



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 12:57 PM UTC

PDB ID : 7ZW0 / pdb_00007zw0
EMDB ID : EMD-14990
Title : FAP-80S Complex - Rotated state
Authors : Ikeuchi, K.; Buschauer, R.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2022-05-17
Resolution : 2.40 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:

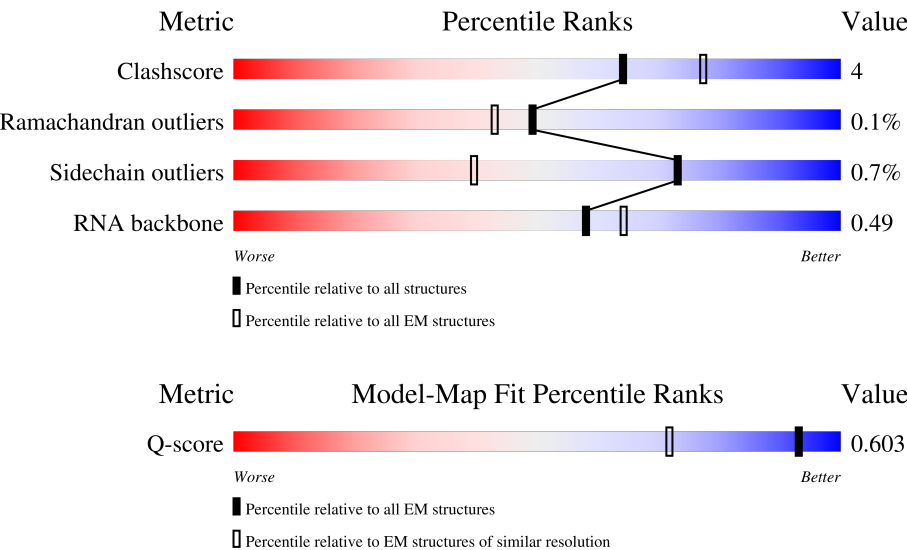
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.40 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	5628 (1.90 - 2.90)

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	LA	3396	
2	LB	217	
3	2	1800	

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Mol	Chain	Length	Quality of chain
4	sP	252	
5	sQ	255	
6	sE	142	
7	sR	254	
8	sA	240	
9	sS	261	
10	sB	225	
11	sT	236	
12	sU	190	
13	sV	200	
14	sW	197	
15	sC	105	
16	sX	156	
17	sD	143	
18	sY	151	
19	sZ	137	
20	sF	143	
21	sG	136	
22	sH	146	
23	sI	144	
24	sJ	121	
25	sa	87	
26	sb	130	
27	sc	145	
28	sd	135	

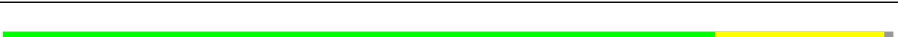
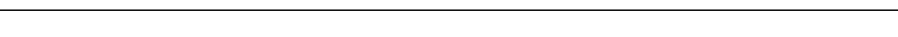
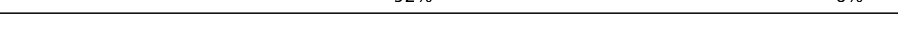
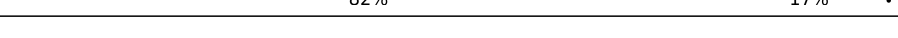
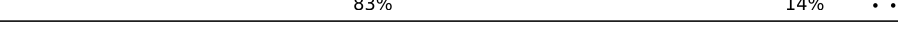
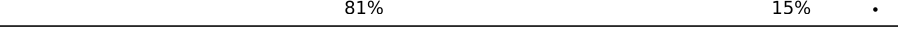
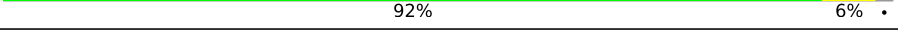
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Mol	Chain	Length	Quality of chain
29	sK	108	
30	se	119	
31	sf	82	
32	sM	56	
33	sg	63	
34	sN	76	
35	sO	319	
36	sL	67	
37	sj	235	
38	sk	114	
39	sm	29	
40	sl	76	
40	sn	76	
41	LC	121	
42	LD	158	
43	LE	254	
44	LF	387	
45	LG	362	
46	LH	297	
47	LI	176	
48	LJ	244	
49	LK	256	
50	LL	191	
51	LM	221	
52	LN	174	

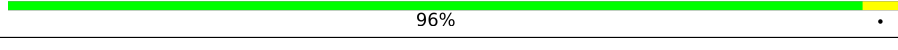
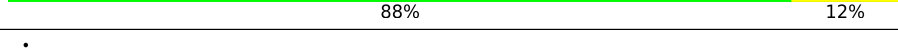
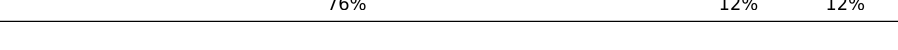
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Mol	Chain	Length	Quality of chain
53	LO	199	 86% 11% .
54	LP	138	 92% 6% ..
55	LQ	204	 90% 9%
56	LR	199	 89% 10% .
57	LS	184	 90% 9% .
58	LT	186	 90% 9% .
59	LU	189	 86% 14% .
60	LV	172	 87% 13% .
61	LW	160	 91% 8% .
62	LX	121	 74% 8% 17%
63	LY	137	 80% 19% .
64	LZ	155	 7% 76% 5% 19%
65	La	142	 71% 14% 15%
66	Lb	127	 92% 6% .
67	Lc	136	 82% 17% .
68	Ld	149	 91% 8% .
69	Le	59	 83% 14% ..
70	Lf	105	 78% 13% 9%
71	Lg	113	 81% 15% .
72	Lh	130	 92% 6% .
73	Li	107	 91% 8% .
74	Lj	121	 84% 8% 7%
75	Lk	120	 90% 9% .
76	Ll	100	 91% 8% .
77	Lm	88	 84% 8% 8%

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Mol	Chain	Length	Quality of chain
78	Ln	78	
79	Lo	51	
80	Lp	52	
81	Lq	25	
81	Lt	25	
82	Lr	106	
83	Ls	92	
84	sh	965	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
87	ZN	sh	1004	-	-	X	-
87	ZN	sh	1015	-	-	X	-

2 Entry composition

There are 87 unique types of molecules in this entry. The entry contains 214001 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 25S ribosomal RNA (RDN25-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	3217	Total	C	N	O	P	0	0
			68809	30735	12400	22457	3217		

- Molecule 2 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	LB	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 3 is a RNA chain called 18S ribosomal RNA (RDN18-1).

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	1765	Total	C	N	O	P	0	0
			37614	16816	6663	12370	1765		

- Molecule 4 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 6 is a protein called RPS15 isoform 1.

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

- Molecule 7 is a protein called 40S ribosomal protein S2.

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

- Molecule 8 is a protein called 40S ribosomal protein S3.

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

- Molecule 9 is a protein called 40S ribosomal protein S4-B.

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

- Molecule 10 is a protein called 40S ribosomal protein S5.

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

- Molecule 11 is a protein called 40S ribosomal protein S6-B.

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

- Molecule 12 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	sC	92	Total	C	N	O	S	0	0
			752	487	122	141	2		

- Molecule 16 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 17 is a protein called 40S ribosomal protein S12.

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

- Molecule 18 is a protein called 40S ribosomal protein S13.

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

- Molecule 19 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	sG	125	Total	C	N	O	S	0	0
			979	613	187	177	2		

- Molecule 22 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S20.

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

- Molecule 25 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	sd	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 29 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	sK	70	Total	C	N	O	0	0
			563	360	104	99		

- Molecule 30 is a protein called 40S ribosomal protein S26-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 32 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	sM	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 33 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	sg	58	Total	C	N	O	S	0	0
			451	284	92	74	1		

- Molecule 34 is a protein called 40S ribosomal protein S31.

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

- Molecule 35 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 36 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 37 is a protein called Uncharacterized protein YIL161W.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	sj	135	Total	C	N	O	S	0	0
			1128	725	190	208	5		

- Molecule 38 is a protein called FK506-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	sk	114	Total	C	N	O	S	0	0
			858	548	144	164	2		

- Molecule 39 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	sm	29	Total	C	N	O	P	0	0
			632	286	135	182	29		

- Molecule 40 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	sl	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		
40	sn	76	Total	C	N	O	P	0	0
			1622	721	285	540	76		

- Molecule 41 is a RNA chain called 5S ribosomal RNA (RDN5-1).

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

- Molecule 42 is a RNA chain called 5.8S ribosomal RNA (RDN58-1).

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

- Molecule 43 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LF	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 45 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LG	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 46 is a protein called 60S ribosomal protein L5.

