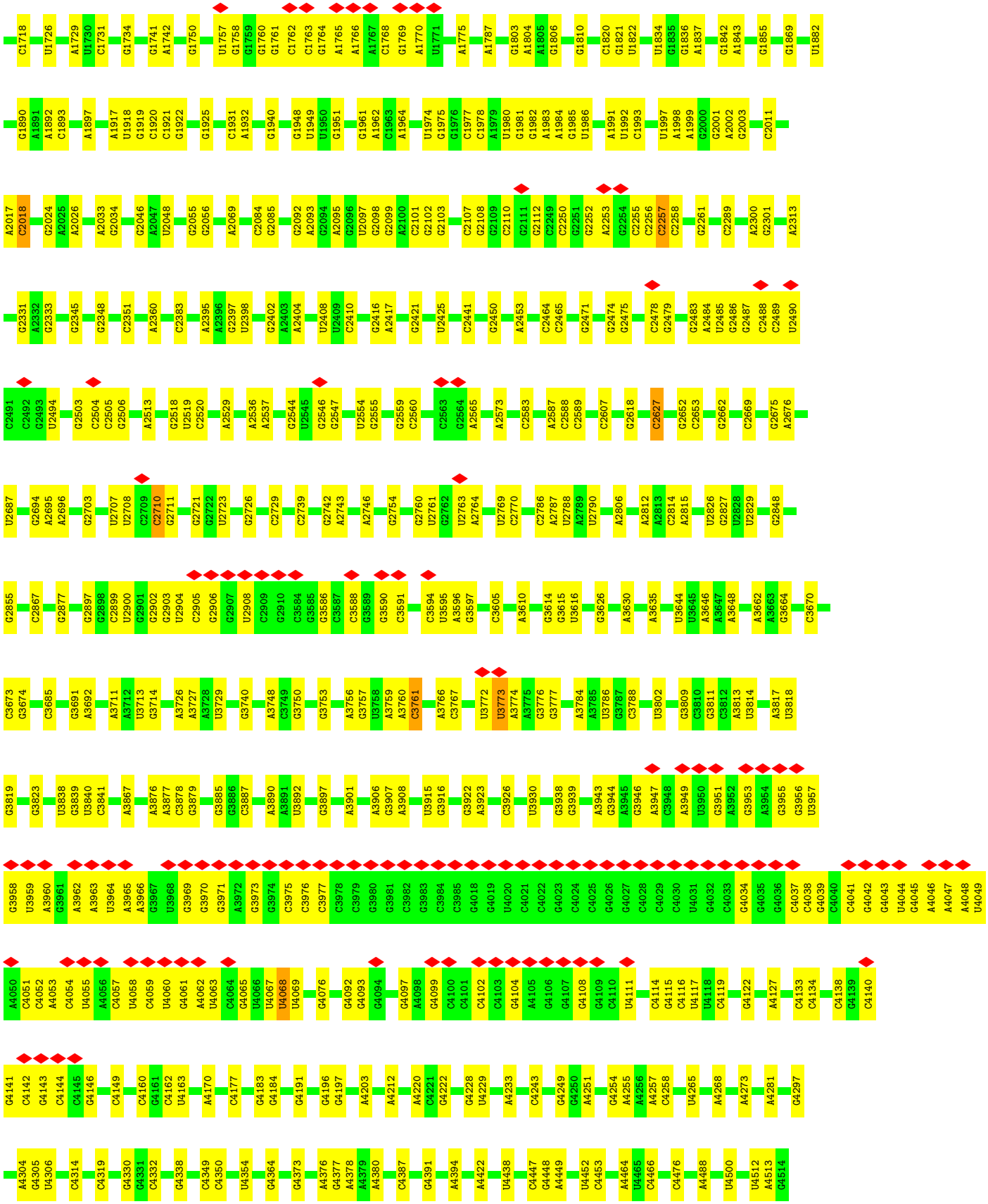


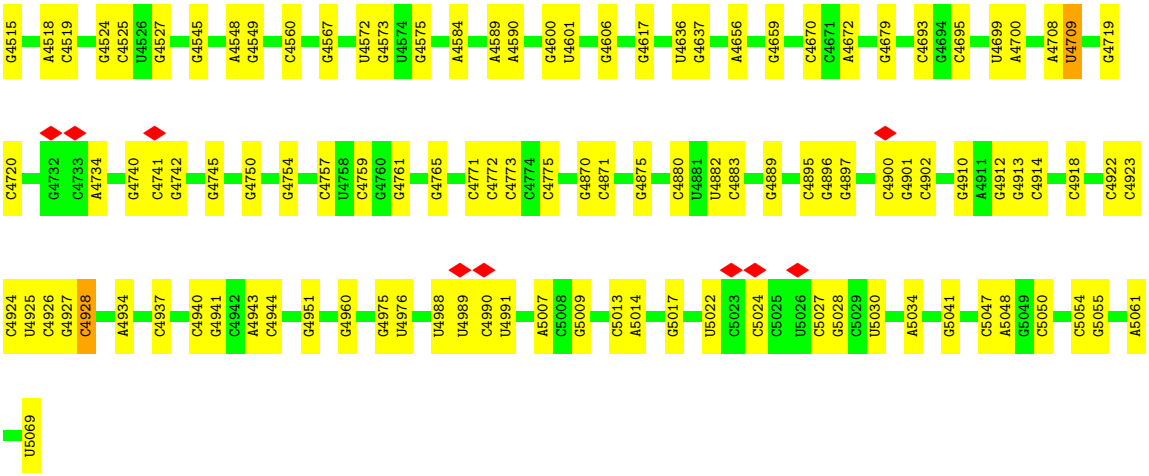


• Molecule 19: 28S rRNA

Chain L5:

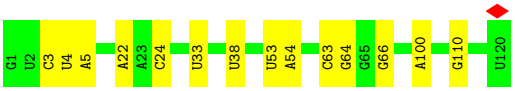



C1718 U1726 A1729 U1730 C1731 G1734 G1741 A1742 G1750 U1757 G1758 G1759 G1760 G1761 C1762 C1763 G1764 A1765 A1766 A1767 C1768 G1769 A1770 U1771 A1775 A1787 G1803 A1804 A1805 G1806 G1810 C1820 G1821 U1822 U1834 G1835 G1836 A1837 G1842 A1843 G1855 G1869 U1882
G1890 A1891 A1892 C1893 A1897 A1917 U1918 G1919 C1920 C1921 G1922 G1925 C1931 A1932 G1940 G1948 U1949 U1950 G1951 G1961 A1962 C1963 A1964 U1974 G1975 G1976 C1977 C1978 A1979 U1980 G1981 G1982 A1983 A1984 G1985 U1986 A1991 U1992 C1993 U1997 A1998 A1999 G2000 G2001 A2002 G2003 C2011
A2017 C2018 G2024 A2025 A2026 A2033 G2034 G2046 A2047 U2048 G2055 G2056 A2069 C2084 G2085 G2092 A2093 G2094 A2095 G2096 U2097 G2098 G2099 A2100 C2101 G2102 G2103 C2107 G2108 G2109 C2110 G2111 G2112 C2249 C2250 G2251 G2252 A2253 G2254 C2255 C2256 C2257 C2258 G2261 C2289 A2300 G2301 A2313
G2331 A2332 G2333 G2345 G2348 C2351 A2360 C2383 A2395 A2396 G2397 U2398 G2402 A2403 A2404 U2408 U2409 C2410 G2416 A2417 G2421 U2425 C2441 G2450 A2453 C2464 C2465 G2471 G2474 G2475 C2478 C2479 G2483 A2484 U2485 G2486 G2487 C2488 C2489 U2490
C2491 C2492 G2493 U2494 G2503 C2504 C2505 G2506 A2513 G2518 U2519 C2520 A2529 A2536 A2537 G2544 U2545 G2546 G2547 U2554 G2555 G2559 C2560 C2563 G2564 A2565 A2573 C2583 A2587 C2588 C2589 C2607 G2618 C2627 G2652 C2653 G2662 C2669 G2675 A2676
U2687 G2694 A2695 A2696 G2703 U2707 U2708 C2709 C2710 G2711 G2721 G2722 U2723 G2726 C2729 C2739 G2742 A2743 A2746 G2754 G2760 U2761 G2762 U2763 A2764 U2769 C2770 C2786 A2787 U2788 A2789 U2790 A2806 A2812 A2813 C2814 A2815 U2826 G2827 U2828 U2829 G2848
G2855 C2867 G2877 G2897 G2898 C2899 U2900 G2901 G2902 G2903 U2904 C2905 G2906 G2907 U2908 C2909 G2910 C3584 G3585 G3586 G3587 C3588 G3589 G3590 C3591 C3594 U3595 A3596 G3597 C3605 A3610 G3614 G3615 U3616 G3626 A3630 A3635 U3644 U3645 A3646 A3647 A3648 A3662 A3663 G3664 C3670
C3673 G3674 C3685 G3691 A3692 A3711 A3712 U3713 G3714 A3726 A3727 A3728 U3729 G3740 A3748 C3749 G3750 G3753 A3756 G3757 U3758 A3759 A3760 C3761 A3766 C3767 U3772 U3773 A3774 A3775 G3776 G3777 A3784 A3785 U3786 G3787 C3788 U3802 G3809 C3810 G3811 C3812 A3813 U3814 A3817 U3818
G3819 G3823 U3838 G3839 U3840 C3841 A3867 A3876 A3877 C3878 G3879 G3885 G3886 C3887 A3890 A3891 U3892 G3897 A3901 A3906 G3907 A3908 U3915 G3916 G3922 A3923 C3926 U3930 G3938 G3939 A3943 G3944 A3945 G3946 A3947 C3948 A3949 U3950 G3951 A3952 G3953 A3954 G3955 G3956 U3957
G3958 U3959 A3960 G3961 A3962 A3963 U3964 A3965 A3966 G3967 U3968 G3969 G3970 G3971 A3972 G3973 G3974 C3975 C3976 C3977 C3978 C3979 G3980 G3981 C3982 G3983 C3984 C3985 G4018 G4019 U4020 C4021 C4022 G4023 C4024 C4025 G4026 G4027 C4028 C4029 C4030 U4031 G4032 C4033 G4034 G4035 G4036 C4037 C4038 G4039 C4040 C4041 G4042 G4043 U4044 G4045 A4046 A4047 A4048 U4049
A4050 C4051 C4052 A4053 C4054 U4055 A4056 C4057 U4058 C4059 U4060 G4061 A4062 U4063 C4064 G4065 U4066 U4067 U4068 U4069 G4076 G4092 G4093 G4094 G4097 A4098 G4099 C4100 C4101 C4102 C4103 G4104 A4105 G4106 G4107 C4108 G4109 C4110 U4111 C4114 G4115 C4116 U4117 U4118 C4119 G4122 A4127 C4133 C4134 C4138 G4139 C4140
G4141 C4142 G4143 C4144 C4145 G4146 C4149 C4160 G4161 C4162 U4163 A4170 C4177 C4183 G4184 G4191 G4196 G4197 A4203 A4212 A4220 G4221 G4222 G4228 U4229 A4233 C4243 G4249 G4250 A4251 G4254 A4255 A4256 A4257 C4258 U4265 A4268 A4273 A4281 G4297
A4304 G4305 U4306 C4314 C4319 G4330 G4331 C4332 G4338 C4349 C4350 U4354 G4364 G4373 A4376 G4377 A4378 A4379 A4380 C4387 G4391 A4394 A4422 U4438 C4447 G4448 A4449 U4452 C4453 A4464 U4465 C4466 C4476 A4488 U4500 U4512 A4513 G4514



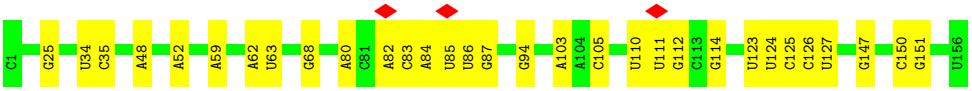
• Molecule 20: 5S rRNA

Chain L7:



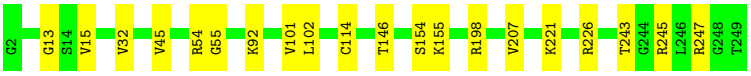
• Molecule 21: 5.8S rRNA

Chain L8:



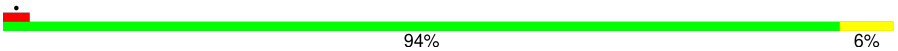
• Molecule 22: 60S ribosomal protein L8

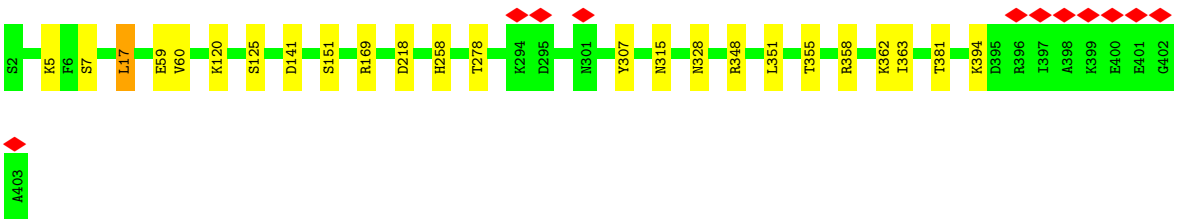
Chain LA:



• Molecule 23: Large ribosomal subunit protein uL3

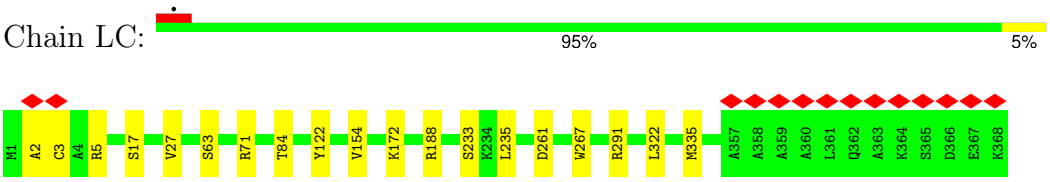
Chain LB:





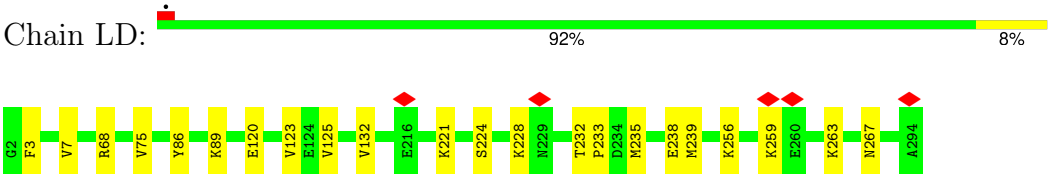
• Molecule 24: 60S ribosomal protein L4

Chain LC:



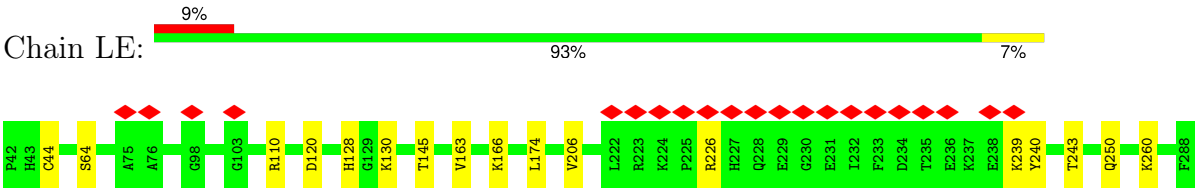
• Molecule 25: Large ribosomal subunit protein uL18

Chain LD:



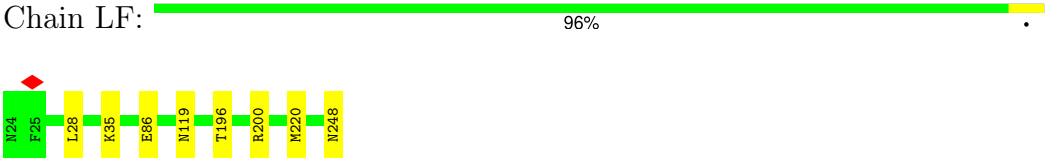
• Molecule 26: 60S ribosomal protein L6

Chain LE:



