wwPDB EM Validation Summary Report (i)

May 19, 2024 – 11:03 am BST

PDB ID	:	6Y2L
EMDB ID	:	EMD-10674
Title	:	Structure of human ribosome in POST state
Authors	:	Bhaskar, V.; Schenk, A.D.; Cavadini, S.; von Loeffelholz, O.; Natchiar, S.K.; Klaholz, B.P.; Chao, J.A.
Deposited on	:	2020-02-16
Resolution	:	3.00 Å(reported)
Based on initial models	:	5LKS, 6QZP, 5AJ0

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:

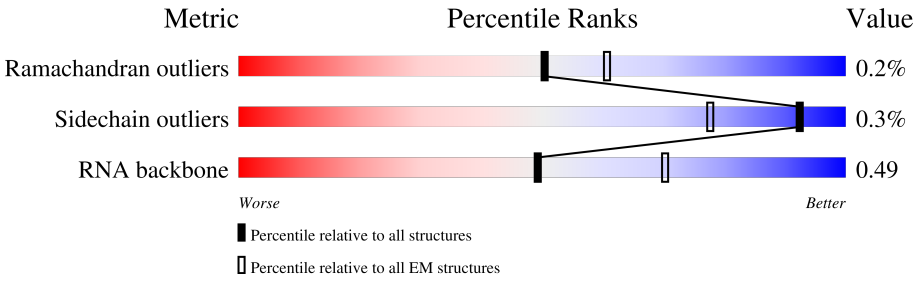
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance

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

The reported resolution of this entry is 3.00 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	A4	28	29% 25% 46%
2	B4	76	70% 30%
3	C4	2	100%
4	L5	5070	55% 16% 29%
5	L7	120	85% 15%
6	L8	156	79% 21%
7	LA	257	96% .
8	LB	403	98% .

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Mol	Chain	Length	Quality of chain
9	LC	427	84% 15%
10	LD	297	99%
11	LE	288	75% 24%
12	LF	248	91% 9%
13	LG	266	86% 14%
14	LH	192	98%
15	LI	214	96%
16	LJ	178	95% 5%
17	LL	211	96%
18	LM	215	64% 35%
19	LN	204	99%
20	LO	203	99%
21	LP	184	83% 17%
22	LQ	188	99%
23	LR	196	90% 10%
24	LS	176	99%
25	LT	160	99%
26	LU	128	79% 21%
27	LV	140	93% 6%
28	LW	157	71% 27%
29	LX	156	77% 23%
30	LY	145	92% 8%
31	LZ	136	99%
32	La	148	99%
33	Lb	159	47% 53%

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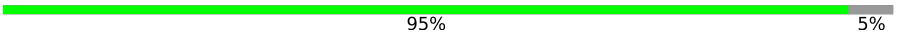
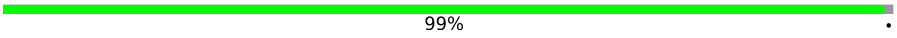
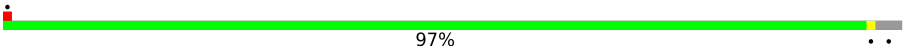
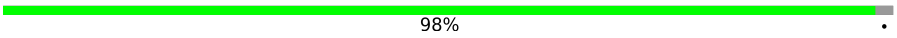
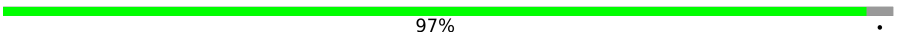
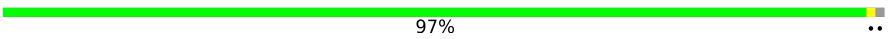
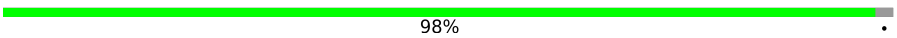
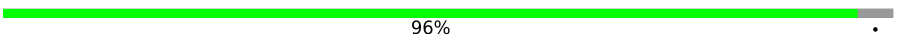
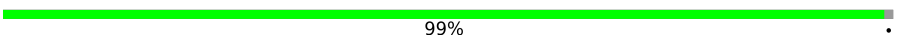
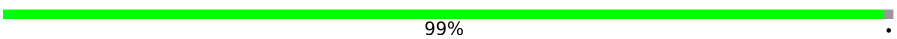
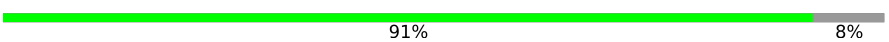
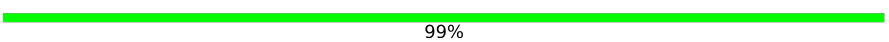
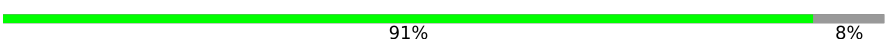
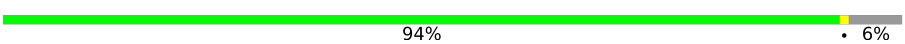
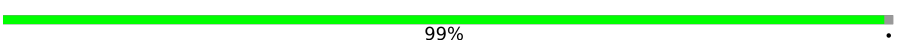
Mol	Chain	Length	Quality of chain
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SC	293	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	

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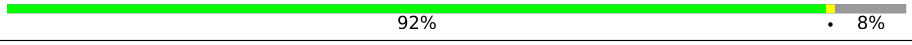
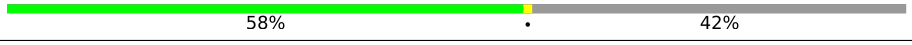
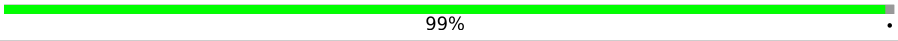
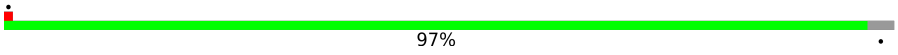
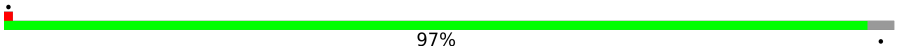
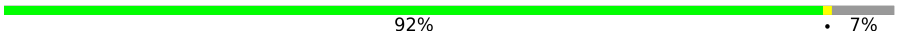
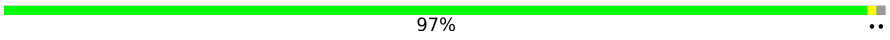
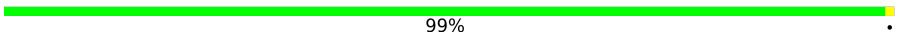
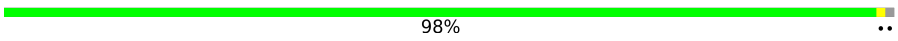
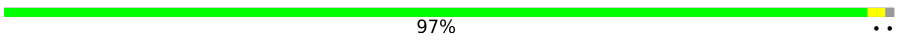
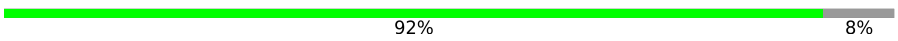
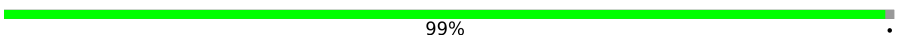
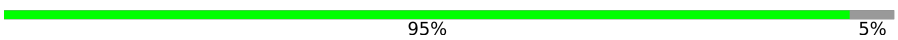
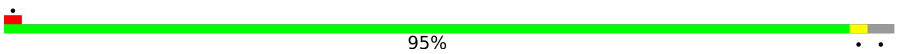
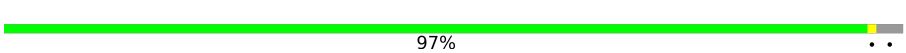
Mol	Chain	Length	Quality of chain
59	SJ	194	
60	SK	165	
61	SL	158	
62	SN	151	
63	SO	151	
64	SP	145	
65	SQ	146	
66	SR	135	
67	SS	152	
68	ST	145	
69	SU	119	
70	SV	83	
71	SW	130	
72	SX	143	
73	SY	133	
74	SZ	125	
75	Sa	115	
76	Sb	84	
77	Sc	69	
78	Sd	56	
79	Se	59	
80	Sg	317	

2 Entry composition (i)

There are 84 unique types of molecules in this entry. The entry contains 208946 atoms, of which 23 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A4	15	300	135	30	120	15	0	0

- Molecule 2 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B4	76	1623	723	290	534	76	0	0

- Molecule 3 is a protein called Nascent polypeptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	C4	2	10	6	2	2	0	0

- Molecule 4 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	L5	3613	77447	34487	14167	25181	3612	0	0

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

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

- Molecule 6 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 12 is a protein called 60S ribosomal protein L7.

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

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 15 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	206	Total	C	N	O	S	0	0
			1651	1051	318	268	14		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			799	515	140	142	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 41 is a protein called 60S ribosomal protein L37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	105	Total	C	N	O	S	0	0
			848	532	173	137	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1713	Total	C	N	O	P	0	0
			36560	16319	6563	11966	1712		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

- Molecule 52 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

- Molecule 53 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SD	223	Total	C	N	O	S	0	0
			1580	1016	286	271	7		

- Molecule 54 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 55 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SF	187	Total	C	N	O	S	0	0
			1416	886	269	254	7		

- Molecule 56 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

- Molecule 57 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	SH	183	Total	C	N	O	0	0
			1274	819	242	213		

- Molecule 58 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SI	206	Total	C	N	O	S	0	0
			1574	989	308	272	5		

- Molecule 59 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

- Molecule 60 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- Molecule 61 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

- Molecule 62 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SN	150	Total	C	N	O	S	0	0
			1182	758	226	197	1		

- Molecule 63 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 64 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SP	128	Total	C	N	O	S	0	0
			975	617	185	167	6		

- Molecule 65 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SQ	142	Total	C	N	O	S	0	0
			1071	687	204	177	3		

- Molecule 66 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

- Molecule 67 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SS	141	Total	C	N	O	S	0	0
			1118	706	226	185	1		

- Molecule 68 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	ST	143	Total	C	N	O	S	0	0
			1081	679	210	189	3		

- Molecule 69 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	4		

- Molecule 70 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SV	83	Total	C	N	O	S	0	0
			618	385	115	113	5		

- Molecule 71 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SW	129	Total	C	N	O	S	0	0
			1026	655	193	172	6		

- Molecule 72 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SX	141	Total	C	N	O	S	0	0
			1078	682	212	181	3		

- Molecule 73 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- Molecule 74 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SZ	75	Total	C	N	O	S	0	0
			559	361	105	92	1		

- Molecule 75 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	5		

- Molecule 76 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sb	83	Total	C	N	O	S	0	0
			618	386	118	107	7		

- Molecule 77 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sc	63	Total 472	C 289	N 92	O 89	S 2	0	0

- Molecule 78 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sd	53	Total 433	C 271	N 87	O 70	S 5	0	0

- Molecule 79 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Se	57	Total 426	C 259	N 96	O 70	S 1	0	0

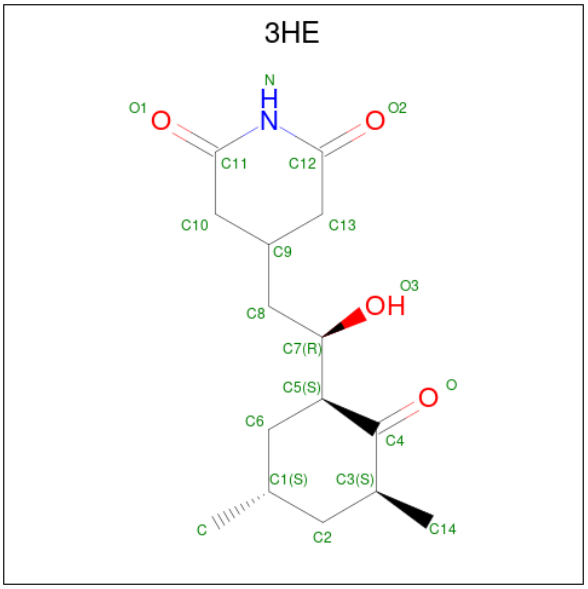
- Molecule 80 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sg	308	Total 2172	C 1388	N 379	O 394	S 11	0	0

- Molecule 81 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	B4	1	Total 1	Mg 1	0
81	L5	129	Total 129	Mg 129	0
81	L7	3	Total 3	Mg 3	0
81	L8	3	Total 3	Mg 3	0
81	LA	1	Total 1	Mg 1	0
81	LN	1	Total 1	Mg 1	0
81	LP	1	Total 1	Mg 1	0
81	LV	1	Total 1	Mg 1	0
81	S2	53	Total 53	Mg 53	0

- Molecule 82 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: $C_{15}H_{23}NO_4$).



Mol	Chain	Residues	Atoms					AltConf
82	L5	1	Total	C	H	N	O	0
			43	15	23	1	4	

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

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

- Molecule 84 is water.