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

- Molecule 47 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	LI	167	Total	C	N	O	0	0
			1307	843	234	230		

- Molecule 48 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	LM	211	Total	C	N	O	S	0	0
			1719	1093	324	296	6		

- Molecule 52 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LN	172	Total	C	N	O	S	0	0
			1365	855	256	250	4		

- Molecule 53 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LO	193	Total	C	N	O	S	0	0
			1543	962	315	266			

- Molecule 54 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LU	188	Total	C	N	O		0	0
			1521	935	326	260			

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

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

- Molecule 61 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	LZ	126	Total	C	N	O	S	0	0
			869	547	174	147	1		

- Molecule 65 is a protein called 60S ribosomal protein L25.

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

- Molecule 66 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 67 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L28.

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

- Molecule 69 is a protein called 60S ribosomal protein L29.

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

- Molecule 70 is a protein called 60S ribosomal protein L30.

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

- Molecule 71 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lh	127	Total	C	N	O	S	0	0
			1013	642	205	165	1		

- Molecule 73 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 75 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 76 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L38.

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

- Molecule 79 is a protein called 60S ribosomal protein L39.

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

- Molecule 80 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 81 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Lq	25	Total	C	N	O	S	0	0
			229	139	62	27	1		
81	Lt	22	Total	C	N	O	S	0	0
			207	127	56	23	1		

- Molecule 82 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 83 is a protein called 60S ribosomal protein L43-A.

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

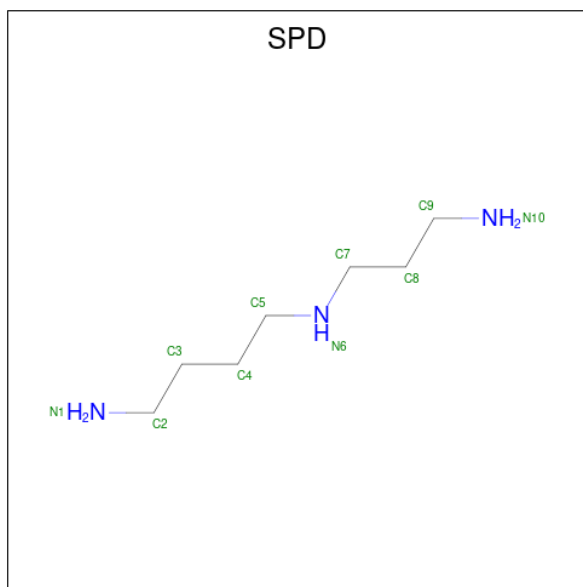
- Molecule 84 is a protein called FAP1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	sh	776	Total	C	N	O	S	0	0
			6024	3719	1092	1108	105		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	LA	220	Total	Mg	0
			220	220	
85	2	87	Total	Mg	0
			87	87	
85	sS	1	Total	Mg	0
			1	1	
85	sB	1	Total	Mg	0
			1	1	
85	sc	1	Total	Mg	0
			1	1	
85	sm	1	Total	Mg	0
			1	1	
85	LC	1	Total	Mg	0
			1	1	
85	LE	2	Total	Mg	0
			2	2	
85	LF	1	Total	Mg	0
			1	1	
85	LQ	1	Total	Mg	0
			1	1	
85	LS	1	Total	Mg	0
			1	1	
85	LU	2	Total	Mg	0
			2	2	
85	LW	1	Total	Mg	0
			1	1	
85	LY	1	Total	Mg	0
			1	1	
85	Lh	1	Total	Mg	0
			1	1	
85	Lj	1	Total	Mg	0
			1	1	
85	Lm	1	Total	Mg	0
			1	1	

- Molecule 86 is SPERMIDINE (CCD ID: SPD) (formula: C₇H₁₉N₃).



Mol	Chain	Residues	Atoms			AltConf
86	LA	1	Total	C	N	0
			10	7	3	

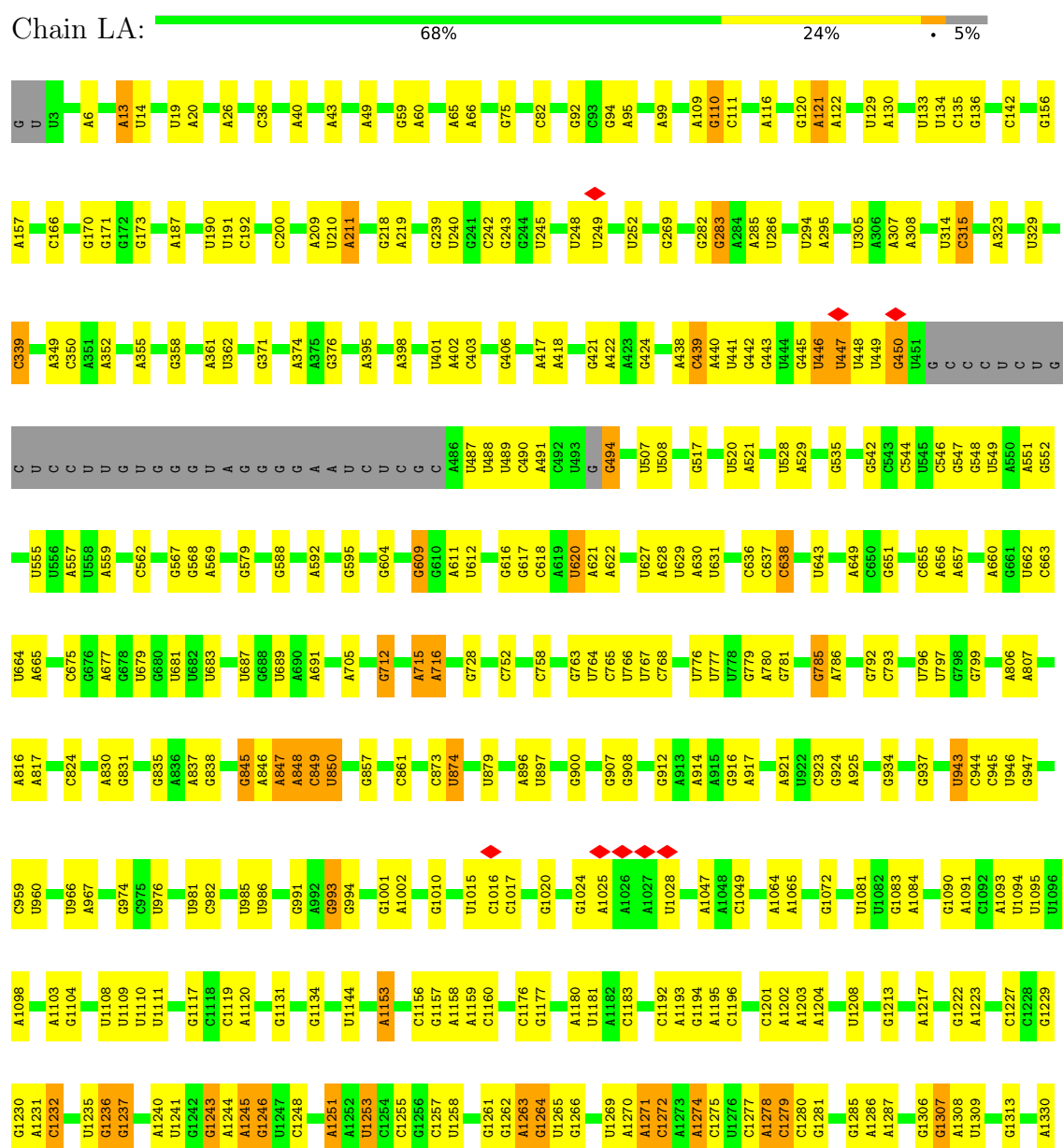
- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
87	sM	1	Total	Zn	0
			1	1	
87	sN	1	Total	Zn	0
			1	1	
87	Lj	1	Total	Zn	0
			1	1	
87	Lm	1	Total	Zn	0
			1	1	
87	Lp	1	Total	Zn	0
			1	1	
87	Lr	1	Total	Zn	0
			1	1	
87	Ls	1	Total	Zn	0
			1	1	
87	sh	27	Total	Zn	0
			27	27	

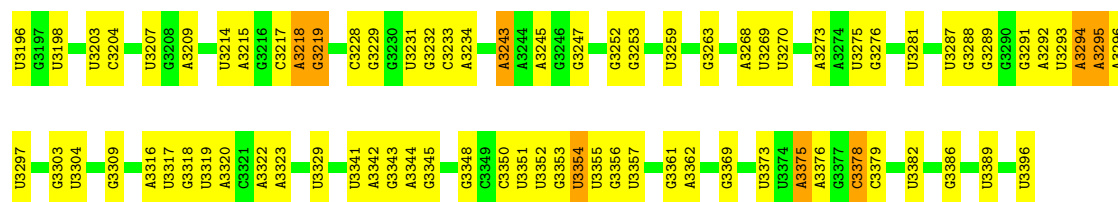
3 Residue-property plots

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.

