



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 05:39 PM UTC

PDB ID : 8UT0 / pdb_00008ut0
EMDB ID : EMD-42525
Title : Eukaryotic 80S ribosome with Reh1, eIF5A and A/P site tRNA
Authors : Yelland, J.N.; Taylor, D.W.; Johnson, A.W.
Deposited on : 2023-10-30
Resolution : 3.22 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

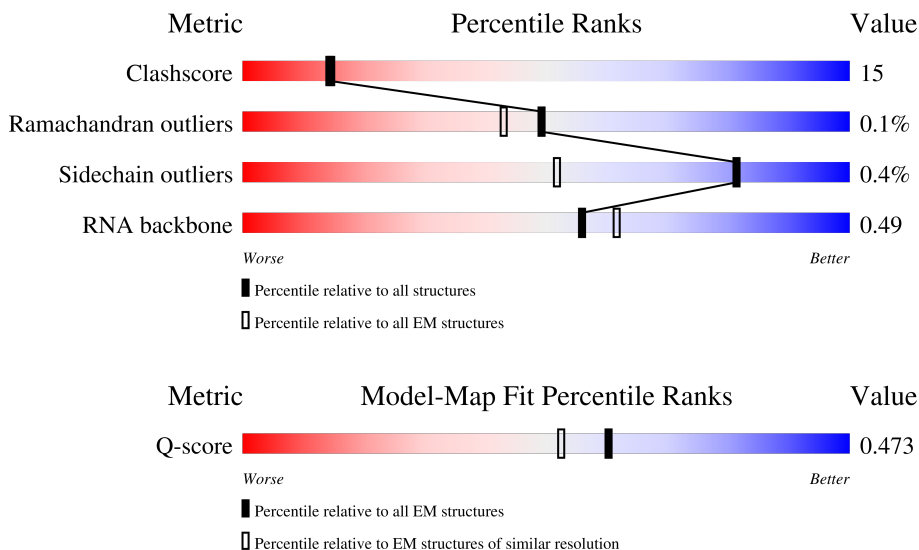
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.22 Å.

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



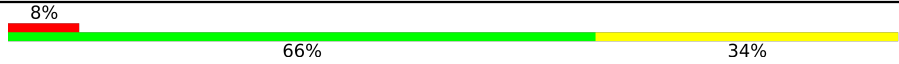







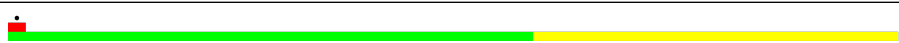

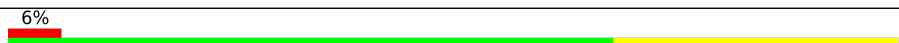


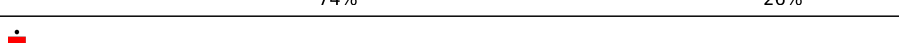
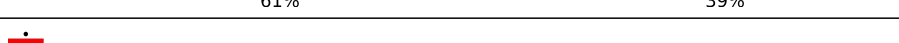
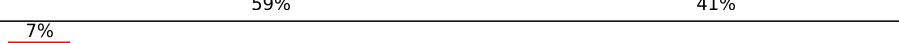
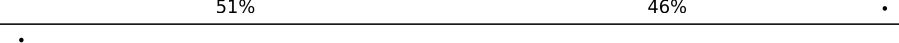
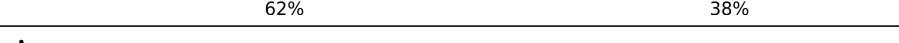
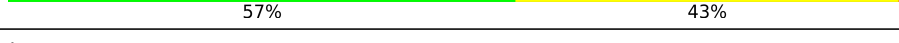






Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14612 (2.72 - 3.72)

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

Mol	Chain	Length	Quality of chain
1	2	1800	
2	SP	206	
3	SQ	232	

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Mol	Chain	Length	Quality of chain
4	SE	117	
5	SR	216	
6	SA	222	
7	SS	258	
8	SB	206	
9	ST	228	
10	SU	184	
11	SV	187	
12	SW	184	
13	SC	92	
14	SX	142	
15	SD	121	
16	SY	150	
17	SZ	127	
18	SF	141	
19	SG	125	
20	SH	145	
21	SI	143	
22	SJ	100	
23	Sa	87	
24	Sb	129	
25	Sc	144	
26	Sd	134	
27	Se	97	
28	Sf	81	

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Mol	Chain	Length	Quality of chain
29	SM	53	66% 34%
30	Sg	57	7% 68% 32%
31	SN	73	26% 53% 47%
32	SO	312	6% 58% 42%
33	SL	63	8% 60% 40%
34	AA	102	15% 54% 39% 7%
35	A	3394	39% 46% 9% 6%
36	B	121	36% 55% 9%
37	C	158	46% 44% 10%
38	LD	251	71% 29%
39	LE	386	64% 36%
40	LF	361	78% 22%
41	LG	294	66% 34%
42	LH	175	73% 22% 5%
43	LI	222	69% 31%
44	LJ	233	5% 68% 32%
45	LK	191	72% 28%
46	LL	218	67% 33%
47	LM	169	59% 41%
48	LN	193	65% 34%
49	LO	136	73% 26%
50	LP	203	61% 38%
51	LQ	197	75% 24%
52	LR	183	5% 76% 23%
53	LS	185	63% 37%

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Mol	Chain	Length	Quality of chain
54	LT	188	72% 28%
55	LU	171	65% 35%
56	LV	159	58% 42%
57	LW	100	63% 37%
58	LX	136	68% 32%
59	LY	65	65% 35%
60	LZ	121	75% 25%
61	La	125	75% 25%
62	Lb	135	70% 30%
63	Lc	148	59% 41%
64	Ld	58	7% 72% 26%
65	Le	96	66% 34%
66	Lf	109	5% 77% 23%
67	Lg	127	72% 28%
68	Lh	106	72% 28%
69	Li	112	75% 25%
70	Lj	119	75% 24%
71	Lk	99	6% 65% 35%
72	Ll	81	67% 33%
73	Lm	77	57% 43%
74	Ln	50	66% 34%
75	Lo	52	79% 19%
76	Lp	25	36% 72% 28%
77	Lq	103	63% 37%
78	Lr	91	78% 22%

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Mol	Chain	Length	Quality of chain
79	Ls	157	
80	z	588	
81	m	76	
82	n	75	
83	D	10	
84	E	210	

2 Entry composition [i](#)

There are 85 unique types of molecules in this entry. The entry contains 205193 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1771	37739	16872	6683	12413	1771	0	0

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 4 is a protein called 40S ribosomal protein S15.

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

- Molecule 5 is a protein called 40S ribosomal protein S2.

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

- Molecule 6 is a protein called 40S ribosomal protein S3.

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

- Molecule 7 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S5.

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

- Molecule 9 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	SC	92	754	489	122	141	2	0	0

- Molecule 14 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SX	142	Total	C	N	O	S	0	0
			1142	733	217	189	3		

- Molecule 15 is a protein called 40S ribosomal protein S12.

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

- Molecule 16 is a protein called 40S ribosomal protein S13.

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

- Molecule 17 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SZ	127	Total	C	N	O	S	0	0
			923	568	185	167	3		

- Molecule 18 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	SF	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 19 is a protein called 40S ribosomal protein S17-B.

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

- Molecule 20 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SH	145	Total	C	N	O	S	0	0
			1188	741	237	208	2		

- Molecule 21 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 22 is a protein called 40S ribosomal protein S20.

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

- Molecule 23 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	Sd	134	1032	651	195	186	0	0

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Se	97	765	473	160	127	5	0	0

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	SM	53	443	275	92	72	4	0	0

- Molecule 30 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	Sg	57	451	284	93	73	1	0	0

- Molecule 31 is a protein called 40S ribosomal protein S31.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SN	97	ALA	LYS	conflict	UNP A0A6A5PU37

- Molecule 32 is a protein called 40S ribosomal protein ASC1.

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

- Molecule 33 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 34 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	AA	95	Total	C	N	O	0	0
			737	466	139	132		

- Molecule 35 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	A	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 36 is a RNA chain called 5S rRNA.

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

- Molecule 37 is a RNA chain called 5.8S rRNA.

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

- Molecule 38 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 39 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LE	386	Total	C	N	O	S	0	0
			3079	1954	584	533	8		

- Molecule 40 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LF	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 41 is a protein called 60S ribosomal protein L5.

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

- Molecule 42 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LH	167	Total	C	N	O	S	0	0
			1307	843	234	230			

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L10.

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

- Molecule 47 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LM	169	Total	C	N	O	S	0	0
			1346	843	252	247	4		

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	LN	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	LR	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	LT	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 55 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	LV	159	1272	802	245	221	4	0	0

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
57	LW	100	796	516	131	149	0	0

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	LY	65	528	339	104	84	1	0	0

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

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

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
62	Lb	135	1080	701	199	180	0	0

- Molecule 63 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Lc	148	1169	747	231	188	3	0	0

- Molecule 64 is a protein called 60S ribosomal protein L29.

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

- Molecule 65 is a protein called 60S ribosomal protein L30.

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

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L32.

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

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ll	81	Total	C	N	O	S	0	0
			645	393	141	106	5		

- Molecule 73 is a protein called 60S ribosomal protein L38.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Lo	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called Translation factor eIF5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Ls	143	Total	C	N	O	S	0	0
			1081	672	181	219	9		

- Molecule 80 is a protein called Cytoplasmic 60S subunit biogenesis factor REH1 (N-terminal 3xFLAG tag).

Mol	Chain	Residues	Atoms					AltConf	Trace
80	z	57	Total	C	N	O	S	0	0
			480	295	96	86	3		

- Molecule 81 is a RNA chain called A site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	m	76	Total	C	N	O	P	0	0
			1611	721	281	534	75		

- Molecule 82 is a RNA chain called P site initiator tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	n	75	Total	C	N	O	P	0	0
			1606	716	297	518	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	10	A	G	conflict	GB 176433

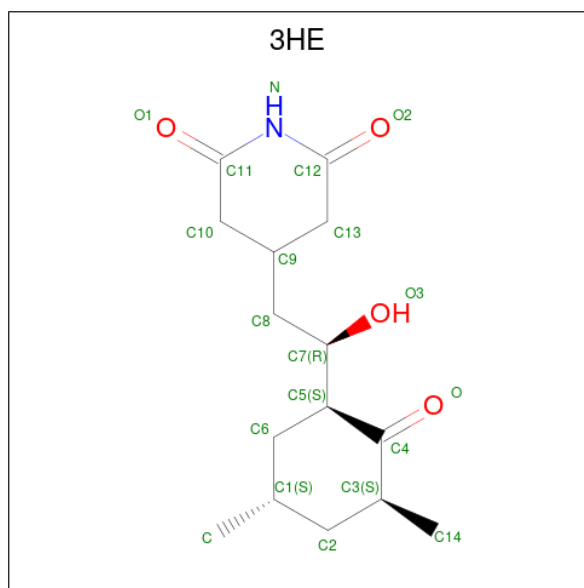
- Molecule 83 is a RNA chain called Messenger RNA (5'-R(P*AP*AP*UP*AP*UP*GP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms				AltConf	Trace	
			Total	C	N	O			P
83	D	10	213	98	44	61	10	0	0

- Molecule 84 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
84	E	210	1051	630	210	211	0	0

- Molecule 85 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (CCD ID: 3HE) (formula: C₁₅H₂₃NO₄).

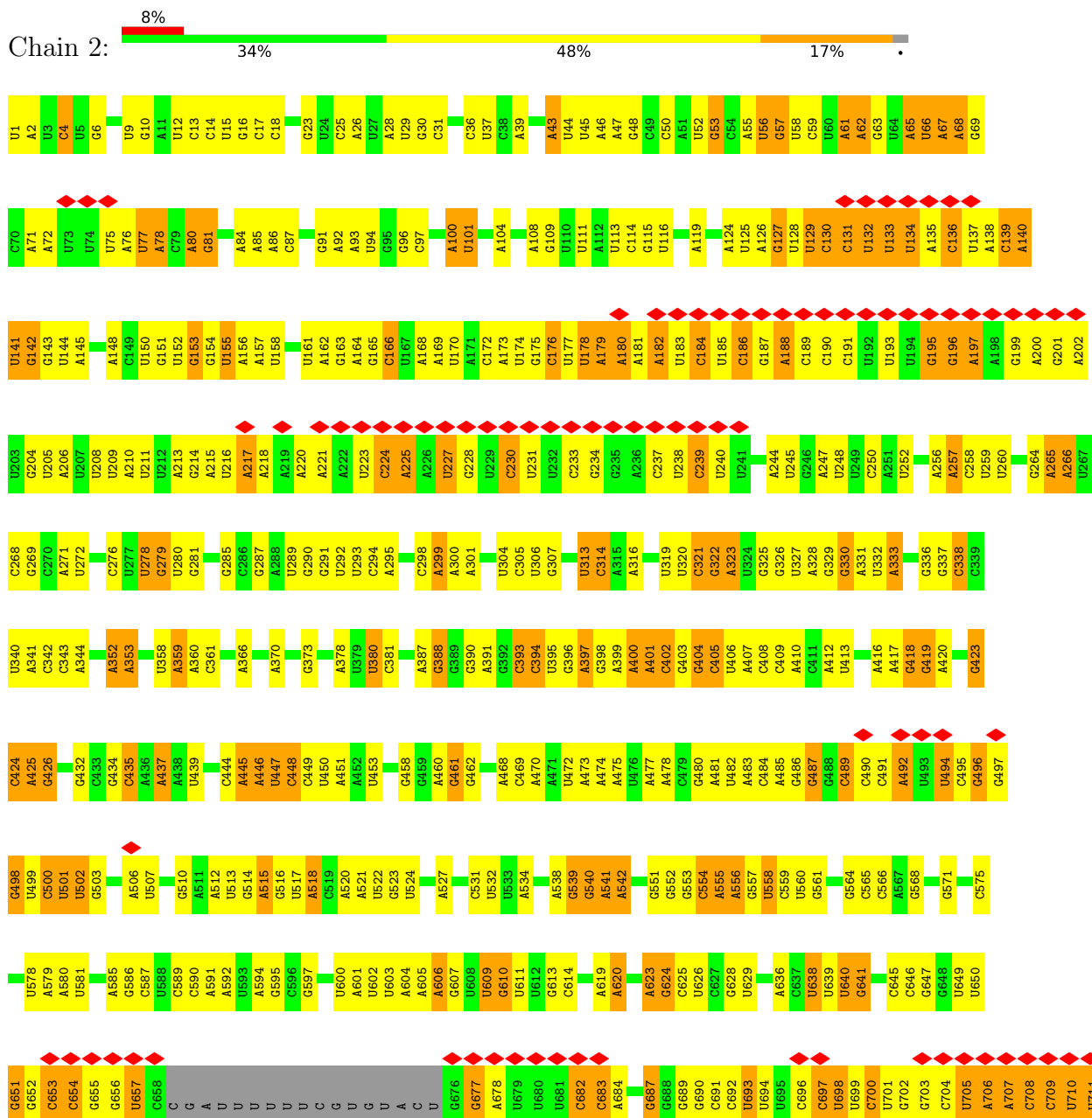


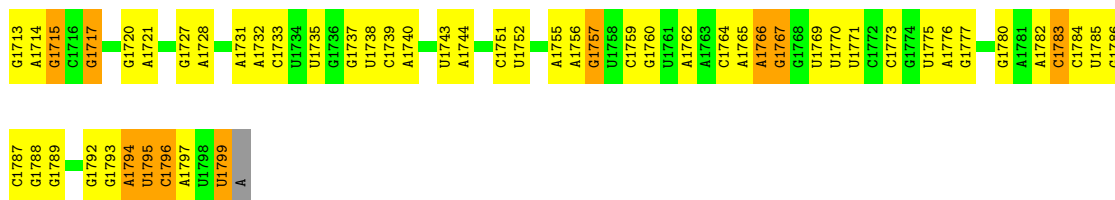
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
85	A	1	20	15	1	4	0

3 Residue-property plots

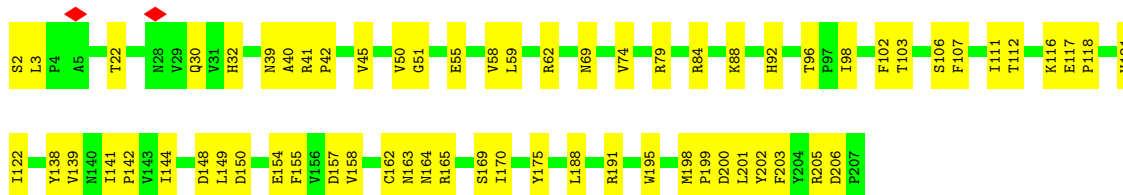
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: 18S rRNA