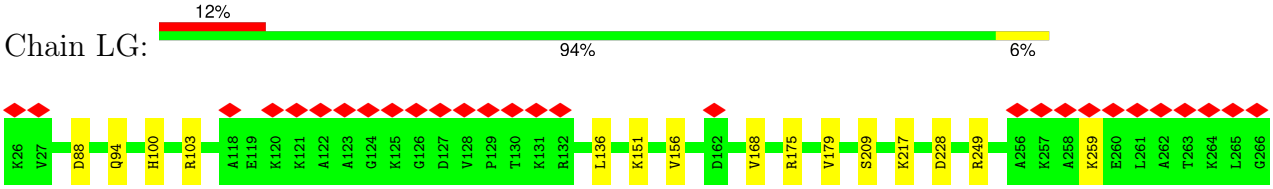
• Molecule 27: 60S ribosomal protein L7

Chain LF:



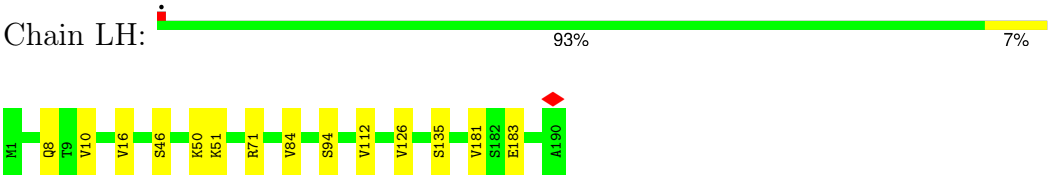
• Molecule 28: 60S ribosomal protein L7a

Chain LG:



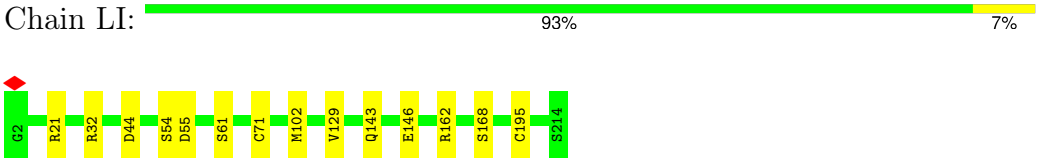
• Molecule 29: 60S ribosomal protein L9

Chain LH:



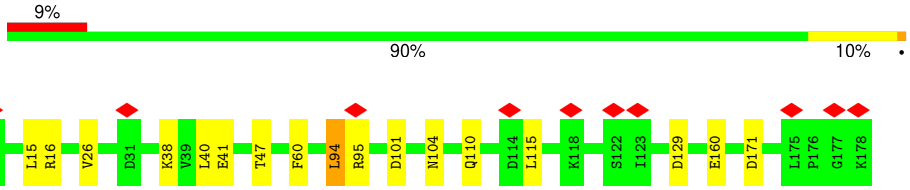
• Molecule 30: 60S ribosomal protein L10-like

Chain LI:



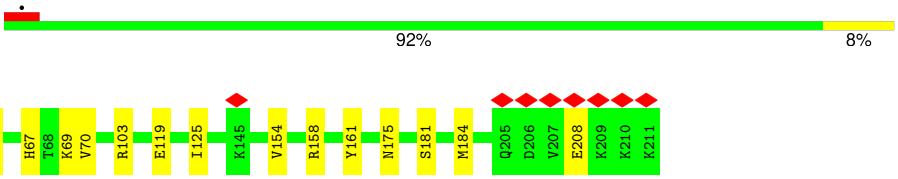
• Molecule 31: 60S ribosomal protein L11

Chain LJ:



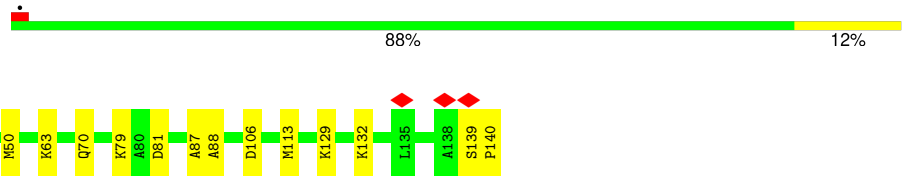
• Molecule 32: Large ribosomal subunit protein eL13

Chain LL:



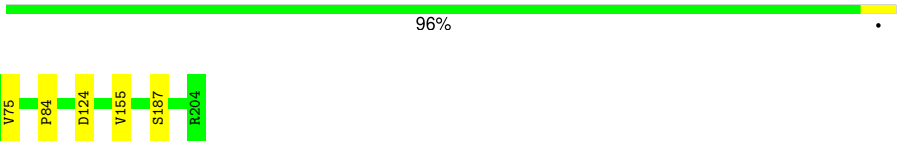
• Molecule 33: 60S ribosomal protein L14

Chain LM:



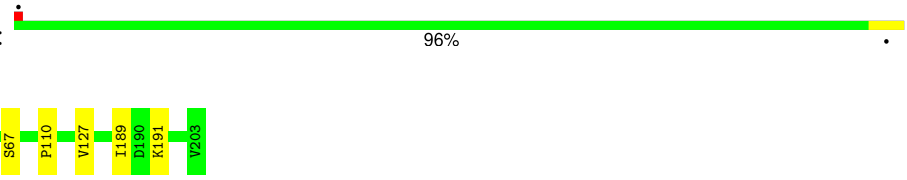
• Molecule 34: 60S ribosomal protein L15

Chain LN:



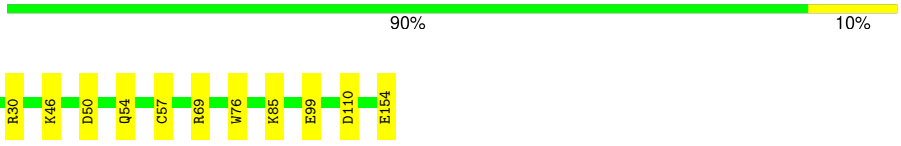
• Molecule 35: 60S ribosomal protein L13a

Chain LO:



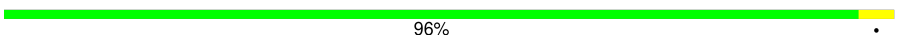
• Molecule 36: 60S ribosomal protein L17

Chain LP:



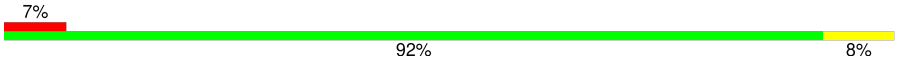
• Molecule 37: 60S ribosomal protein L18

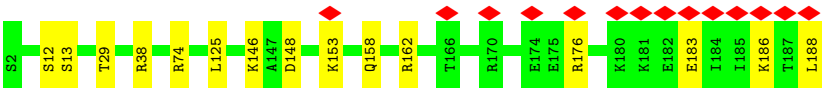
Chain LQ:



• Molecule 38: 60S ribosomal protein L19

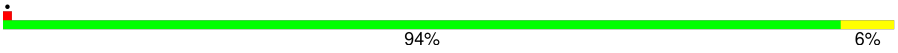
Chain LR:

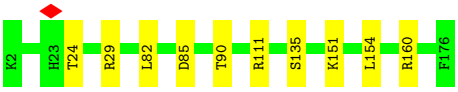




• Molecule 39: 60S ribosomal protein L18a

Chain LS:



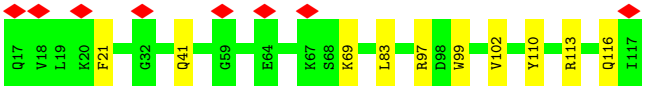


• Molecule 40: 60S ribosomal protein L21

Chain LT:

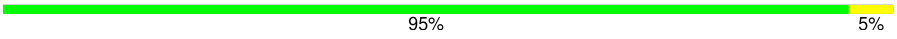
• Molecule 41: Heparin-binding protein HBp15

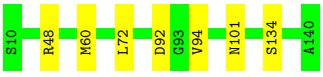
Chain LU:



• Molecule 42: 60S ribosomal protein L23

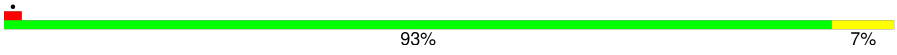
Chain LV:

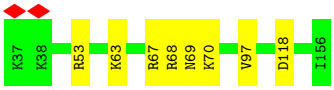




• Molecule 43: 60S ribosomal protein L23a

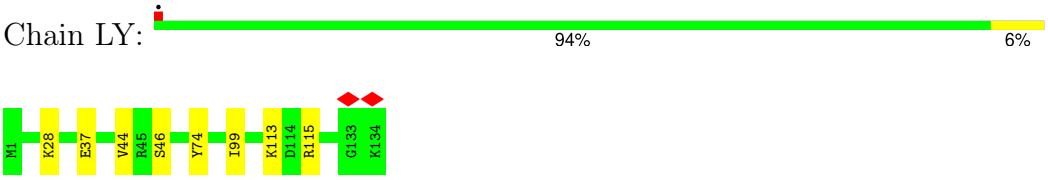
Chain LX:





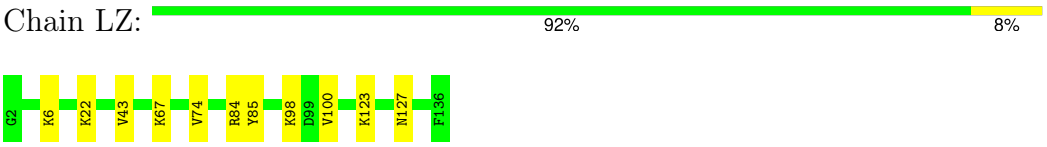
• Molecule 44: 60S ribosomal protein L26

Chain LY:



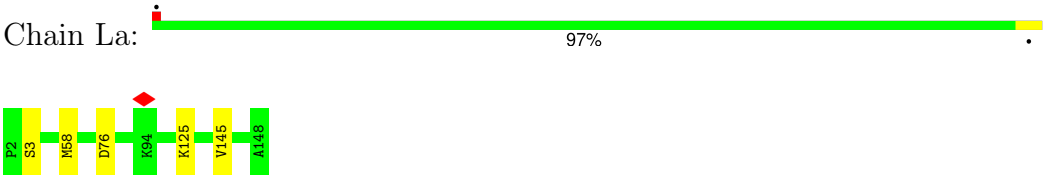
• Molecule 45: 60S ribosomal protein L27

Chain LZ:



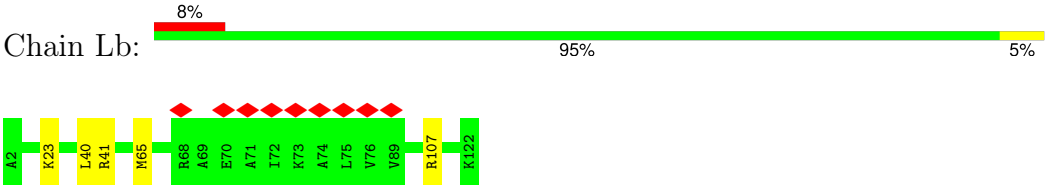
• Molecule 46: 60S ribosomal protein L27a

Chain La:



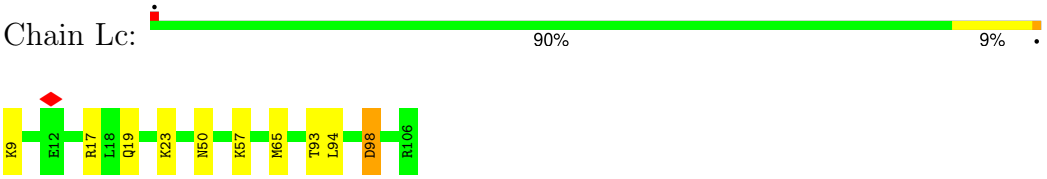
• Molecule 47: 60S ribosomal protein L29

Chain Lb:



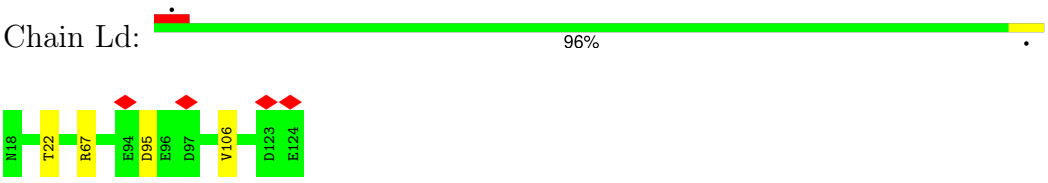
• Molecule 48: 60S ribosomal protein L30

Chain Lc:



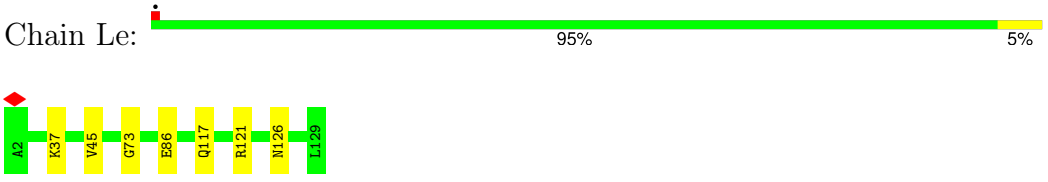
• Molecule 49: 60S ribosomal protein L31

Chain Ld:



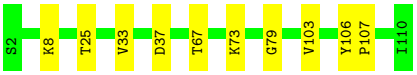
• Molecule 50: 60S ribosomal protein L32

Chain Le:



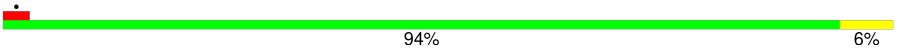
• Molecule 51: 60S ribosomal protein L35a

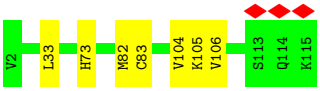
Chain Lf:



• Molecule 52: 60S ribosomal protein L34

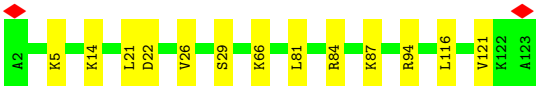
Chain Lg:





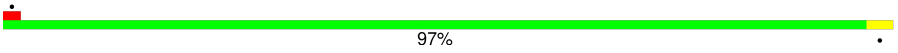
• Molecule 53: 60S ribosomal protein L35

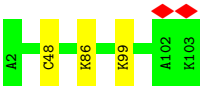
Chain Lh:



• Molecule 54: 60S ribosomal protein L36

Chain Li:



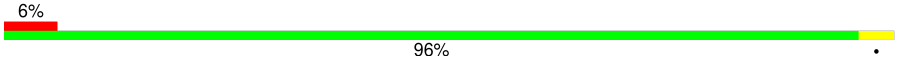


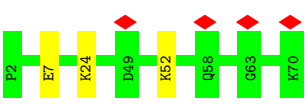
• Molecule 55: 60S ribosomal protein L37

Chain Lj:

• Molecule 56: 60S ribosomal protein L38

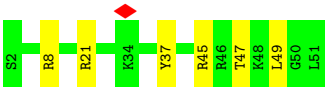
Chain Lk:





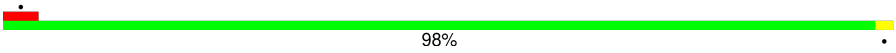
• Molecule 57: 60S ribosomal protein L39

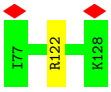
Chain Ll:



• Molecule 58: Large ribosomal subunit protein eL40

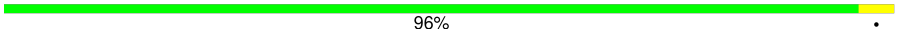
Chain Lm:





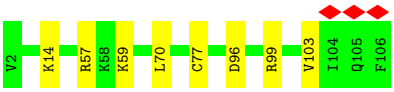
• Molecule 59: 60S ribosomal protein L41

Chain Ln:



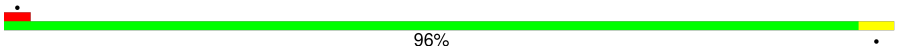
• Molecule 60: 60S ribosomal protein L36a

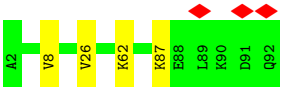
Chain Lo:



• Molecule 61: 60S ribosomal protein L37a

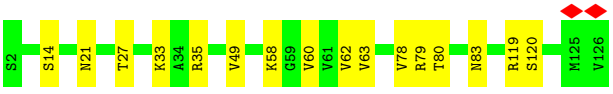
Chain Lp:





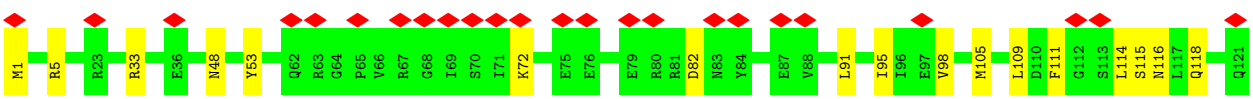
• Molecule 62: 60S ribosomal protein L28