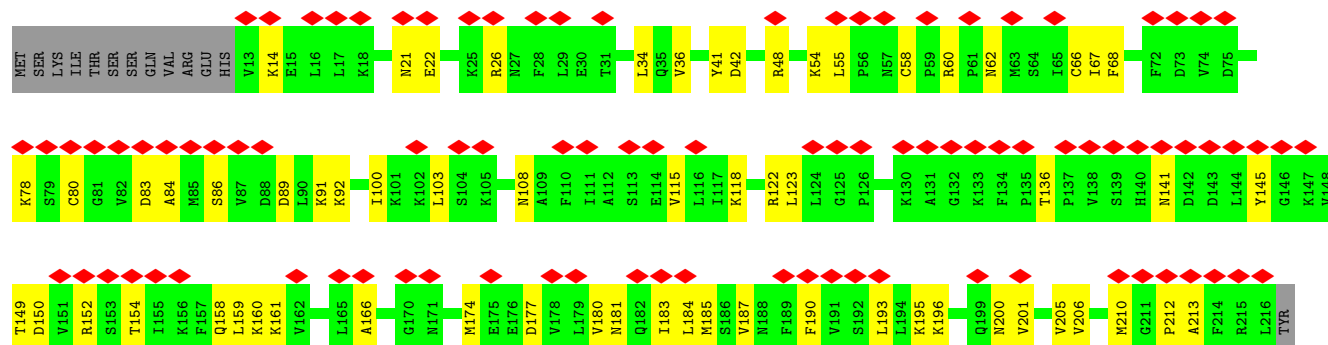
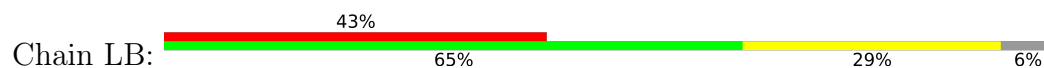
- Molecule 1: 25S ribosomal RNA (RDN25-1)



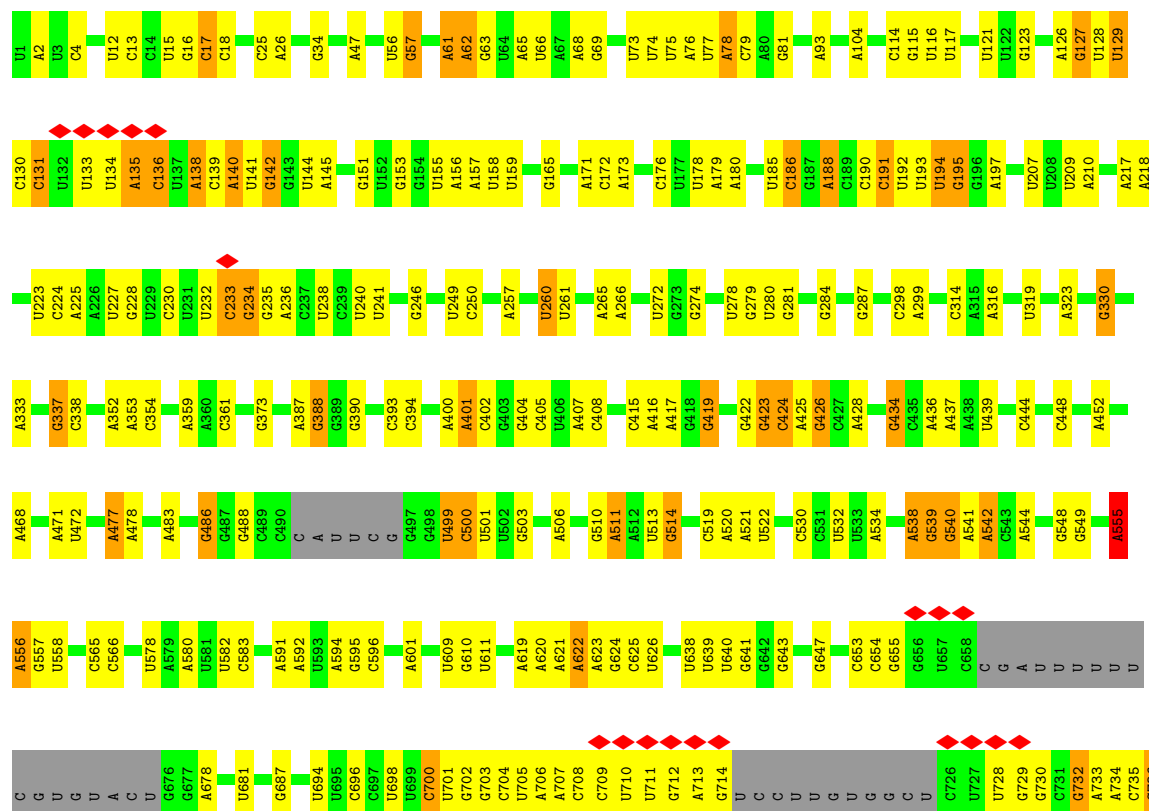
U3068	G2898	U2768	A2637	G2503	C2420	G2273	A2158	U1955	G1952	A1797	G1646	U1554
U3078	C2899	A2769	A2642	U2504	U2426	C2277	U2159	G1953	G1954	A1798	C1657	U1555
U3079	A2900	G2777	U2506	U2505	U2427	C2281	G2160	A1800	A1800	A1799	C1658	C1556
A3086	A2911	G2778	C2507	C2507	U2428	U2282	G2161	A1805	A1805	A1800	U1659	A1557
C3092	G2914	C2788	U2514	U2515	U2433	U2288	G2169	A1806	A1806	A1800	G1661	G1560
C3096	U2923	G2796	A2515	A2515	A2439	G2288	U2170	A1807	A1807	A1800	G1662	G1561
C3097	G2923	A2799	A2522	A2522	A2447	A2303	G2177	A1808	A1808	A1800	U1666	C1562
U3104	A2930	G2800	A2524	A2524	G2450	G2307	G2180	A1814	A1814	A1805	G1667	G1563
U3121	C2931	A2801	G2525	G2525	U2450	C2308	G2181	U1815	U1815	A1806	U1667	U1564
U3122	U2935	A2802	C2526	C2526	U2453	A2309	G2185	A1816	A1816	A1807	G1668	A1566
A3129	A2936	C2810	G2534	G2534	G2454	U2310	G2189	U1816	U1816	A1808	U1675	U1567
A3130	C2942	G2814	A2535	A2535	U2455	U2313	U2189	U1817	U1817	A1809	A1676	U1568
C3115	C2947	A2817	A2536	A2536	G2456	U2314	G2192	U1820	U1820	A1810	U1676	U1569
U3119	G2947	U2818	U	U	G2457	G2315	U2193	U1821	U1821	A1811	A1682	A1570
C3120	U2953	A2819	C	C	A2458	U2334	G2194	A1835	A1835	A1812	A1683	A1571
A3122	U2954	A2820	A	A	U2459	U2335	U2199	G1838	G1838	A1813	A1697	A1572
A3129	G2957	C2821	U	U	U2460	U2336	G2201	U1840	U1840	A1814	U1716	C1574
A3130	C2960	G2828	U2543	U2543	A2461	U2336	G2204	A1842	A1842	A1815	U1717	C1575
U3131	G2961	U2834	C2546	C2546	U2462	U2344	U2205	A1580	A1580	A1816	G1718	C1581
A3139	A2969	G2835	U2549	U2549	G2465	A2345	G2207	C1582	C1582	A1581	A1418	C1582
C2970	C2970	U2836	U2550	U2550	A2466	C2354	A2207	A1583	A1583	A1582	A1419	A1583
A2971	G2971	A2837	U2551	U2551	U2467	U2355	U2208	A1589	A1589	A1583	G1434	G1434
U3151	C2972	U2842	U2552	U2552	C2470	A2356	U2209	G1590	G1590	A1589	A1435	A1435
U3153	G2973	U2843	U2553	U2553	U2471	U2373	G2210	G1591	G1591	A1589	A1436	C1437
C3154	U2983	A2845	C2554	C2554	G2475	C2375	C2212	G1592	G1592	A1589	A1446	A1446
U3155	G2990	C2852	U2557	U2557	U2476	G2385	U2211	G1593	G1593	A1589	G1447	G1447
U3156	U2996	U2853	A2561	A2561	G2477	U2388	G2218	A1597	A1597	A1589	G1450	G1450
U3157	G2997	U2854	C2568	C2568	A2480	C2389	A2219	C1597	C1597	A1589	C1469	C1469
A3165	A3012	A2864	U2569	U2569	U2481	A2390	A2223	U1605	U1605	A1589	U1470	U1470
U3170	U3013	G2871	C2569	C2569	U2482	G2391	A2224	U1606	U1606	A1589	U1471	U1471
U3171	U3014	A2872	G2606	G2606	G2483	C2392	U2225	U1607	U1607	A1589	A1474	A1474
A3172	G3015	U2875	G2607	G2607	A2484	G2393	A2228	C1615	C1615	A1589	A1481	A1481
G3173	A3016	C2876	U2611	U2611	U2485	A2397	A2229	U1620	U1620	A1589	A1482	A1482
A3174	A3017	G2877	U2612	U2612	U2486	A2402	G2236	U1621	U1621	A1589	G1483	G1483
U3175	U3024	U2878	U2613	U2613	U2487	G2403	G2237	U1622	U1622	A1589	G1488	G1488
G3176	A3024	C2879	G2614	G2614	A2488	A2404	A2244	U1629	U1629	A1589	U1495	U1495
U3179	U3041	U2880	U2615	U2615	A2491	C2405	C2245	U1630	U1630	A1589	C1508	C1508
A3180	U3050	C2881	U2616	U2616	U2492	C2406	A2252	C1631	C1631	A1589	A1534	A1534
C3181	U3053	U2882	U2617	U2617	U2493	U2411	A2255	G1634	G1634	A1589	A1535	A1535
A3187	G3053	G2883	U2618	U2618	C2496	G2412	A2256	C1639	C1639	A1589	G1536	G1536
U3192	U3056	U2884	U2619	U2619	U2497	A2413	A2270	A1643	A1643	A1589	A1539	A1539
C3193	G3059	G2885	U2620	U2620	U2498	G2414	A2271	C1644	C1644	A1589	U1645	U1645
		A2886	U2501	U2501	U2499	U2418	G2272			A1589		
		U2887	G2614	G2614	A2502	A2419				A1589		