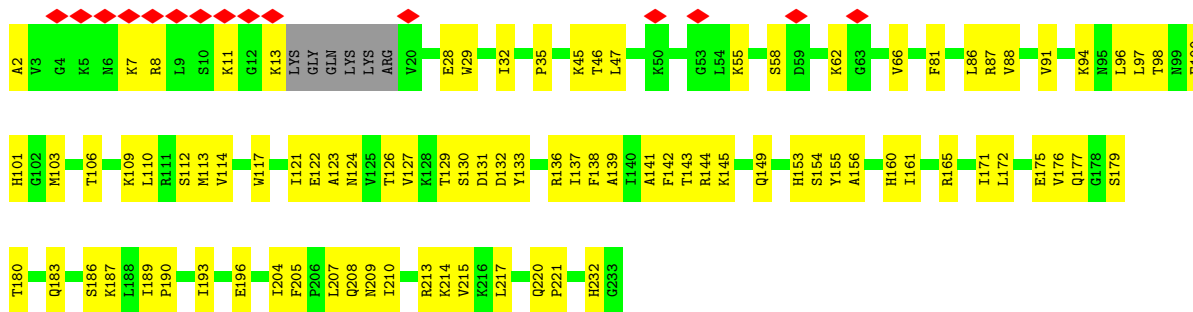




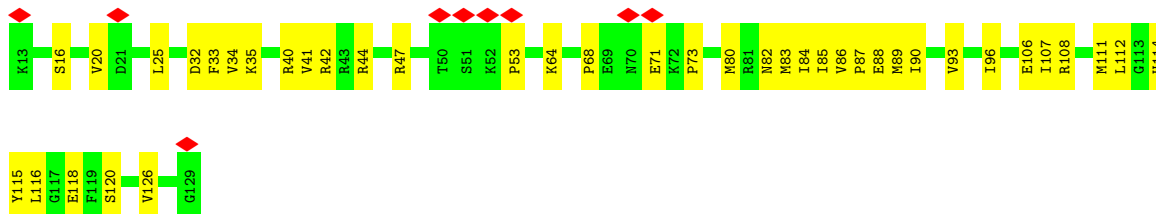
• Molecule 2: 40S ribosomal protein S0-A



• Molecule 3: 40S ribosomal protein S1-A



• Molecule 4: 40S ribosomal protein S15

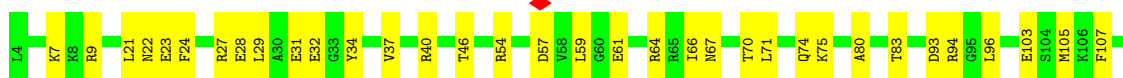
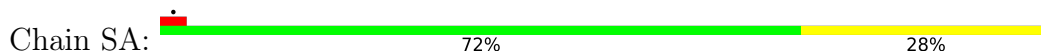


• Molecule 5: 40S ribosomal protein S2

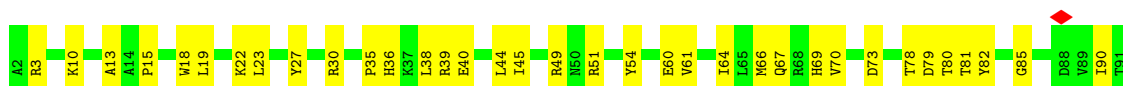




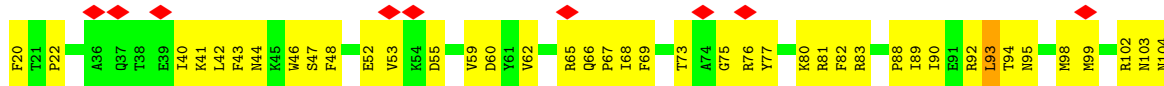
• Molecule 6: 40S ribosomal protein S3



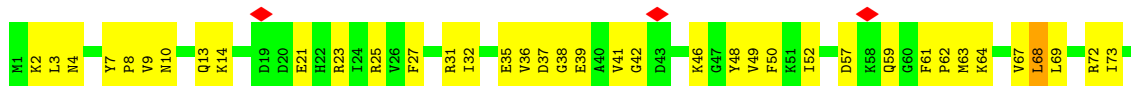
• Molecule 7: 40S ribosomal protein S4-A

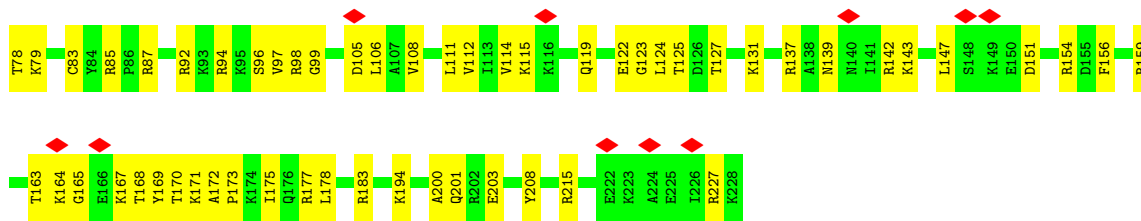


• Molecule 8: 40S ribosomal protein S5

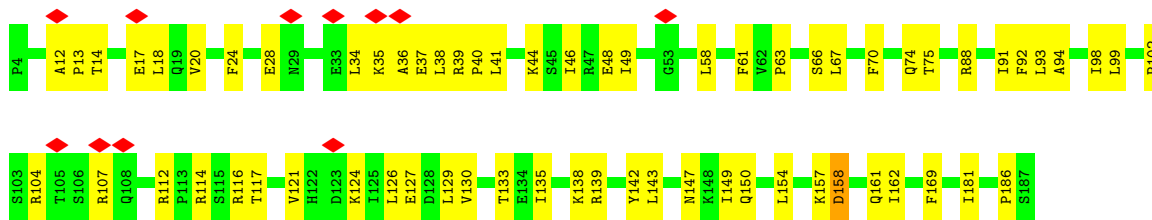


• Molecule 9: 40S ribosomal protein S6-A

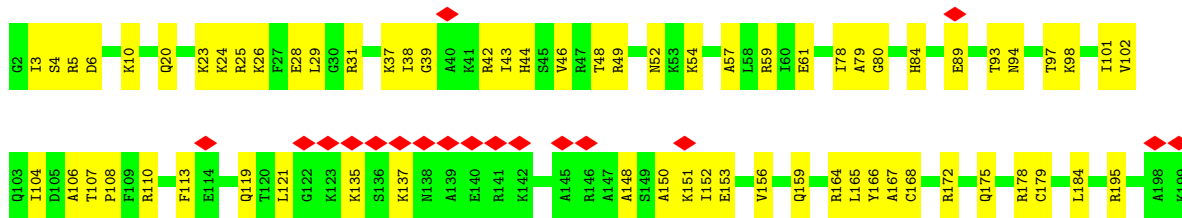




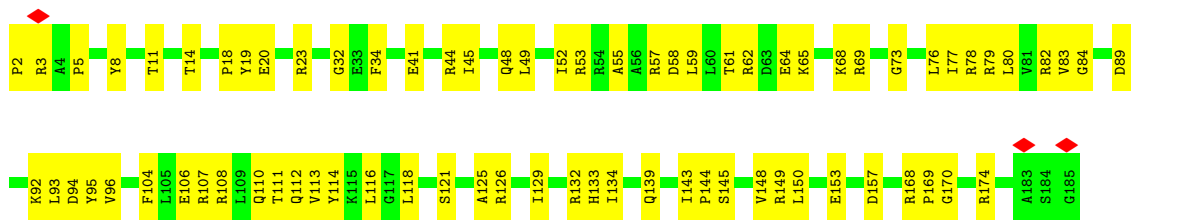
• Molecule 10: 40S ribosomal protein S7-A



• Molecule 11: 40S ribosomal protein S8-A

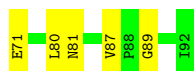


• Molecule 12: 40S ribosomal protein S9-A

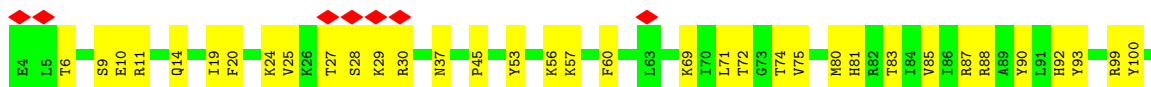


• Molecule 13: 40S ribosomal protein S10-A

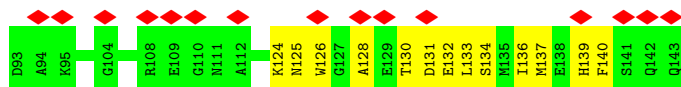
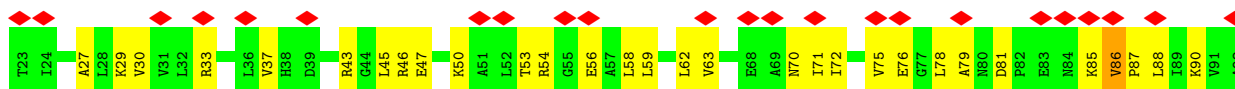




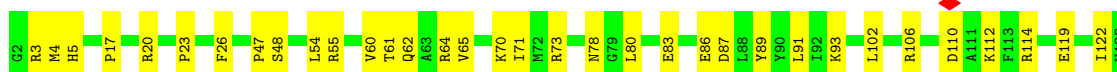
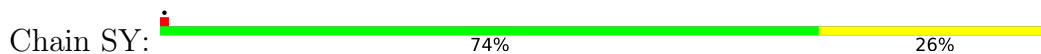
- Molecule 14: 40S ribosomal protein S11-A



- Molecule 15: 40S ribosomal protein S12



- Molecule 16: 40S ribosomal protein S13

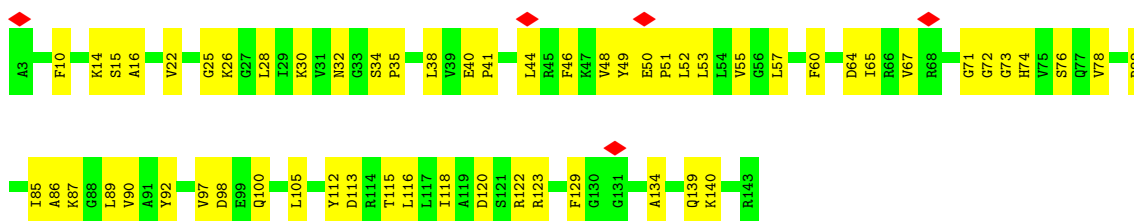


- Molecule 17: 40S ribosomal protein S14-B



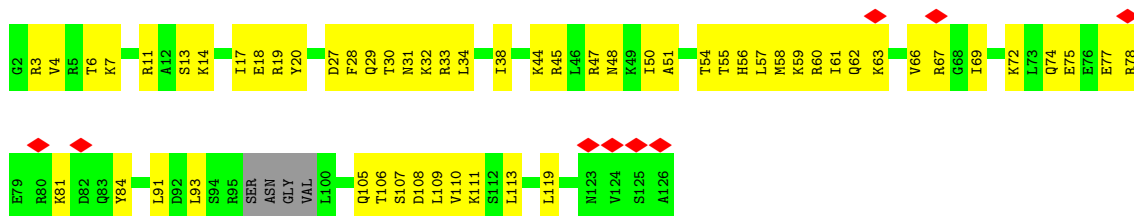
- Molecule 18: 40S ribosomal protein S16-A

Chain SF:  59% 41%



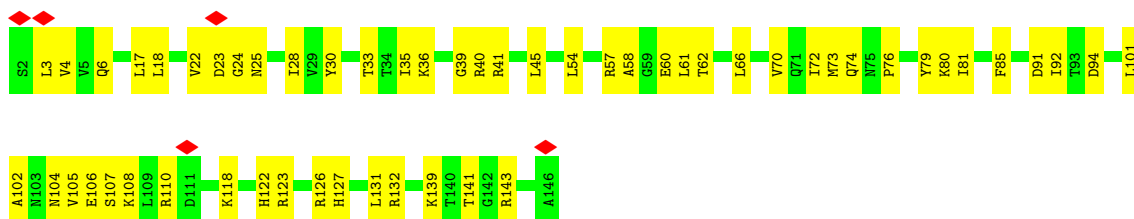
- Molecule 19: 40S ribosomal protein S17-B

Chain SG:  7% 51% 46%



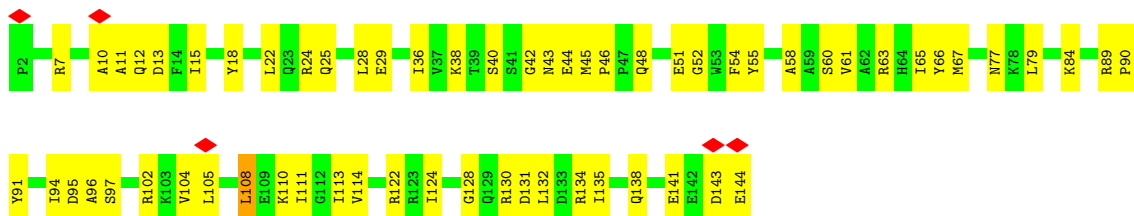
- Molecule 20: 40S ribosomal protein S18-A

Chain SH:  62% 38%



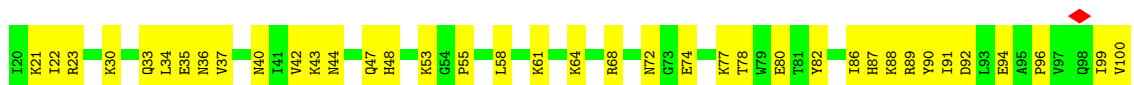
- Molecule 21: 40S ribosomal protein S19-A

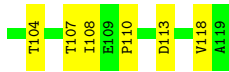
Chain SI:  57% 43%



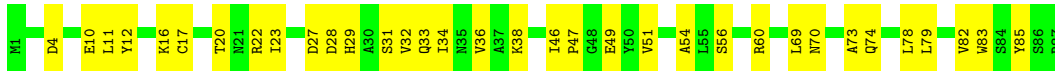
- Molecule 22: 40S ribosomal protein S20

Chain SJ:  56% 44%

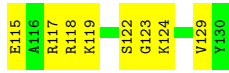
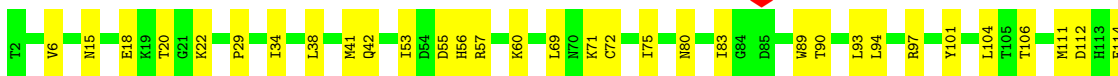




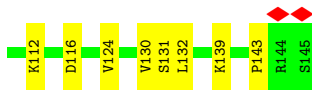
- Molecule 23: 40S ribosomal protein S21-A



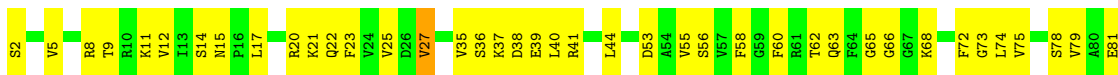
- Molecule 24: 40S ribosomal protein S22-A



- Molecule 25: 40S ribosomal protein S23-A



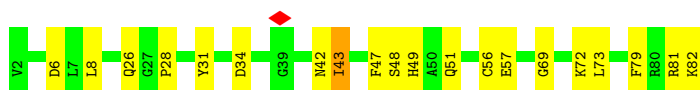
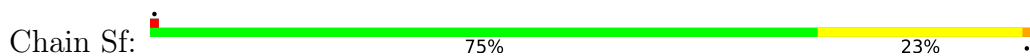
- Molecule 26: 40S ribosomal protein S24-A



- Molecule 27: 40S ribosomal protein S26-B



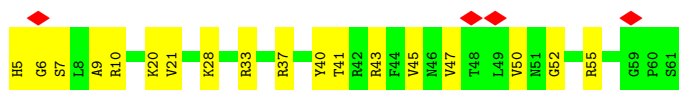
• Molecule 28: 40S ribosomal protein S27-A



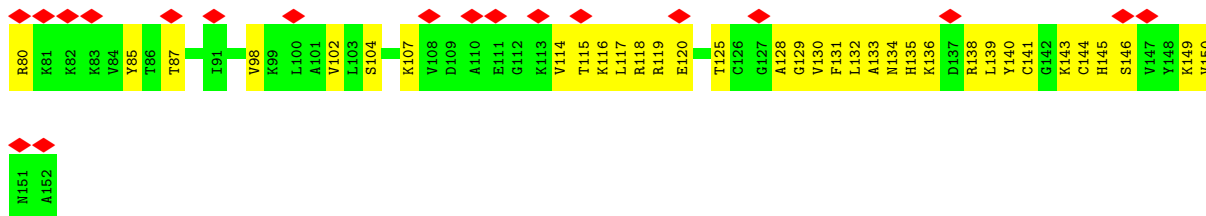
• Molecule 29: 40S ribosomal protein S29-A