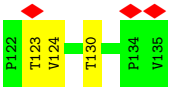
Chain Lr:



• Molecule 63: 40S ribosomal protein S17

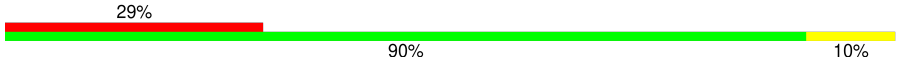
Chain SR:

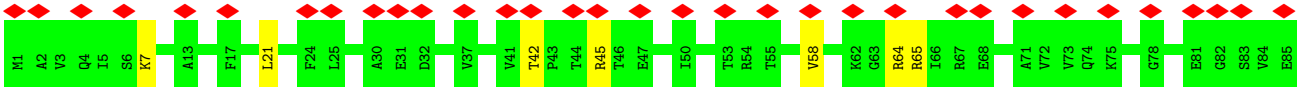


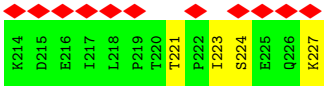


• Molecule 64: Small ribosomal subunit protein uS3

Chain SD:

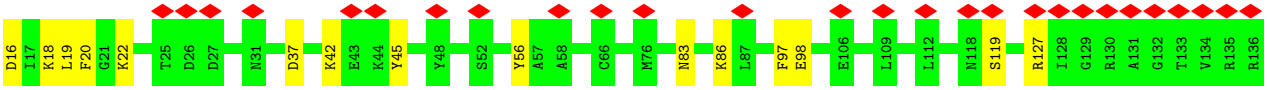


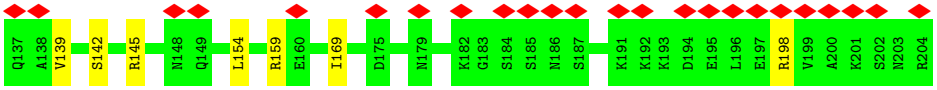




• Molecule 65: 40S ribosomal protein S5

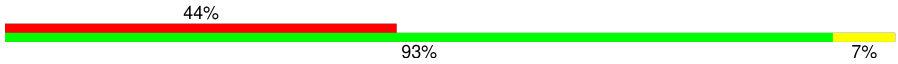
Chain SF:

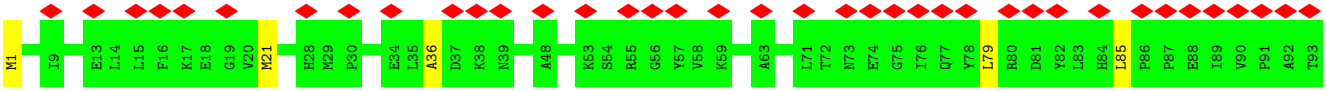




• Molecule 66: 40S ribosomal protein S10

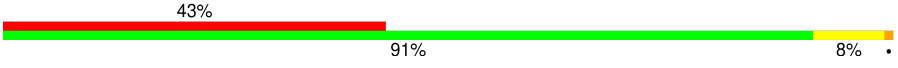
Chain SK:

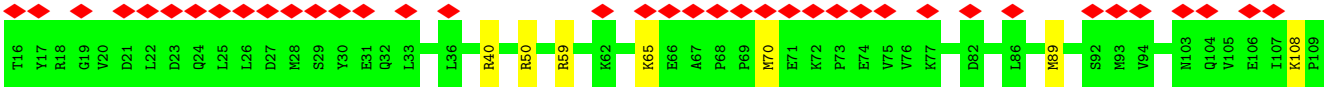


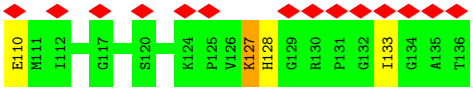


• Molecule 67: Small ribosomal subunit protein uS19

Chain SP:

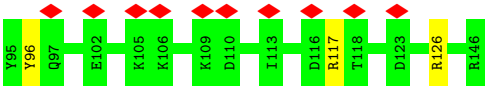






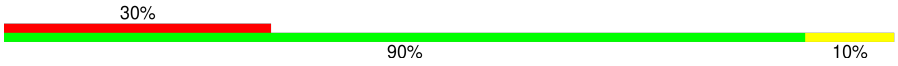
• Molecule 68: Small ribosomal subunit protein uS9

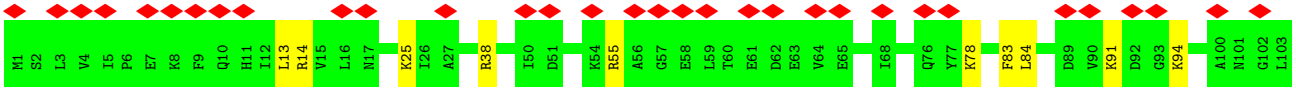
Chain SQ:

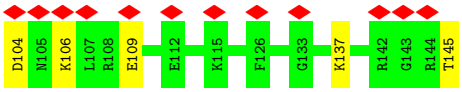


• Molecule 69: 40S ribosomal protein S18

Chain SS:

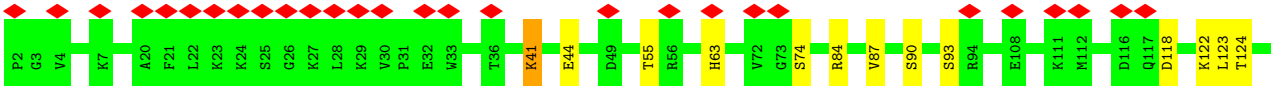


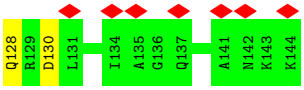




• Molecule 70: 40S ribosomal protein S19

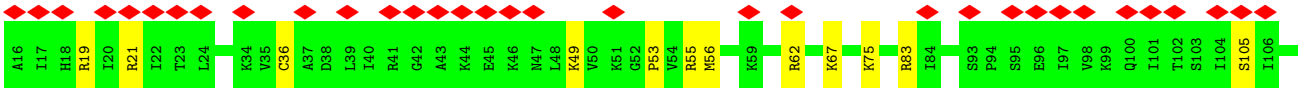
Chain ST:

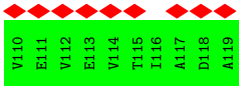




• Molecule 71: 40S ribosomal protein S20

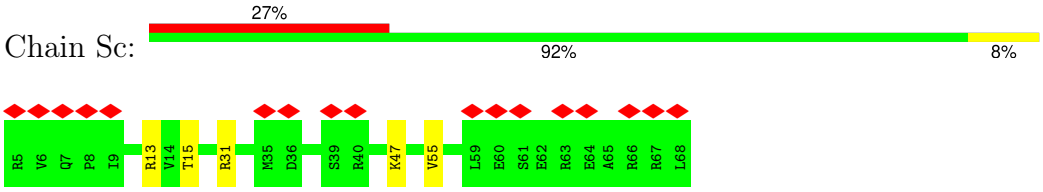
Chain SU:





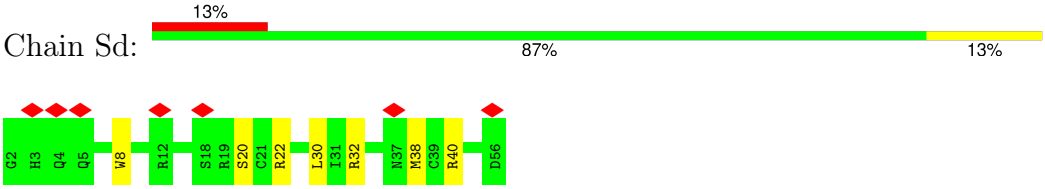
• Molecule 72: 40S ribosomal protein S28

Chain Sc:



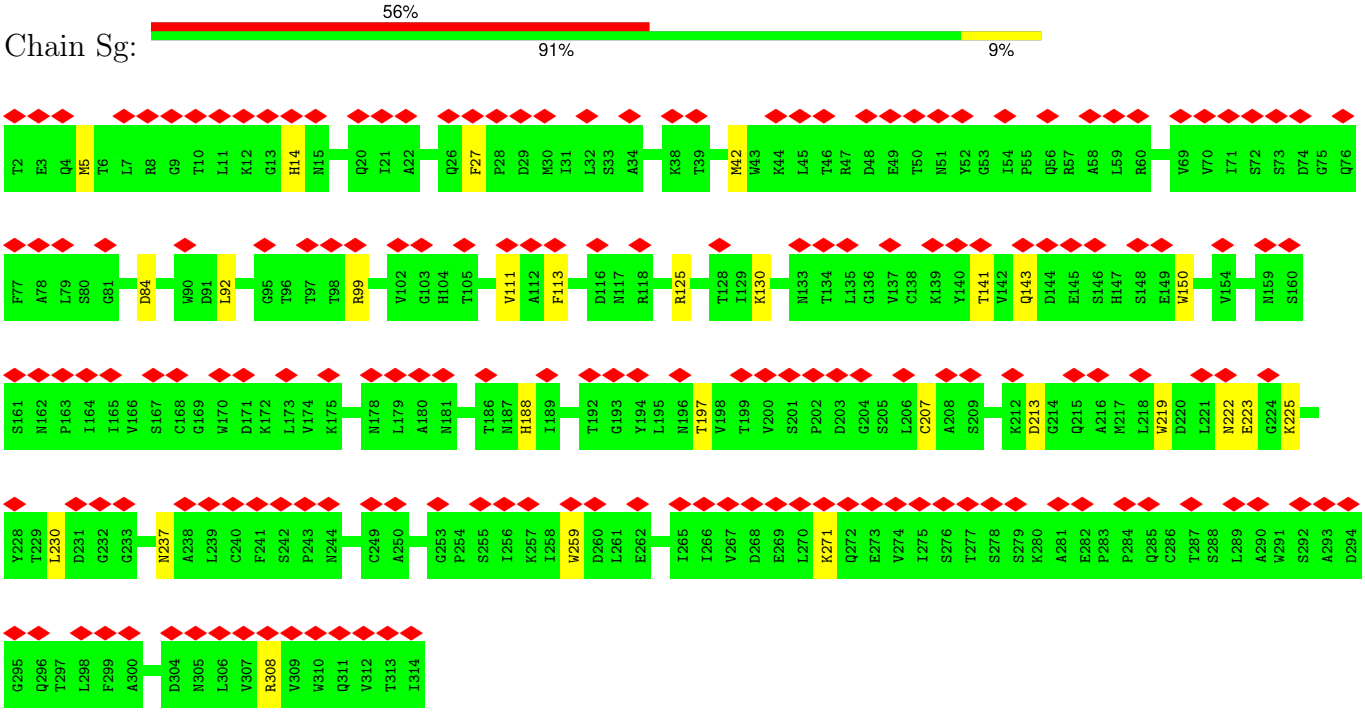
• Molecule 73: 40S ribosomal protein S29

Chain Sd:



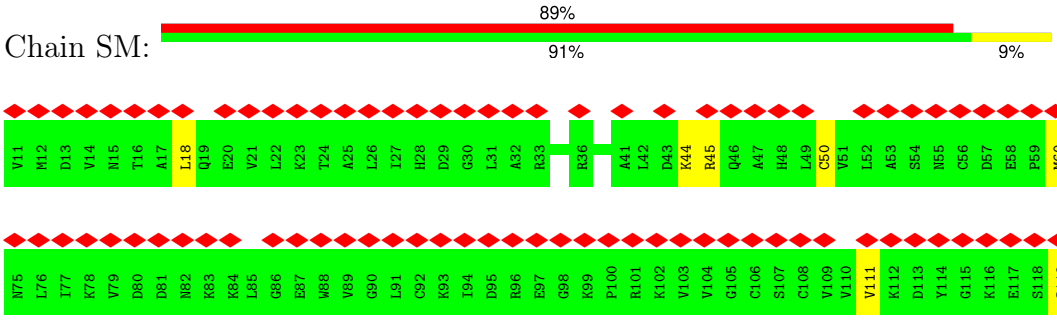
• Molecule 74: Receptor of activated protein C kinase 1

Chain Sg:



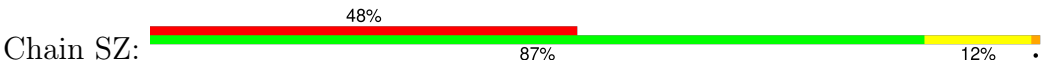
• Molecule 75: Small ribosomal subunit protein eS12

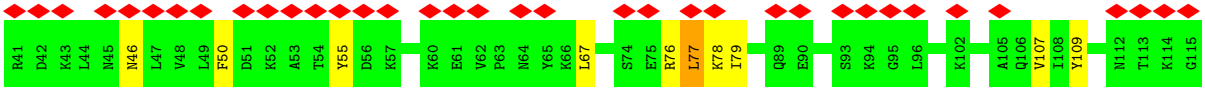
Chain SM:



• Molecule 76: Small ribosomal subunit protein eS25

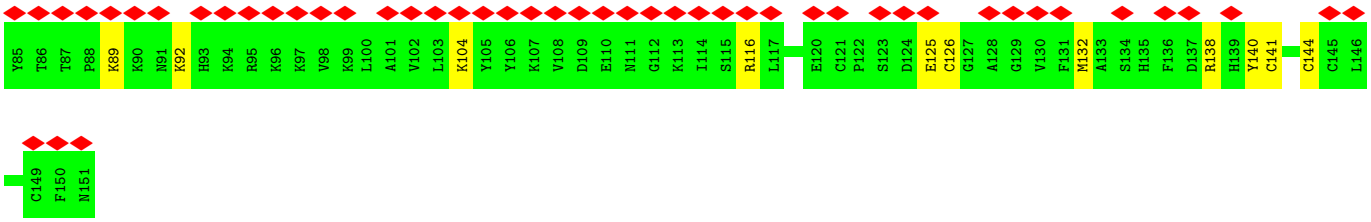
Chain SZ:





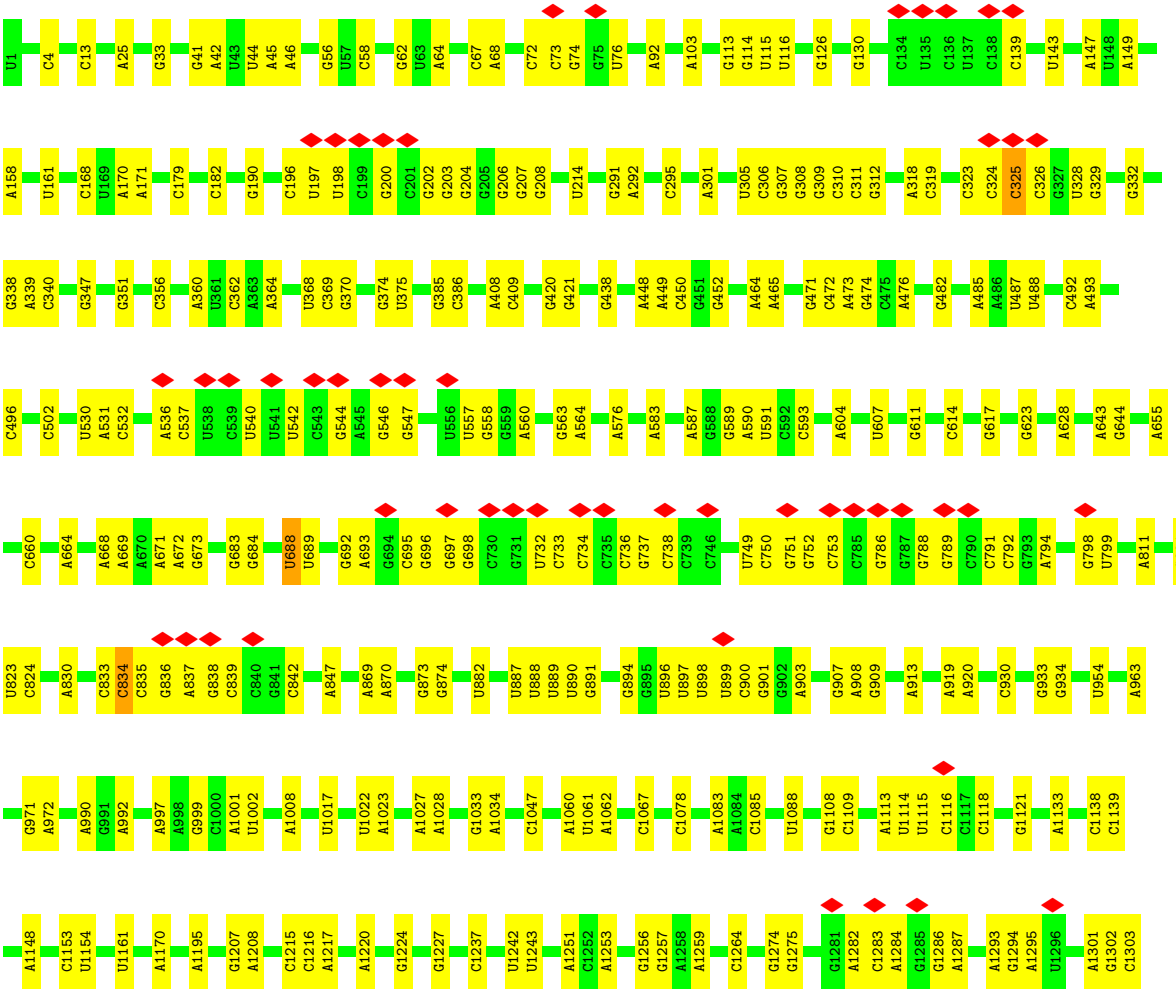
• Molecule 77: Ubiquitin-40S ribosomal protein S27a