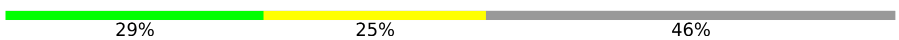
Mol	Chain	Residues	Atoms	AltConf
84	L5	3	Total O 3 3	0
84	LD	1	Total O 1 1	0
84	LI	1	Total O 1 1	0
84	LN	1	Total O 1 1	0
84	La	1	Total O 1 1	0
84	Lp	1	Total O 1 1	0
84	S2	3	Total O 3 3	0

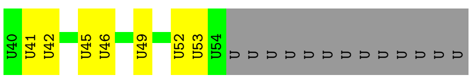
3 Residue-property plots ⓘ

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

- Molecule 1: mRNA

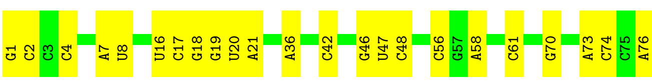
Chain A4:





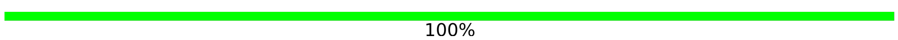
- Molecule 2: tRNA

Chain B4:



- Molecule 3: Nascent polypeptide

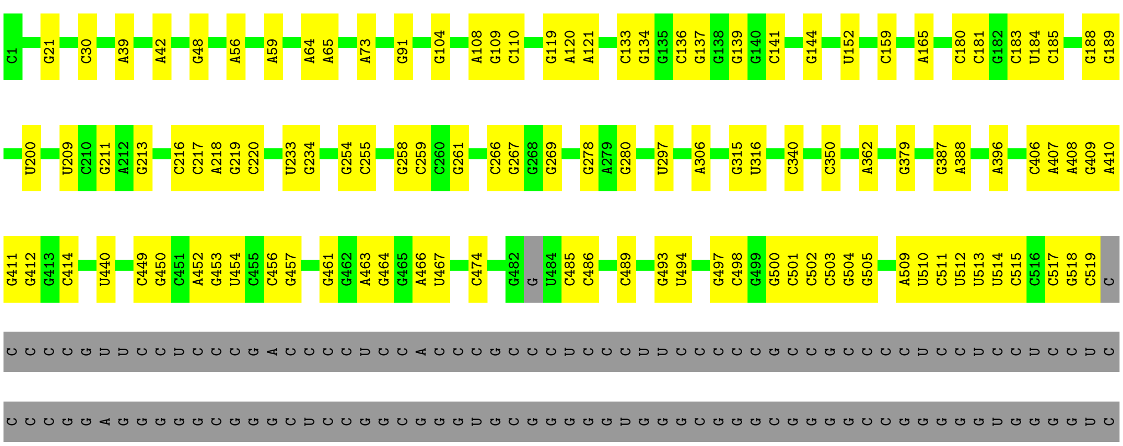
Chain C4:

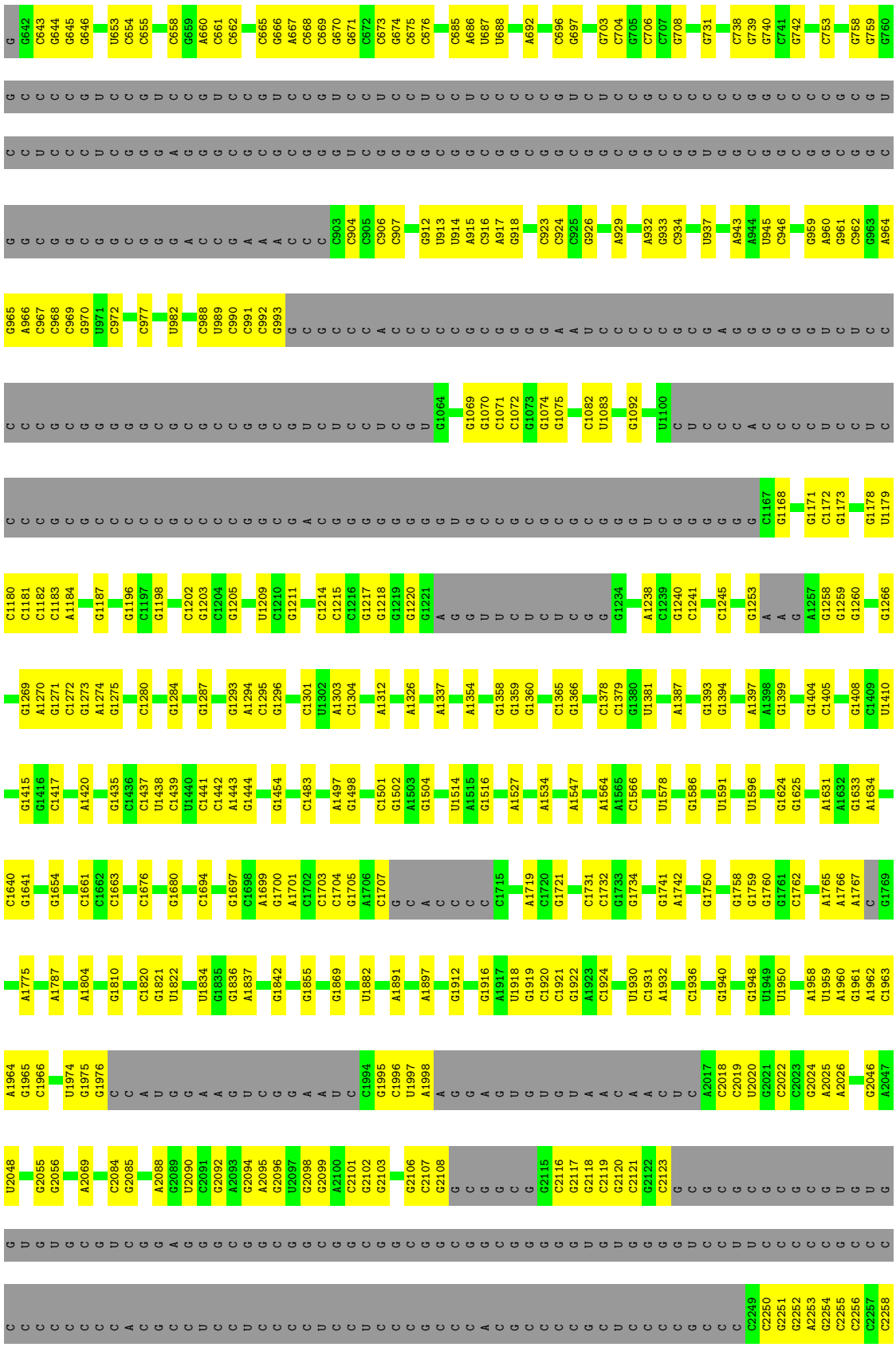


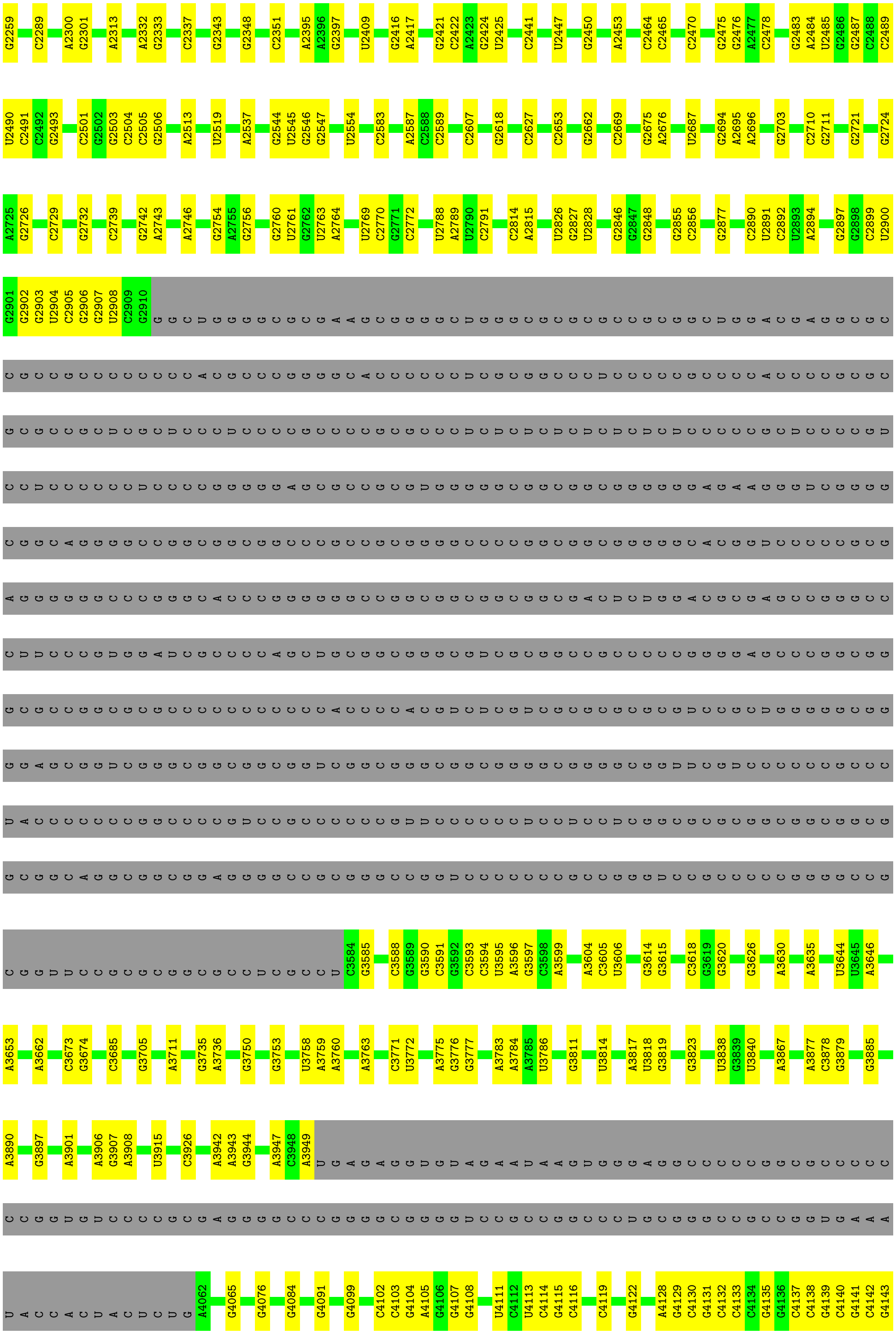
There are no outlier residues recorded for this chain.

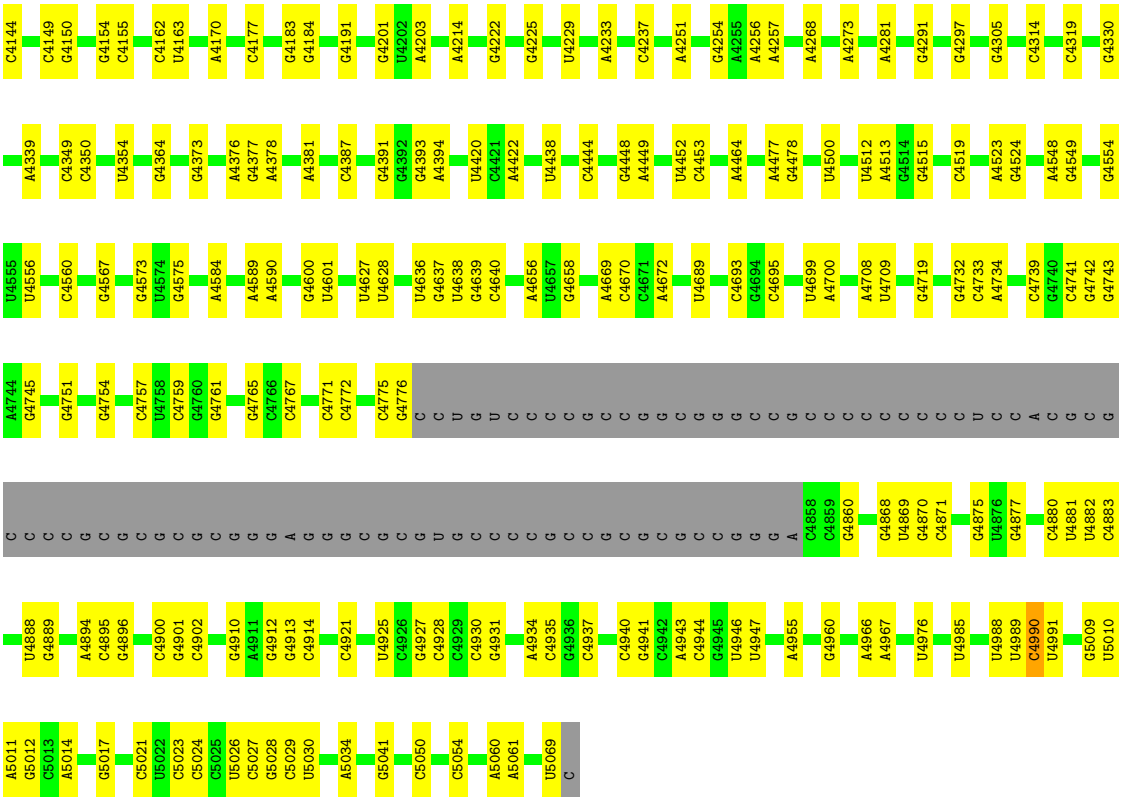
- Molecule 4: 28S ribosomal RNA

Chain L5:



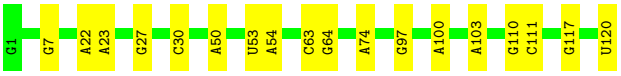






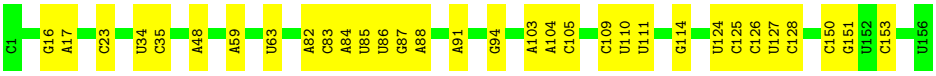
• Molecule 5: 5S ribosomal RNA

Chain L7:



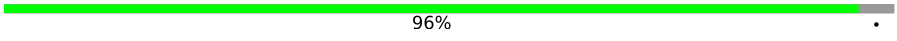
• Molecule 6: 5.8S ribosomal RNA

Chain L8:



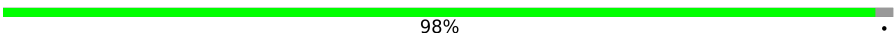
• Molecule 7: 60S ribosomal protein L8

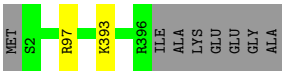
Chain LA:



• Molecule 8: 60S ribosomal protein L3

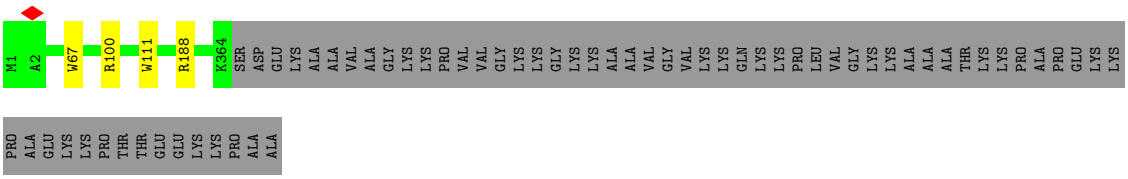
Chain LB:





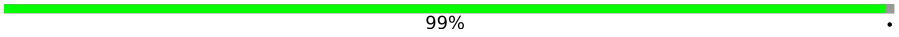
• Molecule 9: 60S ribosomal protein L4

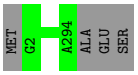
Chain LC:



• Molecule 10: 60S ribosomal protein L5

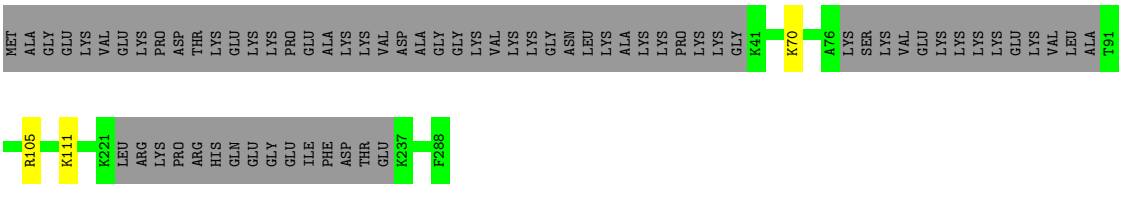
Chain LD:





• Molecule 11: 60S ribosomal protein L6

Chain LE:

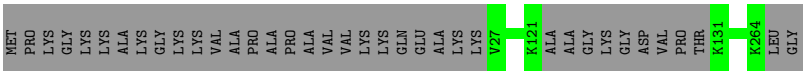


• Molecule 12: 60S ribosomal protein L7

Chain LF:

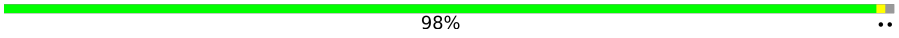
• Molecule 13: 60S ribosomal protein L7a

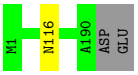
Chain LG:



• Molecule 14: 60S ribosomal protein L9

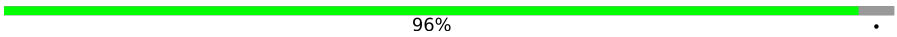
Chain LH:





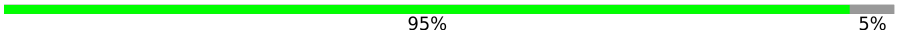
• Molecule 15: 60S ribosomal protein L10-like

Chain LI:



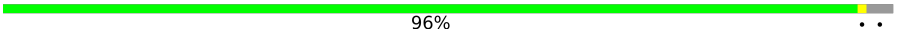
• Molecule 16: 60S ribosomal protein L11

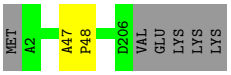
Chain LJ:



• Molecule 17: 60S ribosomal protein L13

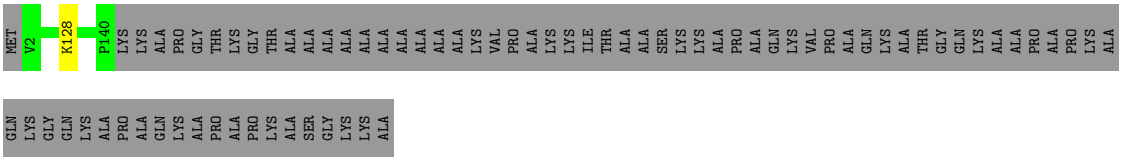
Chain LL:





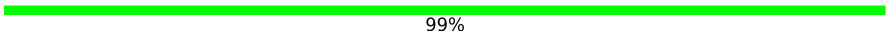
• Molecule 18: 60S ribosomal protein L14

Chain LM:



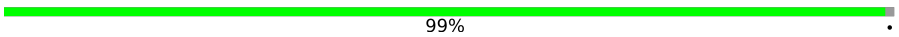
• Molecule 19: 60S ribosomal protein L15

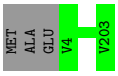
Chain LN:



• Molecule 20: 60S ribosomal protein L13a

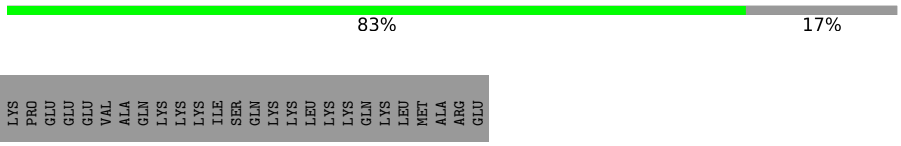
Chain LO:





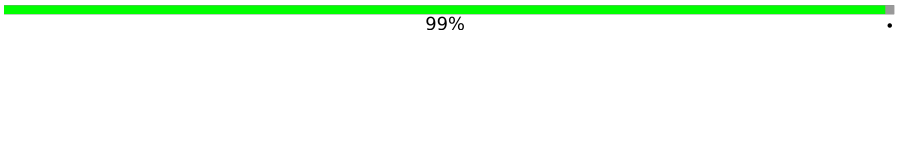
• Molecule 21: 60S ribosomal protein L17

Chain LP:



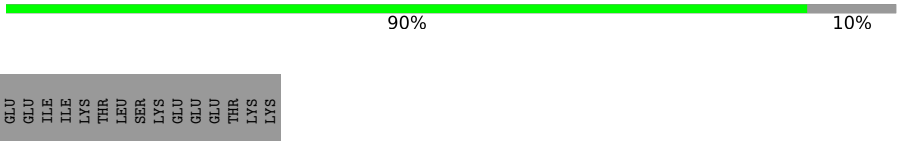
• Molecule 22: 60S ribosomal protein L18

Chain LQ:



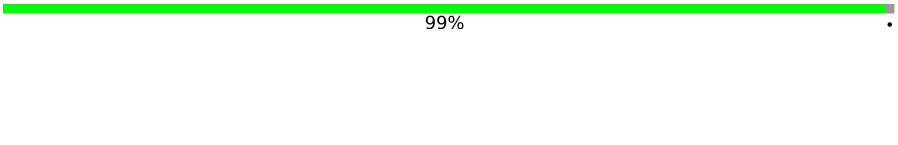
• Molecule 23: 60S ribosomal protein L19

Chain LR:



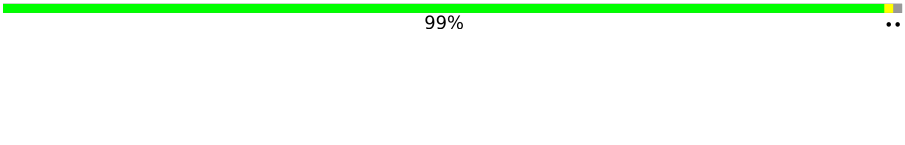
• Molecule 24: 60S ribosomal protein L18a

Chain LS:



• Molecule 25: 60S ribosomal protein L21

Chain LT:

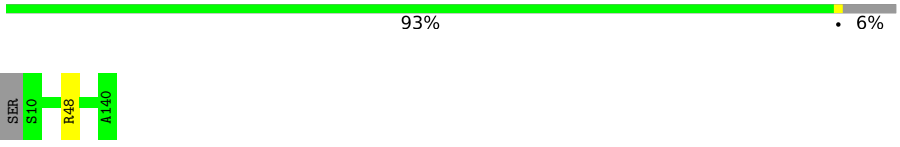


• Molecule 26: 60S ribosomal protein L22

Chain LU:

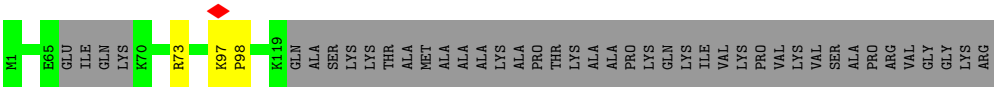
• Molecule 27: 60S ribosomal protein L23

Chain LV:



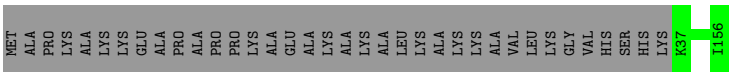
• Molecule 28: 60S ribosomal protein L24

Chain LW:



• Molecule 29: 60S ribosomal protein L23a

Chain LX:

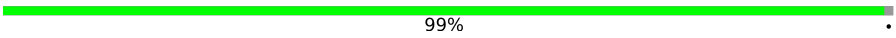


• Molecule 30: 60S ribosomal protein L26

Chain LY:

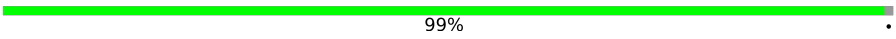
• Molecule 31: 60S ribosomal protein L27

Chain LZ:



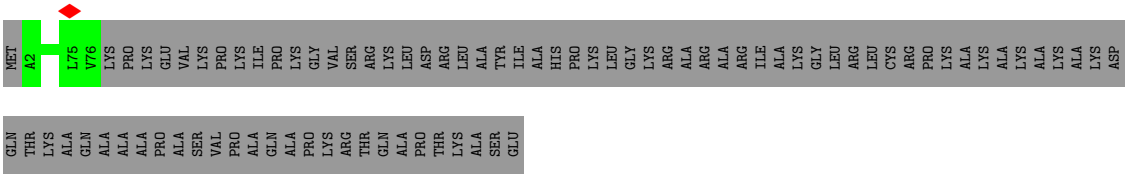
• Molecule 32: 60S ribosomal protein L27a

Chain La:



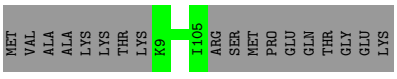
• Molecule 33: 60S ribosomal protein L29

Chain Lb:



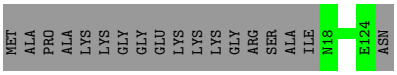
• Molecule 34: 60S ribosomal protein L30

Chain Lc:



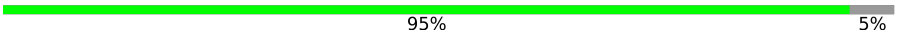
• Molecule 35: 60S ribosomal protein L31

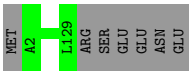
Chain Ld:



• Molecule 36: 60S ribosomal protein L32

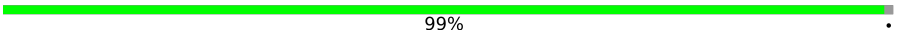
Chain Le:





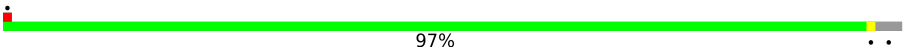
• Molecule 37: 60S ribosomal protein L35a

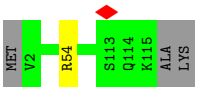
Chain Lf:



• Molecule 38: 60S ribosomal protein L34

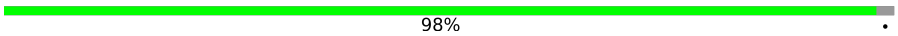
Chain Lg:





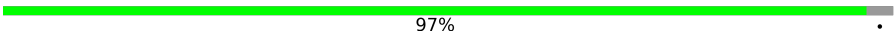
• Molecule 39: 60S ribosomal protein L35

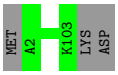
Chain Lh:



• Molecule 40: 60S ribosomal protein L36

Chain Li:



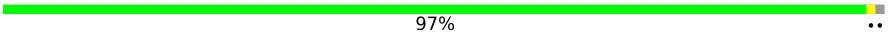


• Molecule 41: 60S ribosomal protein L37

Chain Lj:

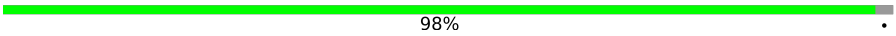
• Molecule 42: 60S ribosomal protein L38

Chain Lk:



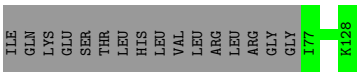
• Molecule 43: 60S ribosomal protein L39

Chain Ll:



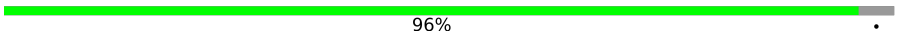
• Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:



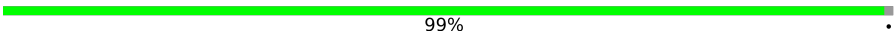
• Molecule 45: 60S ribosomal protein L41

Chain Ln:



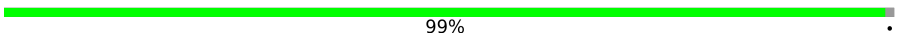
• Molecule 46: 60S ribosomal protein L36a

Chain Lo:



• Molecule 47: 60S ribosomal protein L37a

Chain Lp:

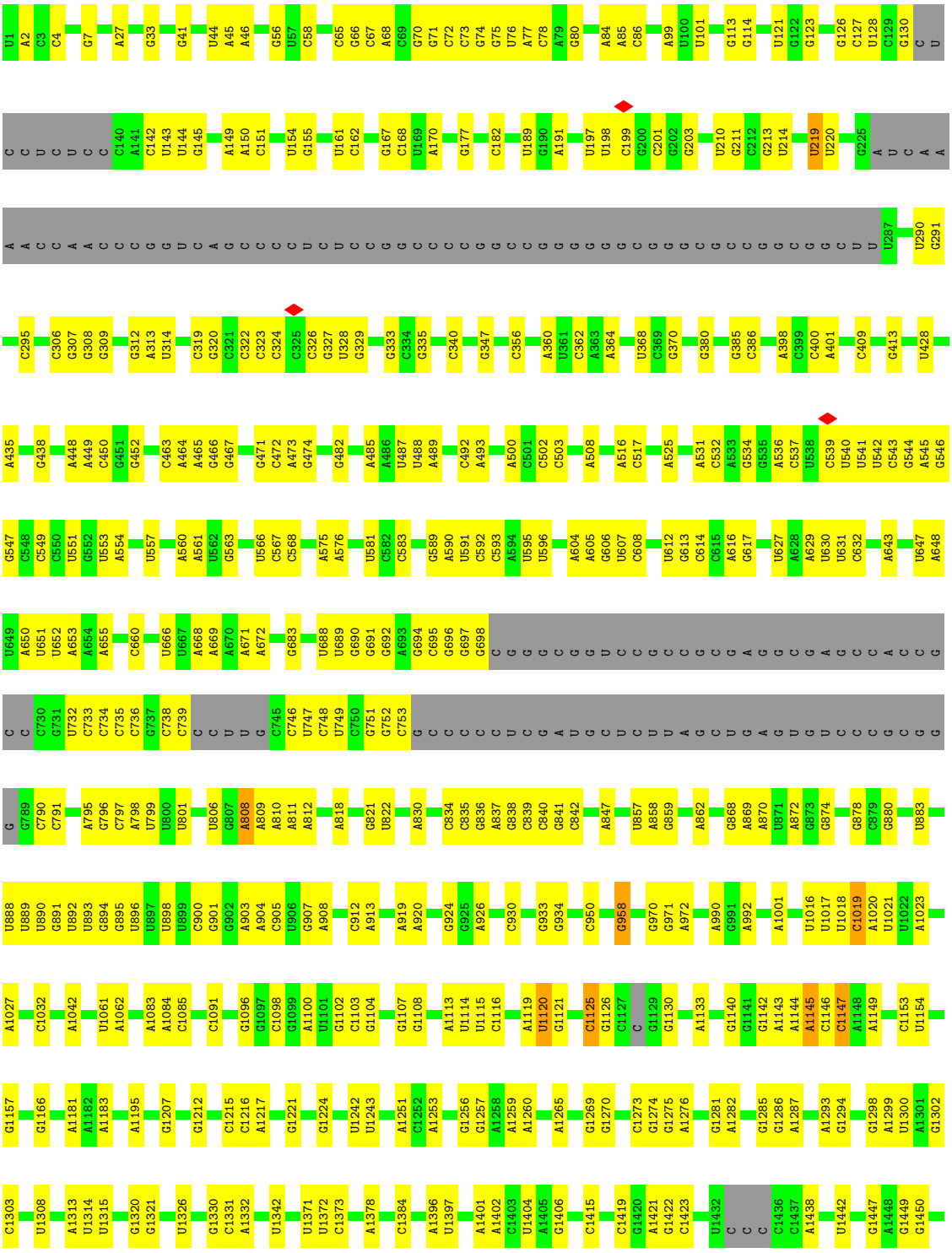


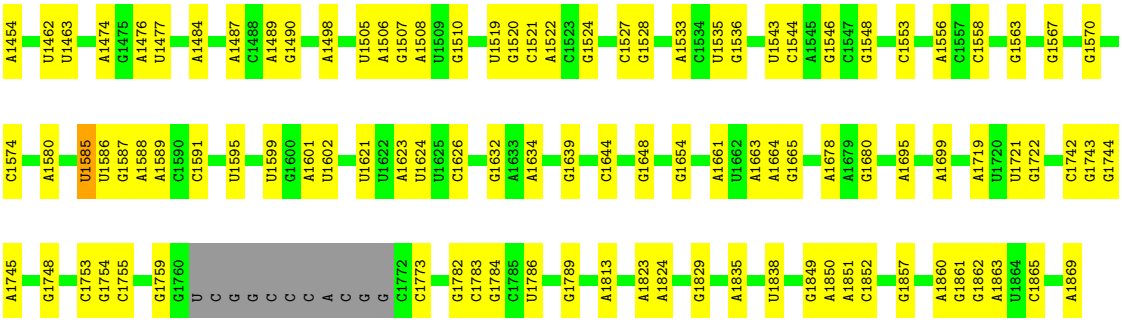
• Molecule 48: 60S ribosomal protein L28

Chain Lr:

• Molecule 49: 18S ribosomal RNA

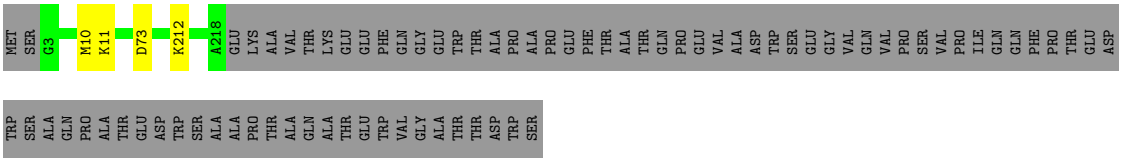
Chain S2:





• Molecule 50: 40S ribosomal protein SA

Chain SA:

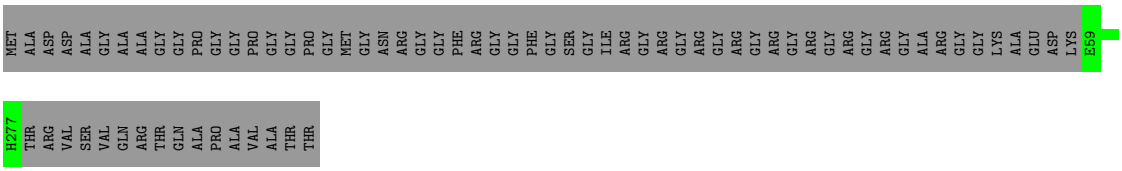


• Molecule 51: 40S ribosomal protein S3a

Chain SB:

• Molecule 52: 40S ribosomal protein S2

Chain SC:

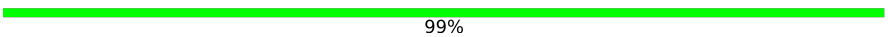


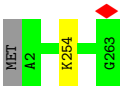
• Molecule 53: 40S ribosomal protein S3

Chain SD:

• Molecule 54: 40S ribosomal protein S4, X isoform

Chain SE:





• Molecule 55: 40S ribosomal protein S5

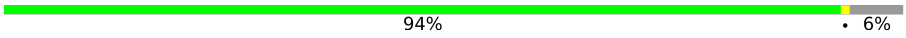
Chain SF:

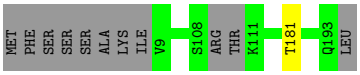
• Molecule 56: 40S ribosomal protein S6

Chain SG:

• Molecule 57: 40S ribosomal protein S7

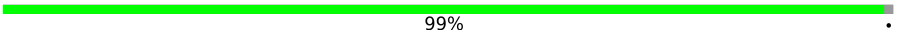
Chain SH:





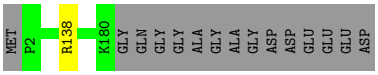
• Molecule 58: 40S ribosomal protein S8

Chain SI:



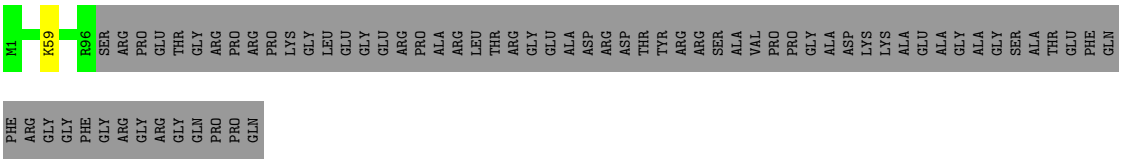
• Molecule 59: 40S ribosomal protein S9

Chain SJ:



• Molecule 60: 40S ribosomal protein S10

Chain SK:

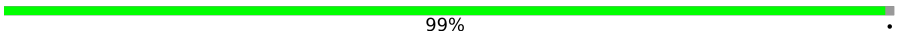


• Molecule 61: 40S ribosomal protein S11

Chain SL:

• Molecule 62: 40S ribosomal protein S13

Chain SN:

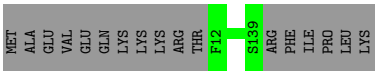


• Molecule 63: 40S ribosomal protein S14

Chain SO:

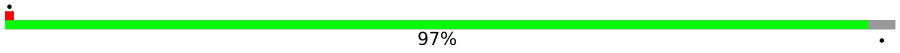
• Molecule 64: 40S ribosomal protein S15

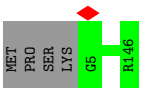
Chain SP:



• Molecule 65: 40S ribosomal protein S16

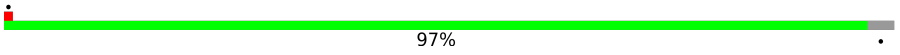
Chain SQ:

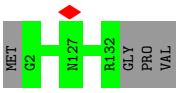




• Molecule 66: 40S ribosomal protein S17

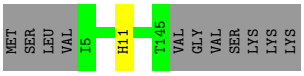
Chain SR:





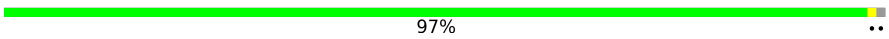
• Molecule 67: 40S ribosomal protein S18

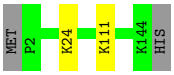
Chain SS:



• Molecule 68: 40S ribosomal protein S19

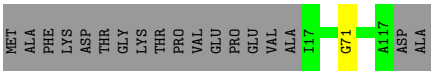
Chain ST:





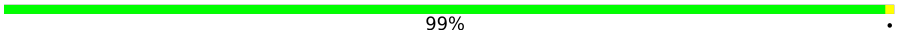
• Molecule 69: 40S ribosomal protein S20

Chain SU:



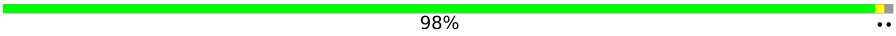
• Molecule 70: 40S ribosomal protein S21

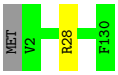
Chain SV:



• Molecule 71: 40S ribosomal protein S15a

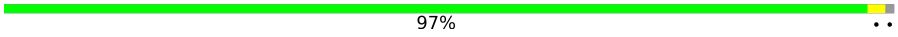
Chain SW:

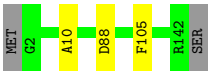




• Molecule 72: 40S ribosomal protein S23

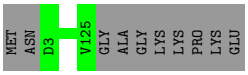
Chain SX:





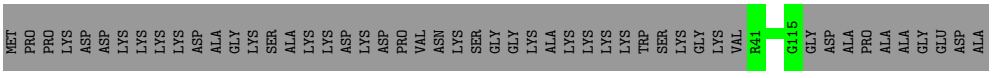
• Molecule 73: 40S ribosomal protein S24

Chain SY:



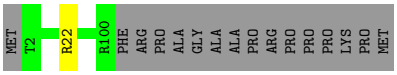
• Molecule 74: 40S ribosomal protein S25

Chain SZ:



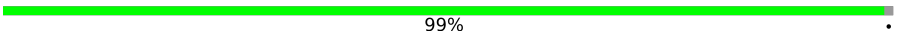
• Molecule 75: 40S ribosomal protein S26

Chain Sa:



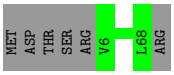
• Molecule 76: 40S ribosomal protein S27

Chain Sb:



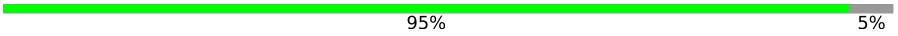
• Molecule 77: 40S ribosomal protein S28

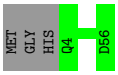
Chain Sc:



• Molecule 78: 40S ribosomal protein S29

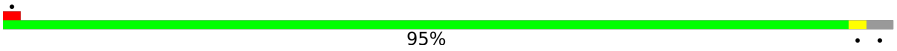
Chain Sd:

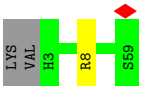




• Molecule 79: 40S ribosomal protein S30

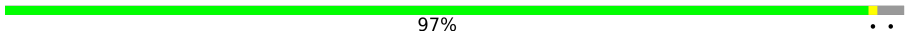
Chain Se:





• Molecule 80: Receptor of activated protein C kinase 1

Chain Sg:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	64926	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.115	Depositor
Minimum map value	-0.028	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	473.0, 473.0, 473.0	wwPDB
Map dimensions	550, 550, 550	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.86, 0.86, 0.86	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, 3HE

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	A4	0.30	0/329	0.75	0/506
2	B4	0.44	1/1813 (0.1%)	0.73	0/2823
4	L5	0.66	0/86626	0.75	6/135120 (0.0%)
5	L7	0.65	0/2858	0.73	3/4455 (0.1%)
6	L8	0.69	0/3701	0.75	0/5766
7	LA	0.39	0/1936	0.49	0/2596
8	LB	0.37	0/3251	0.47	0/4352
9	LC	0.38	0/2938	0.46	0/3947
10	LD	0.37	0/2407	0.44	0/3227
11	LE	0.34	0/1788	0.47	0/2399
12	LF	0.39	0/1905	0.43	0/2539
13	LG	0.35	0/1849	0.46	0/2496
14	LH	0.34	0/1529	0.48	0/2058
15	LI	0.36	0/1690	0.43	0/2258
16	LJ	0.33	0/1352	0.46	0/1813
17	LL	0.37	0/1661	0.44	0/2229
18	LM	0.36	0/1145	0.43	0/1536
19	LN	0.43	0/1746	0.47	1/2338 (0.0%)
20	LO	0.37	0/1665	0.43	0/2229
21	LP	0.38	0/1260	0.44	0/1692
22	LQ	0.39	0/1526	0.45	0/2038
23	LR	0.33	0/1468	0.41	0/1945
24	LS	0.40	0/1492	0.44	0/2003
25	LT	0.38	0/1310	0.49	0/1752
26	LU	0.34	0/813	0.44	0/1093
27	LV	0.37	0/985	0.46	0/1323
28	LW	0.35	0/820	0.45	0/1104
29	LX	0.35	0/998	0.43	0/1341
30	LY	0.38	0/1128	0.45	0/1500
31	LZ	0.38	0/1130	0.45	0/1507
32	La	0.41	0/1183	0.47	0/1582
33	Lb	0.32	0/600	0.41	0/796

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
34	Lc	0.39	0/752	0.43	0/1011
35	Ld	0.36	0/889	0.44	0/1198
36	Le	0.37	0/1067	0.45	0/1425
37	Lf	0.40	0/891	0.50	0/1194
38	Lg	0.39	0/899	0.48	0/1200
39	Lh	0.36	0/1014	0.42	0/1340
40	Li	0.33	0/824	0.40	0/1093
41	Lj	0.40	0/720	0.48	0/952
42	Lk	0.34	0/548	0.45	0/730
43	Ll	0.35	0/454	0.45	0/599
44	Lm	0.33	0/431	0.42	0/570
45	Ln	0.32	0/231	0.39	0/294
46	Lo	0.39	0/861	0.44	0/1137
47	Lp	0.40	0/706	0.47	0/939
48	Lr	0.37	0/1012	0.47	0/1358
49	S2	0.56	0/40879	0.77	27/63710 (0.0%)
50	SA	0.33	0/1708	0.44	0/2324
51	SB	0.34	0/1745	0.45	0/2337
52	SC	0.35	0/1697	0.46	0/2301
53	SD	0.31	0/1606	0.45	0/2181
54	SE	0.31	0/2014	0.47	0/2726
55	SF	0.30	0/1437	0.45	0/1936
56	SG	0.29	0/1657	0.46	0/2247
57	SH	0.29	0/1295	0.44	0/1763
58	SI	0.34	0/1603	0.45	0/2161
59	SJ	0.31	0/1456	0.41	0/1957
60	SK	0.29	0/750	0.41	0/1026
61	SL	0.38	0/1163	0.49	0/1562
62	SN	0.34	0/1206	0.46	0/1626
63	SO	0.33	0/982	0.47	0/1320
64	SP	0.30	0/995	0.43	0/1344
65	SQ	0.33	0/1089	0.47	0/1465
66	SR	0.30	0/955	0.49	0/1294
67	SS	0.30	0/1136	0.47	0/1528
68	ST	0.29	0/1100	0.42	0/1479
69	SU	0.30	0/722	0.52	0/983
70	SV	0.32	0/625	0.45	0/837
71	SW	0.36	0/1043	0.47	0/1396
72	SX	0.34	0/1096	0.49	0/1467
73	SY	0.29	0/944	0.45	0/1271
74	SZ	0.30	0/565	0.45	0/764
75	Sa	0.36	0/794	0.46	0/1065
76	Sb	0.32	0/632	0.46	0/851

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
77	Sc	0.30	0/474	0.52	0/638
78	Sd	0.32	0/443	0.41	0/589
79	Se	0.30	0/431	0.44	0/570
80	Sg	0.29	0/2227	0.54	0/3059
All	All	0.54	1/224670 (0.0%)	0.66	37/331180 (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
17	LL	0	1
56	SG	0	1
67	SS	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B4	1	G	OP3-P	-10.67	1.48	1.61

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
49	S2	219	U	N3-C2-O2	-7.50	116.95	122.20
19	LN	135	ILE	C-N-CA	-7.37	103.28	121.70
49	S2	219	U	N1-C2-O2	7.26	127.88	122.80
49	S2	219	U	C2-N1-C1'	6.86	125.93	117.70
49	S2	1016	U	N1-C2-O2	6.79	127.55	122.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	LL	47	ALA	Peptide
56	SG	32	MET	Peptide
67	SS	11	HIS	Peptide

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	LA	246/257 (96%)	229 (93%)	17 (7%)	0	100	100
8	LB	393/403 (98%)	363 (92%)	29 (7%)	1 (0%)	41	76
9	LC	362/427 (85%)	335 (92%)	25 (7%)	2 (1%)	25	64
10	LD	291/297 (98%)	268 (92%)	23 (8%)	0	100	100
11	LE	213/288 (74%)	188 (88%)	24 (11%)	1 (0%)	29	68
12	LF	223/248 (90%)	208 (93%)	15 (7%)	0	100	100
13	LG	225/266 (85%)	208 (92%)	17 (8%)	0	100	100
14	LH	188/192 (98%)	174 (93%)	13 (7%)	1 (0%)	29	68
15	LI	202/214 (94%)	187 (93%)	15 (7%)	0	100	100
16	LJ	167/178 (94%)	158 (95%)	9 (5%)	0	100	100
17	LL	203/211 (96%)	190 (94%)	12 (6%)	1 (0%)	29	68
18	LM	137/215 (64%)	126 (92%)	11 (8%)	0	100	100
19	LN	201/204 (98%)	196 (98%)	5 (2%)	0	100	100
20	LO	198/203 (98%)	195 (98%)	3 (2%)	0	100	100
21	LP	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
22	LQ	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
23	LR	174/196 (89%)	172 (99%)	2 (1%)	0	100	100
24	LS	173/176 (98%)	157 (91%)	16 (9%)	0	100	100
25	LT	157/160 (98%)	142 (90%)	14 (9%)	1 (1%)	25	64
26	LU	99/128 (77%)	89 (90%)	10 (10%)	0	100	100
27	LV	129/140 (92%)	117 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
28	LW	111/157 (71%)	97 (87%)	12 (11%)	2 (2%)	8 37
29	LX	118/156 (76%)	107 (91%)	11 (9%)	0	100 100
30	LY	132/145 (91%)	122 (92%)	10 (8%)	0	100 100
31	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100 100
32	La	145/148 (98%)	132 (91%)	13 (9%)	0	100 100
33	Lb	73/159 (46%)	68 (93%)	5 (7%)	0	100 100
34	Lc	95/115 (83%)	87 (92%)	8 (8%)	0	100 100
35	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100 100
36	Le	126/135 (93%)	120 (95%)	6 (5%)	0	100 100
37	Lf	107/110 (97%)	99 (92%)	8 (8%)	0	100 100
38	Lg	112/117 (96%)	104 (93%)	8 (7%)	0	100 100
39	Lh	119/123 (97%)	114 (96%)	5 (4%)	0	100 100
40	Li	100/105 (95%)	97 (97%)	3 (3%)	0	100 100
41	Lj	84/97 (87%)	82 (98%)	2 (2%)	0	100 100
42	Lk	67/70 (96%)	59 (88%)	8 (12%)	0	100 100
43	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100 100
44	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100 100
45	Ln	22/25 (88%)	21 (96%)	1 (4%)	0	100 100
46	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100 100
47	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100 100
48	Lr	123/137 (90%)	117 (95%)	6 (5%)	0	100 100
50	SA	214/295 (72%)	200 (94%)	12 (6%)	2 (1%)	17 55
51	SB	211/264 (80%)	199 (94%)	12 (6%)	0	100 100
52	SC	217/293 (74%)	204 (94%)	13 (6%)	0	100 100
53	SD	219/243 (90%)	198 (90%)	21 (10%)	0	100 100
54	SE	260/263 (99%)	249 (96%)	11 (4%)	0	100 100
55	SF	185/204 (91%)	168 (91%)	16 (9%)	1 (0%)	29 68
56	SG	229/249 (92%)	208 (91%)	19 (8%)	2 (1%)	17 55
57	SH	179/194 (92%)	169 (94%)	10 (6%)	0	100 100
58	SI	204/208 (98%)	191 (94%)	13 (6%)	0	100 100
59	SJ	177/194 (91%)	172 (97%)	4 (2%)	1 (1%)	25 64

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	SK	94/165 (57%)	89 (95%)	5 (5%)	0	100	100
61	SL	140/158 (89%)	130 (93%)	10 (7%)	0	100	100
62	SN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
63	SO	132/151 (87%)	116 (88%)	16 (12%)	0	100	100
64	SP	126/145 (87%)	116 (92%)	10 (8%)	0	100	100
65	SQ	140/146 (96%)	127 (91%)	13 (9%)	0	100	100
66	SR	129/135 (96%)	113 (88%)	16 (12%)	0	100	100
67	SS	139/152 (91%)	122 (88%)	17 (12%)	0	100	100
68	ST	141/145 (97%)	135 (96%)	6 (4%)	0	100	100
69	SU	99/119 (83%)	90 (91%)	8 (8%)	1 (1%)	15	53
70	SV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
71	SW	127/130 (98%)	120 (94%)	7 (6%)	0	100	100
72	SX	139/143 (97%)	123 (88%)	14 (10%)	2 (1%)	11	43
73	SY	121/133 (91%)	115 (95%)	6 (5%)	0	100	100
74	SZ	73/125 (58%)	65 (89%)	8 (11%)	0	100	100
75	Sa	97/115 (84%)	84 (87%)	13 (13%)	0	100	100
76	Sb	81/84 (96%)	76 (94%)	5 (6%)	0	100	100
77	Sc	61/69 (88%)	52 (85%)	9 (15%)	0	100	100
78	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
79	Se	55/59 (93%)	44 (80%)	11 (20%)	0	100	100
80	Sg	304/317 (96%)	242 (80%)	61 (20%)	1 (0%)	41	76
All	All	10952/12400 (88%)	10126 (92%)	807 (7%)	19 (0%)	50	82

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	LB	393	LYS
9	LC	111	TRP
14	LH	116	ASN
28	LW	98	PRO
55	SF	80	GLY