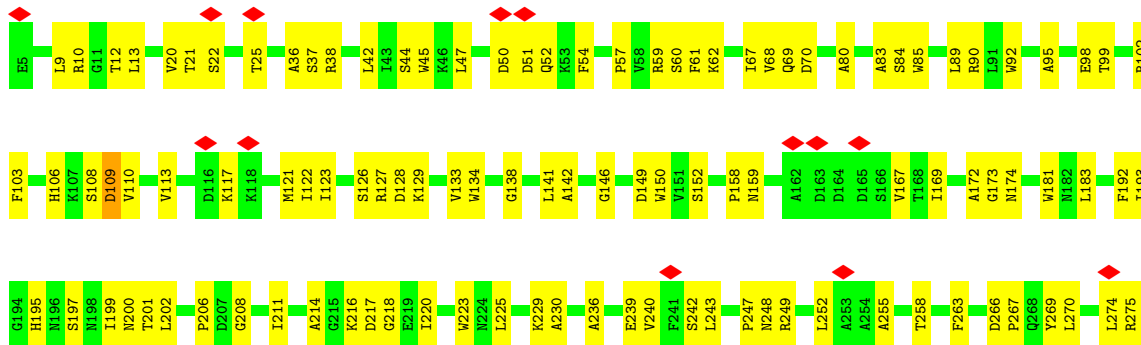
• Molecule 30: 40S ribosomal protein S30-A



• Molecule 31: 40S ribosomal protein S31



• Molecule 32: 40S ribosomal protein ASC1

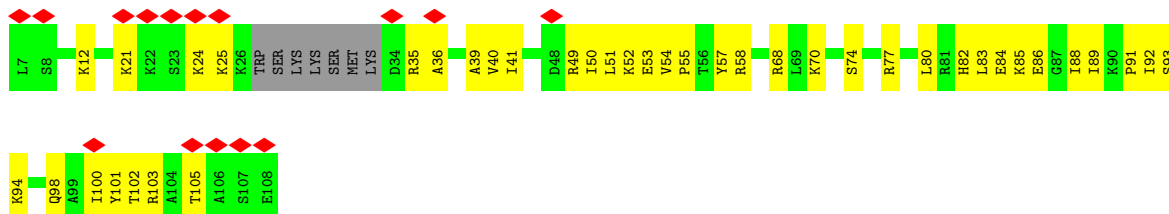




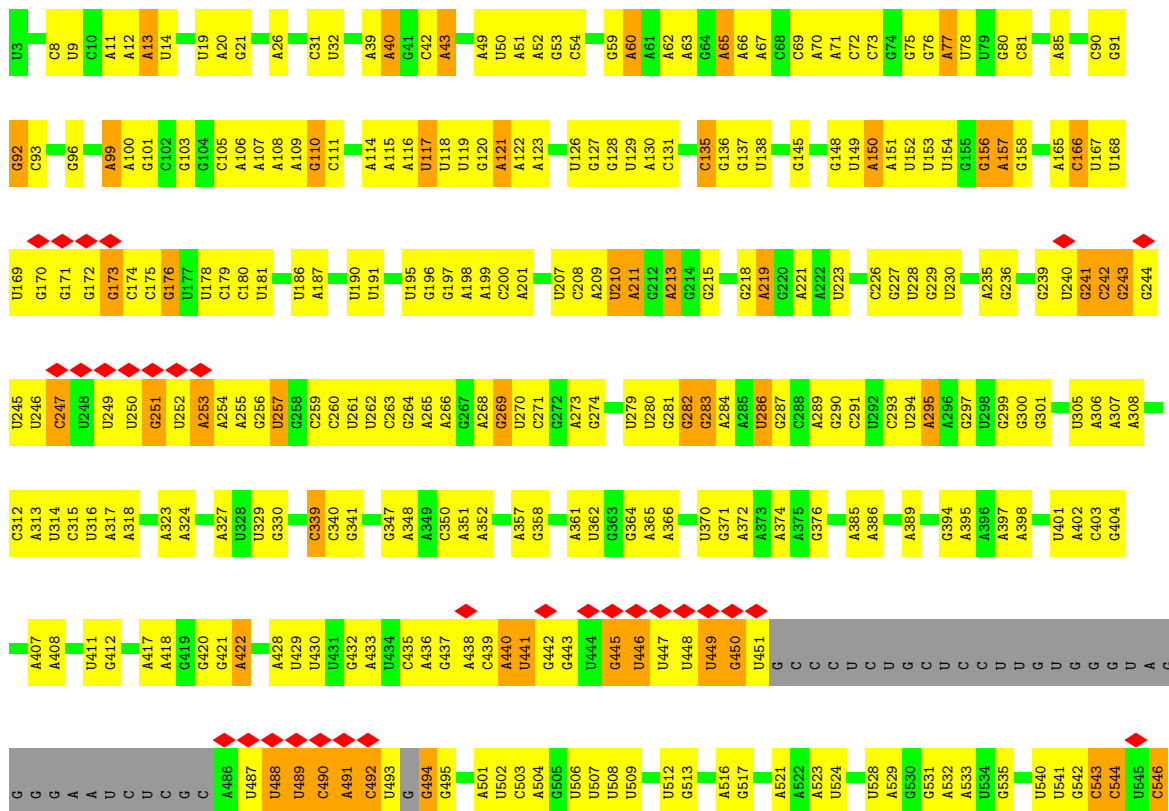
• Molecule 33: 40S ribosomal protein S28-A

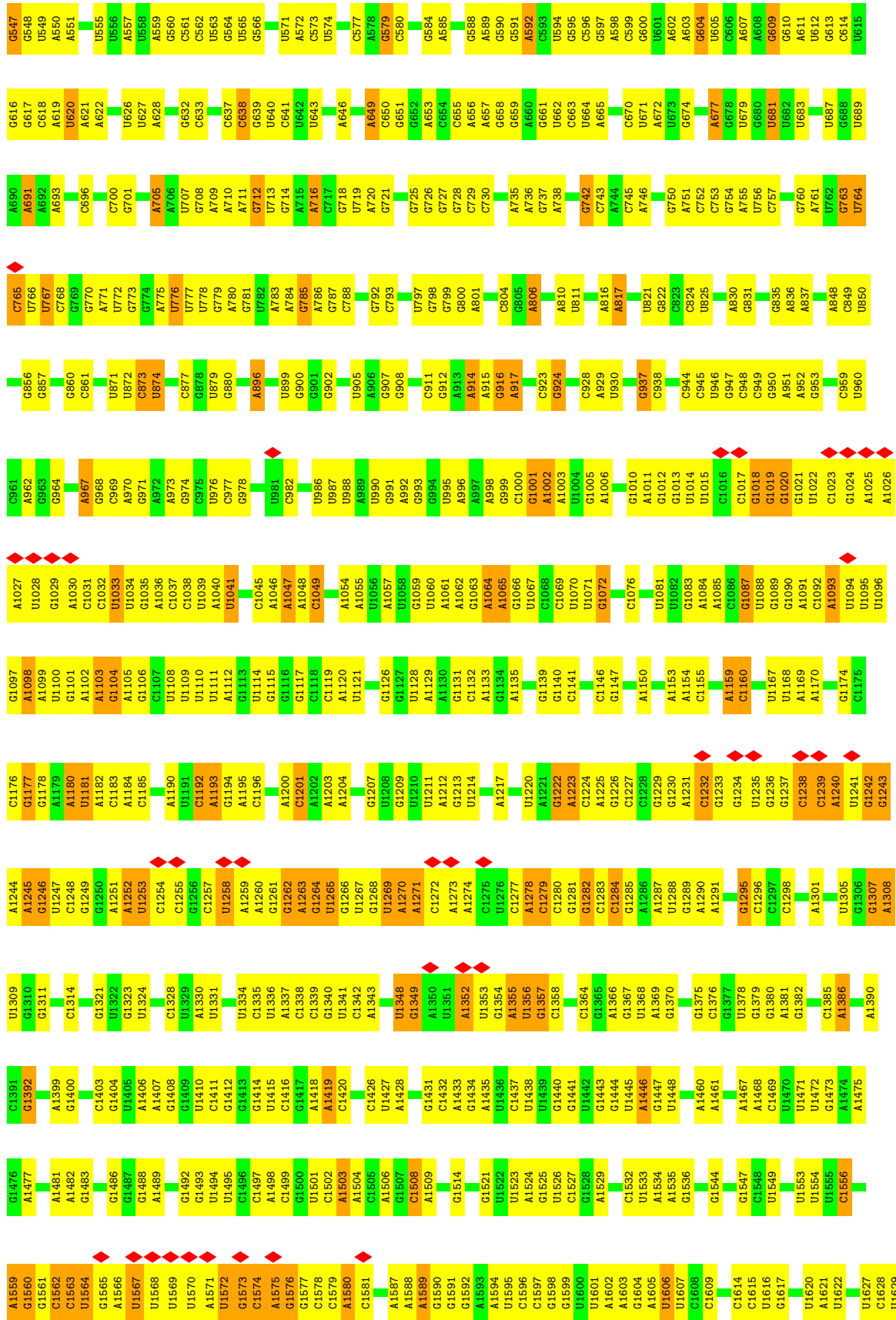


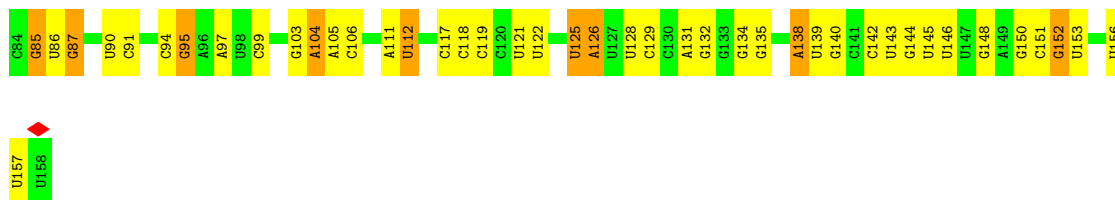
• Molecule 34: 40S ribosomal protein S25-A



• Molecule 35: 25S rRNA



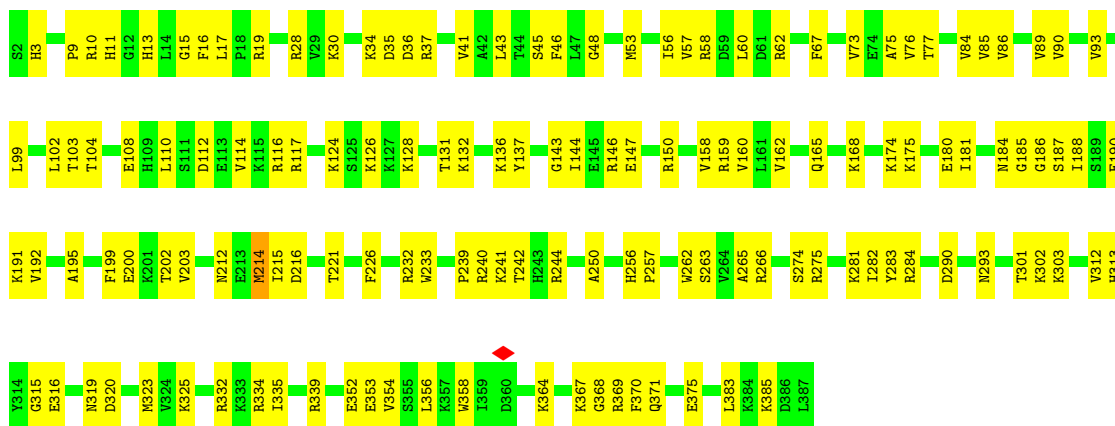




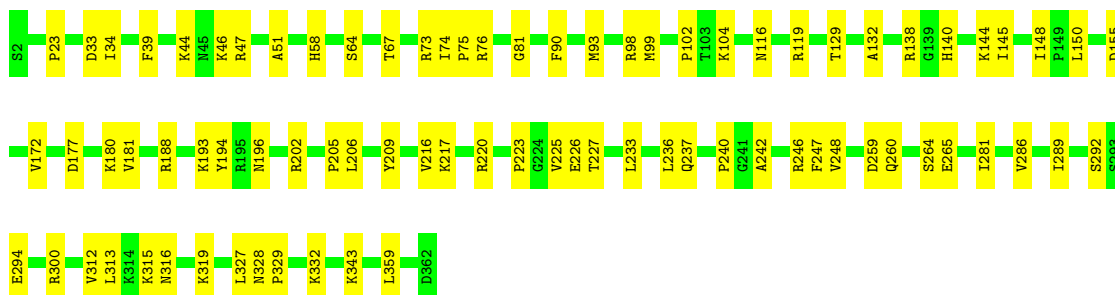
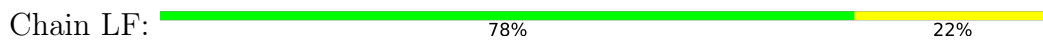
• Molecule 38: 60S ribosomal protein L2-A



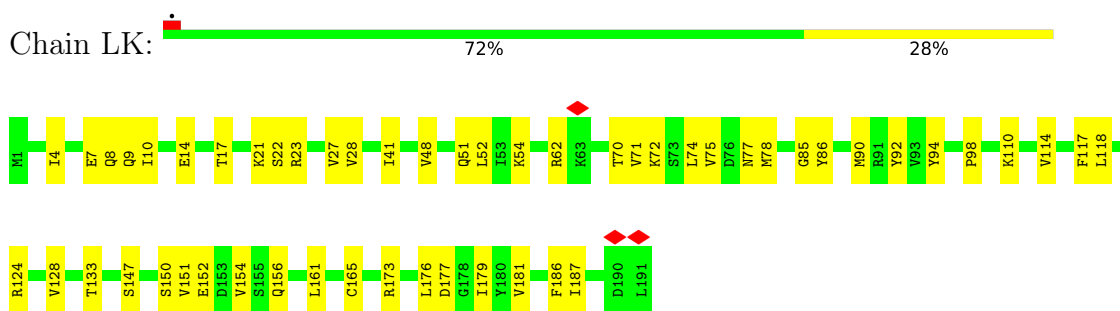
• Molecule 39: 60S ribosomal protein L3



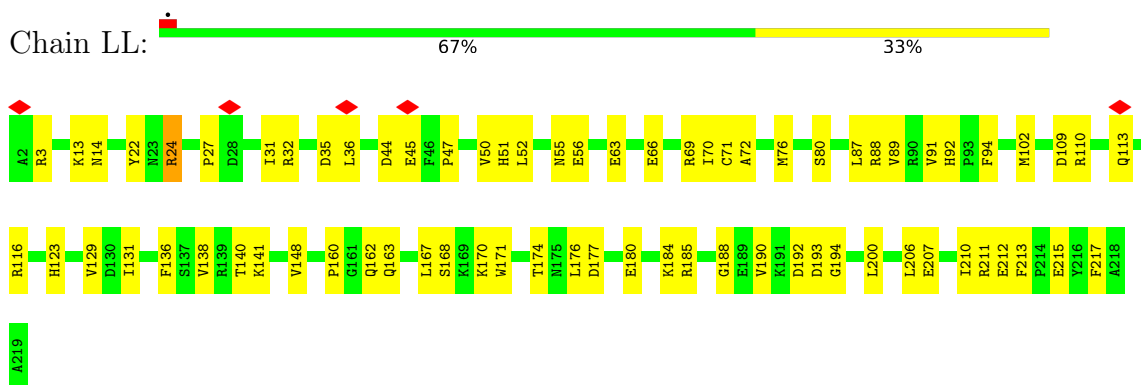
• Molecule 40: 60S ribosomal protein L4-A



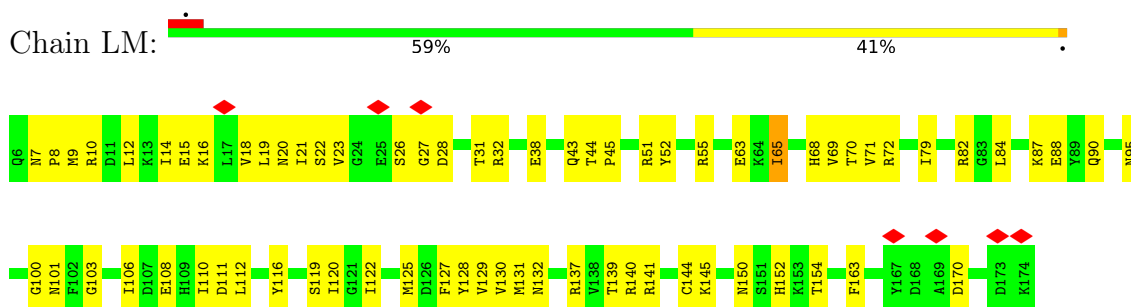
- Molecule 45: 60S ribosomal protein L9-A



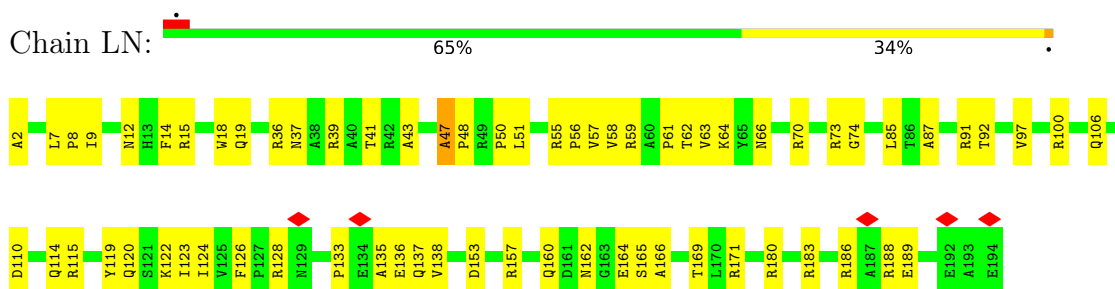
- Molecule 46: 60S ribosomal protein L10