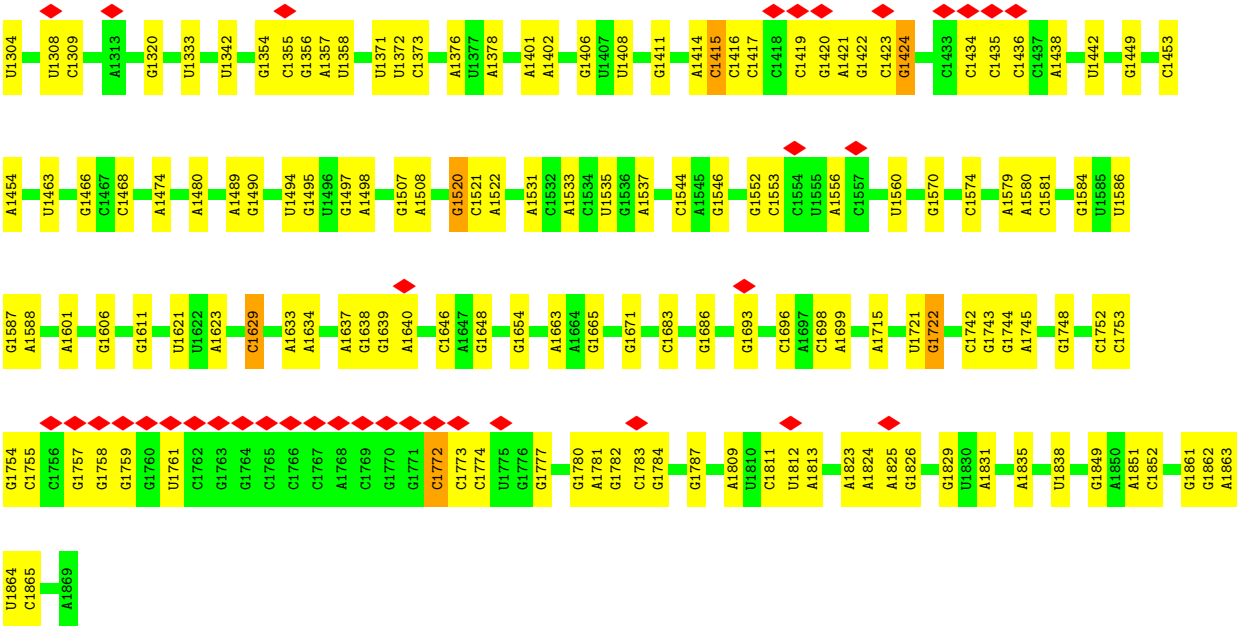
Chain Sf:



• Molecule 78: 18S rRNA

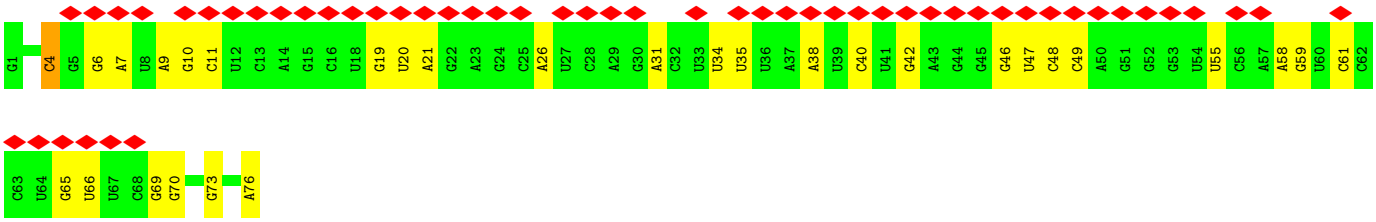
Chain S2:





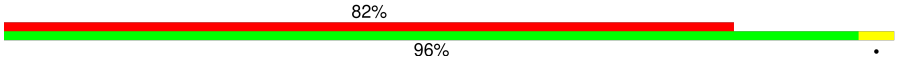
• Molecule 79: E site tRNA

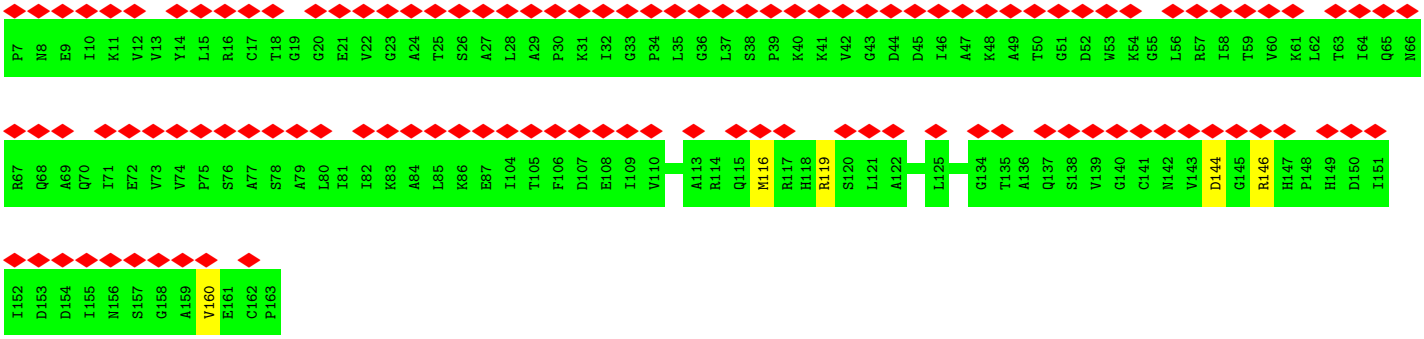
Chain Et:



• Molecule 80: 60S ribosomal protein L12

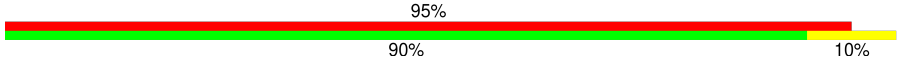
Chain Lt:

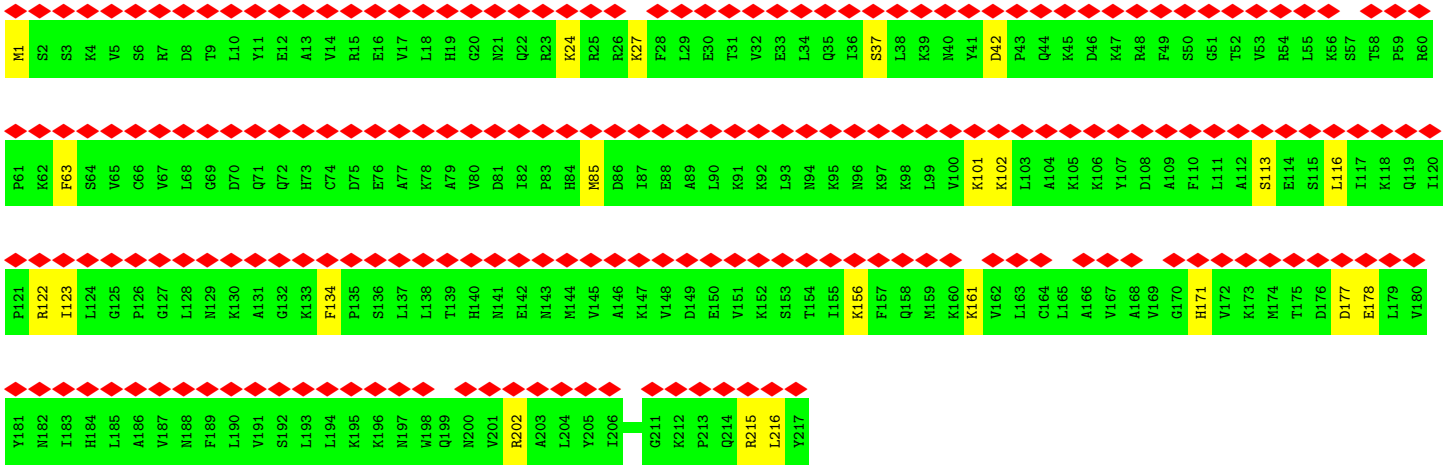




• Molecule 81: 60S ribosomal protein L10a

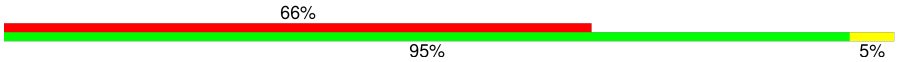
Chain Lz:

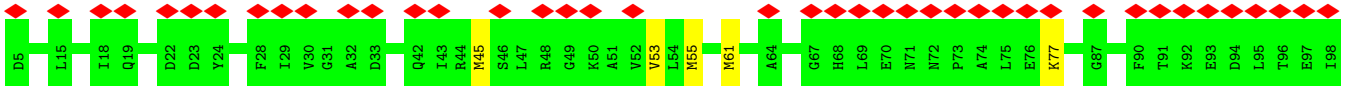


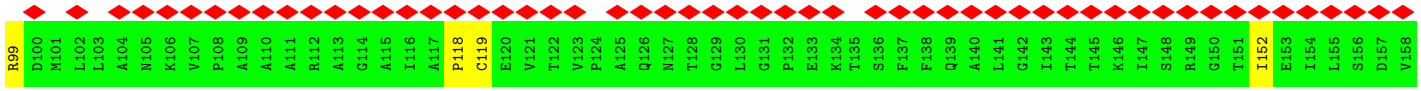


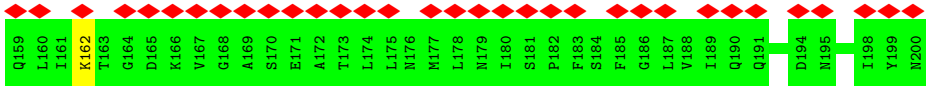
• Molecule 82: 60S acidic ribosomal protein P0

Chain Ls:



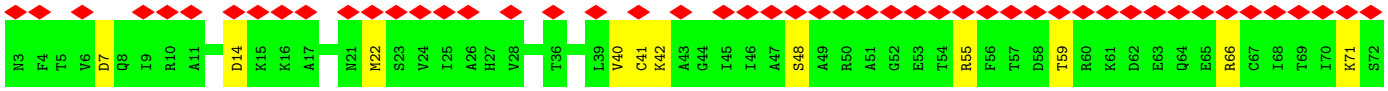


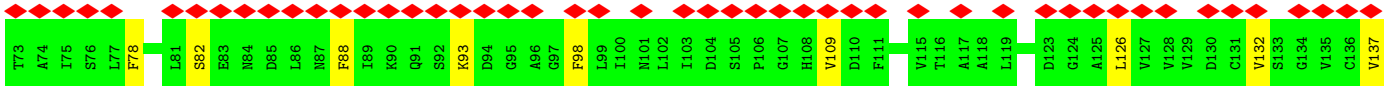


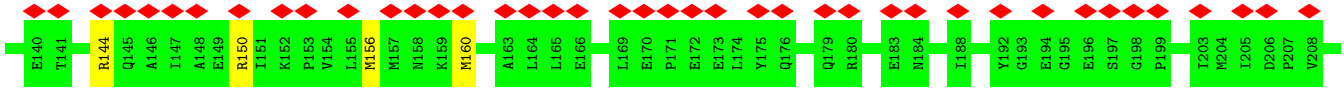


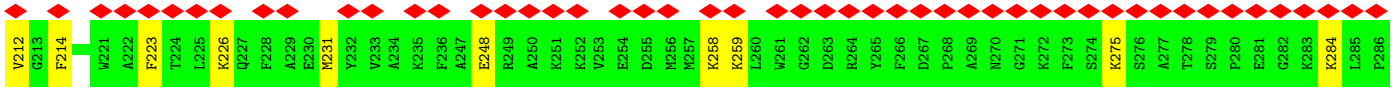
• Molecule 83: eEF2

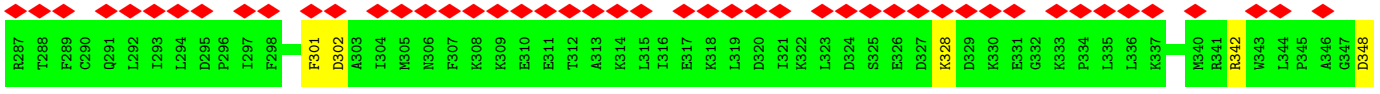
Chain CB:

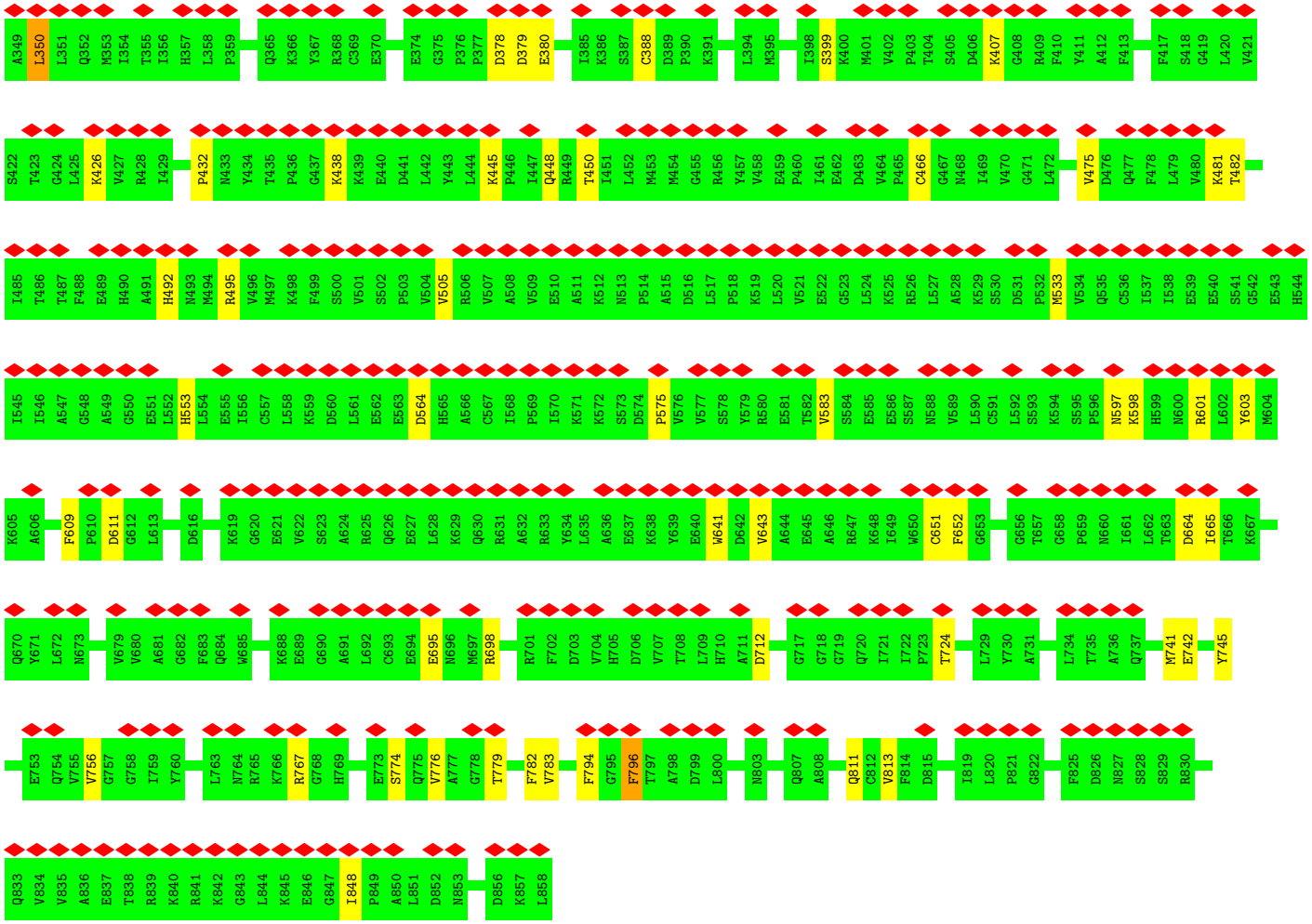






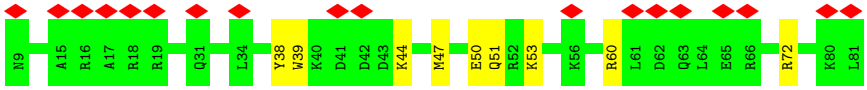






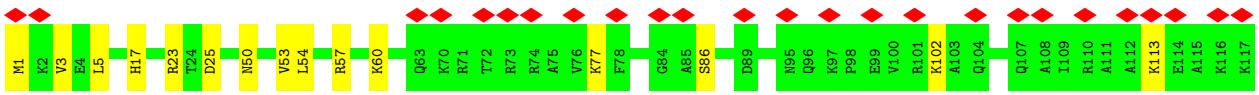
• Molecule 84: Coiled-coil domain-containing protein 124