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	
7	LA	190/199 (96%)	190 (100%)	0	100	100
8	LB	343/349 (98%)	342 (100%)	1 (0%)	92	97
9	LC	299/348 (86%)	297 (99%)	2 (1%)	84	94
10	LD	241/250 (96%)	241 (100%)	0	100	100
11	LE	191/252 (76%)	189 (99%)	2 (1%)	76	91
12	LF	194/215 (90%)	194 (100%)	0	100	100
13	LG	188/223 (84%)	188 (100%)	0	100	100
14	LH	167/171 (98%)	167 (100%)	0	100	100
15	LI	172/181 (95%)	171 (99%)	1 (1%)	86	95
16	LJ	136/149 (91%)	136 (100%)	0	100	100
17	LL	164/177 (93%)	164 (100%)	0	100	100
18	LM	114/161 (71%)	113 (99%)	1 (1%)	78	92
19	LN	171/172 (99%)	171 (100%)	0	100	100
20	LO	170/174 (98%)	170 (100%)	0	100	100
21	LP	132/163 (81%)	132 (100%)	0	100	100
22	LQ	161/165 (98%)	161 (100%)	0	100	100
23	LR	150/175 (86%)	150 (100%)	0	100	100
24	LS	156/157 (99%)	156 (100%)	0	100	100
25	LT	135/140 (96%)	135 (100%)	0	100	100
26	LU	84/115 (73%)	84 (100%)	0	100	100
27	LV	99/107 (92%)	98 (99%)	1 (1%)	76	91
28	LW	61/126 (48%)	60 (98%)	1 (2%)	62	86
29	LX	107/133 (80%)	107 (100%)	0	100	100
30	LY	123/135 (91%)	123 (100%)	0	100	100
31	LZ	117/118 (99%)	117 (100%)	0	100	100
32	La	118/121 (98%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	Lb	59/126 (47%)	59 (100%)	0	100	100
34	Lc	79/97 (81%)	79 (100%)	0	100	100
35	Ld	94/110 (86%)	94 (100%)	0	100	100
36	Le	113/121 (93%)	113 (100%)	0	100	100
37	Lf	87/89 (98%)	87 (100%)	0	100	100
38	Lg	93/100 (93%)	92 (99%)	1 (1%)	73	90
39	Lh	108/110 (98%)	108 (100%)	0	100	100
40	Li	81/89 (91%)	81 (100%)	0	100	100
41	Lj	73/80 (91%)	72 (99%)	1 (1%)	67	88
42	Lk	57/65 (88%)	56 (98%)	1 (2%)	59	85
43	Ll	47/48 (98%)	47 (100%)	0	100	100
44	Lm	47/116 (40%)	47 (100%)	0	100	100
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	90/94 (96%)	90 (100%)	0	100	100
47	Lp	71/75 (95%)	71 (100%)	0	100	100
48	Lr	107/121 (88%)	107 (100%)	0	100	100
50	SA	170/243 (70%)	168 (99%)	2 (1%)	71	90
51	SB	191/231 (83%)	191 (100%)	0	100	100
52	SC	175/225 (78%)	175 (100%)	0	100	100
53	SD	145/202 (72%)	144 (99%)	1 (1%)	84	94
54	SE	196/225 (87%)	195 (100%)	1 (0%)	88	96
55	SF	139/170 (82%)	139 (100%)	0	100	100
56	SG	138/218 (63%)	137 (99%)	1 (1%)	84	94
57	SH	109/174 (63%)	108 (99%)	1 (1%)	78	92
58	SI	149/180 (83%)	149 (100%)	0	100	100
59	SJ	143/168 (85%)	143 (100%)	0	100	100
60	SK	65/136 (48%)	64 (98%)	1 (2%)	65	87
61	SL	121/142 (85%)	119 (98%)	2 (2%)	60	85
62	SN	123/131 (94%)	123 (100%)	0	100	100
63	SO	95/119 (80%)	95 (100%)	0	100	100
64	SP	96/130 (74%)	96 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
65	SQ	102/121 (84%)	102 (100%)	0	100 100
66	SR	84/122 (69%)	84 (100%)	0	100 100
67	SS	110/132 (83%)	110 (100%)	0	100 100
68	ST	105/115 (91%)	103 (98%)	2 (2%)	57 84
69	SU	68/107 (64%)	68 (100%)	0	100 100
70	SV	62/67 (92%)	61 (98%)	1 (2%)	62 86
71	SW	110/113 (97%)	109 (99%)	1 (1%)	78 92
72	SX	109/115 (95%)	108 (99%)	1 (1%)	78 92
73	SY	86/115 (75%)	86 (100%)	0	100 100
74	SZ	56/103 (54%)	56 (100%)	0	100 100
75	Sa	83/98 (85%)	82 (99%)	1 (1%)	71 90
76	Sb	65/76 (86%)	65 (100%)	0	100 100
77	Sc	51/62 (82%)	51 (100%)	0	100 100
78	Sd	44/49 (90%)	44 (100%)	0	100 100
79	Se	39/48 (81%)	38 (97%)	1 (3%)	46 78
80	Sg	199/275 (72%)	198 (100%)	1 (0%)	88 96
All	All	8840/10553 (84%)	8811 (100%)	29 (0%)	92 97

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	SD	76	ARG
79	Se	8	ARG
57	SH	181	THR
71	SW	28	ARG
56	SG	218	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 131 such sidechains are listed below:

Mol	Chain	Res	Type
67	SS	125	HIS
71	SW	82	GLN
80	Sg	117	ASN
23	LR	121	HIS
23	LR	75	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A4	14/28 (50%)	7 (50%)	0
2	B4	75/76 (98%)	22 (29%)	0
4	L5	3596/5070 (70%)	814 (22%)	29 (0%)
49	S2	1704/1869 (91%)	505 (29%)	22 (1%)
5	L7	119/120 (99%)	17 (14%)	0
6	L8	155/156 (99%)	31 (20%)	3 (1%)
All	All	5663/7319 (77%)	1396 (24%)	54 (0%)

5 of 1396 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A4	41	U
1	A4	42	U
1	A4	45	U
1	A4	46	U
1	A4	49	U

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L5	5027	C
49	S2	213	G
49	S2	1535	U
6	L8	16	G
49	S2	85	A

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 201 ligands modelled in this entry, 200 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
82	3HE	L5	5101	-	21,21,21	0.92	2 (9%)	19,30,30	1.79	4 (21%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
82	3HE	L5	5101	-	-	1/8/36/36	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	L5	5101	3HE	C12-N	-2.54	1.33	1.37
82	L5	5101	3HE	C11-N	-2.44	1.33	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
82	L5	5101	3HE	C13-C12-N	3.82	120.64	115.95
82	L5	5101	3HE	C10-C11-N	3.30	119.99	115.95
82	L5	5101	3HE	C11-N-C12	-3.10	122.02	125.78
82	L5	5101	3HE	C-C1-C2	-2.44	107.03	111.18

There are no chirality outliers.

All (1) torsion outliers are listed below:

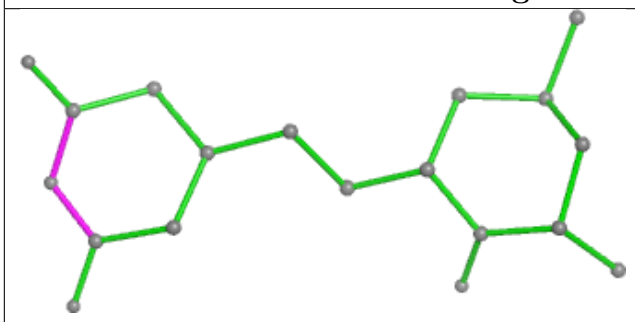
Mol	Chain	Res	Type	Atoms
82	L5	5101	3HE	C7-C8-C9-C10

There are no ring outliers.

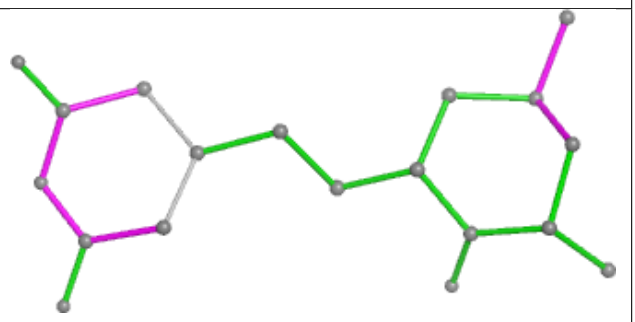
No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

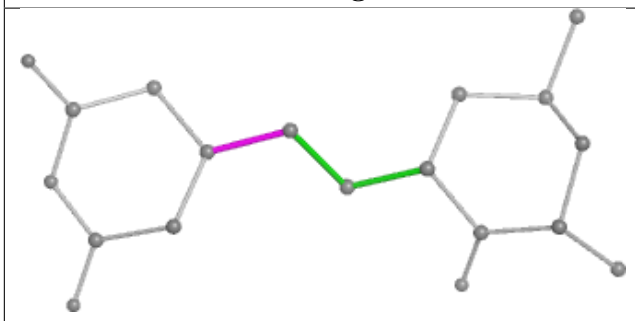
Ligand 3HE L5 5101



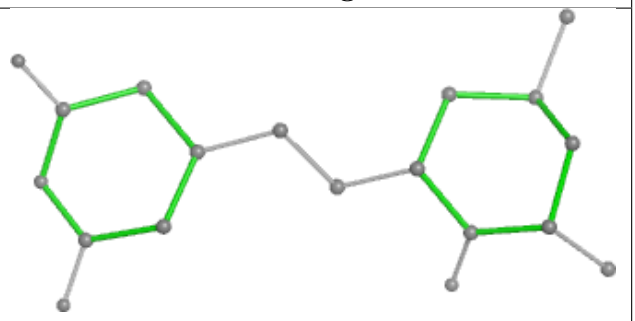
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

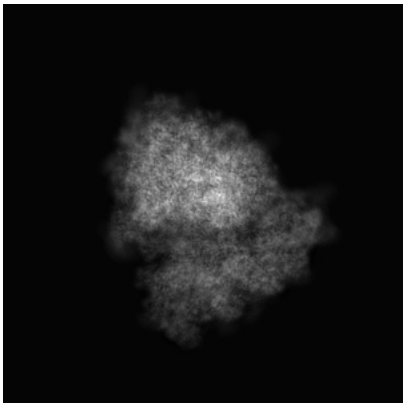
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10674. These allow visual inspection of the internal detail of the map and identification of artifacts.

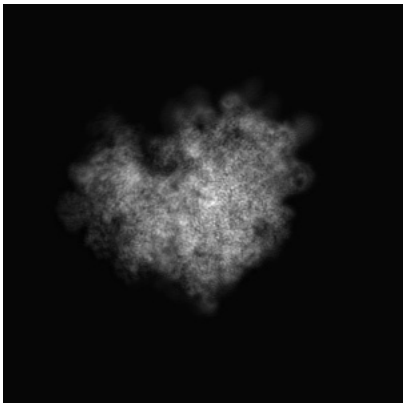
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

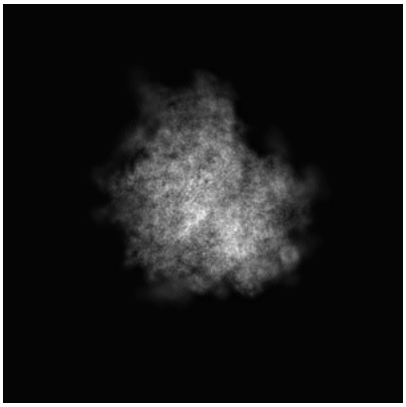
6.1.1 Primary map



X



Y

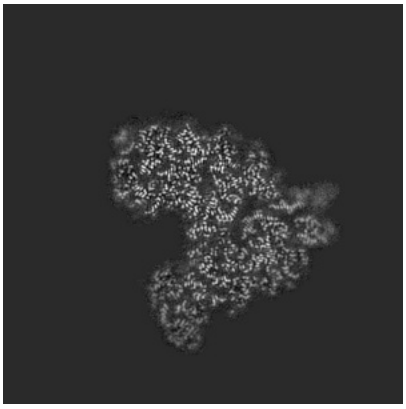


Z

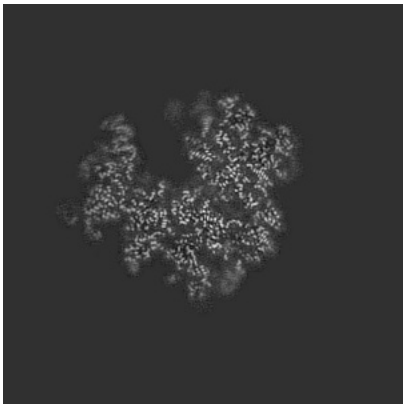
The images above show the map projected in three orthogonal directions.

6.2 Central slices

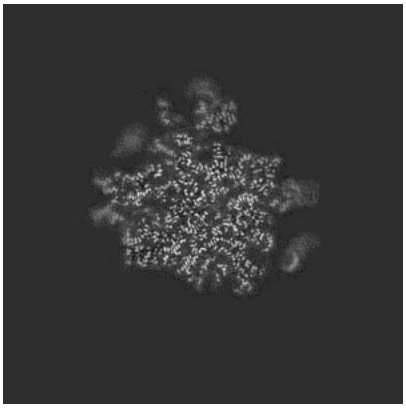
6.2.1 Primary map



X Index: 275



Y Index: 275

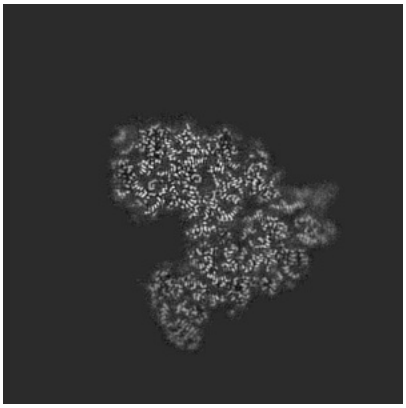


Z Index: 275

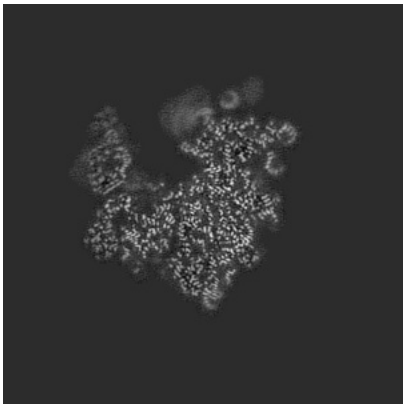
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

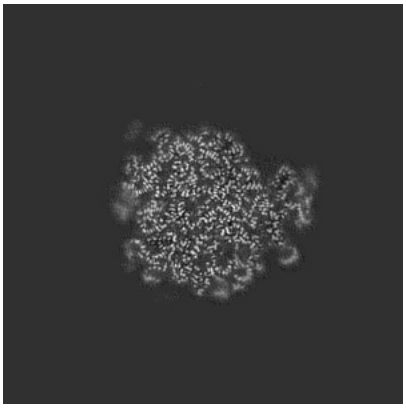
6.3.1 Primary map



X Index: 276



Y Index: 297

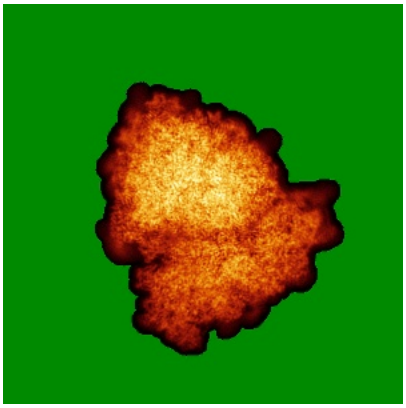


Z Index: 308

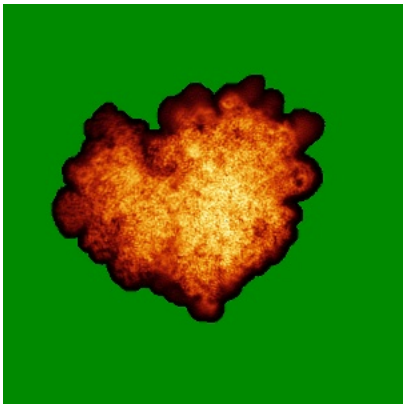
The images above show the largest variance slices of the map in three orthogonal directions.