- Molecule 47: 60S ribosomal protein L11-B

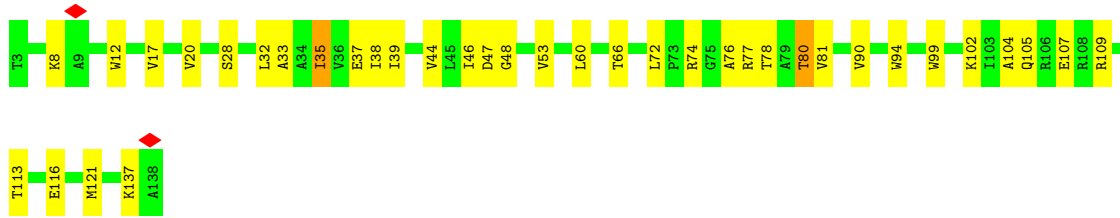


- Molecule 48: 60S ribosomal protein L13-A



- Molecule 49: 60S ribosomal protein L14-A

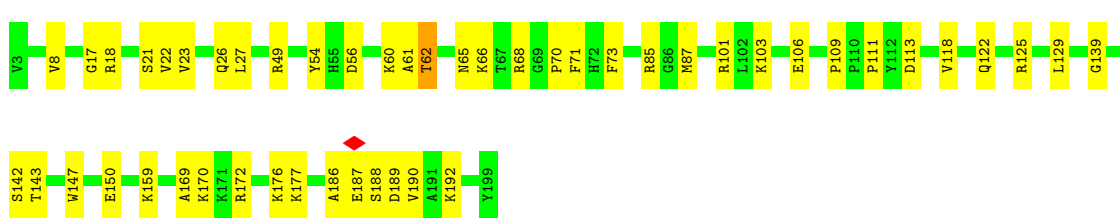
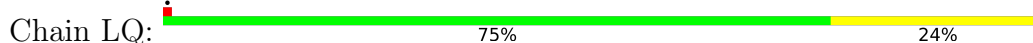




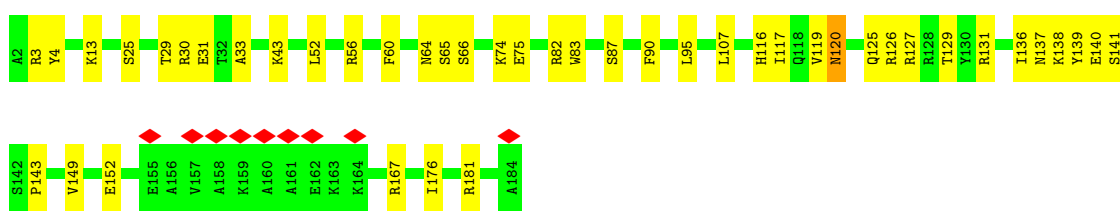
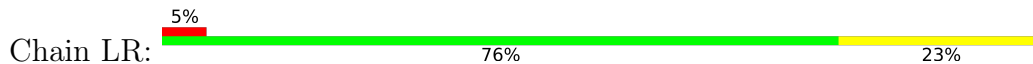
• Molecule 50: 60S ribosomal protein L15-A



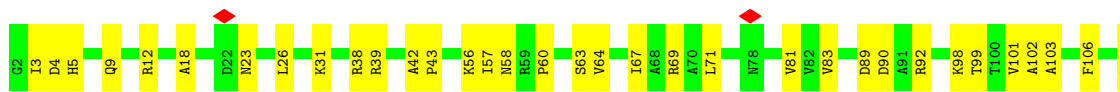
• Molecule 51: 60S ribosomal protein L16-A



• Molecule 52: 60S ribosomal protein L17-A

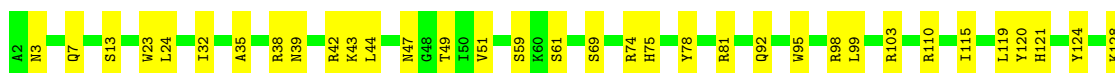
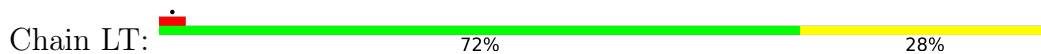


• Molecule 53: 60S ribosomal protein L18-A





- Molecule 54: 60S ribosomal protein L19-A



- Molecule 55: 60S ribosomal protein L20-A



- Molecule 56: 60S ribosomal protein L21-A



- Molecule 57: 60S ribosomal protein L22-A

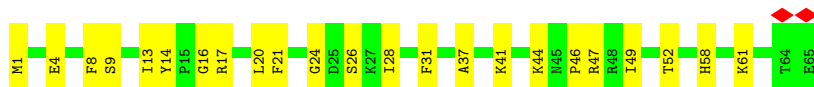


- Molecule 58: 60S ribosomal protein L23-A

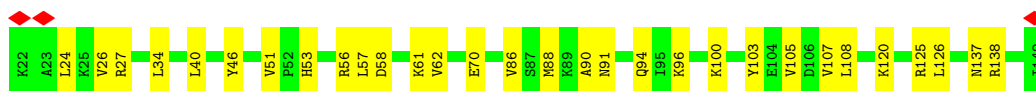
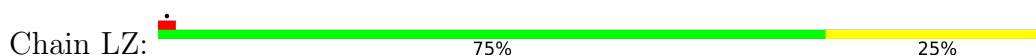




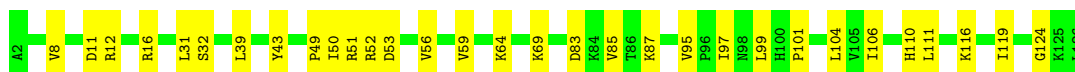
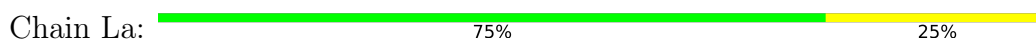
- Molecule 59: 60S ribosomal protein L24-A



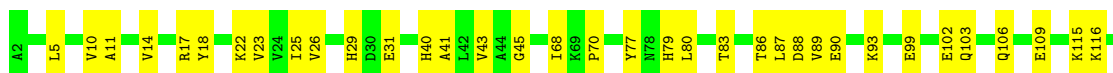
- Molecule 60: 60S ribosomal protein L25



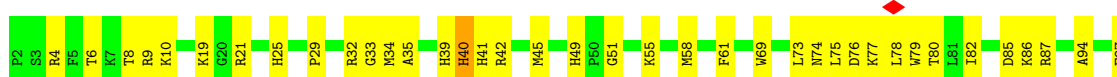
- Molecule 61: 60S ribosomal protein L26-A



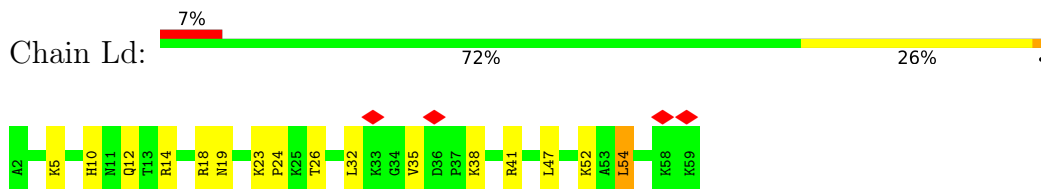
- Molecule 62: 60S ribosomal protein L27-A



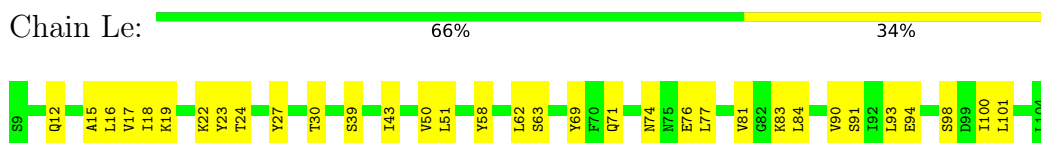
- Molecule 63: 60S ribosomal protein L28



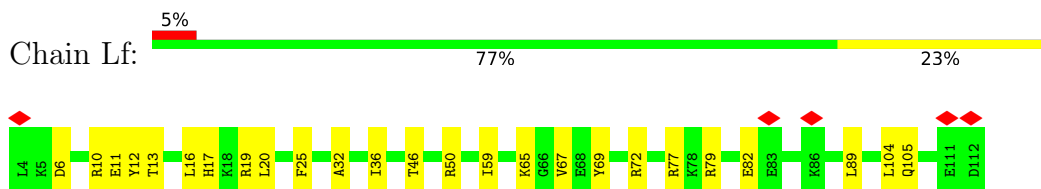
- Molecule 64: 60S ribosomal protein L29



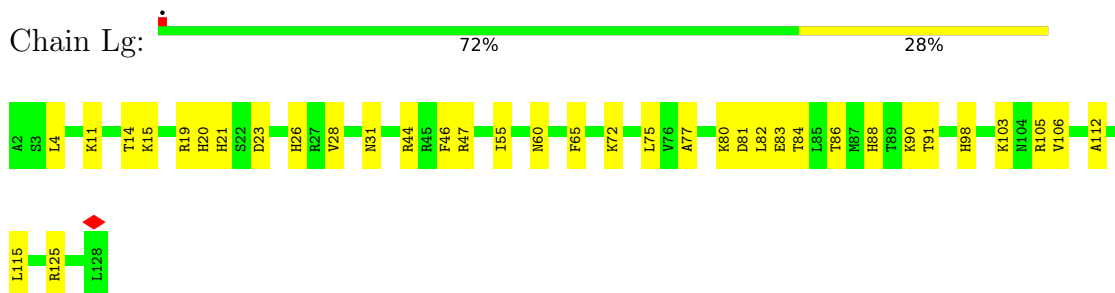
- Molecule 65: 60S ribosomal protein L30



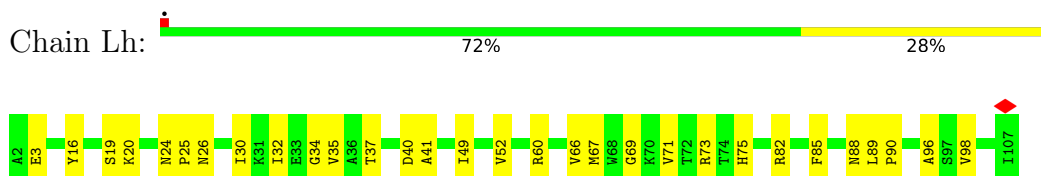
- Molecule 66: 60S ribosomal protein L31-A



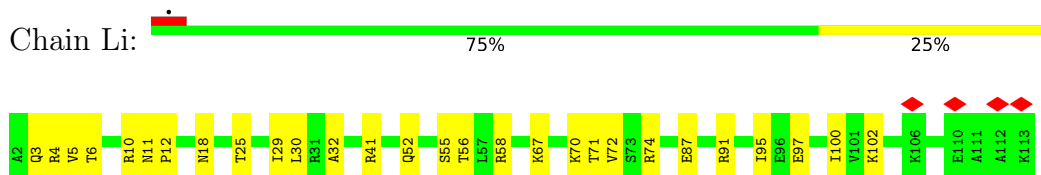
- Molecule 67: 60S ribosomal protein L32



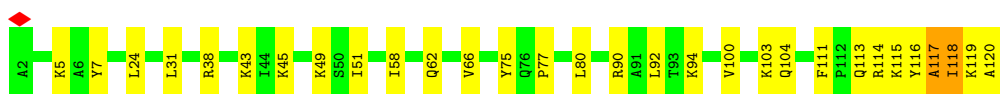
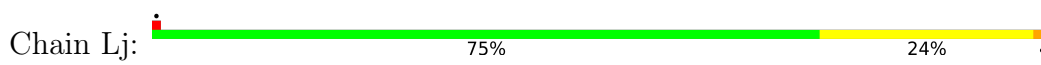
- Molecule 68: 60S ribosomal protein L33-A



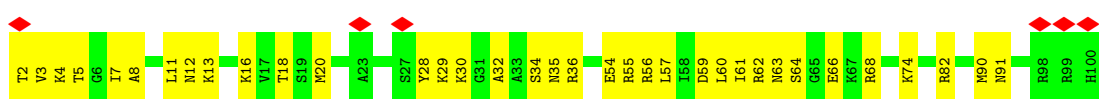
- Molecule 69: 60S ribosomal protein L34-A



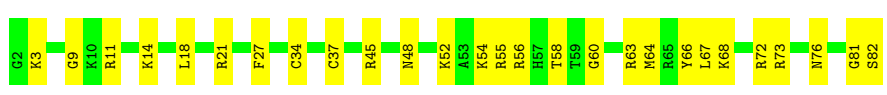
- Molecule 70: 60S ribosomal protein L35-A



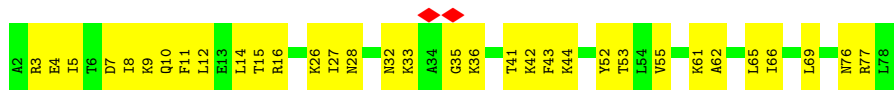
• Molecule 71: 60S ribosomal protein L36-A



• Molecule 72: 60S ribosomal protein L37-A



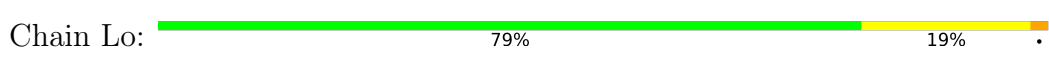
• Molecule 73: 60S ribosomal protein L38



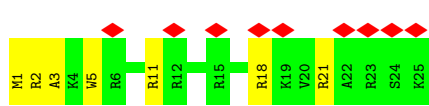
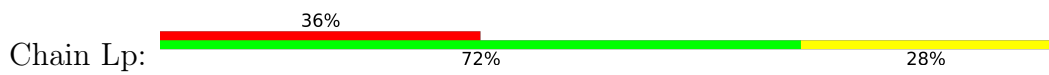
• Molecule 74: 60S ribosomal protein L39

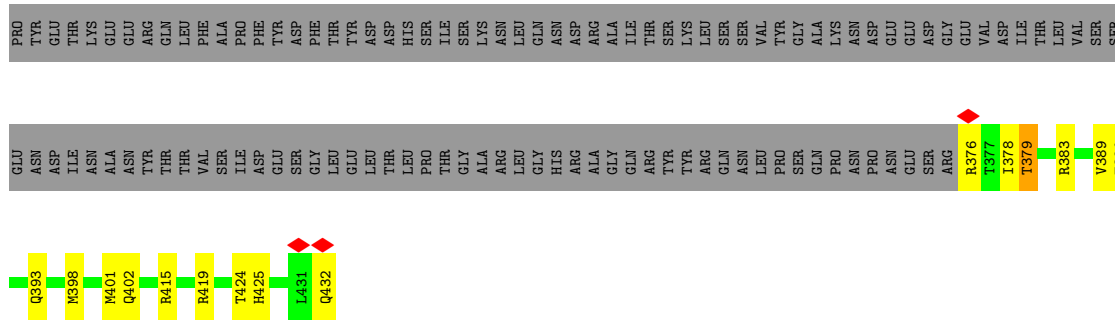


• Molecule 75: 60S ribosomal protein L40-A

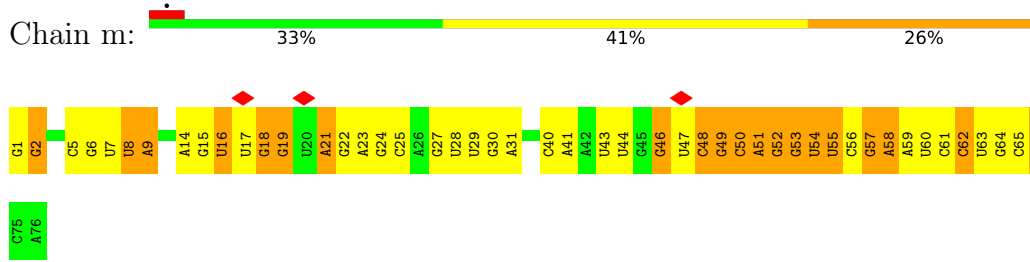


• Molecule 76: 60S ribosomal protein L41-A

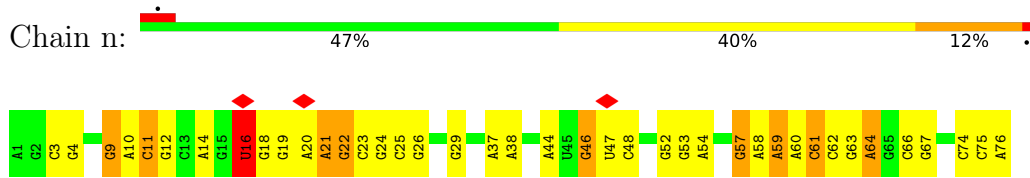




• Molecule 81: A site tRNA



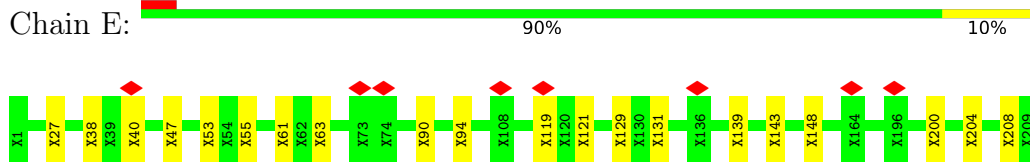
• Molecule 82: P site initiator tRNA



• Molecule 83: Messenger RNA (5'-R(P*AP*AP*UP*AP*UP*GP*AP*AP*AP*A)-3')