Chain CE:



• Molecule 85: 60S ribosomal protein L24

Chain LW:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	86934	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.283	Depositor
Minimum map value	-0.113	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.0253	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	SE	0.29	0/2118	0.59	1/2849 (0.0%)
2	SI	0.35	1/1715 (0.1%)	0.64	1/2287 (0.0%)
3	SL	0.31	0/1268	0.64	1/1696 (0.1%)
4	SX	0.29	0/1116	0.60	0/1490
5	SG	0.68	4/1946 (0.2%)	0.95	4/2590 (0.2%)
6	SJ	0.29	0/1550	0.61	0/2069
7	SY	0.35	0/1083	0.64	1/1438 (0.1%)
8	Se	0.30	0/465	0.65	0/612
9	SA	0.31	0/1778	0.62	2/2416 (0.1%)
10	SB	0.29	0/1765	0.56	0/2362
11	SH	0.30	0/1519	0.61	0/2033
12	SV	0.28	0/643	0.58	0/860
13	Sa	0.28	0/836	0.61	0/1121
14	SC	0.29	0/1762	0.56	0/2381
15	SN	0.63	2/1232 (0.2%)	1.06	5/1656 (0.3%)
16	SO	0.28	0/1062	0.63	1/1425 (0.1%)
17	SW	0.29	0/1051	0.58	0/1406
18	Sb	0.30	0/665	0.58	0/891
19	L5	0.32	0/89312	0.86	73/139287 (0.1%)
20	L7	0.28	0/2861	0.79	0/4459
21	L8	0.31	0/3701	0.81	0/5766
22	LA	0.31	0/1936	0.63	0/2596
23	LB	0.31	0/3306	0.60	1/4424 (0.0%)
24	LC	0.29	0/2981	0.60	1/4002 (0.0%)
25	LD	0.43	3/2428 (0.1%)	0.81	4/3252 (0.1%)
26	LE	0.30	0/1942	0.60	0/2606
27	LF	0.31	0/1905	0.56	0/2539
28	LG	0.30	0/1960	0.58	1/2637 (0.0%)
29	LH	0.31	0/1537	0.61	0/2066
30	LI	0.30	0/1673	0.58	0/2233
31	LJ	0.31	0/1433	0.63	0/1915
32	LL	0.29	0/1732	0.58	0/2315

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	LM	0.69	3/1161 (0.3%)	1.04	5/1554 (0.3%)
34	LN	0.30	0/1746	0.61	0/2338
35	LO	0.30	0/1682	0.56	0/2250
36	LP	0.29	0/1268	0.56	0/1701
37	LQ	0.30	0/1537	0.64	0/2052
38	LR	0.27	0/1581	0.60	0/2088
39	LS	0.32	0/1493	0.60	0/2003
40	LT	0.32	0/1326	0.59	0/1770
41	LU	0.45	0/839	0.66	0/1126
42	LV	0.31	0/993	0.60	0/1332
43	LX	0.28	0/1002	0.56	0/1345
44	LY	0.30	0/1132	0.59	0/1504
45	LZ	0.35	0/1130	0.56	0/1507
46	La	0.30	0/1191	0.57	0/1591
47	Lb	0.28	0/889	0.60	0/1175
48	Lc	0.34	0/774	0.63	1/1038 (0.1%)
49	Ld	0.30	0/903	0.62	0/1216
50	Le	0.31	0/1071	0.58	0/1429
51	Lf	0.32	0/895	0.64	0/1198
52	Lg	0.28	0/916	0.61	0/1220
53	Lh	0.28	0/1023	0.58	0/1351
54	Li	0.29	0/843	0.60	0/1115
55	Lj	0.39	0/720	0.83	3/952 (0.3%)
56	Lk	0.28	0/575	0.52	0/761
57	Ll	0.28	0/454	0.59	0/599
58	Lm	0.26	0/435	0.54	0/575
59	Ln	0.29	0/231	0.76	0/294
60	Lo	0.30	0/876	0.59	0/1156
61	Lp	0.31	0/718	0.56	0/953
62	Lr	0.29	0/1017	0.59	0/1364
63	SR	0.31	0/1105	0.67	1/1484 (0.1%)
64	SD	0.30	0/1793	0.60	0/2414
65	SF	0.36	1/1516 (0.1%)	0.64	1/2037 (0.0%)
66	SK	0.29	0/851	0.59	0/1147
67	SP	0.54	2/1003 (0.2%)	0.73	1/1342 (0.1%)
68	SQ	0.75	4/1160 (0.3%)	0.99	5/1553 (0.3%)
69	SS	0.29	0/1216	0.65	0/1628
70	ST	0.30	0/1131	0.59	0/1515
71	SU	0.25	0/831	0.56	0/1115
72	Sc	0.27	0/508	0.69	0/680
73	Sd	0.30	0/470	0.59	0/623
74	Sg	0.30	0/2493	0.59	1/3394 (0.0%)
75	SM	0.26	0/950	0.52	0/1275

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	SZ	0.29	0/604	0.76	2/810 (0.2%)
77	Sf	0.28	0/560	0.62	0/745
78	S2	0.25	0/41242	0.82	39/64255 (0.1%)
79	Et	0.26	0/1778	0.89	1/2767 (0.0%)
80	Lt	0.25	0/1058	0.57	0/1430
81	Lz	0.38	2/1769 (0.1%)	0.63	1/2371 (0.0%)
82	Ls	0.28	0/1519	0.57	0/2052
83	CB	0.42	6/6734 (0.1%)	0.64	7/9094 (0.1%)
84	CE	0.63	2/616 (0.3%)	0.70	1/812 (0.1%)
85	LW	0.31	0/979	0.61	0/1295
All	All	0.32	30/244588 (0.0%)	0.77	165/358074 (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
4	SX	0	1
11	SH	0	1
22	LA	0	1
23	LB	0	2
31	LJ	0	1
32	LL	0	1
33	LM	0	1
35	LO	0	1
51	Lf	0	3
55	Lj	0	2
62	Lr	0	1
67	SP	0	1
68	SQ	0	1
76	SZ	0	1
All	All	0	18

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	SG	130	PRO	CB-CG	21.28	2.56	1.50
68	SQ	38	PRO	CG-CD	-18.38	0.90	1.50
15	SN	23	PRO	CB-CG	17.41	2.37	1.50
33	LM	140	PRO	CB-CG	16.55	2.32	1.50
83	CB	575	PRO	CB-CG	11.72	2.08	1.50

The worst 5 of 165 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
15	SN	23	PRO	CA-N-CD	-23.22	78.99	111.50
5	SG	130	PRO	N-CD-CG	-22.13	70.01	103.20
33	LM	140	PRO	CA-N-CD	-20.97	82.14	111.50
68	SQ	38	PRO	N-CD-CG	-19.84	73.44	103.20
33	LM	140	PRO	CB-CG-CD	-19.79	29.34	106.50

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	LA	13	GLY	Peptide
23	LB	17	LEU	Peptide
23	LB	258	HIS	Peptide
11	SH	15	LYS	Peptide
4	SX	126	ALA	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
1	SE	260/262 (99%)	243 (94%)	17 (6%)	0	100 100
2	SI	204/206 (99%)	194 (95%)	10 (5%)	0	100 100
3	SL	151/153 (99%)	138 (91%)	13 (9%)	0	100 100
4	SX	139/282 (49%)	127 (91%)	11 (8%)	1 (1%)	19 36
5	SG	235/237 (99%)	225 (96%)	10 (4%)	0	100 100
6	SJ	183/185 (99%)	170 (93%)	13 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	SY	129/131 (98%)	118 (92%)	11 (8%)	0	100	100
8	Se	56/58 (97%)	48 (86%)	8 (14%)	0	100	100
9	SA	219/221 (99%)	193 (88%)	26 (12%)	0	100	100
10	SB	212/214 (99%)	201 (95%)	11 (5%)	0	100	100
11	SH	182/186 (98%)	165 (91%)	17 (9%)	0	100	100
12	SV	81/83 (98%)	71 (88%)	10 (12%)	0	100	100
13	Sa	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	13	25
14	SC	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
15	SN	148/150 (99%)	146 (99%)	2 (1%)	0	100	100
16	SO	138/140 (99%)	124 (90%)	14 (10%)	0	100	100
17	SW	127/129 (98%)	122 (96%)	5 (4%)	0	100	100
18	Sb	81/83 (98%)	70 (86%)	11 (14%)	0	100	100
22	LA	246/248 (99%)	224 (91%)	21 (8%)	1 (0%)	30	49
23	LB	400/402 (100%)	371 (93%)	29 (7%)	0	100	100
24	LC	366/368 (100%)	337 (92%)	29 (8%)	0	100	100
25	LD	291/293 (99%)	273 (94%)	18 (6%)	0	100	100
26	LE	232/236 (98%)	203 (88%)	29 (12%)	0	100	100
27	LF	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
28	LG	239/241 (99%)	224 (94%)	15 (6%)	0	100	100
29	LH	188/190 (99%)	177 (94%)	11 (6%)	0	100	100
30	LI	198/202 (98%)	186 (94%)	12 (6%)	0	100	100
31	LJ	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
32	LL	208/210 (99%)	197 (95%)	11 (5%)	0	100	100
33	LM	137/139 (99%)	126 (92%)	10 (7%)	1 (1%)	19	36
34	LN	201/203 (99%)	191 (95%)	8 (4%)	2 (1%)	13	25
35	LO	199/201 (99%)	187 (94%)	12 (6%)	0	100	100
36	LP	151/153 (99%)	138 (91%)	13 (9%)	0	100	100
37	LQ	185/187 (99%)	178 (96%)	7 (4%)	0	100	100
38	LR	183/187 (98%)	175 (96%)	8 (4%)	0	100	100
39	LS	173/175 (99%)	161 (93%)	12 (7%)	0	100	100
40	LT	157/159 (99%)	149 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	LU	99/101 (98%)	81 (82%)	18 (18%)	0	100	100
42	LV	129/131 (98%)	124 (96%)	5 (4%)	0	100	100
43	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
44	LY	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
45	LZ	133/135 (98%)	124 (93%)	9 (7%)	0	100	100
46	La	145/147 (99%)	136 (94%)	9 (6%)	0	100	100
47	Lb	105/109 (96%)	97 (92%)	8 (8%)	0	100	100
48	Lc	96/98 (98%)	90 (94%)	6 (6%)	0	100	100
49	Ld	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
50	Le	126/128 (98%)	117 (93%)	8 (6%)	1 (1%)	16	32
51	Lf	107/109 (98%)	96 (90%)	10 (9%)	1 (1%)	14	28
52	Lg	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
53	Lh	120/122 (98%)	116 (97%)	4 (3%)	0	100	100
54	Li	100/102 (98%)	95 (95%)	5 (5%)	0	100	100
55	Lj	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
56	Lk	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
57	Ll	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
58	Lm	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
59	Ln	22/24 (92%)	22 (100%)	0	0	100	100
60	Lo	103/105 (98%)	100 (97%)	3 (3%)	0	100	100
61	Lp	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
62	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
63	SR	133/135 (98%)	118 (89%)	14 (10%)	1 (1%)	16	32
64	SD	225/227 (99%)	205 (91%)	20 (9%)	0	100	100
65	SF	187/189 (99%)	166 (89%)	21 (11%)	0	100	100
66	SK	96/98 (98%)	86 (90%)	8 (8%)	2 (2%)	5	12
67	SP	119/121 (98%)	109 (92%)	10 (8%)	0	100	100
68	SQ	142/144 (99%)	120 (84%)	21 (15%)	1 (1%)	19	36
69	SS	143/145 (99%)	137 (96%)	6 (4%)	0	100	100
70	ST	141/143 (99%)	127 (90%)	13 (9%)	1 (1%)	19	36
71	SU	102/104 (98%)	96 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
72	Sc	62/64 (97%)	52 (84%)	10 (16%)	0	100 100
73	Sd	53/55 (96%)	49 (92%)	4 (8%)	0	100 100
74	Sg	311/313 (99%)	277 (89%)	34 (11%)	0	100 100
75	SM	120/122 (98%)	109 (91%)	11 (9%)	0	100 100
76	SZ	73/75 (97%)	59 (81%)	14 (19%)	0	100 100
77	Sf	65/67 (97%)	56 (86%)	9 (14%)	0	100 100
80	Lt	137/141 (97%)	102 (74%)	34 (25%)	1 (1%)	19 36
81	Lz	215/217 (99%)	164 (76%)	51 (24%)	0	100 100
82	Ls	194/196 (99%)	175 (90%)	19 (10%)	0	100 100
83	CB	842/846 (100%)	772 (92%)	66 (8%)	4 (0%)	25 44
84	CE	71/73 (97%)	69 (97%)	2 (3%)	0	100 100
85	LW	114/118 (97%)	108 (95%)	6 (5%)	0	100 100
All	All	12774/13091 (98%)	11759 (92%)	997 (8%)	18 (0%)	50 69

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
83	CB	779	THR
4	SX	127	ASN
33	LM	88	ALA
34	LN	124	ASP
63	SR	124	VAL