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

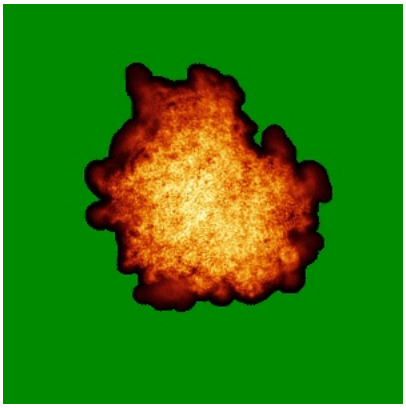
6.4.1 Primary map



X



Y

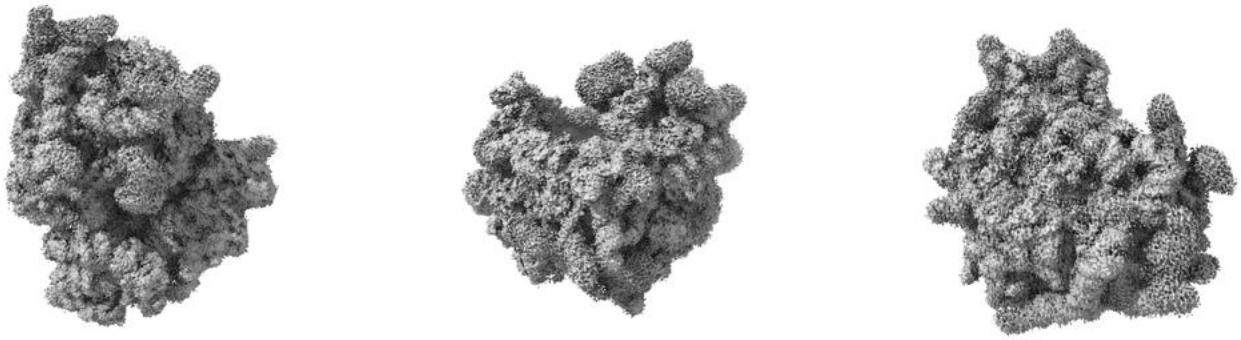


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

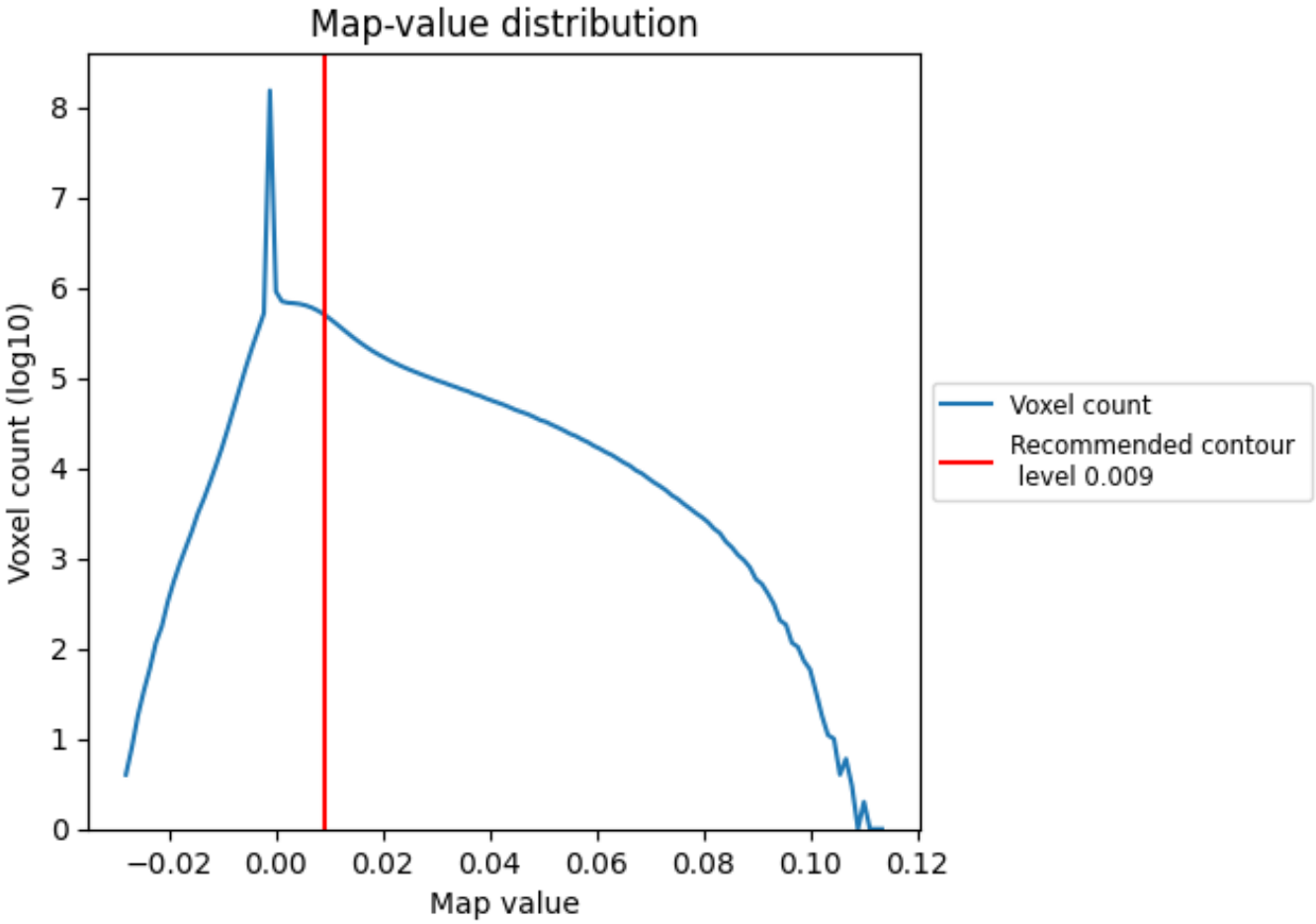
6.6 Mask visualisation (i)

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

7 Map analysis

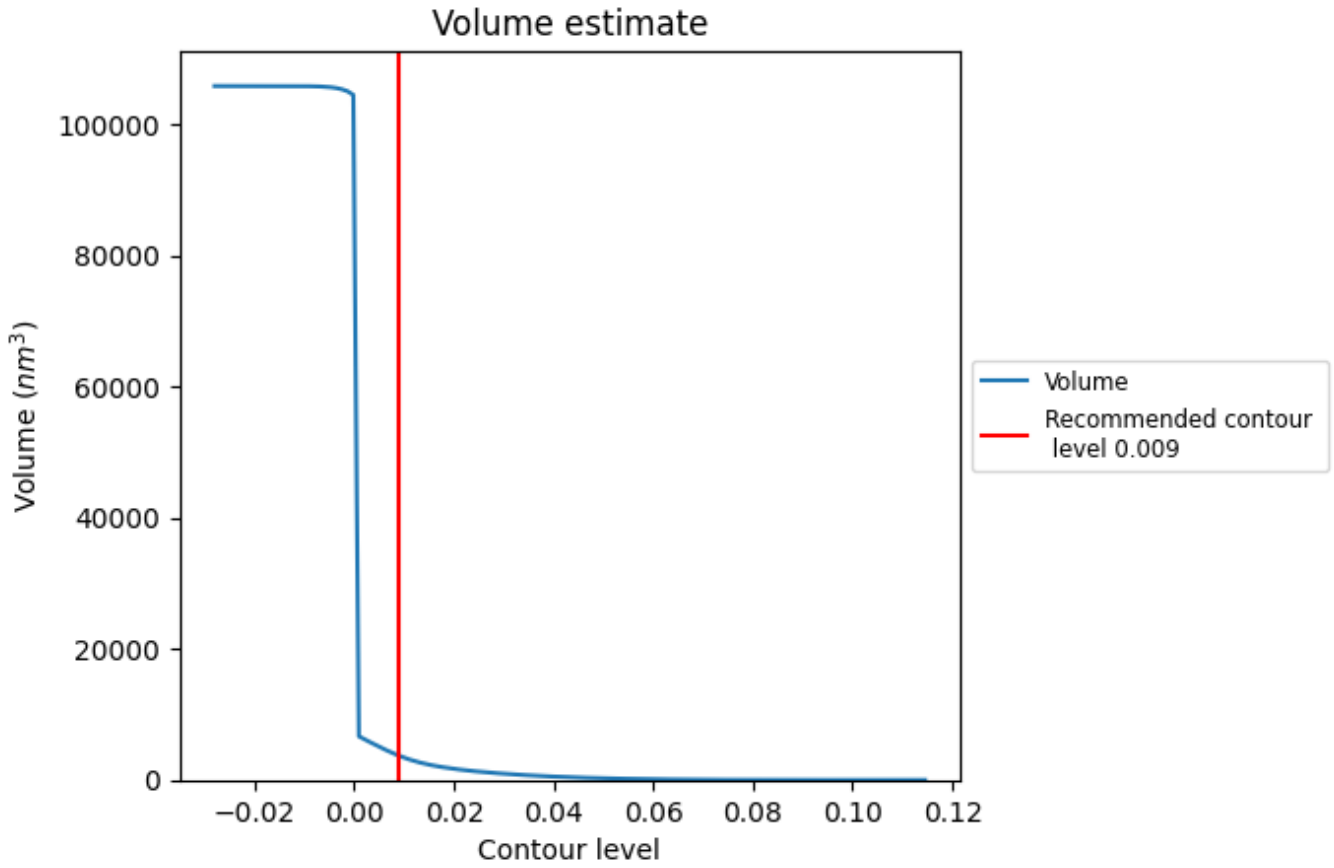
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

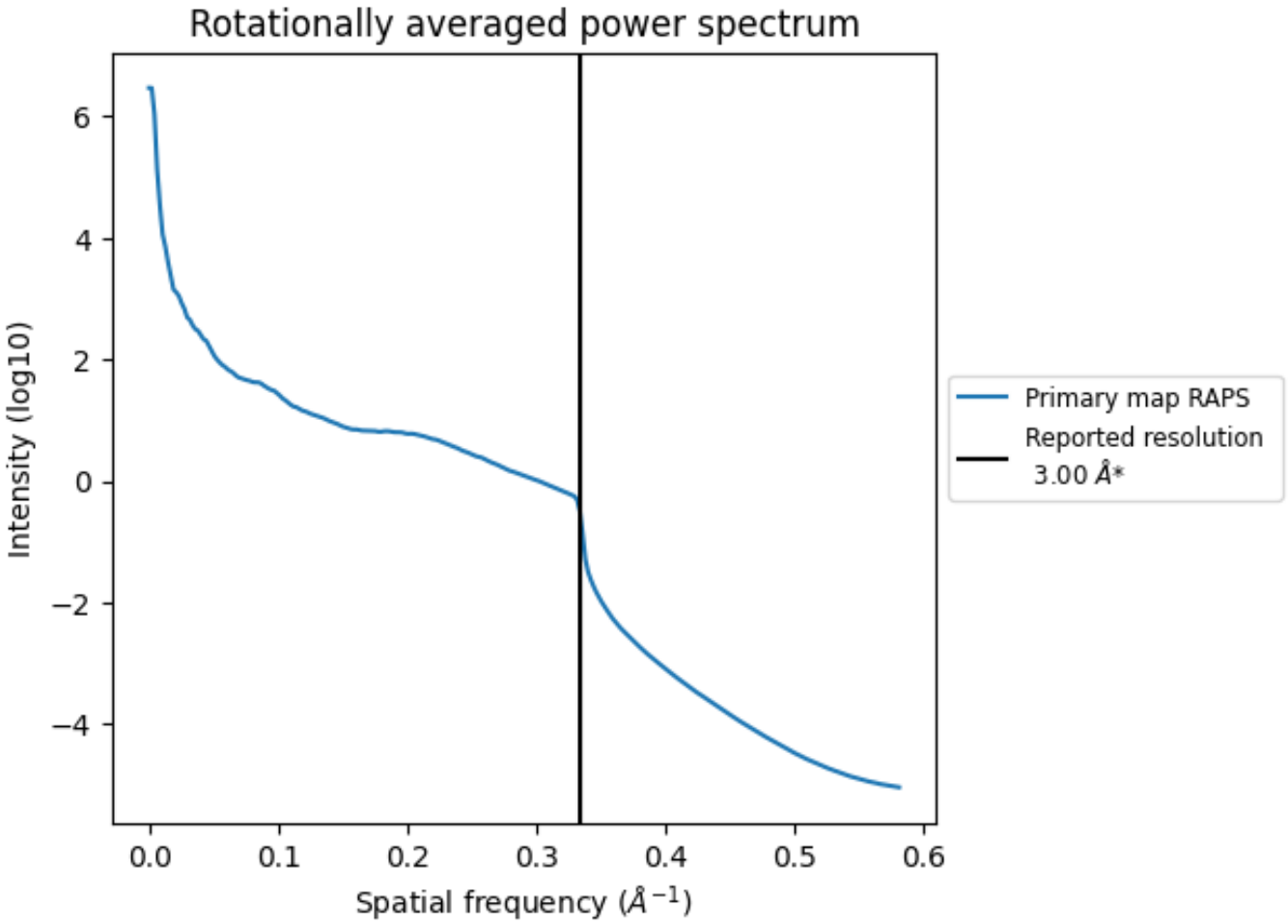
7.2 Volume estimate (i)



The volume at the recommended contour level is 3703 nm^3; this corresponds to an approximate mass of 3345 kDa.