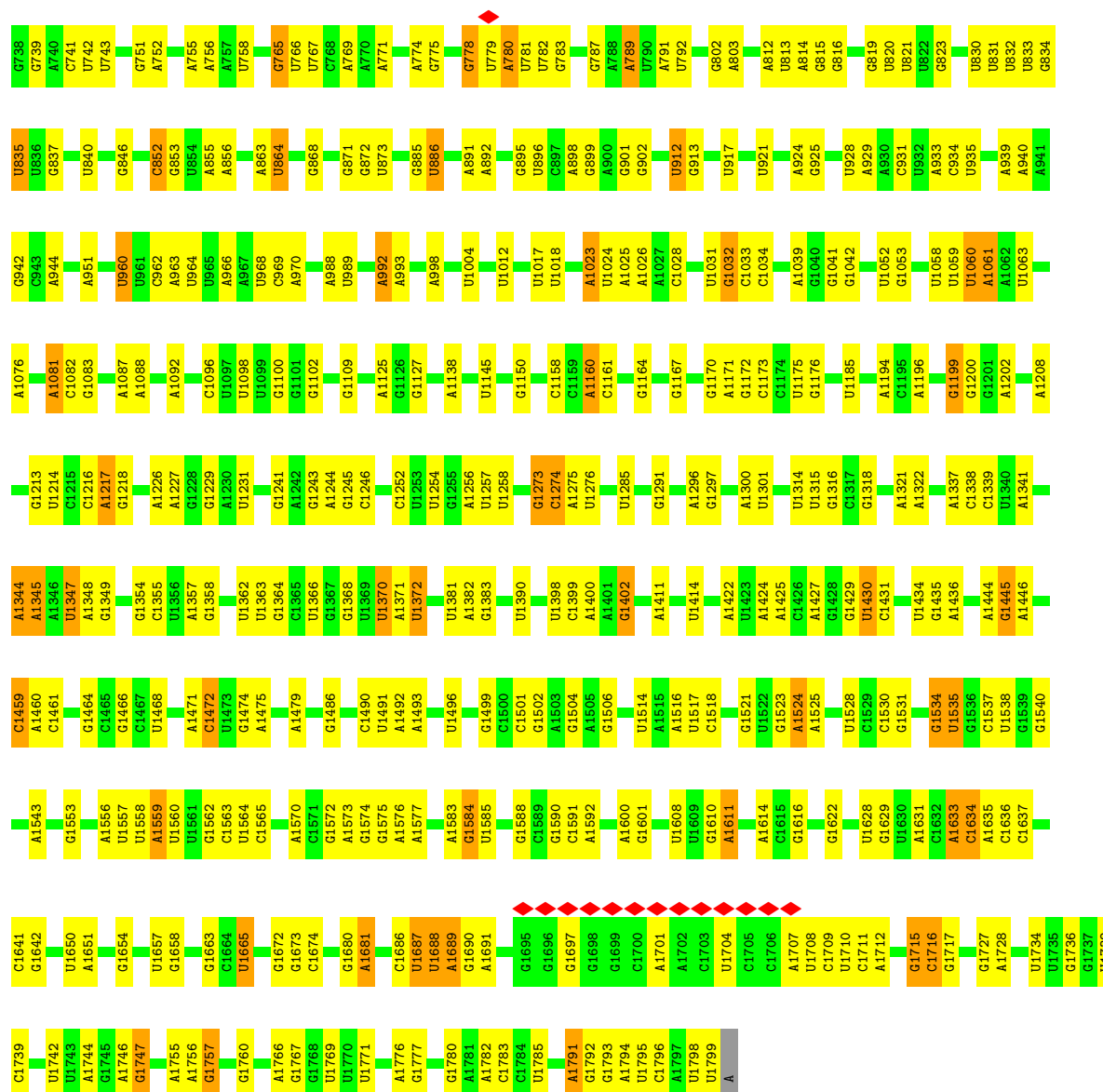


• Molecule 2: 60S ribosomal protein L1-A



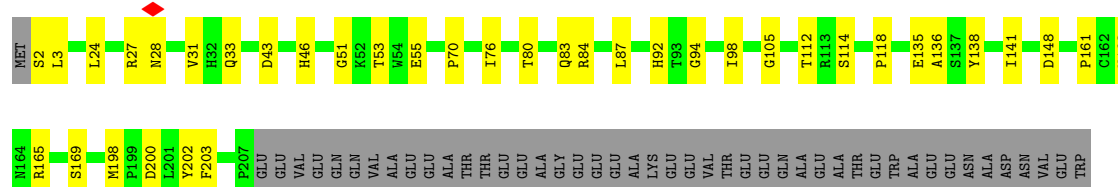
• Molecule 3: 18S ribosomal RNA (RDN18-1)





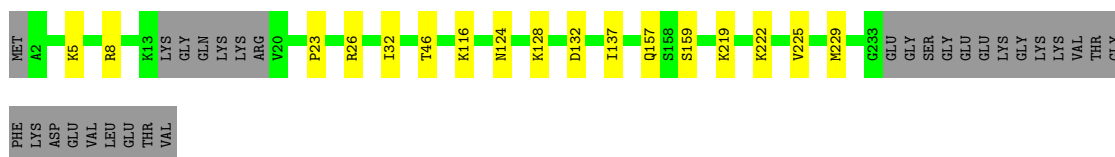
- Molecule 4: 40S ribosomal protein S0-A

Chain sP:



- Molecule 5: 40S ribosomal protein S1-A

Chain sQ:



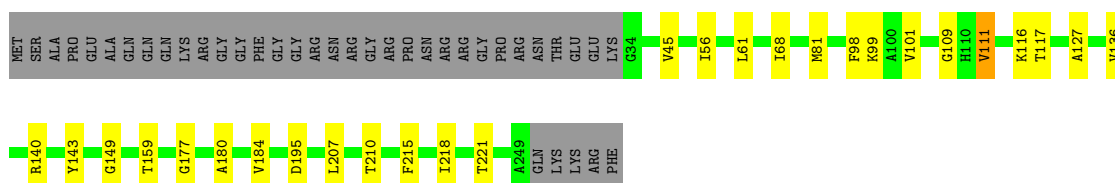
- Molecule 6: RPS15 isoform 1

Chain sE: 74% 8% 18%



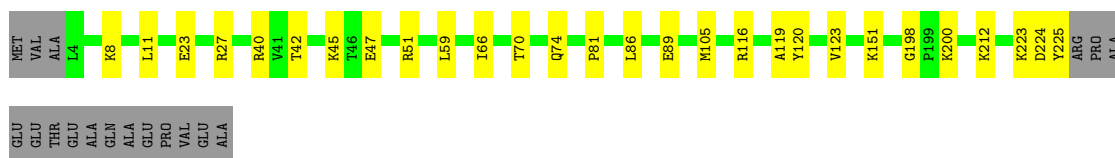
- Molecule 7: 40S ribosomal protein S2

Chain sR: 74% 10% 15%



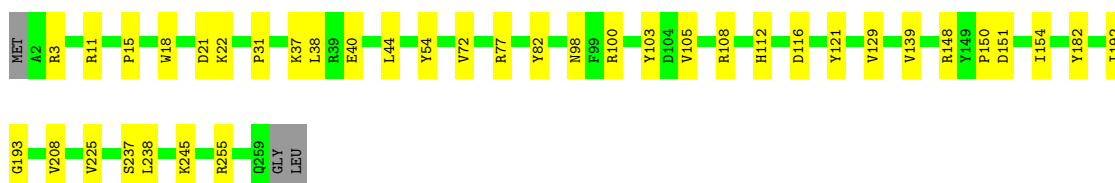
- Molecule 8: 40S ribosomal protein S3

Chain sA: 81% 12% 8%



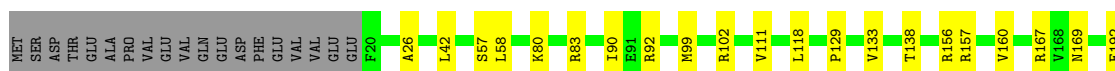
- Molecule 9: 40S ribosomal protein S4-B

Chain sS: 84% 15% 1%



- Molecule 10: 40S ribosomal protein S5

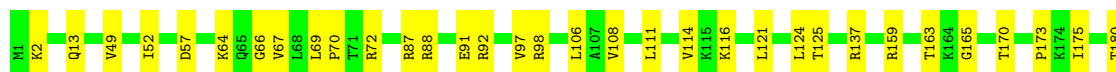
Chain sB: 80% 11% 8%





- Molecule 11: 40S ribosomal protein S6-B

Chain sT: 80% 17% .