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	SE	224/224 (100%)	203 (91%)	21 (9%)	7 15
2	SI	178/178 (100%)	158 (89%)	20 (11%)	5 10
3	SL	137/137 (100%)	115 (84%)	22 (16%)	2 3
4	SX	113/226 (50%)	105 (93%)	8 (7%)	12 26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
5	SG	207/207 (100%)	192 (93%)	15 (7%)	12 25
6	SJ	161/161 (100%)	146 (91%)	15 (9%)	7 15
7	SY	113/113 (100%)	91 (80%)	22 (20%)	1 1
8	Se	47/47 (100%)	44 (94%)	3 (6%)	14 30
9	SA	183/183 (100%)	168 (92%)	15 (8%)	9 20
10	SB	195/195 (100%)	182 (93%)	13 (7%)	13 28
11	SH	166/166 (100%)	147 (89%)	19 (11%)	4 9
12	SV	67/67 (100%)	53 (79%)	14 (21%)	1 1
13	Sa	89/89 (100%)	78 (88%)	11 (12%)	4 7
14	SC	188/188 (100%)	165 (88%)	23 (12%)	4 8
15	SN	130/130 (100%)	117 (90%)	13 (10%)	6 13
16	SO	110/110 (100%)	93 (84%)	17 (16%)	2 3
17	SW	112/112 (100%)	104 (93%)	8 (7%)	12 26
18	Sb	75/75 (100%)	68 (91%)	7 (9%)	7 15
22	LA	190/190 (100%)	172 (90%)	18 (10%)	7 14
23	LB	348/348 (100%)	326 (94%)	22 (6%)	15 30
24	LC	306/306 (100%)	288 (94%)	18 (6%)	16 33
25	LD	246/247 (100%)	226 (92%)	20 (8%)	9 20
26	LE	209/209 (100%)	192 (92%)	17 (8%)	9 20
27	LF	194/194 (100%)	186 (96%)	8 (4%)	26 50
28	LG	203/205 (99%)	189 (93%)	14 (7%)	13 26
29	LH	169/169 (100%)	155 (92%)	14 (8%)	9 20
30	LI	172/172 (100%)	158 (92%)	14 (8%)	9 20
31	LJ	148/148 (100%)	130 (88%)	18 (12%)	4 8
32	LL	176/176 (100%)	160 (91%)	16 (9%)	7 16
33	LM	118/118 (100%)	106 (90%)	12 (10%)	6 12
34	LN	171/171 (100%)	165 (96%)	6 (4%)	31 56
35	LO	173/173 (100%)	166 (96%)	7 (4%)	27 51
36	LP	134/134 (100%)	119 (89%)	15 (11%)	5 10
37	LQ	164/164 (100%)	157 (96%)	7 (4%)	25 48
38	LR	166/166 (100%)	151 (91%)	15 (9%)	8 16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
39	LS	156/156 (100%)	146 (94%)	10 (6%)	14 30
40	LT	139/139 (100%)	125 (90%)	14 (10%)	6 12
41	LU	91/91 (100%)	81 (89%)	10 (11%)	5 10
42	LV	101/101 (100%)	94 (93%)	7 (7%)	13 26
43	LX	108/108 (100%)	100 (93%)	8 (7%)	11 24
44	LY	124/124 (100%)	116 (94%)	8 (6%)	14 29
45	LZ	117/117 (100%)	106 (91%)	11 (9%)	7 15
46	La	120/120 (100%)	115 (96%)	5 (4%)	25 49
47	Lb	88/90 (98%)	83 (94%)	5 (6%)	17 34
48	Lc	83/83 (100%)	73 (88%)	10 (12%)	4 8
49	Ld	98/98 (100%)	94 (96%)	4 (4%)	26 50
50	Le	114/114 (100%)	108 (95%)	6 (5%)	19 38
51	Lf	88/88 (100%)	82 (93%)	6 (7%)	13 27
52	Lg	98/98 (100%)	91 (93%)	7 (7%)	12 26
53	Lh	109/109 (100%)	96 (88%)	13 (12%)	4 8
54	Li	86/86 (100%)	83 (96%)	3 (4%)	31 56
55	Lj	73/73 (100%)	63 (86%)	10 (14%)	3 6
56	Lk	64/64 (100%)	61 (95%)	3 (5%)	22 44
57	Ll	47/47 (100%)	41 (87%)	6 (13%)	3 7
58	Lm	48/48 (100%)	47 (98%)	1 (2%)	48 72
59	Ln	23/23 (100%)	22 (96%)	1 (4%)	25 48
60	Lo	93/93 (100%)	85 (91%)	8 (9%)	8 18
61	Lp	74/74 (100%)	70 (95%)	4 (5%)	18 37
62	Lr	109/109 (100%)	94 (86%)	15 (14%)	3 6
63	SR	122/122 (100%)	104 (85%)	18 (15%)	2 4
64	SD	190/190 (100%)	167 (88%)	23 (12%)	4 8
65	SF	159/159 (100%)	139 (87%)	20 (13%)	3 7
66	SK	89/89 (100%)	84 (94%)	5 (6%)	17 35
67	SP	107/107 (100%)	98 (92%)	9 (8%)	9 19
68	SQ	119/119 (100%)	107 (90%)	12 (10%)	6 12
69	SS	126/126 (100%)	111 (88%)	15 (12%)	4 8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
70	ST	113/113 (100%)	98 (87%)	15 (13%)	3 6
71	SU	94/94 (100%)	82 (87%)	12 (13%)	3 7
72	Sc	57/57 (100%)	52 (91%)	5 (9%)	8 17
73	Sd	48/48 (100%)	41 (85%)	7 (15%)	2 5
74	Sg	272/272 (100%)	246 (90%)	26 (10%)	7 14
75	SM	102/104 (98%)	91 (89%)	11 (11%)	5 11
76	SZ	66/66 (100%)	58 (88%)	8 (12%)	4 8
77	Sf	60/60 (100%)	49 (82%)	11 (18%)	1 1
80	Lt	112/115 (97%)	108 (96%)	4 (4%)	30 55
81	Lz	195/196 (100%)	175 (90%)	20 (10%)	6 12
82	Ls	162/164 (99%)	152 (94%)	10 (6%)	15 30
83	CB	722/723 (100%)	635 (88%)	87 (12%)	4 8
84	CE	62/62 (100%)	55 (89%)	7 (11%)	4 9
85	LW	97/97 (100%)	82 (84%)	15 (16%)	2 3
All	All	11107/11234 (99%)	10085 (91%)	1022 (9%)	10 15

5 of 1022 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
35	LO	3	GLU
81	Lz	37	SER
45	LZ	123	LYS
77	Sf	141	CYS
83	CB	301	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
83	CB	184	ASN
83	CB	553	HIS
83	CB	660	ASN
31	LJ	104	ASN
28	LG	94	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	L5	3704/3740 (99%)	884 (23%)	20 (0%)
20	L7	119/120 (99%)	14 (11%)	0
21	L8	155/156 (99%)	31 (20%)	1 (0%)
78	S2	1715/1740 (98%)	428 (24%)	7 (0%)
79	Et	73/75 (97%)	30 (41%)	0
All	All	5766/5831 (98%)	1387 (24%)	28 (0%)

5 of 1387 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
19	L5	2	G
19	L5	13	U
19	L5	17	A
19	L5	25	A
19	L5	26	C

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
19	L5	2786	C
78	S2	1781	A
19	L5	4600	G
78	S2	688	U
19	L5	3673	C

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 261 ligands modelled in this entry, 261 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
19	L5	12
78	S2	6
47	Lb	1
26	LE	1
83	CB	1
85	LW	1
11	SH	1
80	Lt	1
30	LI	1
79	Et	1
38	LR	1

The worst 5 of 27 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Lb	76:VAL	C	89:VAL	N	33.86
1	S2	753:C	O3'	785:C	P	27.17
1	LE	76:ALA	C	88:VAL	N	23.48
1	L5	2910:G	O3'	3584:C	P	20.84
1	S2	698:G	O3'	730:C	P	16.88

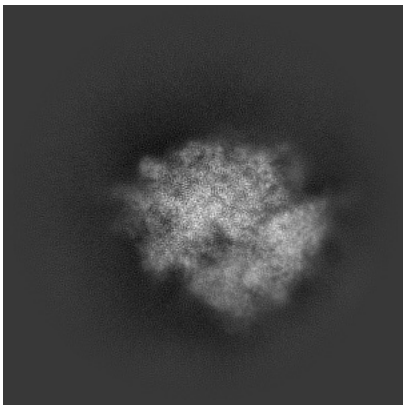
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-44043. These allow visual inspection of the internal detail of the map and identification of artifacts.

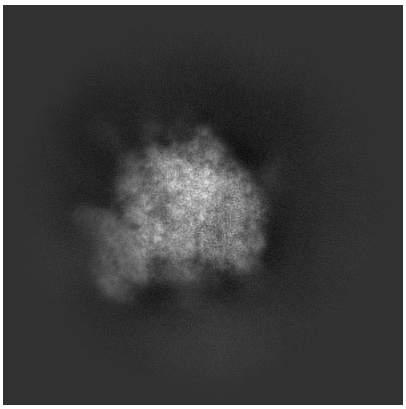
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

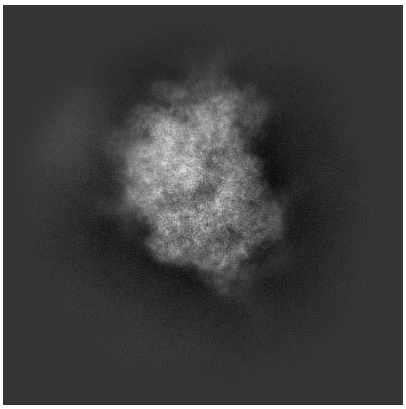
6.1.1 Primary map



X

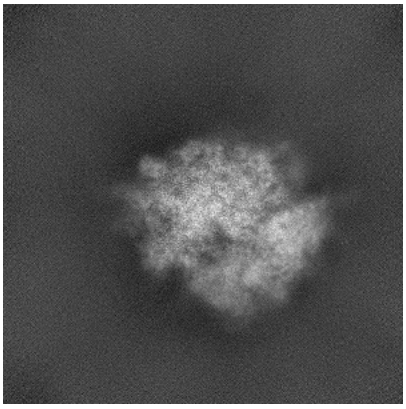


Y

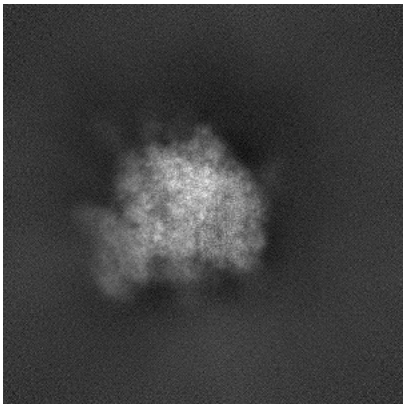


Z

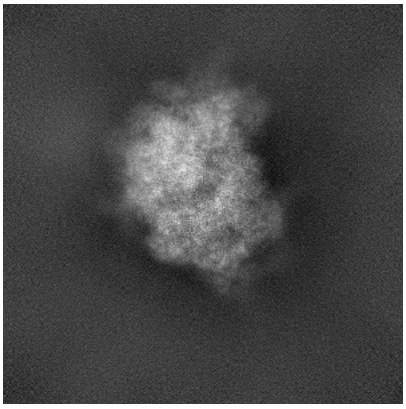
6.1.2 Raw map



X



Y

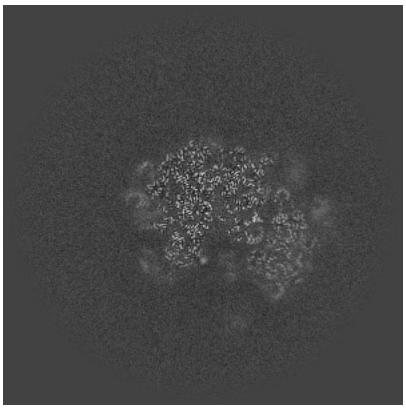


Z

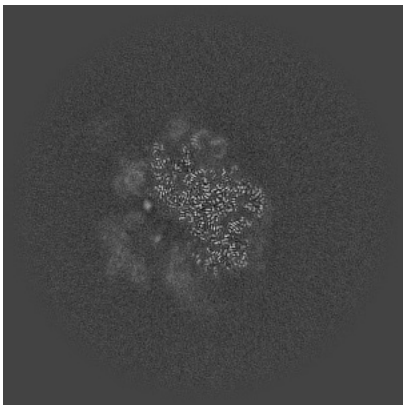
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

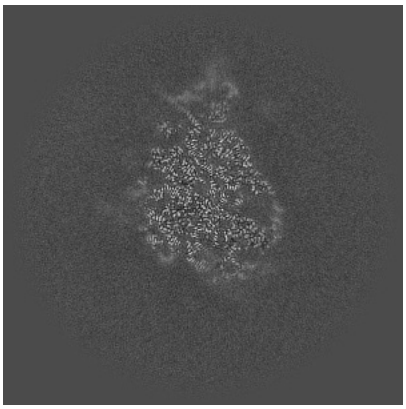
6.2.1 Primary map



X Index: 256

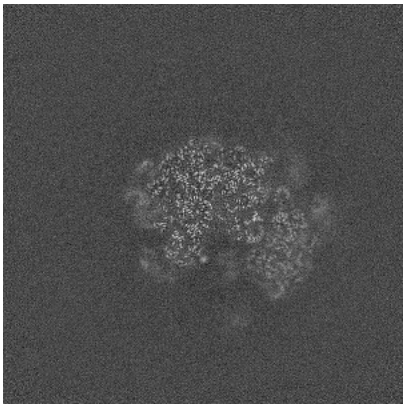


Y Index: 256

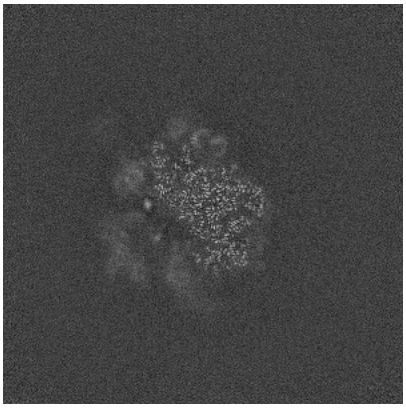


Z Index: 256

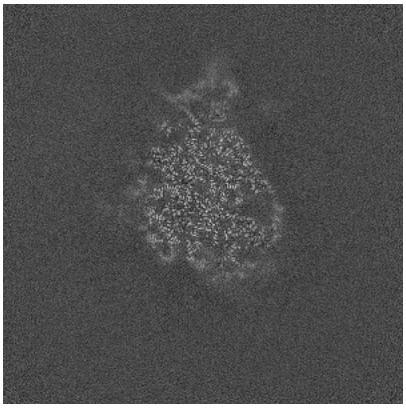
6.2.2 Raw map



X Index: 256



Y Index: 256

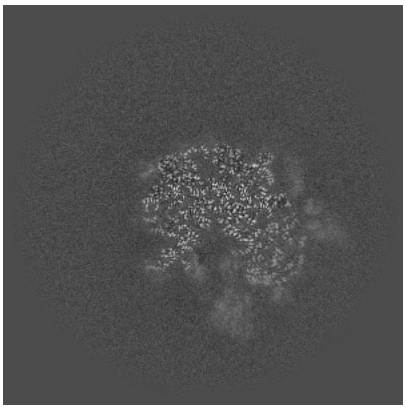


Z Index: 256

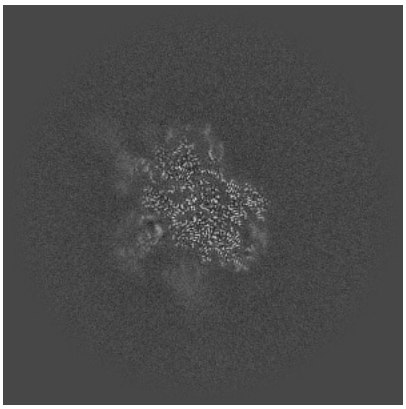
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

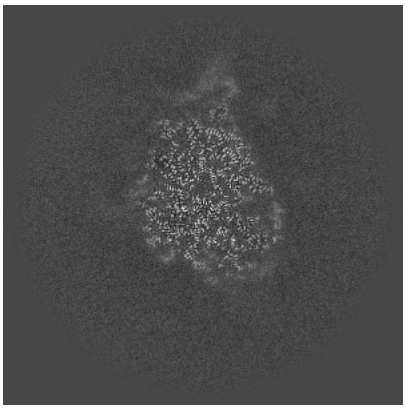
6.3.1 Primary map



X Index: 243

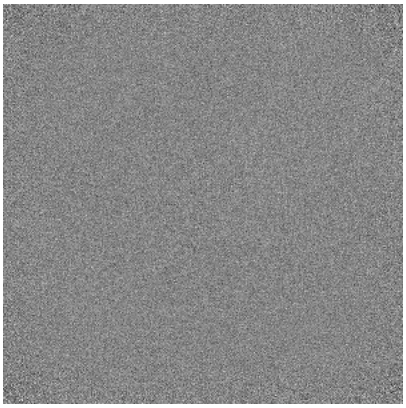


Y Index: 243

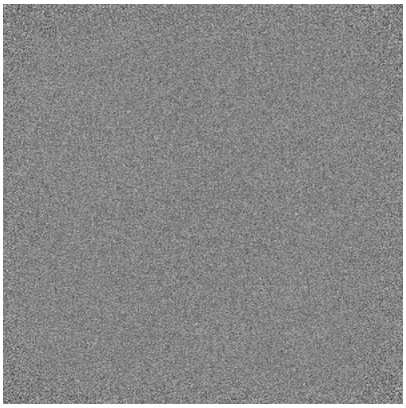


Z Index: 258

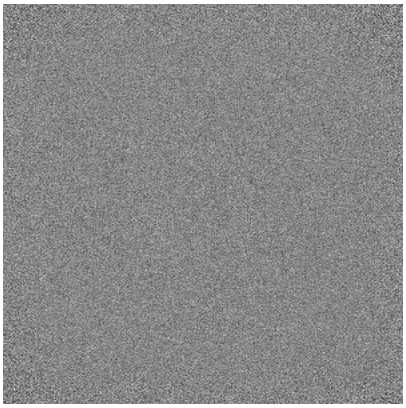
6.3.2 Raw map



X Index: 0



Y Index: 0

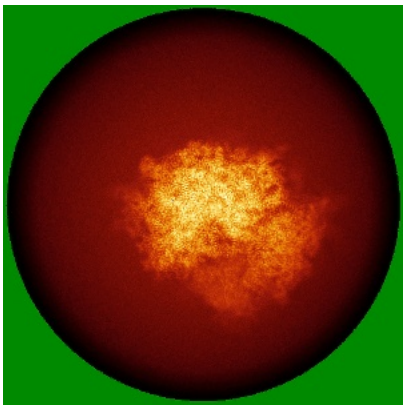


Z Index: 0

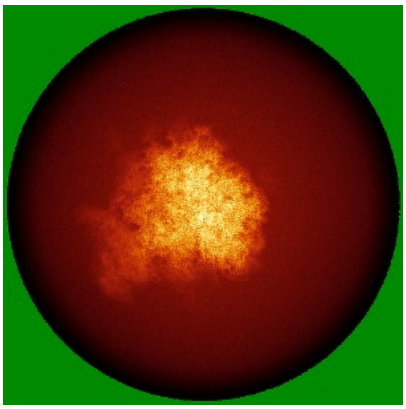
The images above show the largest variance slices of the map in three orthogonal directions.