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.333 Å^{-1}

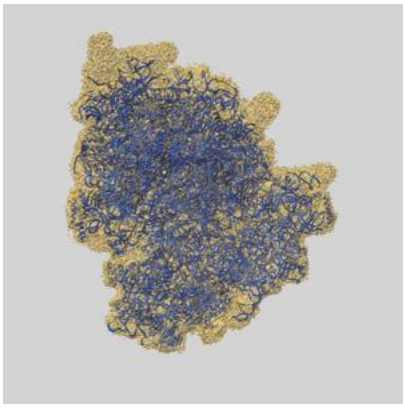
8 Fourier-Shell correlation (i)

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

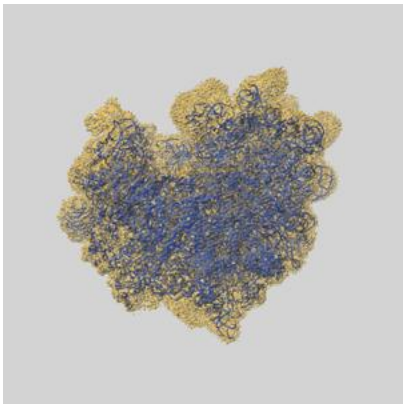
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10674 and PDB model 6Y2L. Per-residue inclusion information can be found in section 3 on page 20.

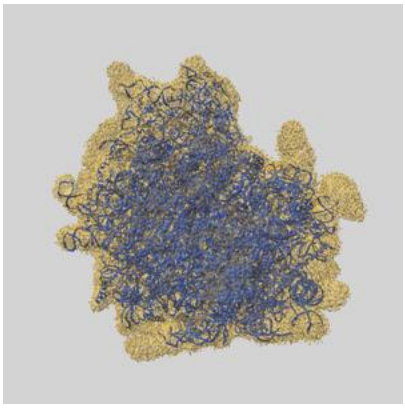
9.1 Map-model overlay



X



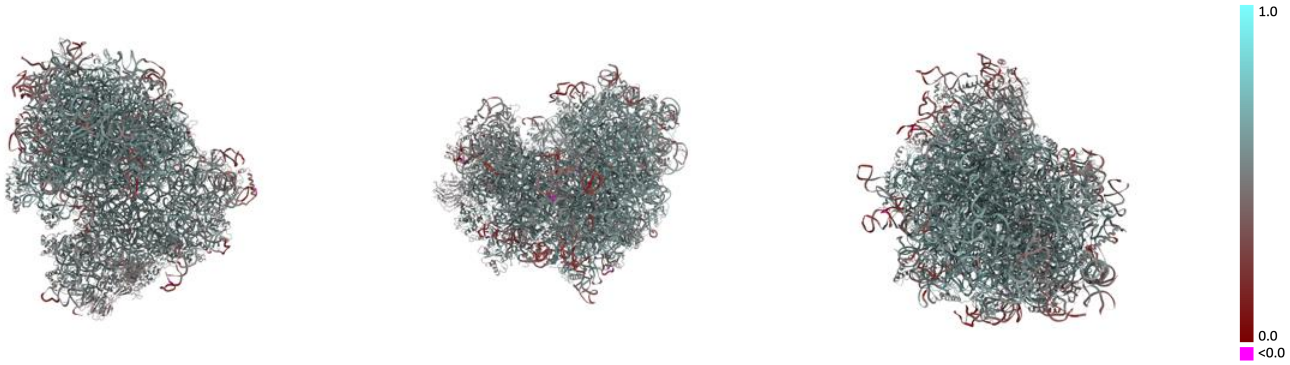
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009 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.

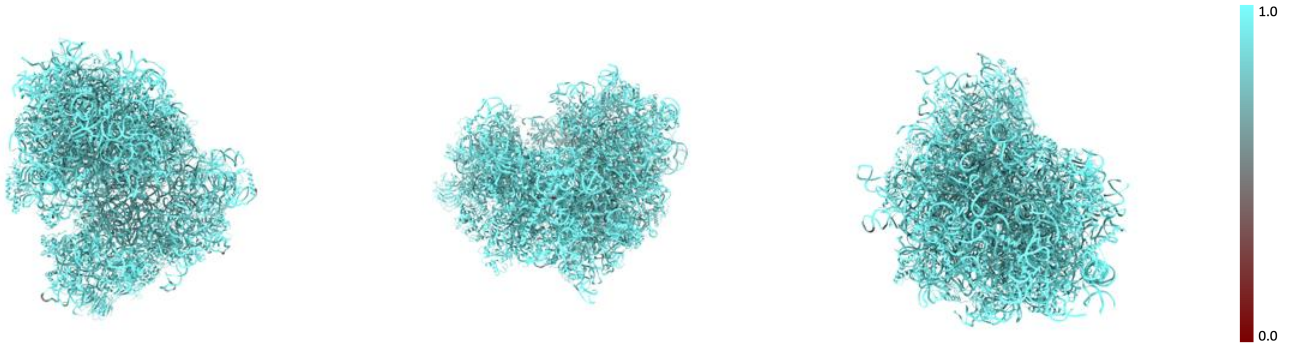
9.2 Q-score mapped to coordinate model



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.

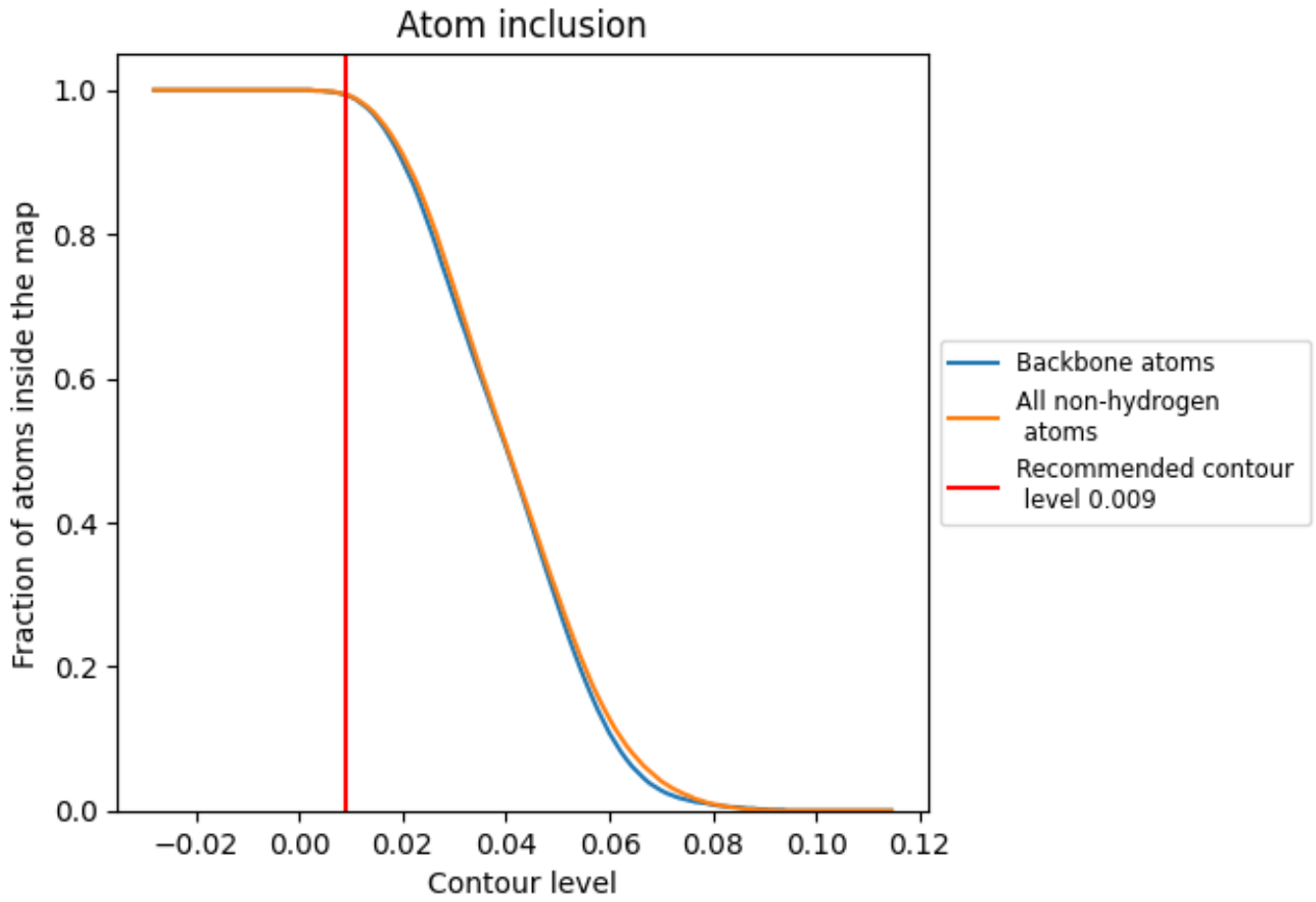
9.3 Atom inclusion mapped to coordinate model



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 (0.009).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9940	0.5370
A4	0.9870	0.4160
B4	0.9870	0.4860
C4	0.9000	0.4000
L5	0.9970	0.5420
L7	0.9990	0.5730
L8	0.9970	0.5640
LA	0.9950	0.5910
LB	0.9940	0.5690
LC	0.9950	0.5740
LD	0.9980	0.5370
LE	0.9940	0.5310
LF	0.9970	0.5730
LG	0.9890	0.5420
LH	0.9920	0.5400
LI	0.9940	0.5570
LJ	0.9880	0.5270
LL	0.9940	0.5630
LM	0.9950	0.5520
LN	0.9980	0.5980
LO	0.9960	0.5700
LP	0.9980	0.5790
LQ	0.9980	0.5870
LR	0.9930	0.5590
LS	0.9970	0.5770
LT	0.9920	0.5590
LU	0.9920	0.5160
LV	0.9970	0.5720
LW	0.9770	0.4750
LX	0.9990	0.5650
LY	0.9950	0.5690
LZ	0.9940	0.5580
La	0.9980	0.5900
Lb	0.9780	0.5280
Lc	0.9960	0.5670

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Chain	Atom inclusion	Q-score
Ld	0.9990	0.5630
Le	0.9980	0.5890
Lf	0.9930	0.5840
Lg	0.9930	0.5600
Lh	0.9960	0.5570
Li	0.9940	0.5480
Lj	0.9970	0.5930
Lk	0.9870	0.5320
Ll	0.9980	0.5660
Lm	0.9880	0.5560
Ln	1.0000	0.5930
Lo	0.9950	0.5710
Lp	0.9970	0.5810
Lr	0.9960	0.5730
S2	0.9920	0.5130
SA	0.9750	0.5240
SB	0.9860	0.5450
SC	0.9870	0.5380
SD	0.9860	0.4900
SE	0.9890	0.5270
SF	0.9890	0.5050
SG	0.9980	0.4830
SH	0.9860	0.5050
SI	0.9950	0.5440
SJ	0.9940	0.5190
SK	0.9900	0.4650
SL	0.9920	0.5580
SN	0.9910	0.5550
SO	0.9870	0.5520
SP	0.9850	0.4910
SQ	0.9860	0.5000
SR	0.9730	0.4870
SS	0.9890	0.4900
ST	0.9860	0.5000
SU	0.9870	0.4770
SV	0.9830	0.5290
SW	0.9950	0.5560
SX	0.9950	0.5470
SY	0.9940	0.5010
SZ	0.9870	0.4800
Sa	0.9960	0.5520
Sb	0.9850	0.5220

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Chain	Atom inclusion	Q-score
Sc	0.9830	0.5090
Sd	0.9980	0.5370
Se	0.9810	0.4750
Sg	0.9750	0.4470