- Molecule 12: 40S ribosomal protein S7-A

Chain sU: 78% 18% . .



- Molecule 13: 40S ribosomal protein S8-A

Chain sV: 74% 20% 6%



- Molecule 14: 40S ribosomal protein S9-A

Chain sW: 83% 10% 7%

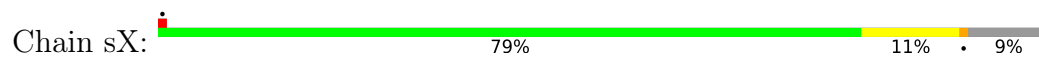


- Molecule 15: 40S ribosomal protein S10-A

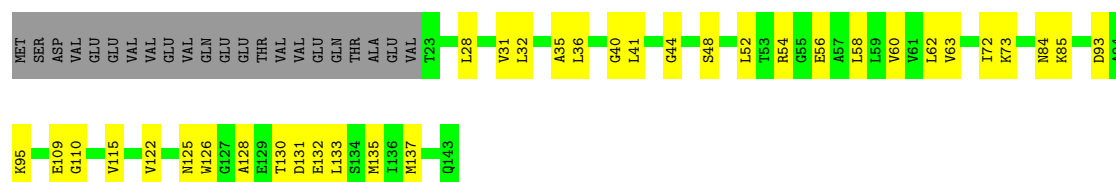
Chain sC: 65% 23% 12%



- Molecule 16: 40S ribosomal protein S11-A



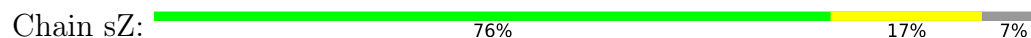
- Molecule 17: 40S ribosomal protein S12



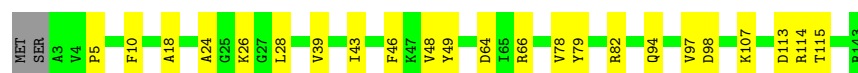
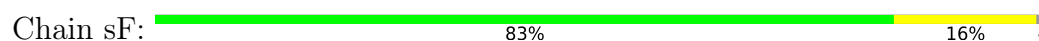
- Molecule 18: 40S ribosomal protein S13



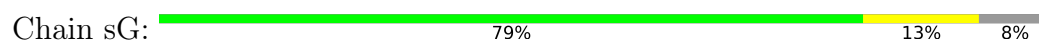
- Molecule 19: 40S ribosomal protein S14-A



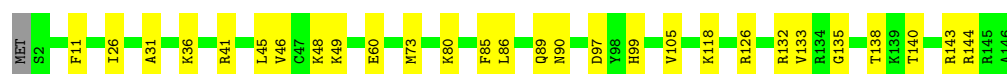
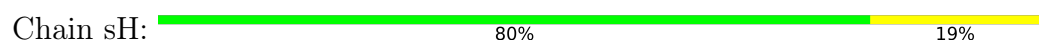
- Molecule 20: 40S ribosomal protein S16-A



- Molecule 21: 40S ribosomal protein S17-A



- Molecule 22: 40S ribosomal protein S18-A



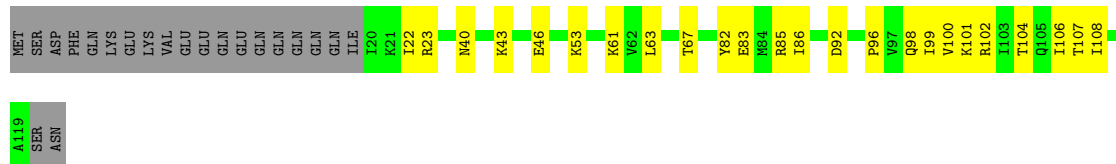
- Molecule 23: 40S ribosomal protein S19-A

Chain sI:  83% 17%

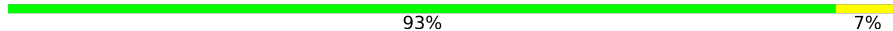


- Molecule 24: 40S ribosomal protein S20

Chain sJ:  63% 20% 17%



- Molecule 25: 40S ribosomal protein S21-A

Chain sa:  93% 7%



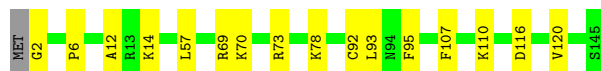
- Molecule 26: 40S ribosomal protein S22-A

Chain sb:  87% 12%



- Molecule 27: 40S ribosomal protein S23-A

Chain sc:  88% 11%



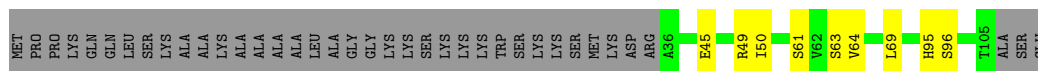
- Molecule 28: 40S ribosomal protein S24-A

Chain sd:  87% 13%



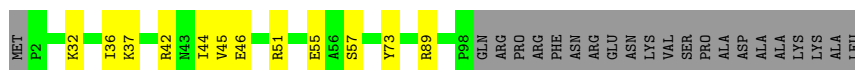
- Molecule 29: 40S ribosomal protein S25-A

Chain sK:  56% 8% 35%



- Molecule 30: 40S ribosomal protein S26-A

Chain se: 71% 10% 18%



- Molecule 31: 40S ribosomal protein S27-A

Chain sf: 90% 9% .



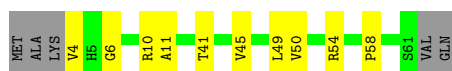
- Molecule 32: RPS29A isoform 1

Chain sM: 86% 9% 5%



- Molecule 33: 40S ribosomal protein S30-A

Chain sg: 76% 16% 8%



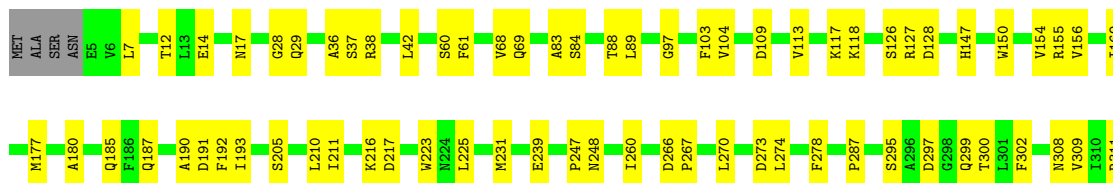
- Molecule 34: 40S ribosomal protein S31

Chain sN: 64% 32% .



- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein

Chain sO: 75% 23% .





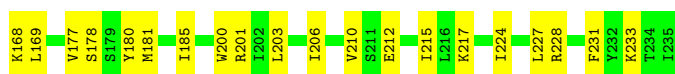
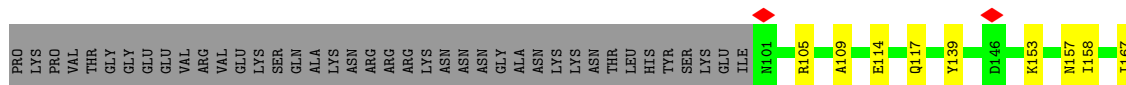
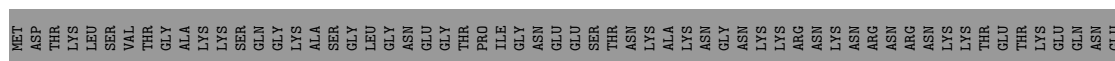
- Molecule 36: 40S ribosomal protein S28-A

Chain sL: 81% 13% 6%



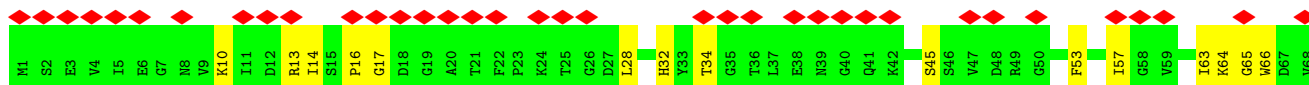
- Molecule 37: Uncharacterized protein YIL161W

Chain sj: 45% 12% 43%



- Molecule 38: FK506-binding protein 1

Chain sk: 39% 77% 23%



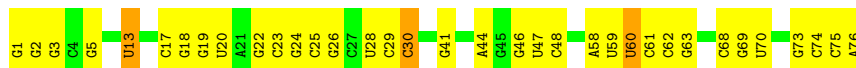
- Molecule 39: mRNA

Chain sm: 41% 48% 10%



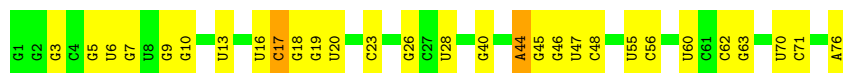
- Molecule 40: tRNA

Chain sl: 54% 42% 4%



- Molecule 40: tRNA

Chain sn:  62% 36% .