• Molecule 84: 60S ribosomal protein L1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23734	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	70	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.629	Depositor
Minimum map value	-0.337	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.0875	Depositor
Map size (\AA)	524.88, 524.88, 524.88	wwPDB
Map dimensions	648, 648, 648	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.81, 0.81, 0.81	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: 3HE, 5CT

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	2	0.32	0/42211	0.39	0/65773
2	SP	0.27	0/1644	0.38	0/2249
3	SQ	0.25	0/1823	0.40	0/2447
4	SE	0.22	0/936	0.39	0/1259
5	SR	0.31	0/1656	0.41	0/2251
6	SA	0.25	0/1754	0.42	0/2361
7	SS	0.29	0/2097	0.42	0/2823
8	SB	0.25	0/1625	0.47	0/2197
9	ST	0.24	0/1839	0.41	0/2460
10	SU	0.24	0/1498	0.43	0/2019
11	SV	0.31	0/1501	0.44	0/2006
12	SW	0.26	0/1504	0.41	0/2016
13	SC	0.27	0/772	0.46	0/1044
14	SX	0.33	0/1168	0.47	0/1575
15	SD	0.17	0/883	0.43	0/1199
16	SY	0.28	0/1215	0.39	0/1638
17	SZ	0.26	0/934	0.39	0/1257
18	SF	0.26	0/1125	0.44	0/1510
19	SG	0.25	0/957	0.45	0/1283
20	SH	0.25	0/1207	0.42	0/1623
21	SI	0.24	0/1130	0.41	0/1517
22	SJ	0.25	0/807	0.41	0/1091
23	Sa	0.29	0/682	0.42	0/921
24	Sb	0.36	0/1038	0.44	0/1395
25	Sc	0.34	0/1139	0.40	0/1518
26	Sd	0.27	0/1046	0.41	0/1401
27	Se	0.29	0/778	0.38	0/1042
28	Sf	0.28	0/620	0.37	0/838
29	SM	0.30	0/453	0.43	0/602
30	Sg	0.24	0/459	0.45	0/611
31	SN	0.21	0/567	0.56	0/764
32	SO	0.22	0/2436	0.45	0/3318

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	SL	0.24	0/493	0.50	0/663
34	AA	0.21	0/744	0.45	0/991
35	A	0.38	0/76214	0.37	0/118821
36	B	0.30	0/2883	0.34	0/4491
37	C	0.41	0/3746	0.36	0/5832
38	LD	0.38	0/1933	0.43	0/2598
39	LE	0.36	0/3150	0.41	0/4236
40	LF	0.35	0/2801	0.41	0/3792
41	LG	0.26	0/2400	0.41	0/3239
42	LH	0.30	0/1329	0.40	0/1794
43	LI	0.32	0/1821	0.37	0/2451
44	LJ	0.31	0/1836	0.43	0/2481
45	LK	0.31	0/1529	0.46	0/2060
46	LL	0.30	0/1801	0.42	0/2416
47	LM	0.26	0/1367	0.46	0/1834
48	LN	0.32	0/1568	0.42	0/2106
49	LO	0.30	0/1068	0.38	0/1438
50	LP	0.39	0/1757	0.43	0/2354
51	LQ	0.34	0/1585	0.39	0/2128
52	LR	0.37	0/1439	0.41	0/1938
53	LS	0.32	0/1465	0.39	0/1965
54	LT	0.32	0/1532	0.35	0/2043
55	LU	0.34	0/1473	0.41	0/1980
56	LV	0.30	0/1296	0.40	0/1739
57	LW	0.30	0/812	0.52	0/1099
58	LX	0.38	0/1018	0.45	0/1369
59	LY	0.33	0/540	0.36	0/717
60	LZ	0.37	0/979	0.43	0/1321
61	La	0.36	0/995	0.35	0/1329
62	Lb	0.34	0/1106	0.42	0/1485
63	Lc	0.35	0/1200	0.47	0/1607
64	Ld	0.25	0/473	0.34	0/629
65	Le	0.32	0/745	0.38	0/1001
66	Lf	0.34	0/890	0.39	0/1196
67	Lg	0.35	0/1038	0.40	0/1390
68	Lh	0.39	0/868	0.44	0/1168
69	Li	0.40	0/890	0.45	0/1189
70	Lj	0.33	0/978	0.40	0/1301
71	Lk	0.26	0/772	0.45	0/1026
72	Ll	0.39	0/660	0.41	0/875
73	Lm	0.32	0/618	0.39	0/826
74	Ln	0.41	0/443	0.45	0/588
75	Lo	0.29	0/416	0.33	0/553

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Lp	0.25	0/230	0.31	0/296
77	Lq	0.30	0/836	0.40	0/1104
78	Lr	0.33	0/701	0.38	0/934
79	Ls	0.25	0/1080	0.43	0/1452
80	z	0.31	0/483	0.42	0/640
81	m	0.29	0/1799	0.44	0/2801
82	n	0.85	1/1796 (0.1%)	0.49	2/2799 (0.1%)
83	D	0.34	0/240	0.44	0/368
All	All	0.34	1/219340 (0.0%)	0.39	2/322461 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
82	n	16	U	O3'-P	34.02	2.12	1.61

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	n	16	U	P-O3'-C3'	-14.11	99.04	120.20
82	n	16	U	O3'-P-O5'	-6.12	94.82	104.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37739	0	18988	1123	0
2	SP	1603	0	1610	57	0
3	SQ	1798	0	1890	78	0
4	SE	916	0	941	40	0
5	SR	1626	0	1715	57	0
6	SA	1729	0	1812	55	0
7	SS	2056	0	2140	77	0
8	SB	1605	0	1669	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	ST	1815	0	1894	78	0
10	SU	1473	0	1555	49	0
11	SV	1476	0	1501	64	0
12	SW	1479	0	1556	70	0
13	SC	754	0	725	45	0
14	SX	1142	0	1209	41	0
15	SD	875	0	878	45	0
16	SY	1192	0	1255	39	0
17	SZ	923	0	948	40	0
18	SF	1105	0	1166	54	0
19	SG	948	0	990	51	0
20	SH	1188	0	1218	58	0
21	SI	1112	0	1124	68	0
22	SJ	797	0	863	34	0
23	Sa	673	0	662	30	0
24	Sb	1021	0	1060	34	0
25	Sc	1121	0	1196	37	0
26	Sd	1032	0	1044	53	0
27	Se	765	0	814	29	0
28	Sf	610	0	633	16	0
29	SM	443	0	436	26	0
30	Sg	451	0	494	18	0
31	SN	556	0	552	34	0
32	SO	2383	0	2332	113	0
33	SL	491	0	524	19	0
34	AA	737	0	799	30	0
35	A	68091	0	34217	1597	0
36	B	2579	0	1304	86	0
37	C	3353	0	1695	72	0
38	LD	1899	0	1957	73	0
39	LE	3079	0	3158	109	0
40	LF	2749	0	2863	84	0
41	LG	2351	0	2294	85	0
42	LH	1307	0	1377	33	0
43	LI	1784	0	1862	59	0
44	LJ	1804	0	1877	57	0
45	LK	1508	0	1572	48	0
46	LL	1764	0	1804	68	0
47	LM	1346	0	1370	61	0
48	LN	1543	0	1608	69	0
49	LO	1053	0	1149	31	0
50	LP	1720	0	1779	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	LQ	1555	0	1659	43	0
52	LR	1416	0	1433	43	0
53	LS	1441	0	1543	58	0
54	LT	1515	0	1606	52	0
55	LU	1437	0	1475	53	0
56	LV	1272	0	1312	68	0
57	LW	796	0	812	25	0
58	LX	1003	0	1048	36	0
59	LY	528	0	546	20	0
60	LZ	964	0	1025	30	0
61	La	984	0	1075	22	0
62	Lb	1080	0	1122	30	0
63	Lc	1169	0	1211	51	0
64	Ld	462	0	491	19	0
65	Le	737	0	792	27	0
66	Lf	876	0	912	21	0
67	Lg	1017	0	1081	33	0
68	Lh	850	0	880	23	0
69	Li	880	0	945	31	0
70	Lj	969	0	1078	30	0
71	Lk	766	0	844	32	0
72	Ll	645	0	649	26	0
73	Lm	612	0	682	36	0
74	Ln	436	0	475	19	0
75	Lo	410	0	446	10	0
76	Lp	229	0	273	10	0
77	Lq	824	0	892	32	0
78	Lr	694	0	738	17	0
79	Ls	1081	0	1071	38	0
80	z	480	0	505	13	0
81	m	1611	0	817	47	0
82	n	1606	0	817	36	0
83	D	213	0	109	1	0
84	E	1051	0	241	12	0
85	A	20	0	23	3	0
All	All	205193	0	150707	5386	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

The worst 5 of 5386 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
82:n:16:U:O3'	82:n:18:G:P	2.12	1.07
1:2:699:U:H3	1:2:739:G:H1	1.11	0.99
1:2:225:A:N6	1:2:837:G:N3	2.14	0.96
11:SV:152:ILE:HD12	14:SX:24:LYS:HE2	1.47	0.94
1:2:647:G:H22	1:2:687:G:H1	1.15	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	SP	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
3	SQ	222/232 (96%)	208 (94%)	14 (6%)	0	100	100
4	SE	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
5	SR	214/216 (99%)	207 (97%)	6 (3%)	1 (0%)	24	58
6	SA	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
7	SS	256/258 (99%)	236 (92%)	20 (8%)	0	100	100
8	SB	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
9	ST	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
10	SU	182/184 (99%)	173 (95%)	8 (4%)	1 (0%)	24	58
11	SV	183/187 (98%)	174 (95%)	9 (5%)	0	100	100
12	SW	182/184 (99%)	177 (97%)	5 (3%)	0	100	100
13	SC	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
14	SX	140/142 (99%)	125 (89%)	15 (11%)	0	100	100
15	SD	119/121 (98%)	106 (89%)	12 (10%)	1 (1%)	16	48
16	SY	148/150 (99%)	138 (93%)	10 (7%)	0	100	100
17	SZ	125/127 (98%)	121 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	SF	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
19	SG	117/125 (94%)	110 (94%)	7 (6%)	0	100	100
20	SH	143/145 (99%)	140 (98%)	3 (2%)	0	100	100
21	SI	141/143 (99%)	138 (98%)	3 (2%)	0	100	100
22	SJ	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
23	Sa	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
24	Sb	127/129 (98%)	120 (94%)	7 (6%)	0	100	100
25	Sc	142/144 (99%)	137 (96%)	5 (4%)	0	100	100
26	Sd	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
27	Se	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
28	Sf	79/81 (98%)	75 (95%)	4 (5%)	0	100	100
29	SM	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
30	Sg	55/57 (96%)	46 (84%)	9 (16%)	0	100	100
31	SN	71/73 (97%)	61 (86%)	10 (14%)	0	100	100
32	SO	310/312 (99%)	289 (93%)	21 (7%)	0	100	100
33	SL	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
34	AA	91/102 (89%)	78 (86%)	12 (13%)	1 (1%)	11	42
38	LD	249/251 (99%)	231 (93%)	18 (7%)	0	100	100
39	LE	384/386 (100%)	364 (95%)	20 (5%)	0	100	100
40	LF	359/361 (99%)	344 (96%)	15 (4%)	0	100	100
41	LG	292/294 (99%)	281 (96%)	11 (4%)	0	100	100
42	LH	163/175 (93%)	152 (93%)	11 (7%)	0	100	100
43	LI	220/222 (99%)	213 (97%)	7 (3%)	0	100	100
44	LJ	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
45	LK	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
46	LL	216/218 (99%)	202 (94%)	13 (6%)	1 (0%)	24	58
47	LM	167/169 (99%)	159 (95%)	8 (5%)	0	100	100
48	LN	191/193 (99%)	174 (91%)	16 (8%)	1 (0%)	24	58
49	LO	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
50	LP	201/203 (99%)	189 (94%)	12 (6%)	0	100	100
51	LQ	195/197 (99%)	190 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	LR	181/183 (99%)	168 (93%)	13 (7%)	0	100	100
53	LS	183/185 (99%)	168 (92%)	14 (8%)	1 (0%)	24	58
54	LT	186/188 (99%)	183 (98%)	3 (2%)	0	100	100
55	LU	169/171 (99%)	158 (94%)	11 (6%)	0	100	100
56	LV	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
57	LW	98/100 (98%)	86 (88%)	12 (12%)	0	100	100
58	LX	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
59	LY	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
60	LZ	119/121 (98%)	112 (94%)	7 (6%)	0	100	100
61	La	123/125 (98%)	122 (99%)	1 (1%)	0	100	100
62	Lb	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
63	Lc	146/148 (99%)	134 (92%)	11 (8%)	1 (1%)	18	52
64	Ld	56/58 (97%)	50 (89%)	6 (11%)	0	100	100
65	Le	94/96 (98%)	94 (100%)	0	0	100	100
66	Lf	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
67	Lg	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
68	Lh	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
69	Li	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
70	Lj	117/119 (98%)	112 (96%)	3 (3%)	2 (2%)	7	33
71	Lk	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
72	Ll	79/81 (98%)	74 (94%)	5 (6%)	0	100	100
73	Lm	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
74	Ln	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
75	Lo	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
76	Lp	23/25 (92%)	23 (100%)	0	0	100	100
77	Lq	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
78	Lr	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
79	Ls	140/157 (89%)	129 (92%)	11 (8%)	0	100	100
80	z	55/588 (9%)	53 (96%)	2 (4%)	0	100	100
All	All	11120/11853 (94%)	10531 (95%)	579 (5%)	10 (0%)	49	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	AA	40	VAL
48	LN	47	ALA
15	SD	86	VAL
63	Lc	40	HIS
5	SR	174	ARG