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

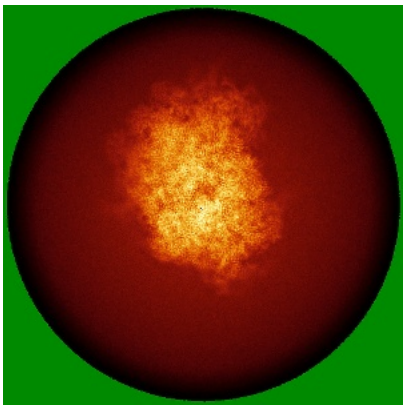
6.4.1 Primary map



X

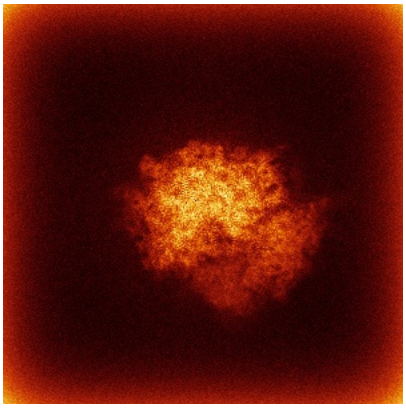


Y

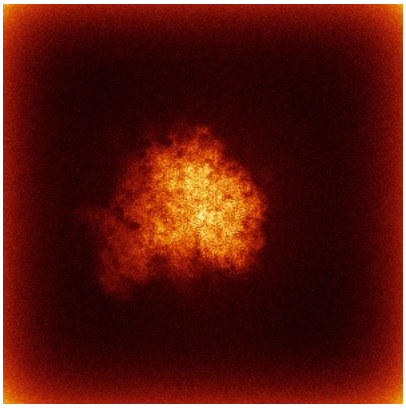


Z

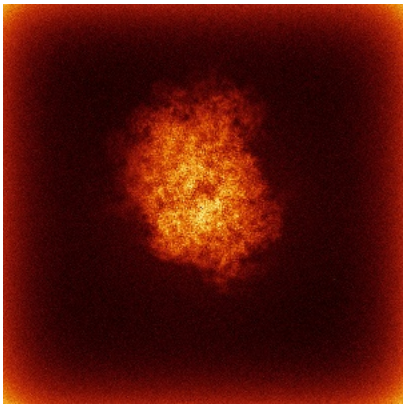
6.4.2 Raw map



X



Y

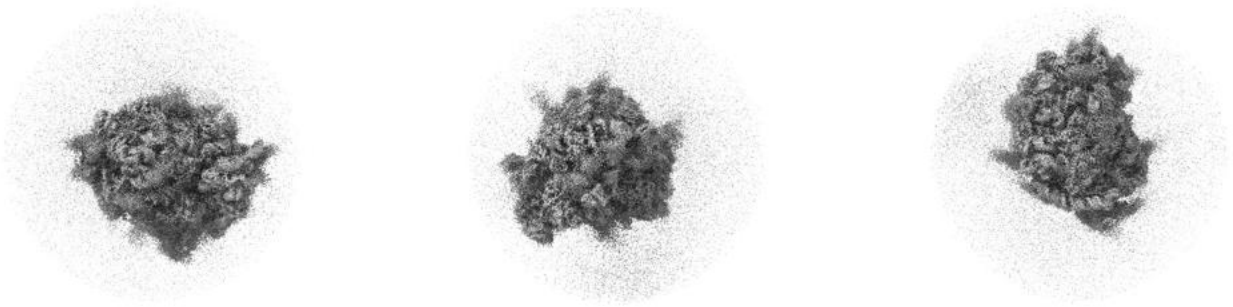


Z

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

6.5 Orthogonal surface views (i)

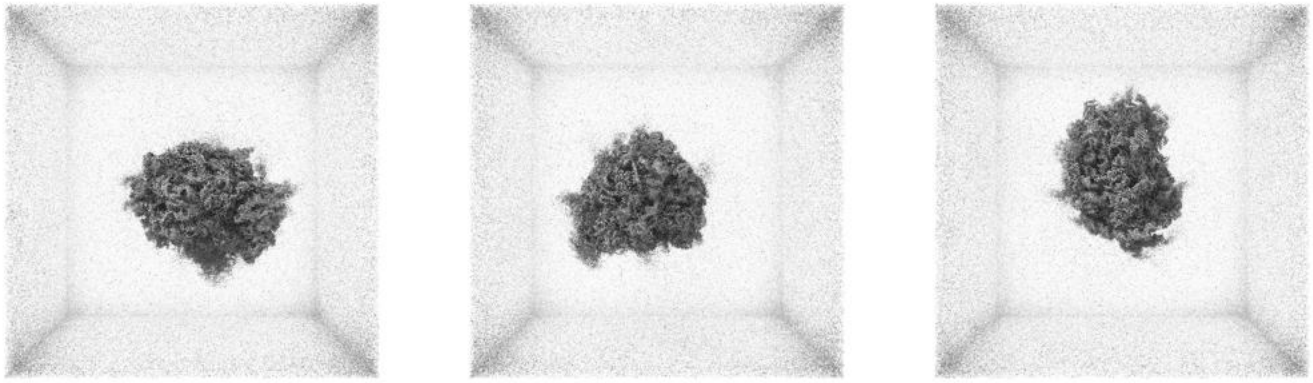
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.0253. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

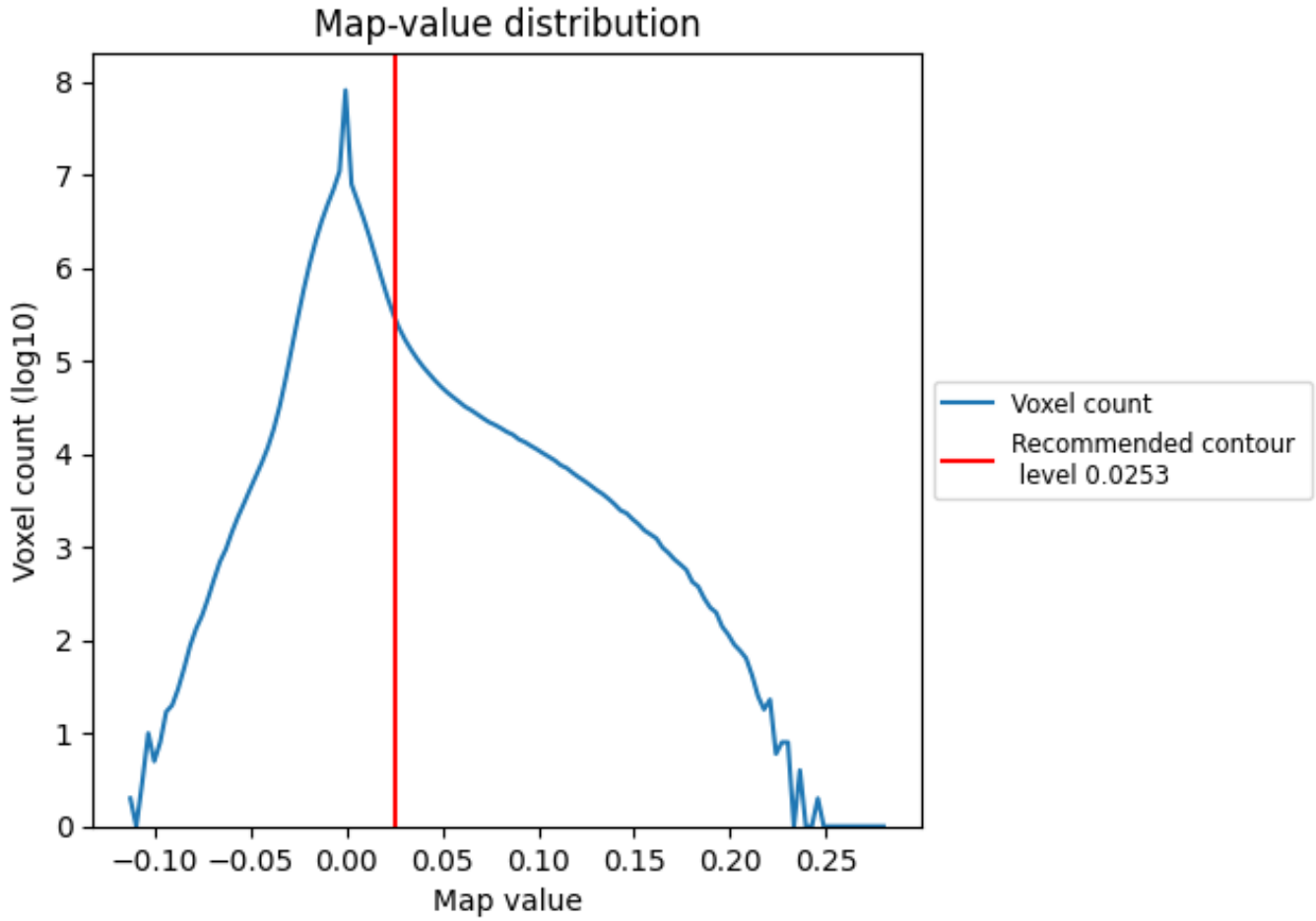
6.6 Mask visualisation (i)

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

7 Map analysis

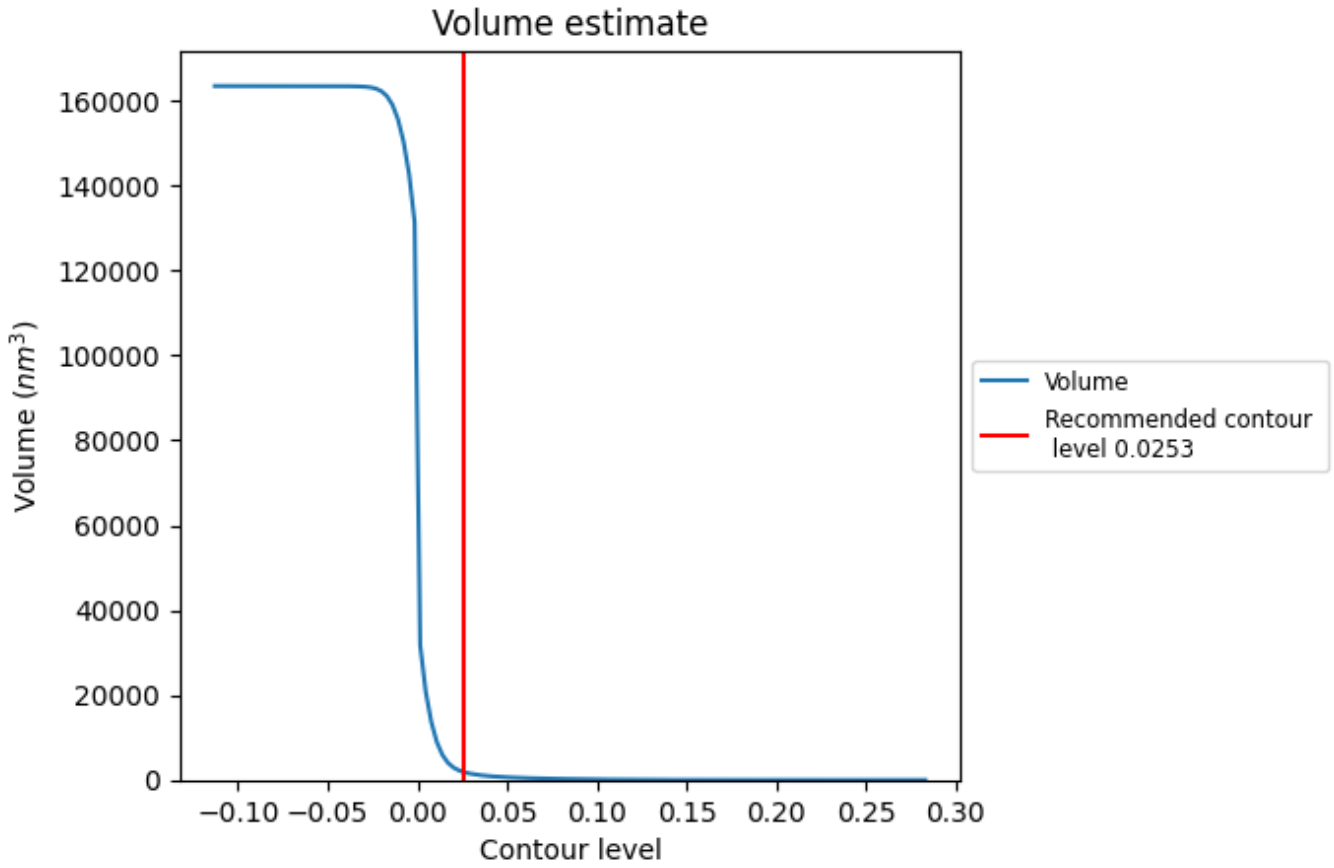
This section contains the results of statistical analysis of the map.

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.

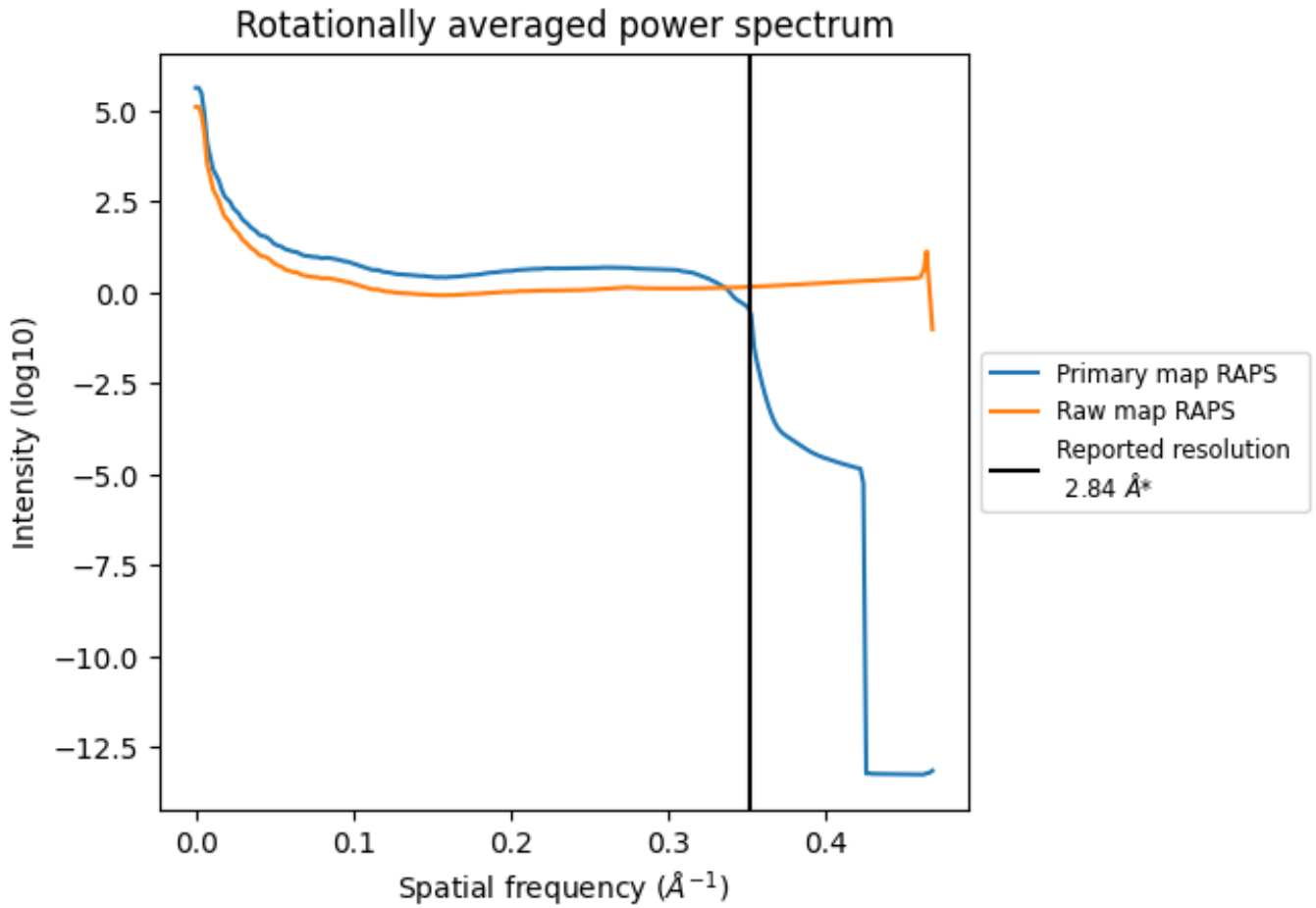
7.2 Volume estimate (i)