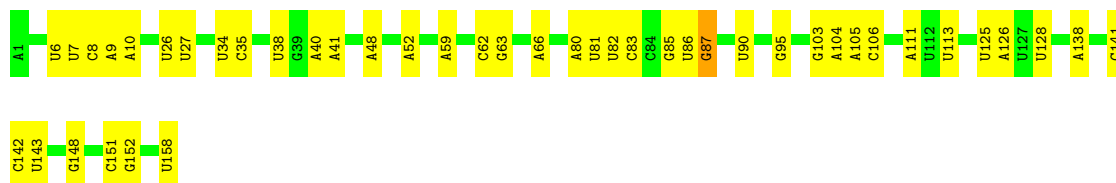
- Molecule 41: 5S ribosomal RNA (RDN5-1)

Chain LC:  85% 14% .



- Molecule 42: 5.8S ribosomal RNA (RDN58-1)

Chain LD:  72% 27% .

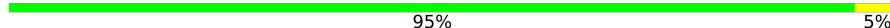


- Molecule 43: 60S ribosomal protein L2-A

Chain LE:  90% 9% .



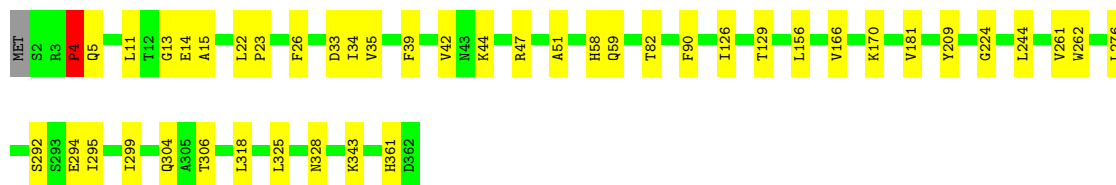
- Molecule 44: 60S ribosomal protein L3

Chain LF:  95% 5% .



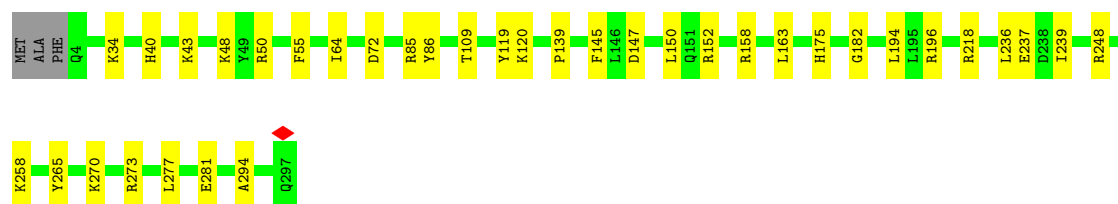
- Molecule 45: 60S ribosomal protein L4-A

Chain LG:  88% 12% .



- Molecule 46: 60S ribosomal protein L5

Chain LH:  87% 12%



- Molecule 47: 60S ribosomal protein L6-B

Chain LI:  84% 11% 5%



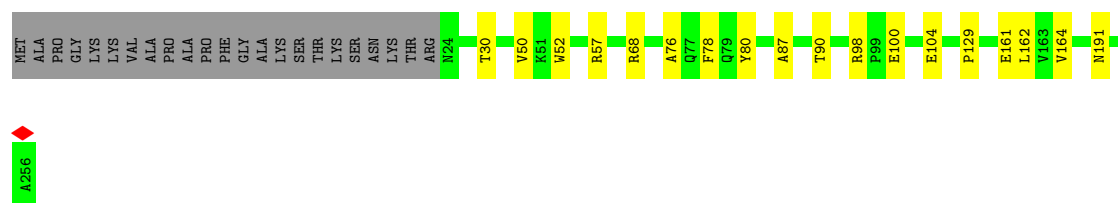
- Molecule 48: 60S ribosomal protein L7-A

Chain LJ:  84% 7% 9%



- Molecule 49: 60S ribosomal protein L8-A

Chain LK:  84% 7% 9%



- Molecule 50: 60S ribosomal protein L9-A

Chain LL:  91% 9%



- Molecule 51: 60S ribosomal protein L10

Chain LM:  85% 10% 5%



- Molecule 52: 60S ribosomal protein L11-A

Chain LN:  91% 8%

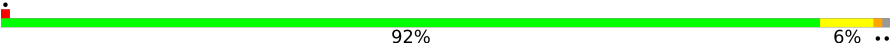


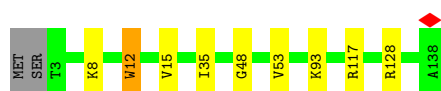
- Molecule 53: 60S ribosomal protein L13-A

Chain LO:  86% 11%



- Molecule 54: 60S ribosomal protein L14-A

Chain LP:  92% 6%



- Molecule 55: 60S ribosomal protein L15-A

Chain LQ:  90% 9%



- Molecule 56: 60S ribosomal protein L16-A

Chain LR:  89% 10%



- Molecule 57: 60S ribosomal protein L17-A

Chain LS:  90% 9%

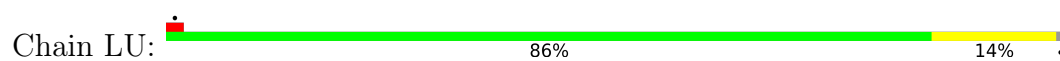


- Molecule 58: 60S ribosomal protein L18-A

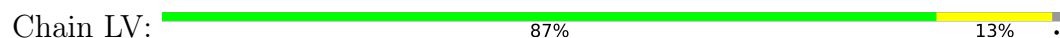
Chain LT:  90% 9%



- Molecule 59: 60S ribosomal protein L19-A



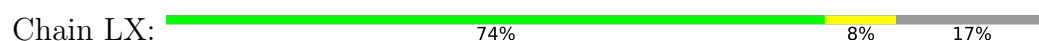
- Molecule 60: 60S ribosomal protein L20-A



- Molecule 61: 60S ribosomal protein L21-A



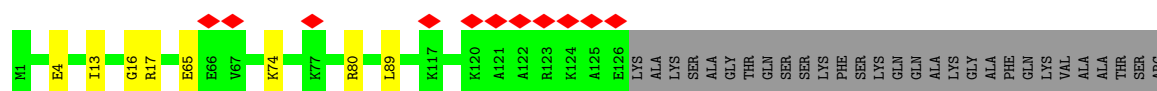
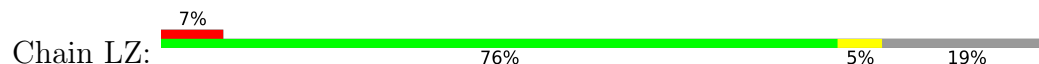
- Molecule 62: 60S ribosomal protein L22-A



- Molecule 63: 60S ribosomal protein L23-A



- Molecule 64: 60S ribosomal protein L24-A



- Molecule 65: 60S ribosomal protein L25



- Molecule 66: 60S ribosomal protein L26-A

Chain Lb:  92% 6% .



- Molecule 67: 60S ribosomal protein L27-A

Chain Lc:  82% 17% .



- Molecule 68: 60S ribosomal protein L28

Chain Ld:  91% 8% .



- Molecule 69: 60S ribosomal protein L29

Chain Le:  83% 14% . .



- Molecule 70: 60S ribosomal protein L30

Chain Lf:  78% 13% 9%



- Molecule 71: 60S ribosomal protein L31-A

Chain Lg:  81% 15% .



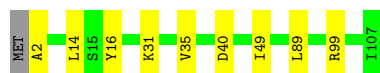
- Molecule 72: 60S ribosomal protein L32

Chain Lh:  92% 6% .



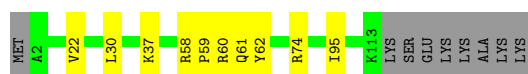
- Molecule 73: 60S ribosomal protein L33-A

Chain Li:  91% 8%



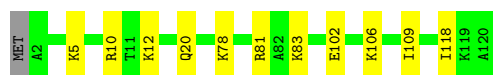
- Molecule 74: 60S ribosomal protein L34-A

Chain Lj:  84% 8% 7%



- Molecule 75: 60S ribosomal protein L35-A

Chain Lk:  90% 9%



- Molecule 76: 60S ribosomal protein L36-A

Chain Ll:  91% 8%



- Molecule 77: 60S ribosomal protein L37-A

Chain Lm:  84% 8% 8%



- Molecule 78: 60S ribosomal protein L38

Chain Ln:  88% 10%

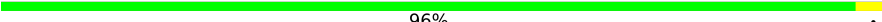


- Molecule 79: 60S ribosomal protein L39

Chain Lo:  88% 10%



- Molecule 80: 60S ribosomal protein L40-A

Chain Lp:  96% .