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	
2	SP	170/173 (98%)	170 (100%)	0	100	100
3	SQ	200/205 (98%)	200 (100%)	0	100	100
4	SE	95/98 (97%)	95 (100%)	0	100	100
5	SR	175/175 (100%)	175 (100%)	0	100	100
6	SA	182/182 (100%)	182 (100%)	0	100	100
7	SS	220/220 (100%)	219 (100%)	1 (0%)	81	84
8	SB	172/173 (99%)	171 (99%)	1 (1%)	78	83
9	ST	189/195 (97%)	187 (99%)	2 (1%)	65	77
10	SU	163/165 (99%)	162 (99%)	1 (1%)	78	83
11	SV	148/149 (99%)	148 (100%)	0	100	100
12	SW	156/157 (99%)	156 (100%)	0	100	100
13	SC	78/85 (92%)	78 (100%)	0	100	100
14	SX	126/127 (99%)	126 (100%)	0	100	100
15	SD	88/98 (90%)	88 (100%)	0	100	100
16	SY	127/127 (100%)	127 (100%)	0	100	100
17	SZ	90/96 (94%)	90 (100%)	0	100	100
18	SF	117/117 (100%)	117 (100%)	0	100	100
19	SG	101/113 (89%)	101 (100%)	0	100	100
20	SH	127/128 (99%)	127 (100%)	0	100	100
21	SI	115/115 (100%)	113 (98%)	2 (2%)	53	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	SJ	93/93 (100%)	93 (100%)	0	100	100
23	Sa	71/74 (96%)	71 (100%)	0	100	100
24	Sb	110/110 (100%)	110 (100%)	0	100	100
25	Sc	119/119 (100%)	117 (98%)	2 (2%)	53	72
26	Sd	102/112 (91%)	101 (99%)	1 (1%)	68	78
27	Se	82/83 (99%)	82 (100%)	0	100	100
28	Sf	70/70 (100%)	69 (99%)	1 (1%)	59	75
29	SM	47/47 (100%)	47 (100%)	0	100	100
30	Sg	48/49 (98%)	48 (100%)	0	100	100
31	SN	56/63 (89%)	55 (98%)	1 (2%)	51	72
32	SO	250/257 (97%)	248 (99%)	2 (1%)	73	80
33	SL	55/56 (98%)	55 (100%)	0	100	100
34	AA	76/83 (92%)	76 (100%)	0	100	100
38	LD	190/193 (98%)	190 (100%)	0	100	100
39	LE	321/322 (100%)	319 (99%)	2 (1%)	78	83
40	LF	288/288 (100%)	288 (100%)	0	100	100
41	LG	241/243 (99%)	239 (99%)	2 (1%)	73	80
42	LH	139/154 (90%)	139 (100%)	0	100	100
43	LI	186/186 (100%)	185 (100%)	1 (0%)	81	84
44	LJ	187/191 (98%)	187 (100%)	0	100	100
45	LK	168/171 (98%)	168 (100%)	0	100	100
46	LL	185/185 (100%)	184 (100%)	1 (0%)	81	84
47	LM	145/147 (99%)	144 (99%)	1 (1%)	76	81
48	LN	154/154 (100%)	154 (100%)	0	100	100
49	LO	107/107 (100%)	104 (97%)	3 (3%)	38	65
50	LP	175/175 (100%)	174 (99%)	1 (1%)	78	83
51	LQ	160/160 (100%)	159 (99%)	1 (1%)	78	83
52	LR	138/145 (95%)	137 (99%)	1 (1%)	76	81
53	LS	150/150 (100%)	150 (100%)	0	100	100
54	LT	152/153 (99%)	152 (100%)	0	100	100
55	LU	155/155 (100%)	154 (99%)	1 (1%)	78	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	LV	135/136 (99%)	134 (99%)	1 (1%)	76	81
57	LW	87/87 (100%)	87 (100%)	0	100	100
58	LX	104/104 (100%)	104 (100%)	0	100	100
59	LY	54/57 (95%)	54 (100%)	0	100	100
60	LZ	104/105 (99%)	104 (100%)	0	100	100
61	La	108/108 (100%)	108 (100%)	0	100	100
62	Lb	112/115 (97%)	111 (99%)	1 (1%)	70	79
63	Lc	117/118 (99%)	116 (99%)	1 (1%)	70	79
64	Ld	46/46 (100%)	45 (98%)	1 (2%)	45	69
65	Le	81/81 (100%)	81 (100%)	0	100	100
66	Lf	92/96 (96%)	91 (99%)	1 (1%)	65	77
67	Lg	108/109 (99%)	108 (100%)	0	100	100
68	Lh	90/90 (100%)	90 (100%)	0	100	100
69	Li	95/95 (100%)	95 (100%)	0	100	100
70	Lj	104/104 (100%)	104 (100%)	0	100	100
71	Lk	80/81 (99%)	80 (100%)	0	100	100
72	Ll	67/67 (100%)	67 (100%)	0	100	100
73	Lm	68/68 (100%)	67 (98%)	1 (2%)	57	74
74	Ln	45/45 (100%)	45 (100%)	0	100	100
75	Lo	45/47 (96%)	44 (98%)	1 (2%)	45	69
76	Lp	22/23 (96%)	22 (100%)	0	100	100
77	Lq	87/88 (99%)	86 (99%)	1 (1%)	65	77
78	Lr	71/71 (100%)	71 (100%)	0	100	100
79	Ls	118/132 (89%)	118 (100%)	0	100	100
80	z	52/523 (10%)	51 (98%)	1 (2%)	50	71
All	All	9351/9989 (94%)	9314 (100%)	37 (0%)	81	85

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	LV	127	GLN
77	Lq	100	LYS
62	Lb	86	THR

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Mol	Chain	Res	Type
66	Lf	46	THR
32	SO	109	ASP

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

Mol	Chain	Res	Type
41	LG	151	GLN
50	LP	86	ASN
75	Lo	90	ASN
43	LI	64	GLN
46	LL	113	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1800 (98%)	447 (25%)	60 (3%)
35	A	3180/3394 (93%)	560 (17%)	38 (1%)
36	B	120/121 (99%)	13 (10%)	2 (1%)
37	C	157/158 (99%)	25 (15%)	1 (0%)
81	m	75/76 (98%)	27 (36%)	0
82	n	74/75 (98%)	18 (24%)	0
83	D	9/10 (90%)	4 (44%)	1 (11%)
All	All	5383/5634 (95%)	1094 (20%)	102 (1%)

5 of 1094 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	43	A

5 of 102 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	1636	C
35	A	1097	G
36	B	120	C
1	2	1688	U

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Mol	Chain	Res	Type
35	A	719	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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
79	5CT	Ls	51	79	13,14,15	0.72	0	8,15,17	1.76	2 (25%)

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
79	5CT	Ls	51	79	-	1/13/14/16	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	Ls	51	5CT	C4-C3-C2	-3.76	105.54	113.47
79	Ls	51	5CT	C1-NZ-CE	-2.35	108.24	113.38

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
79	Ls	51	5CT	C2-C3-C4-N1

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
79	Ls	51	5CT	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	$\# Z > 2$
85	3HE	A	3401	-	21,21,21	0.60	0	23,30,30	0.87	0

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
85	3HE	A	3401	-	-	0/8/36/36	0/2/2/2

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.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
85	A	3401	3HE	3	0

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
11	SV	1
82	n	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	SV	123:LYS	C	135:LYS	N	20.35
1	n	16:U	O3'	18:G	P	2.12

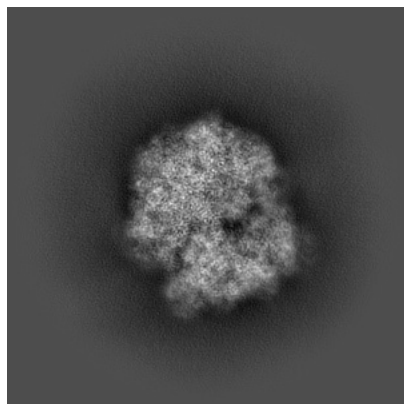
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42525. These allow visual inspection of the internal detail of the map and identification of artifacts.

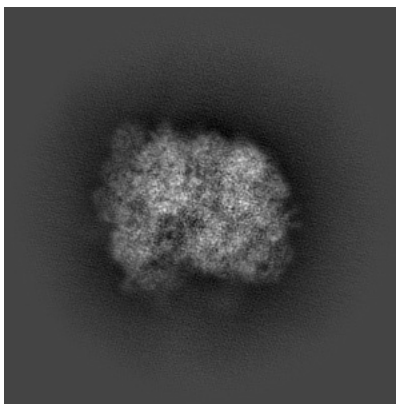
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

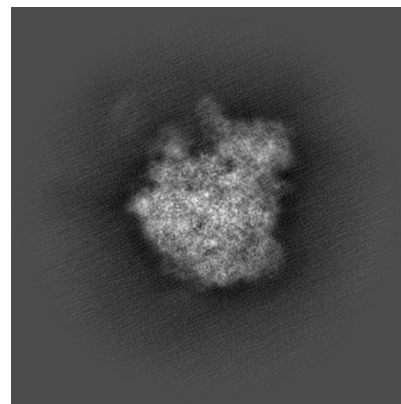
6.1.1 Primary map



X

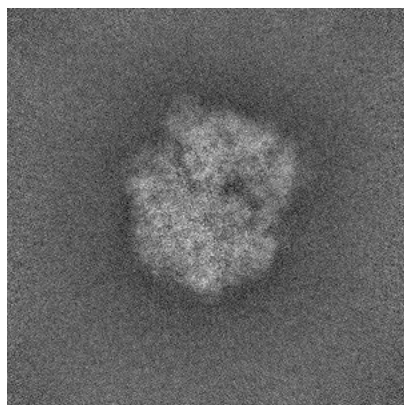


Y

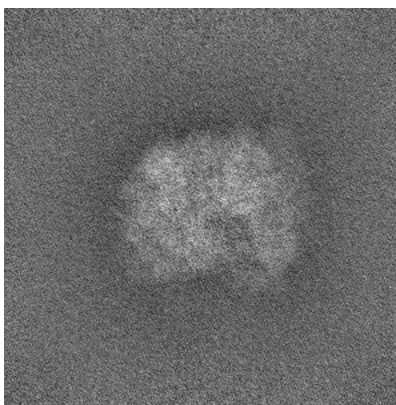


Z

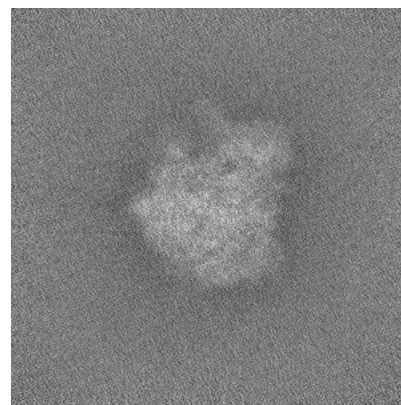
6.1.2 Raw map



X



Y

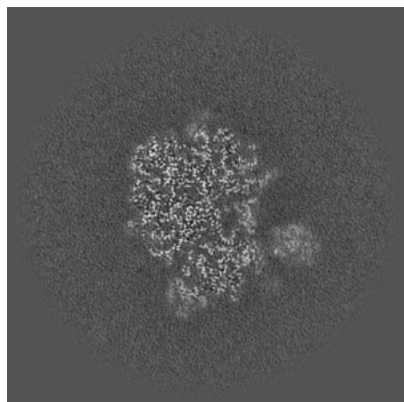


Z

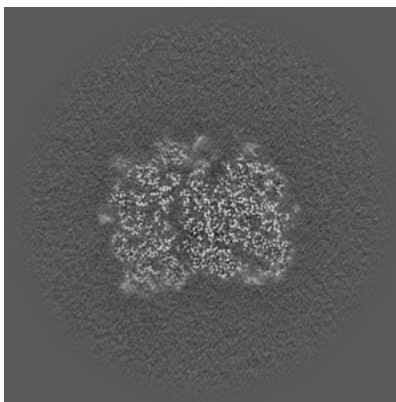
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

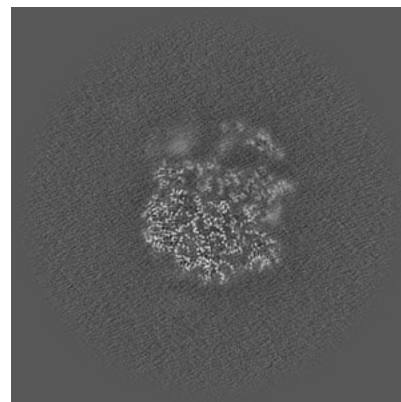
6.2.1 Primary map



X Index: 324

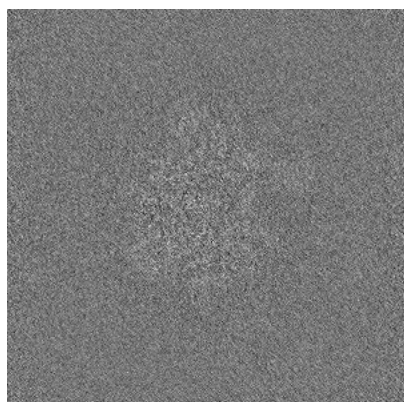


Y Index: 324

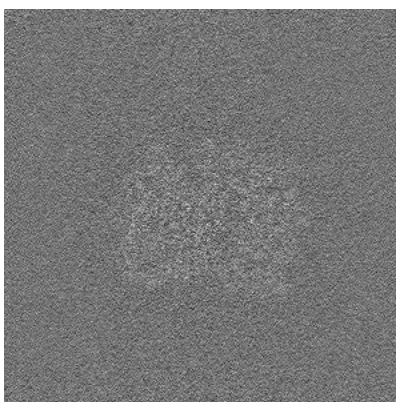


Z Index: 324

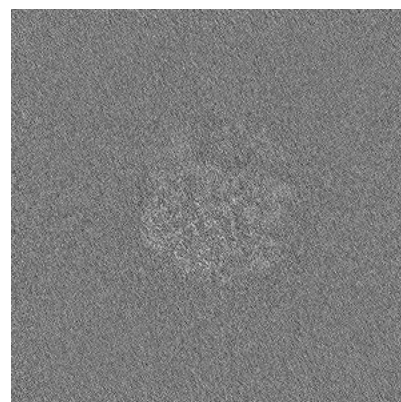
6.2.2 Raw map



X Index: 324



Y Index: 324

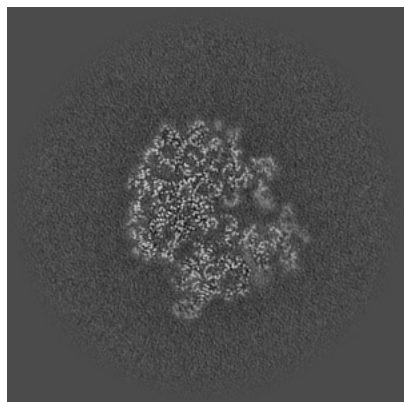


Z Index: 324

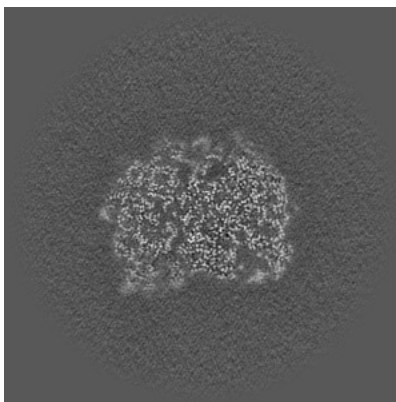
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

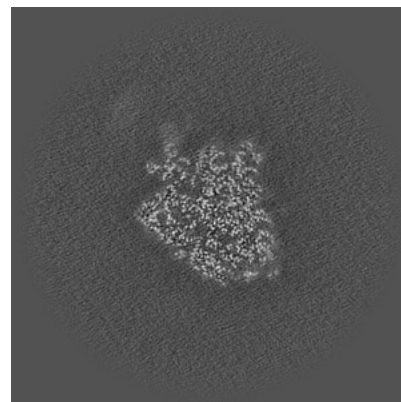
6.3.1 Primary map



X Index: 343

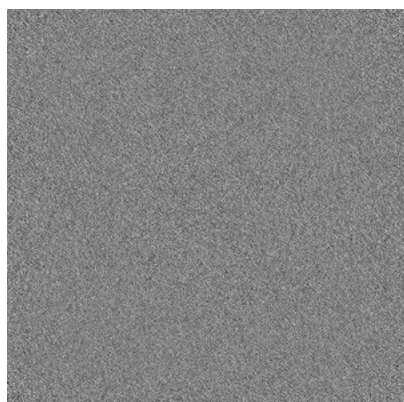


Y Index: 319

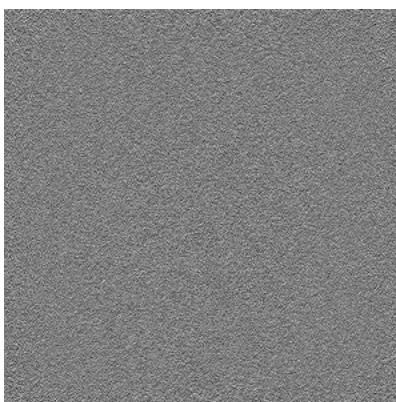


Z Index: 366

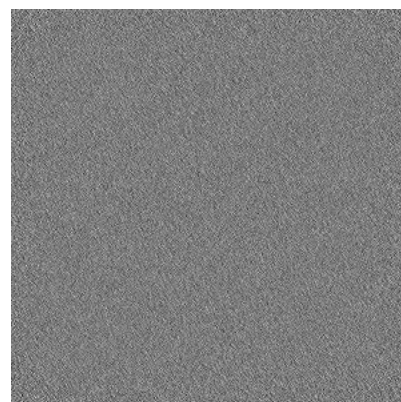
6.3.2 Raw map



X Index: 0



Y Index: 0

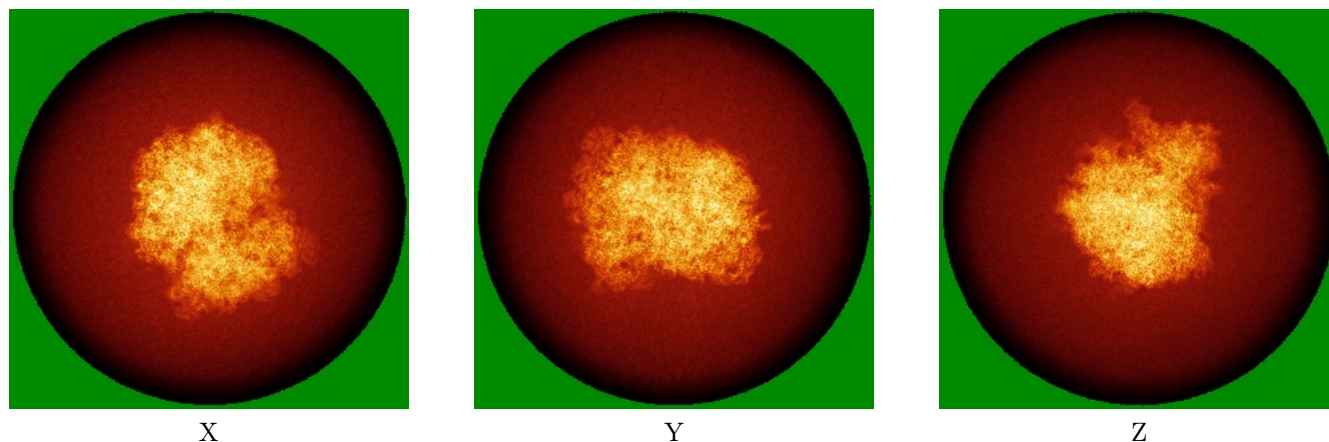


Z Index: 0

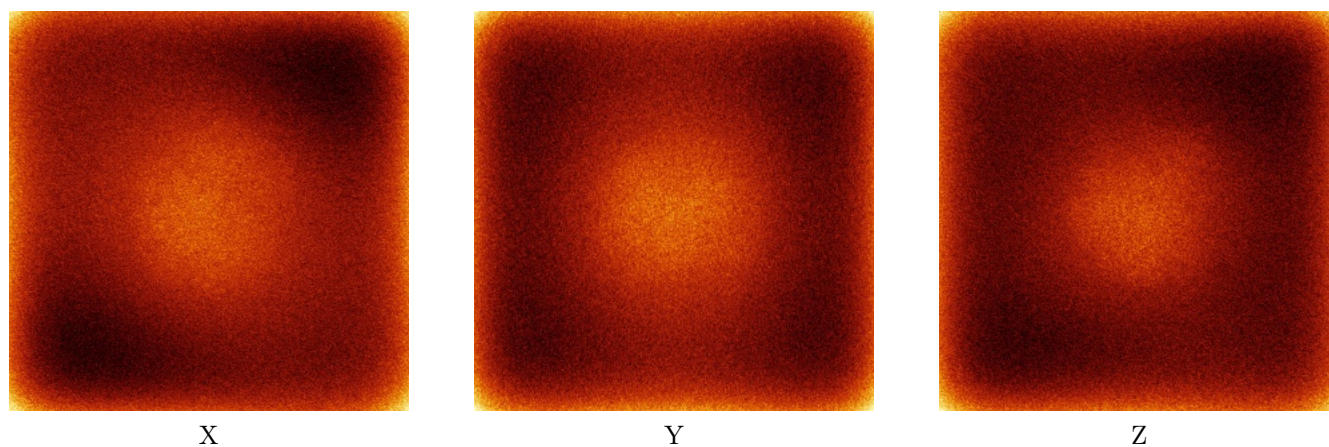
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