The volume at the recommended contour level is 1946 nm^3; this corresponds to an approximate mass of 1758 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)

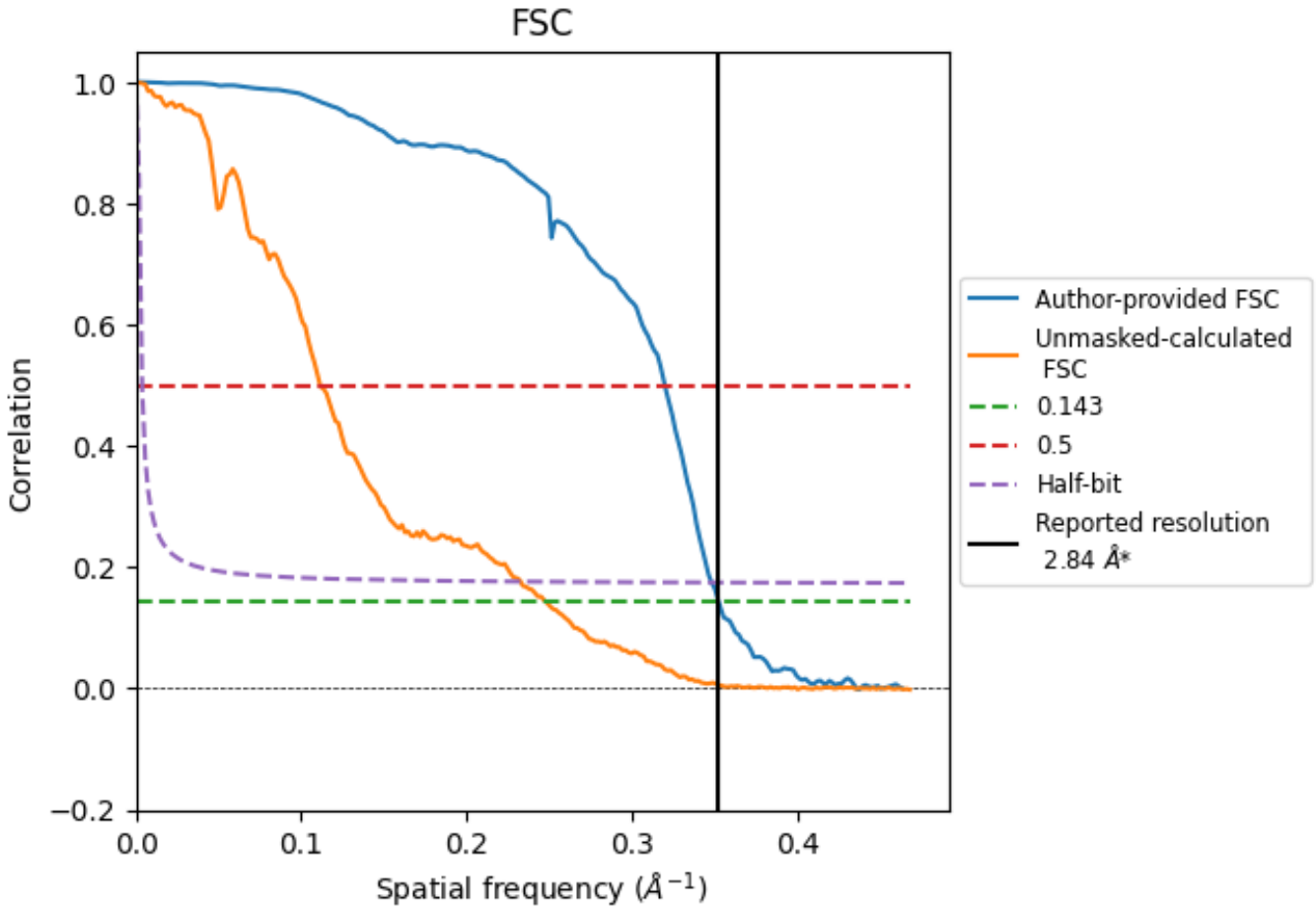


*Reported resolution corresponds to spatial frequency of 0.352 $Å^{-1}$

8 Fourier-Shell correlation

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

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.352 Å^{-1}

8.2 Resolution estimates (i)

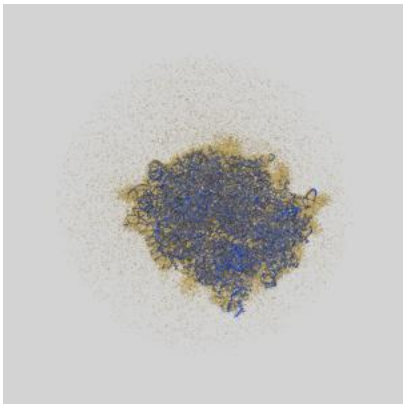
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	2.84	3.12	2.87
Unmasked-calculated*	4.03	8.98	4.30

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.03 differs from the reported value 2.84 by more than 10 %

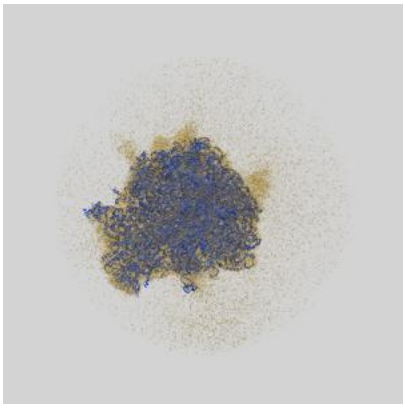
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-44043 and PDB model 9B0J. Per-residue inclusion information can be found in section 3 on page 21.

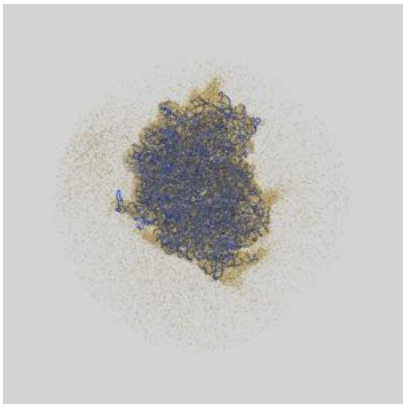
9.1 Map-model overlay



X



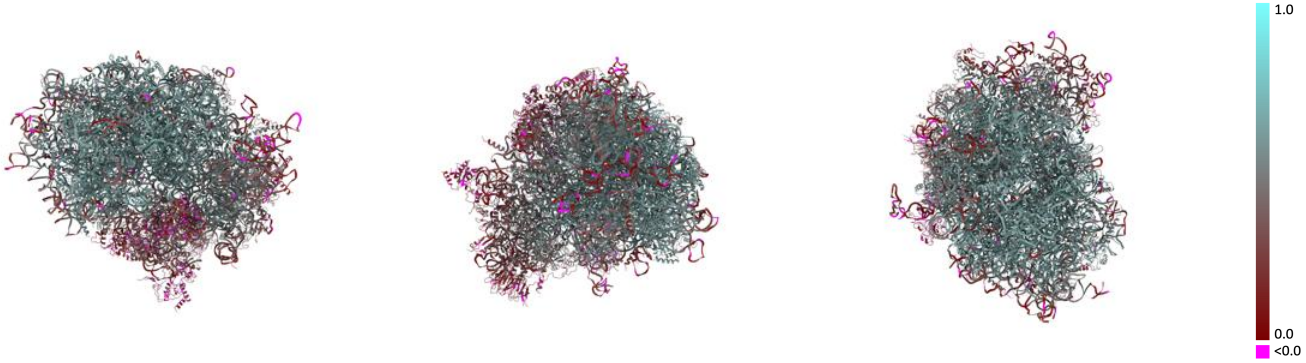
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0253 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.

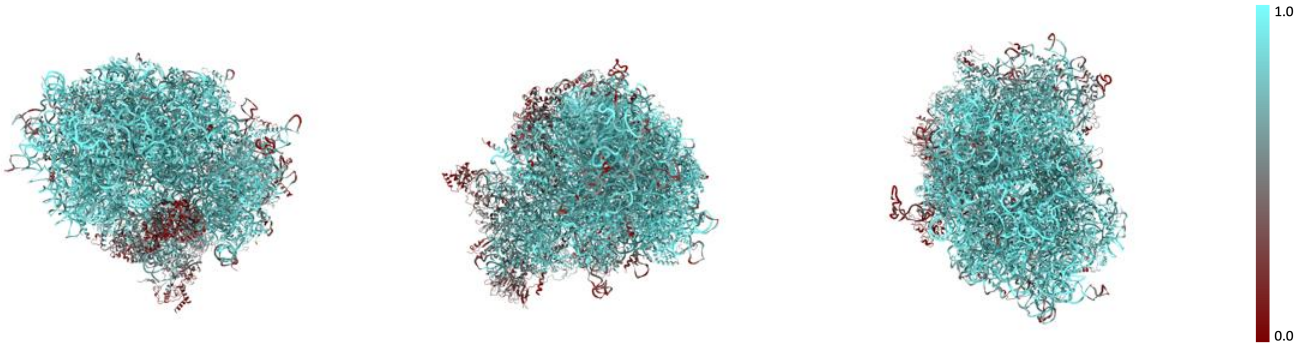
9.2 Q-score mapped to coordinate model



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.

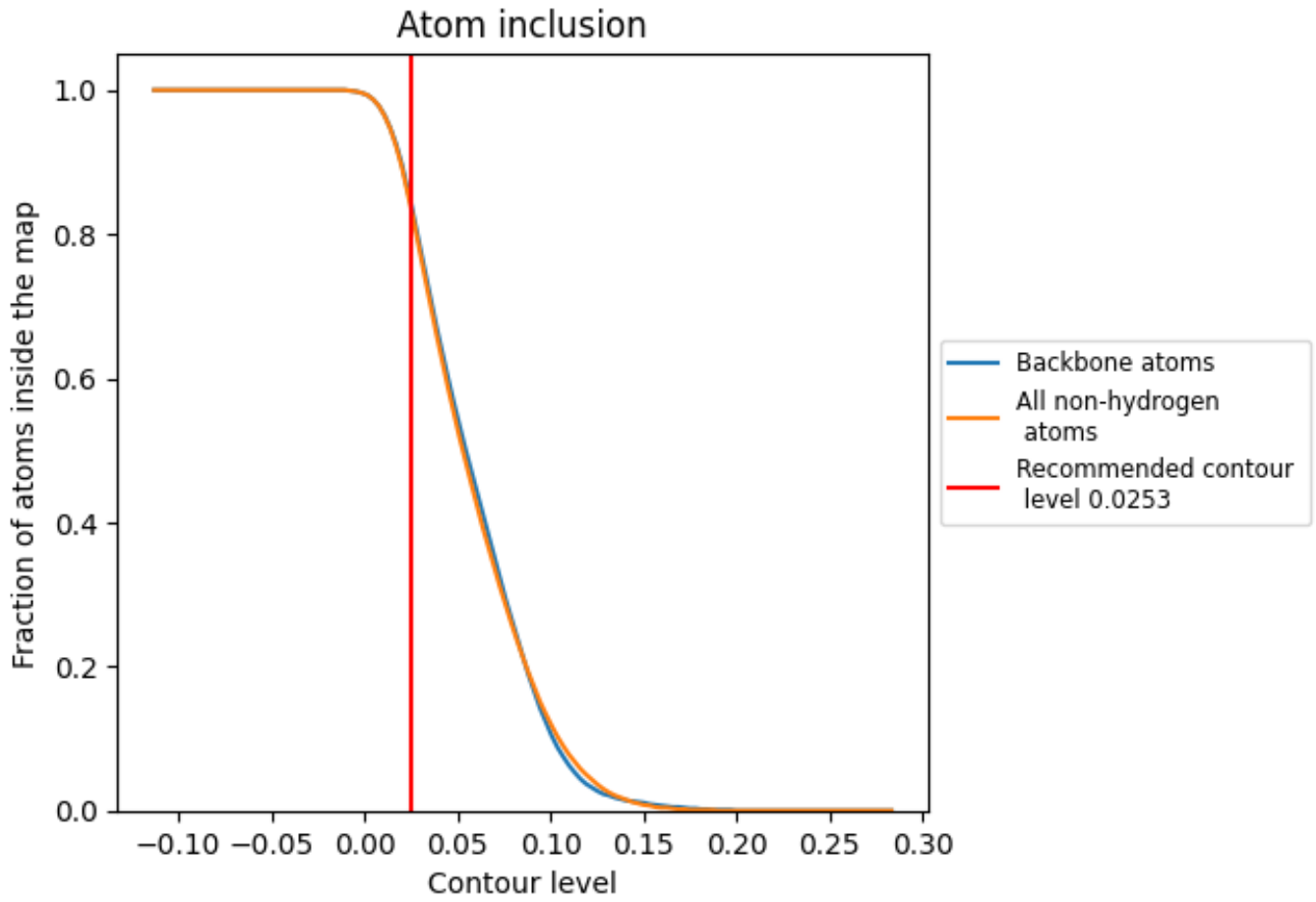
9.3 Atom inclusion mapped to coordinate model



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 (0.0253).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 83% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0253) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8340	0.4860
CB	0.3020	0.2300
CE	0.7070	0.2800
Et	0.3230	0.1680
L5	0.9150	0.5320
L7	0.9860	0.5960
L8	0.9440	0.5690
LA	0.9660	0.6190
LB	0.9300	0.5940
LC	0.9200	0.5920
LD	0.8950	0.5530
LE	0.8400	0.5260
LF	0.9460	0.6010
LG	0.8300	0.5350
LH	0.9140	0.5770
LI	0.9400	0.5940
LJ	0.7870	0.4790
LL	0.8960	0.5660
LM	0.9320	0.5810
LN	0.9810	0.6270
LO	0.9490	0.6040
LP	0.9440	0.6120
LQ	0.9540	0.6200
LR	0.8620	0.5470
LS	0.9540	0.6140
LT	0.9130	0.5780
LU	0.8090	0.4750
LV	0.9550	0.6080
LW	0.6850	0.4280
LX	0.9200	0.5860
LY	0.9210	0.5890
LZ	0.9410	0.5800
La	0.9580	0.6220
Lb	0.8300	0.5170
Lc	0.9210	0.5570

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Chain	Atom inclusion	Q-score
Ld	0.8900	0.5740
Le	0.9520	0.6120
Lf	0.9640	0.6180
Lg	0.9250	0.5900
Lh	0.9090	0.5900
Li	0.9030	0.5780
Lj	0.9630	0.6160
Lk	0.8350	0.5380
Ll	0.9340	0.5860
Lm	0.9300	0.5980
Ln	0.9760	0.6050
Lo	0.9200	0.5950
Lp	0.9160	0.6010
Lr	0.9400	0.6000
Ls	0.3350	0.2160
Lt	0.2110	0.1330
Lz	0.0860	0.1080
S2	0.8800	0.4370
SA	0.7960	0.4690
SB	0.8260	0.5120
SC	0.8690	0.5090
SD	0.5800	0.3170
SE	0.8200	0.4600
SF	0.5890	0.3300
SG	0.6820	0.3690
SH	0.6970	0.4030
SI	0.8210	0.4990
SJ	0.8120	0.4630
SK	0.4770	0.2340
SL	0.8170	0.5000
SM	0.1550	0.1330
SN	0.8980	0.5540
SO	0.8120	0.4970
SP	0.4690	0.2740
SQ	0.6090	0.2910
SR	0.6340	0.3400
SS	0.5450	0.3160
ST	0.5880	0.2760
SU	0.5170	0.2710
SV	0.8550	0.5060
SW	0.9230	0.5560
SX	0.8530	0.5250

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Chain	Atom inclusion	Q-score
SY	0.7290	0.3700
SZ	0.4180	0.2450
Sa	0.8700	0.5360
Sb	0.7900	0.4740
Sc	0.6030	0.3300
Sd	0.7530	0.3430
Se	0.6890	0.4130
Sf	0.2760	0.1630
Sg	0.3650	0.2080