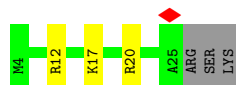
- Molecule 81: 60S ribosomal protein L41-A

Chain Lq:  88% 12%



- Molecule 81: 60S ribosomal protein L41-A

Chain Lt:  76% 12% 12%



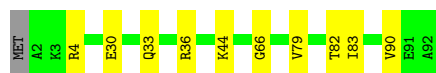
- Molecule 82: 60S ribosomal protein L42-A

Chain Lr:  87% 10% .



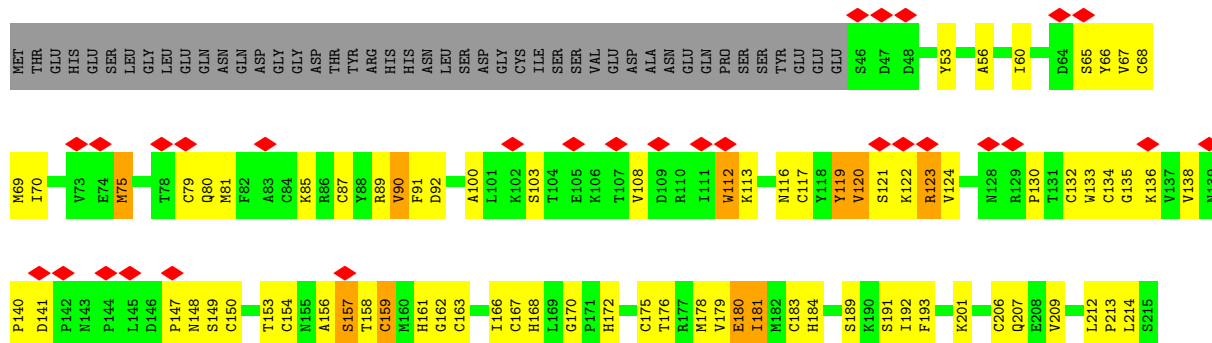
- Molecule 83: 60S ribosomal protein L43-A

Chain Ls:  88% 11% .



- Molecule 84: FAP1 isoform 1

Chain sh:  17% 52% 24% . 20%



GLU	LYS	F714	G654	T589	S488	L360	C287	C216
ASP	LEU	E715	A655	C590	D489	L360	C287	S217
SER	ALA	E716	A655	Q591	D489	L360	C287	I218
PRO	LEU	L717	K656	K592	S490	H365	R291	H219
VAL	PHE	L718	G657	T593	N491	S366	V292	T220
MET	TYR	L719	D658	C594	D492	C367	V293	C221
ASP	PRO	L720	R659	H595	N499	P368	D294	K222
ASN	GLU	E733	V660	L596	N499	F369	D294	K223
ASN	ASN	E733	V660	L596	N499	T370	S296	K224
THR	TYR	Q738	S661	C600	A504	C371	C297	C225
GLU	GLU	Q738	V662	Q601	P505	C371	C297	C225
THR	PRO	L742	T663	C604	P505	C380	R298	L229
ALA	LYS	L742	T663	C604	P505	L381	K299	C230
SER	VAL	M747	E664	K605	G509	Q382	H300	C233
VAL	GLU	M747	S665	Q606	T510	I383	S301	P234
ASN	VAL	T751	S666	T607	K511	D384	F302	E235
ALA	THR	T751	V667	T607	K511	S385	F302	E235
LYS	LYS	S754	L668	Q610	T514	C388	C306	S239
ARG	LYS	S754	L668	Q610	T514	C388	C306	S239
ASP	ASN	K758	D669	K611	C515	A389	I307	K240
MET	GLY	T759	D669	R612	N516	C390	I307	K240
GLU	PHE	M760	C670	L613	N520	C391	P309	D341
LEU	LEU	M760	N671	N614	I520	Q392	P310	S242
VAL	VAL	R765	E672	C615	R524	Q392	P310	S242
GLN	GLN	R765	E672	C615	R524	Q392	P310	S242
GLY	ASN	I768	E673	N616	R524	S396	G314	K245
LEU	LEU	I768	E673	N616	R524	S396	G314	K245
VAL	VAL	L771	E675	E618	K532	V397	A317	I247
ASP	ALA	L771	E675	E618	K532	V397	A317	I247
PHE	ALA	L771	E675	E618	K532	V397	A317	I247
ASP	ALA	L771	E675	E618	K532	V397	A317	I247
PHE	GLY	D783	L677	P620	L541	Q402	P322	C249
MET	ASN	R784	L677	P620	D542	Q403	S323	Y250
ALA	THR	R784	L677	P620	D542	R404	S324	C251
LYS	ALA	R788	K678	K621	E550	P405	L325	C251
GLU	GLU	S789	R679	P622	T551	R406	K326	G252
ALA	ASP	T790	L680	H624	V552	C407	L326	G252
PHE	LEU	F791	K681	G625	F553	N408	T327	T259
LEU	ARG	F791	K681	G625	F553	N408	T327	T259
ALA	ARG	L792	E682	K626	P555	K410	C328	K260
ASP	PHE	K793	L683	T627	C556	M415	C330	K260
SER	PHE	D796	K684	E628	C557	M415	C330	K260
ILE	GLU	D796	K684	E628	C557	M415	C330	K260
SER	PRO	N801	ALA	C629	C558	H420	R332	E263
LEU	HIS	N801	ALA	C629	C558	H420	R332	E263
LEU	LEU	A810	GLY	P630	K563	K438	T333	K265
SER	LYS	A810	ILE	D631	V564	L335	A334	F266
LYS	LYS	A810	ILE	D631	R565	L335	A334	F266
THR	HIS	L813	LYS	C634	T566	N439	L335	P267
GLU	THR	L813	LYS	C634	T566	N439	L335	P267
LEU	LEU	F817	GLU	A635	V567	L440	E336	K268
GLU	LEU	K818	THR	T636	C568	F441	E337	S269
LEU	VAL	K818	ASN	L637	F569	R442	L338	G270
ASN	VAL	K818	ASN	L637	F569	R442	L338	G270
ASN	ASN	R824	ASN	V638	Q570	Q444	T339	K271
ARG	PRO	R824	PHE	K639	S573	D445	K340	S272
GLN	GLN	R824	THR					

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	114964	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 ($e^-/\text{\AA}^2$)	43.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	47.687	Depositor
Minimum map value	-8.227	Depositor
Average map value	0.005	Depositor
Map value standard deviation	1.107	Depositor
Recommended contour level	2	Depositor
Map size (Å)	501.59998, 501.59998, 501.59998	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LA	0.36	0/77021	0.42	2/120082 (0.0%)
2	LB	0.26	0/1634	0.69	1/2195 (0.0%)
3	2	0.38	0/42071	0.46	5/65553 (0.0%)
4	sP	0.29	0/1644	0.49	0/2249
5	sQ	0.30	0/1823	0.54	0/2447
6	sE	0.32	0/936	0.61	0/1259
7	sR	0.41	0/1656	0.68	1/2251 (0.0%)
8	sA	0.30	0/1754	0.57	0/2361
9	sS	0.35	0/2097	0.62	1/2823 (0.0%)
10	sB	0.32	0/1625	0.55	2/2197 (0.1%)
11	sT	0.26	0/1839	0.50	0/2460
12	sU	0.30	0/1498	0.64	1/2019 (0.0%)
13	sV	0.32	0/1501	0.53	0/2006
14	sW	0.31	0/1504	0.58	1/2016 (0.0%)
15	sC	0.35	0/769	0.72	0/1039
16	sX	0.35	0/1168	0.52	0/1575
17	sD	0.31	0/883	0.92	0/1199
18	sY	0.35	0/1215	0.64	0/1638
19	sZ	0.35	0/934	0.63	0/1257
20	sF	0.33	0/1125	0.52	0/1510
21	sG	0.36	0/989	0.69	1/1327 (0.1%)
22	sH	0.37	0/1207	0.59	0/1623
23	sI	0.35	0/1130	0.70	4/1517 (0.3%)
24	sJ	0.34	0/807	0.70	0/1091
25	sa	0.31	0/682	0.57	0/921
26	sb	0.37	0/1038	0.63	0/1395
27	sc	0.33	0/1139	0.54	2/1518 (0.1%)
28	sd	0.30	0/1087	0.54	0/1449
29	sK	0.30	0/571	0.61	0/768
30	se	0.37	0/778	0.66	1/1042 (0.1%)
31	sf	0.32	0/620	0.54	0/838
32	sM	0.47	0/452	0.57	0/600