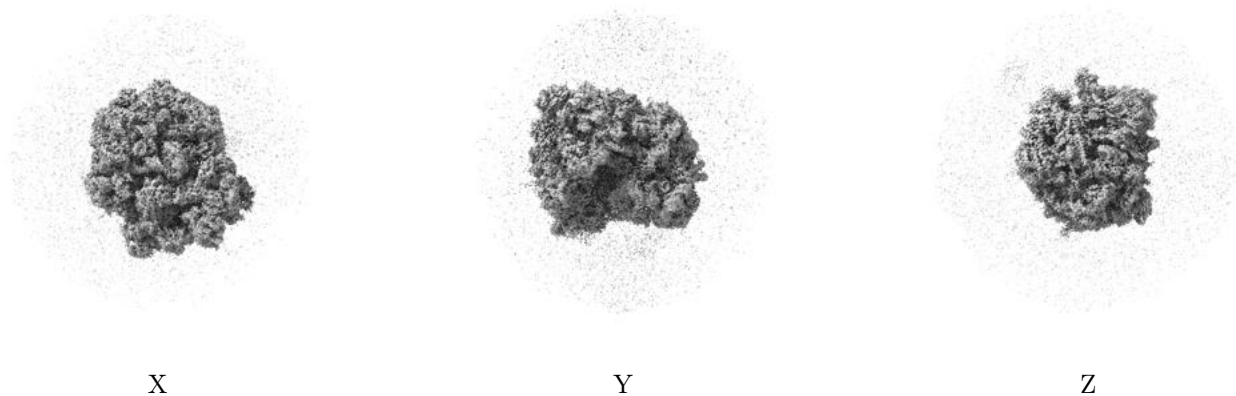
6.4.2 Raw map



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.

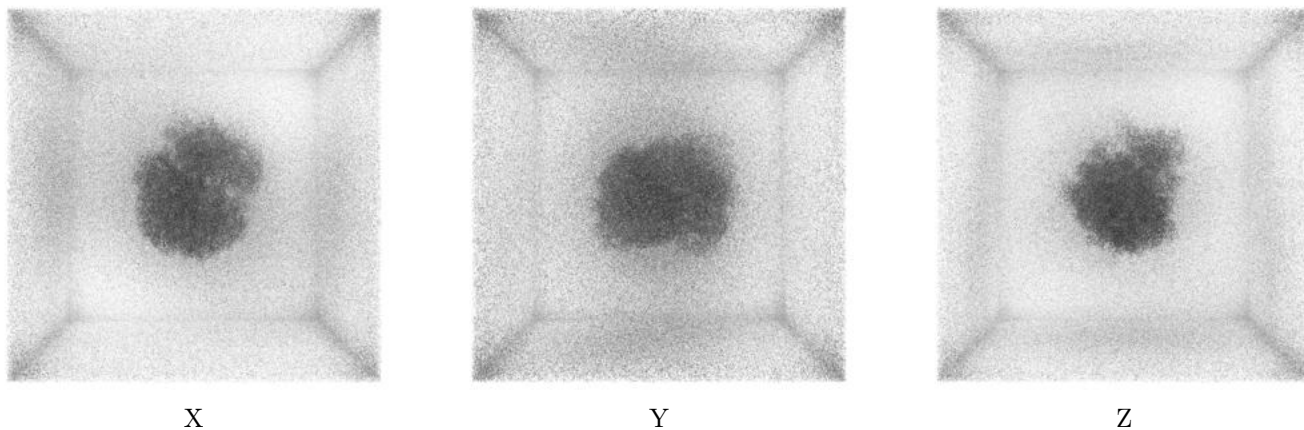
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0875. 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



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.

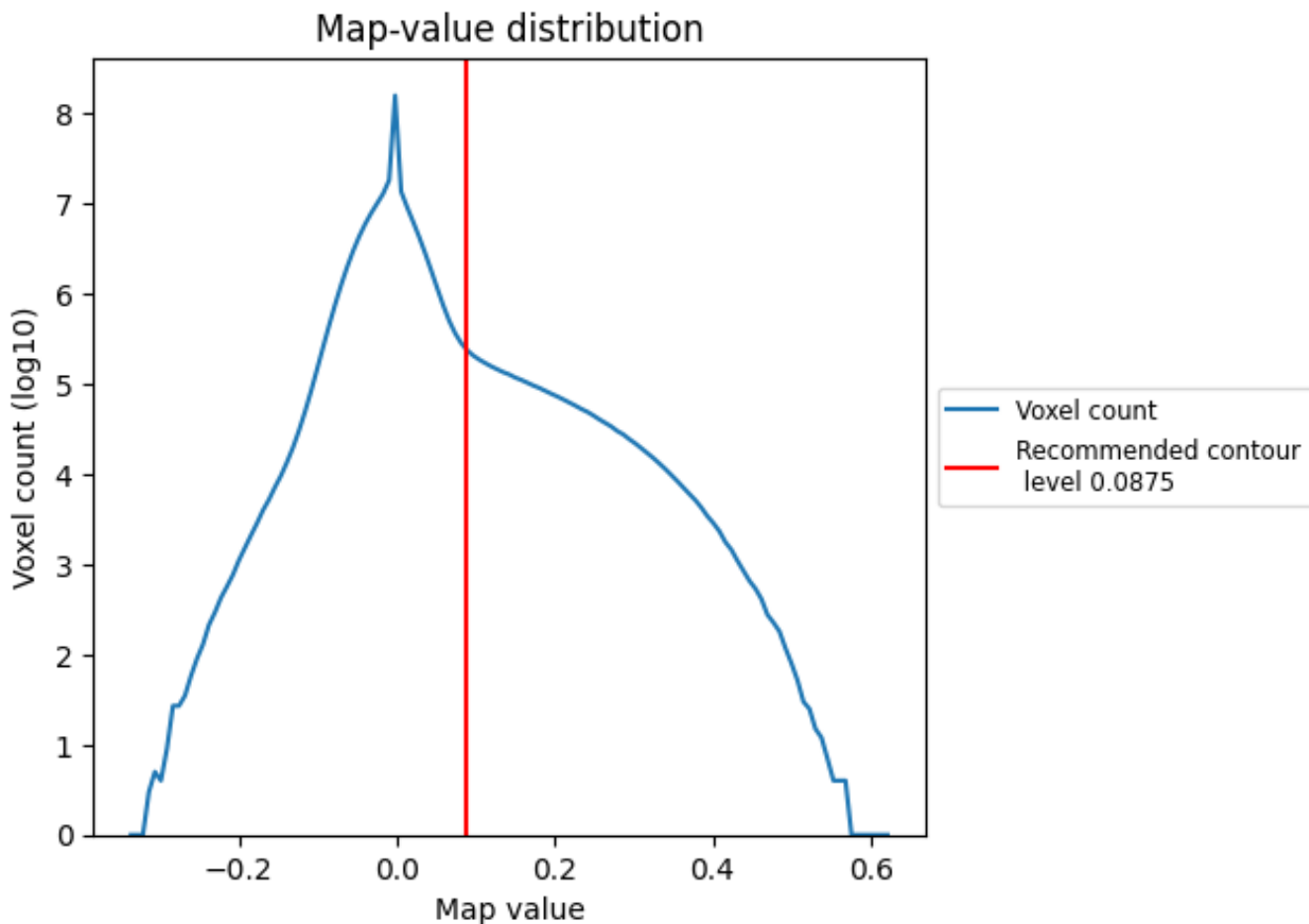
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

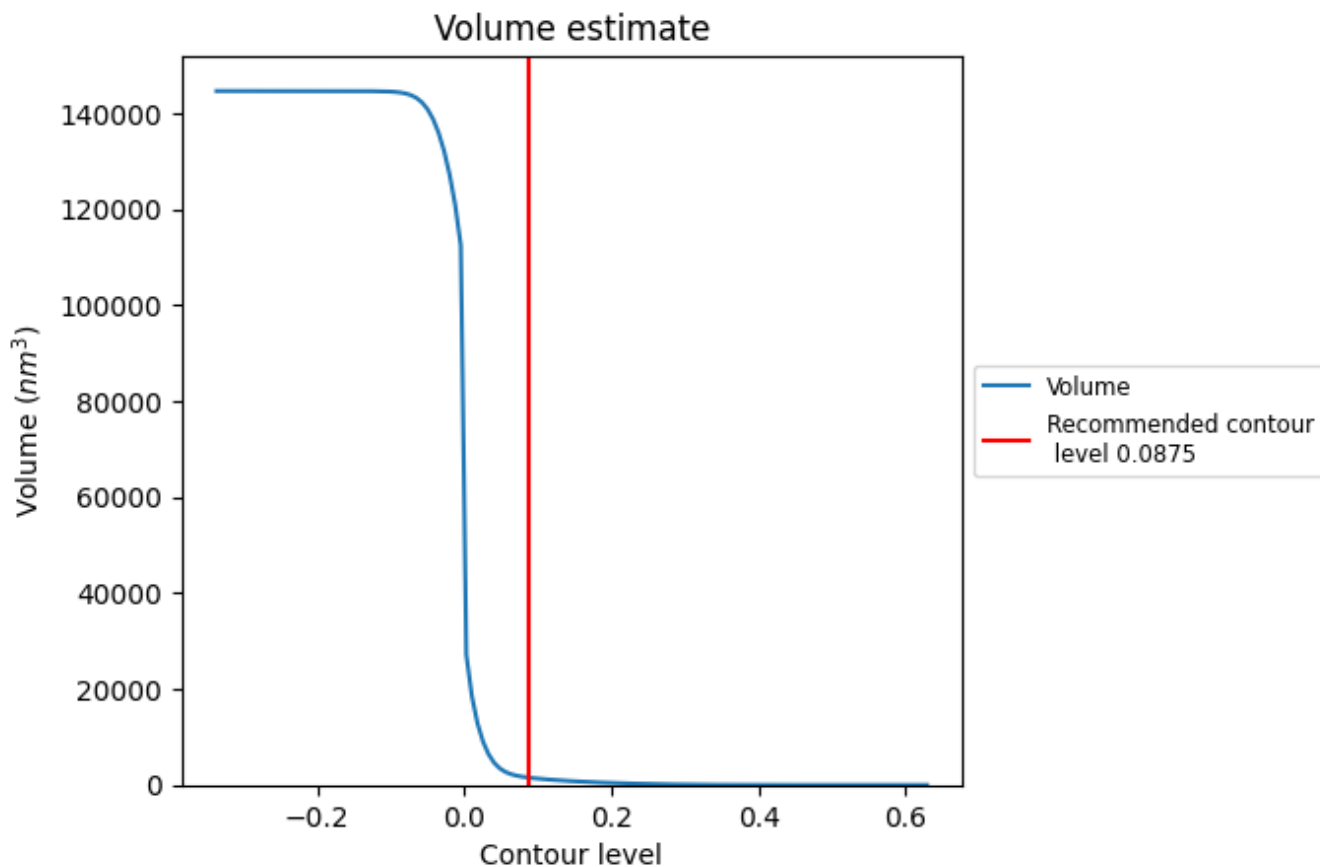
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

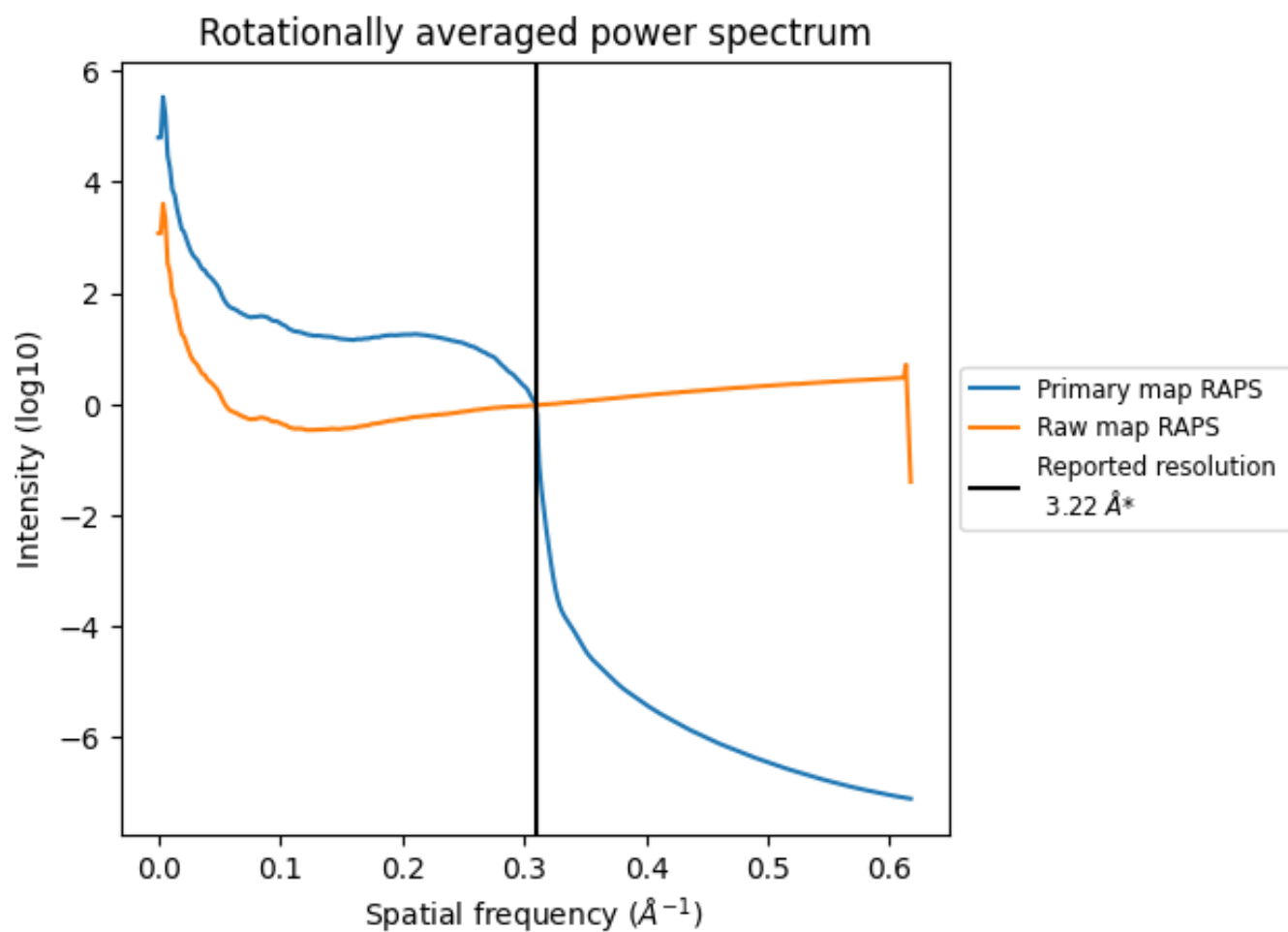
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1531 nm^3 ; this corresponds to an approximate mass of 1383 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

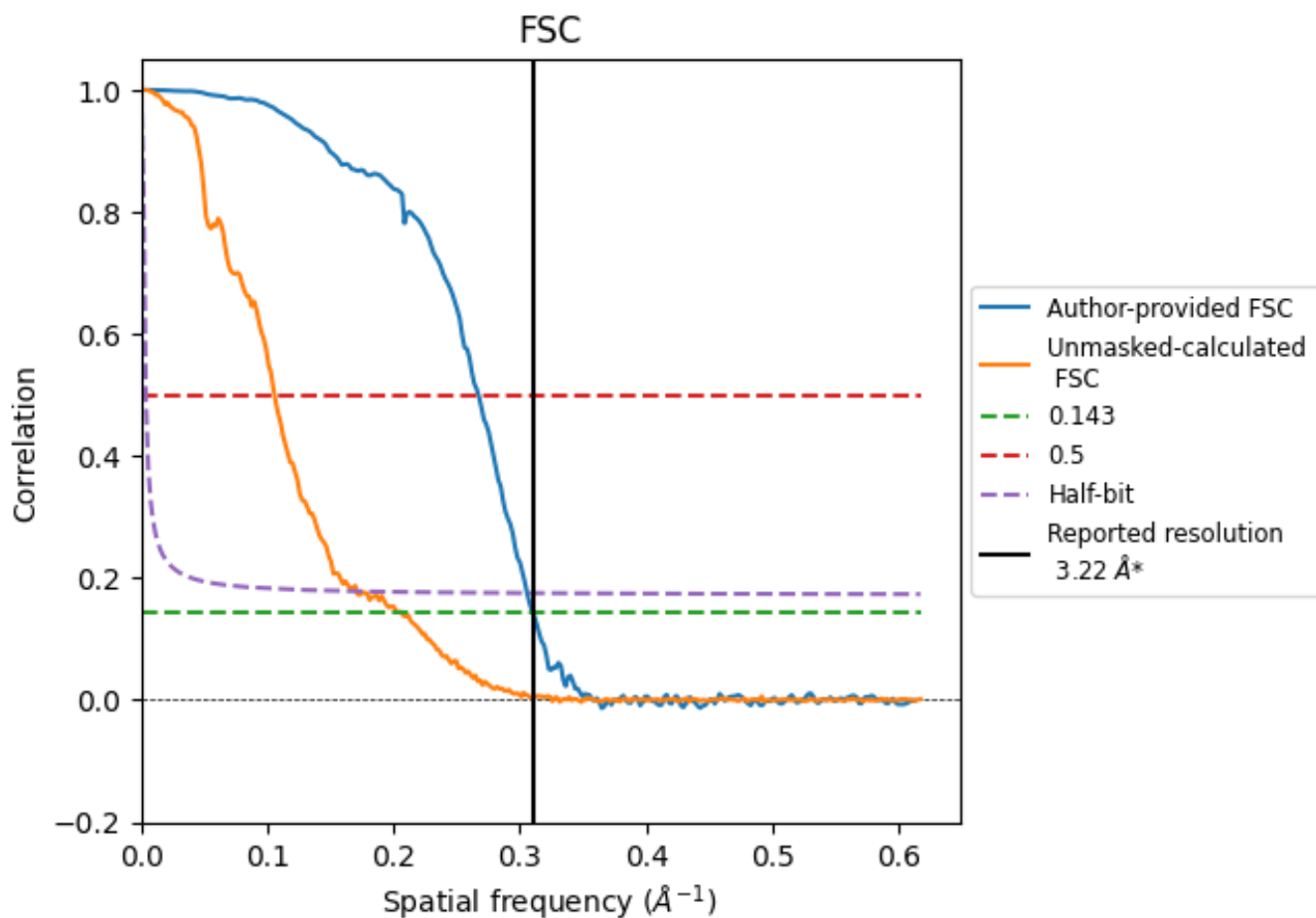


*Reported resolution corresponds to spatial frequency of 0.311 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.311 Å⁻¹

8.2 Resolution estimates [i](#)

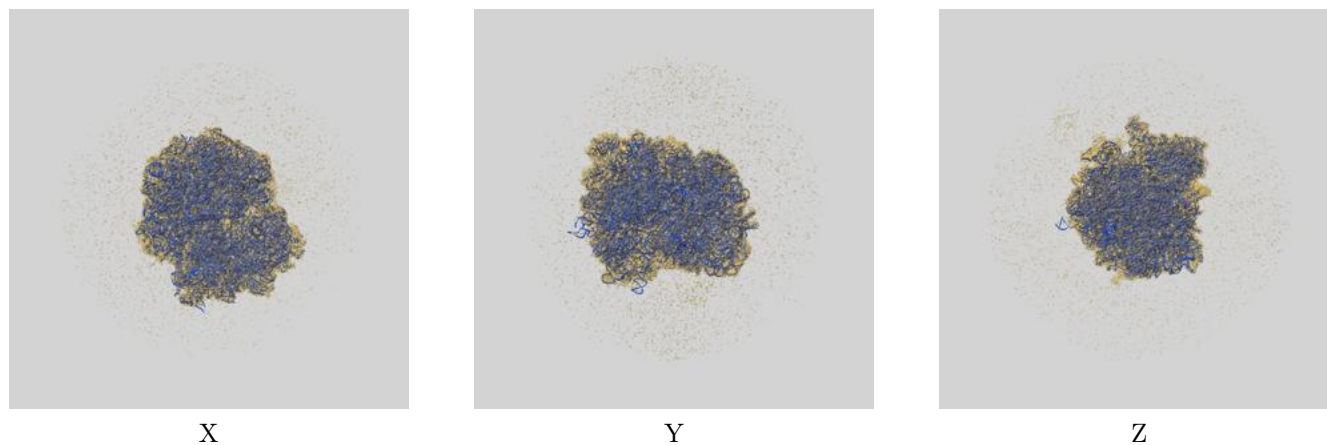
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.22	-	-
Author-provided FSC curve	3.22	3.74	3.27
Unmasked-calculated*	4.85	9.47	5.85

*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 4.85 differs from the reported value 3.22 by more than 10 %

9 Map-model fit [i](#)

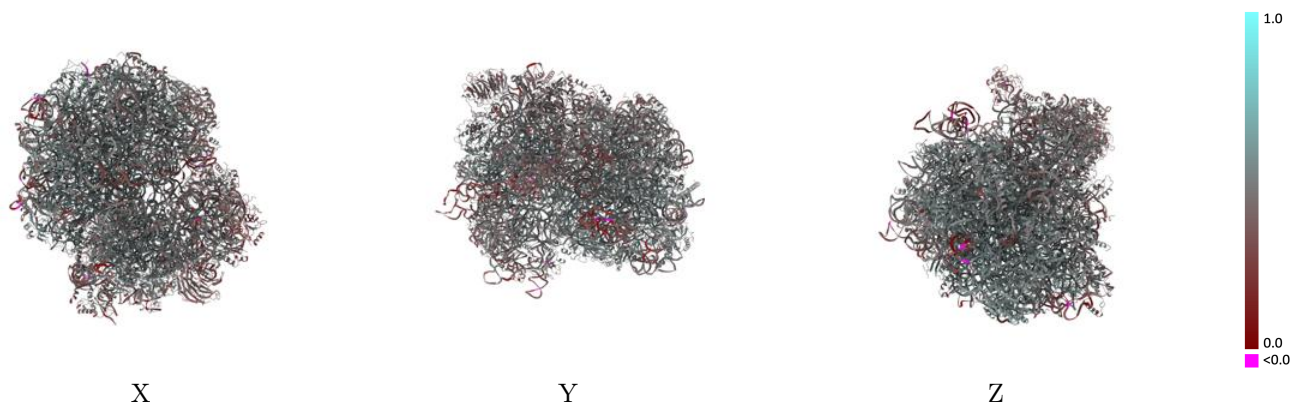
This section contains information regarding the fit between EMDB map EMD-42525 and PDB model 8UT0. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



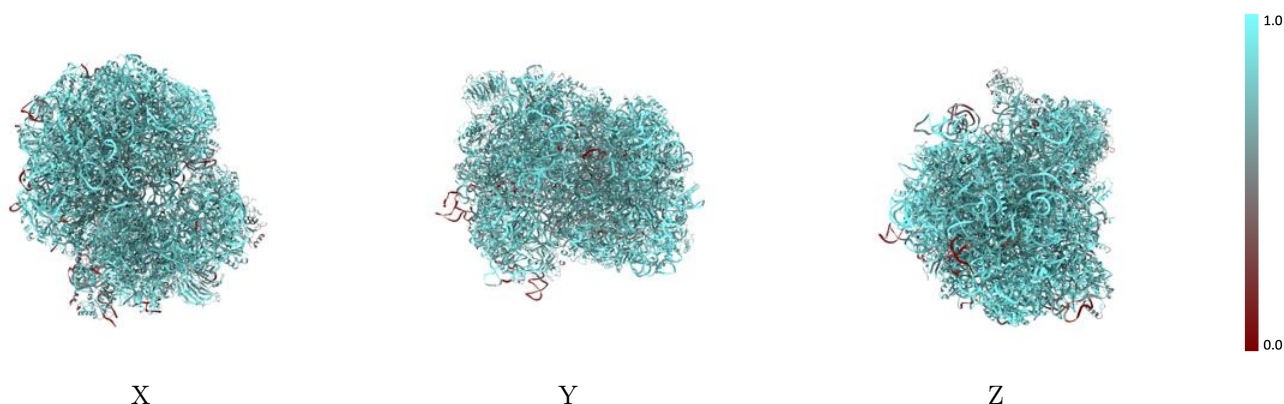
The images above show the 3D surface view of the map at the recommended contour level 0.0875 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



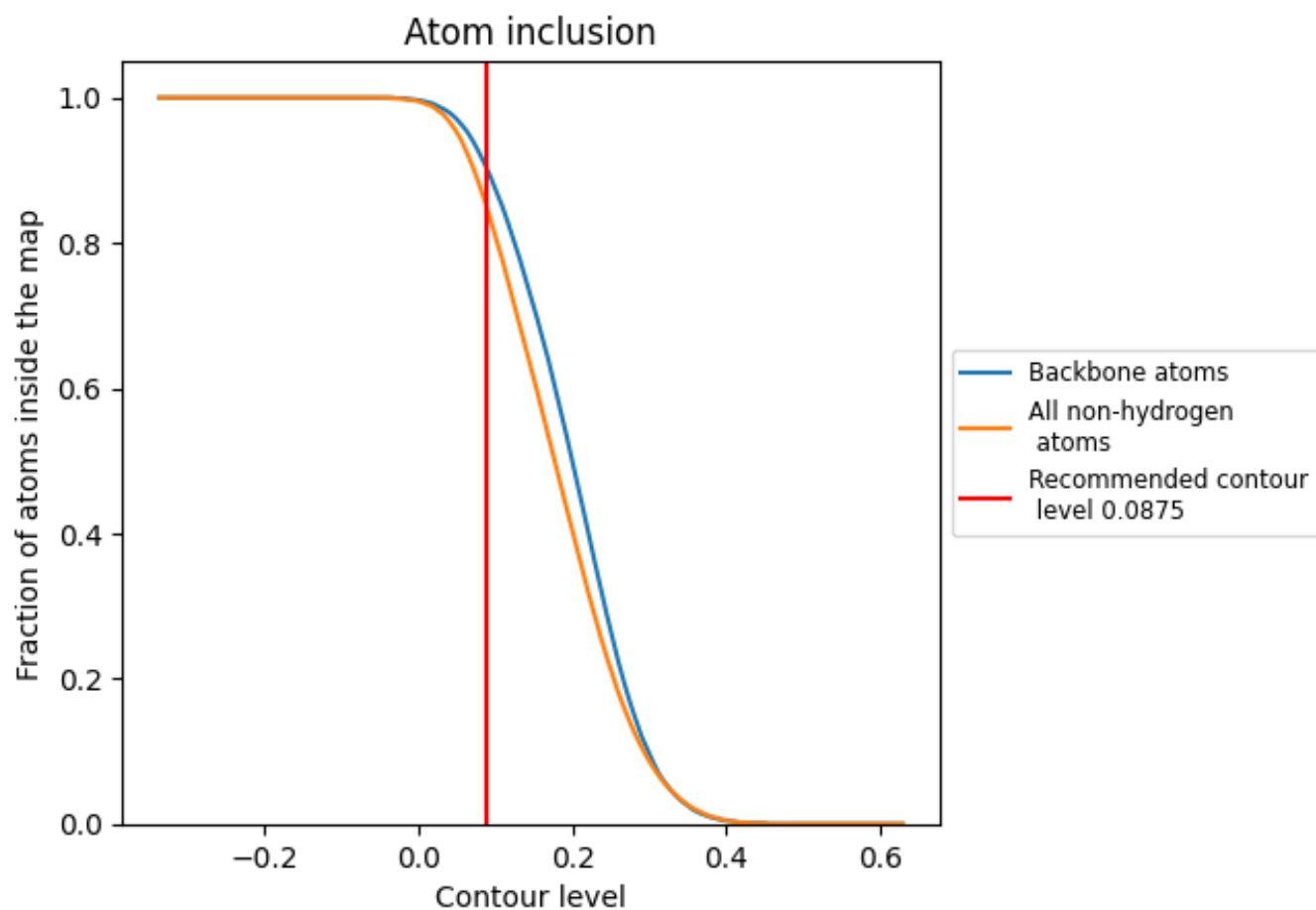
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0875).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 85% 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 (0.0875) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8530	 0.4730
2	 0.8450	 0.4340
A	 0.9010	 0.4750
AA	 0.6400	 0.4220
B	 0.9520	 0.4600
C	 0.9390	 0.5020
D	 0.9110	 0.4860
E	 0.8600	 0.4560
LD	 0.8300	 0.5460
LE	 0.8680	 0.5260
LF	 0.8760	 0.5310
LG	 0.8340	 0.4450
LH	 0.8530	 0.5010
LI	 0.8530	 0.5110
LJ	 0.8140	 0.4870
LK	 0.8370	 0.5030
LL	 0.7960	 0.5050
LM	 0.7770	 0.4490
LN	 0.8510	 0.5030
LO	 0.8630	 0.5000
LP	 0.8550	 0.5350
LQ	 0.8550	 0.5210
LR	 0.8640	 0.5360
LS	 0.8620	 0.5150
LT	 0.8190	 0.5110
LU	 0.8380	 0.5140
LV	 0.8190	 0.5020
LW	 0.8170	 0.4740
LX	 0.7760	 0.5250
LY	 0.8380	 0.5390
LZ	 0.8540	 0.5340
La	 0.8940	 0.5420
Lb	 0.8740	 0.5130
Lc	 0.8720	 0.5170
Ld	 0.7720	 0.4920



















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Chain	Atom inclusion	Q-score
Le	 0.8620	 0.5100
Lf	 0.8620	 0.5190
Lg	 0.8610	 0.5460
Lh	 0.8500	 0.5440
Li	 0.8310	 0.5290
Lj	 0.8800	 0.5300
Lk	 0.7920	 0.4610
Ll	 0.9030	 0.5570
Lm	 0.8280	 0.5030
Ln	 0.9040	 0.5580
Lo	 0.8310	 0.5370
Lp	 0.5480	 0.4930
Lq	 0.8100	 0.4980
Lr	 0.8010	 0.5430
Ls	 0.6590	 0.4950
SA	 0.7580	 0.4660
SB	 0.7050	 0.4290
SC	 0.8310	 0.4390
SD	 0.5530	 0.2860
SE	 0.7620	 0.4310
SF	 0.7910	 0.4420
SG	 0.7850	 0.4390
SH	 0.7890	 0.4460
SI	 0.8060	 0.4300
SJ	 0.7520	 0.4340
SL	 0.7150	 0.4370
SM	 0.8590	 0.4830
SN	 0.5560	 0.3040
SO	 0.7630	 0.3940
SP	 0.8380	 0.4860
SQ	 0.7510	 0.4650
SR	 0.8260	 0.5180
SS	 0.8140	 0.4960
ST	 0.7730	 0.4350
SU	 0.7720	 0.4520
SV	 0.7720	 0.4740
SW	 0.8180	 0.4810
SX	 0.8030	 0.5080
SY	 0.8170	 0.5020
SZ	 0.7740	 0.4770
Sa	 0.8620	 0.5140
Sb	 0.8440	 0.5310

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Chain	Atom inclusion	Q-score
Sc	 0.7810	 0.5350
Sd	 0.8010	 0.4560
Se	 0.8420	 0.5050
Sf	 0.8290	 0.4820
Sg	 0.7630	 0.4830
m	 0.8410	 0.3990
n	 0.8410	 0.4460
z	 0.7630	 0.4980