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	sg	0.29	0/458	0.62	0/610
34	sN	0.28	0/567	0.83	0/764
35	sO	0.32	0/2436	0.65	2/3318 (0.1%)
36	sL	0.33	0/493	0.57	0/663
37	sj	0.17	0/1149	0.55	0/1541
38	sk	0.18	0/878	0.51	0/1192
39	sm	0.24	0/714	0.41	0/1111
40	sl	0.18	0/1810	0.37	0/2821
40	sn	0.26	0/1810	0.38	0/2821
41	LC	0.33	0/2883	0.34	0/4491
42	LD	0.37	0/3746	0.38	0/5832
43	LE	0.36	0/1933	0.56	0/2598
44	LF	0.33	0/3146	0.52	0/4228
45	LG	0.32	0/2800	0.57	2/3790 (0.1%)
46	LH	0.28	0/2400	0.50	0/3239
47	LI	0.29	0/1329	0.55	0/1794
48	LJ	0.33	0/1821	0.56	0/2451
49	LK	0.29	0/1836	0.55	0/2481
50	LL	0.30	0/1529	0.53	0/2060
51	LM	0.33	0/1755	0.50	0/2353
52	LN	0.26	0/1386	0.53	0/1859
53	LO	0.28	0/1568	0.57	0/2106
54	LP	0.33	0/1068	0.51	0/1438
55	LQ	0.33	0/1757	0.52	1/2354 (0.0%)
56	LR	0.34	0/1585	0.53	0/2128
57	LS	0.32	0/1439	0.54	0/1938
58	LT	0.32	0/1465	0.56	0/1965
59	LU	0.42	0/1538	0.56	0/2050
60	LV	0.37	0/1473	0.54	0/1980
61	LW	0.30	0/1296	0.52	0/1739
62	LX	0.26	0/812	0.57	2/1099 (0.2%)
63	LY	0.30	0/1018	0.51	0/1369
64	LZ	0.41	0/883	0.74	1/1193 (0.1%)
65	La	0.45	0/979	0.64	2/1321 (0.2%)
66	Lb	0.29	0/995	0.50	0/1329
67	Lc	0.29	0/1106	0.50	0/1485
68	Ld	0.41	0/1200	0.59	1/1607 (0.1%)
69	Le	0.27	0/473	0.64	2/629 (0.3%)
70	Lf	0.25	0/745	0.45	0/1001
71	Lg	0.31	0/890	0.53	0/1196
72	Lh	0.33	0/1034	0.48	0/1385
73	Li	0.35	0/868	0.54	0/1168
74	Lj	0.31	0/890	0.54	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
75	Lk	0.27	0/978	0.48	0/1301
76	Ll	0.28	0/772	0.51	0/1026
77	Lm	0.36	0/660	0.62	0/875
78	Ln	0.27	0/618	0.42	0/826
79	Lo	0.34	0/443	0.56	0/588
80	Lp	0.27	0/416	0.52	0/553
81	Lq	0.26	0/230	0.41	0/296
81	Lt	0.17	0/208	0.41	0/267
82	Lr	0.29	0/836	0.54	0/1104
83	Ls	0.26	0/701	0.49	0/934
84	sh	0.52	0/6154	1.04	44/8290 (0.5%)
All	All	0.35	0/229174	0.51	79/335971 (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
12	sU	0	1
17	sD	0	2
19	sZ	0	1
20	sF	0	1
26	sb	0	1
35	sO	0	2
44	LF	0	1
45	LG	0	2
49	LK	0	2
50	LL	0	1
54	LP	0	1
64	LZ	0	1
69	Le	0	1
75	Lk	0	1
All	All	0	18

There are no bond length outliers.

The worst 5 of 79 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
84	sh	122	LYS	N-CA-C	10.15	122.34	111.28
84	sh	159	CYS	N-CA-C	-9.47	97.15	110.50
84	sh	158	THR	N-CA-C	-9.14	97.57	111.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	sR	109	GLY	N-CA-C	8.45	124.74	114.69
45	LG	4	PRO	CA-C-N	7.99	136.79	121.54

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
17	sD	110	GLY	Peptide
17	sD	84	ASN	Peptide
20	sF	39	VAL	Peptide
12	sU	64	VAL	Peptide
19	sZ	90	ARG	Peptide

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	LA	68809	0	34575	330	0
2	LB	1609	0	1701	39	0
3	2	37614	0	18925	201	0
4	sP	1603	0	1610	22	0
5	sQ	1798	0	1890	11	0
6	sE	916	0	941	8	0
7	sR	1626	0	1715	15	0
8	sA	1729	0	1812	20	0
9	sS	2056	0	2140	24	0
10	sB	1605	0	1668	15	0
11	sT	1815	0	1894	28	0
12	sU	1473	0	1555	28	0
13	sV	1476	0	1501	25	0
14	sW	1479	0	1556	14	0
15	sC	752	0	719	15	0
16	sX	1142	0	1209	11	0
17	sD	875	0	878	20	0
18	sY	1192	0	1255	8	0
19	sZ	923	0	948	16	0
20	sF	1105	0	1166	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	sG	979	0	1025	8	0
22	sH	1188	0	1218	20	0
23	sI	1112	0	1124	17	0
24	sJ	797	0	863	17	0
25	sa	673	0	662	4	0
26	sb	1021	0	1060	9	0
27	sc	1121	0	1195	11	0
28	sd	1073	0	1132	11	0
29	sK	563	0	603	5	0
30	se	765	0	814	8	0
31	sf	610	0	633	6	0
32	sM	442	0	428	4	0
33	sg	451	0	491	6	0
34	sN	556	0	546	20	0
35	sO	2383	0	2332	47	0
36	sL	491	0	524	10	0
37	sj	1128	0	1161	41	0
38	sk	858	0	863	16	0
39	sm	632	0	318	9	0
40	sl	1622	0	820	11	0
40	sn	1622	0	820	10	0
41	LC	2579	0	1304	6	0
42	LD	3353	0	1695	14	0
43	LE	1899	0	1957	18	0
44	LF	3075	0	3142	12	0
45	LG	2748	0	2859	27	0
46	LH	2351	0	2294	21	0
47	LI	1307	0	1377	12	0
48	LJ	1784	0	1862	12	0
49	LK	1804	0	1877	10	0
50	LL	1508	0	1572	12	0
51	LM	1719	0	1763	15	0
52	LN	1365	0	1393	9	0
53	LO	1543	0	1608	17	0
54	LP	1053	0	1149	7	0
55	LQ	1720	0	1779	14	0
56	LR	1555	0	1659	11	0
57	LS	1416	0	1433	12	0
58	LT	1441	0	1543	12	0
59	LU	1521	0	1617	25	0
60	LV	1437	0	1475	17	0
61	LW	1272	0	1312	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	LX	796	0	812	6	0
63	LY	1003	0	1048	15	0
64	LZ	869	0	783	4	0
65	La	964	0	1025	10	0
66	Lb	984	0	1075	4	0
67	Lc	1080	0	1122	12	0
68	Ld	1169	0	1211	10	0
69	Le	462	0	491	6	0
70	Lf	737	0	792	10	0
71	Lg	876	0	912	10	0
72	Lh	1013	0	1077	6	0
73	Li	850	0	880	6	0
74	Lj	880	0	942	10	0
75	Lk	969	0	1078	7	0
76	Ll	766	0	844	6	0
77	Lm	645	0	645	6	0
78	Ln	612	0	682	5	0
79	Lo	436	0	475	3	0
80	Lp	410	0	442	2	0
81	Lq	229	0	273	3	0
81	Lt	207	0	250	3	0
82	Lr	824	0	888	6	0
83	Ls	694	0	734	10	0
84	sh	6024	0	5965	211	0
85	2	87	0	0	0	0
85	LA	220	0	0	0	0
85	LC	1	0	0	0	0
85	LE	2	0	0	0	0
85	LF	1	0	0	0	0
85	LQ	1	0	0	0	0
85	LS	1	0	0	0	0
85	LU	2	0	0	0	0
85	LW	1	0	0	0	0
85	LY	1	0	0	0	0
85	Lh	1	0	0	0	0
85	Lj	1	0	0	0	0
85	Lm	1	0	0	0	0
85	sB	1	0	0	0	0
85	sS	1	0	0	0	0
85	sc	1	0	0	0	0
85	sm	1	0	0	0	0
86	LA	10	0	19	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Lr	1	0	0	0	0
87	Ls	1	0	0	0	0
87	sM	1	0	0	0	0
87	sN	1	0	0	0	0
87	sh	27	0	0	4	0
All	All	214001	0	159425	1503	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 4.

The worst 5 of 1503 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)
84:sh:249:CYS:SG	84:sh:286:ALA:HA	1.58	1.42
84:sh:219:HIS:CD2	84:sh:235:GLU:HG3	1.61	1.34
39:sm:7:A:H5'	84:sh:788:ARG:NH2	1.65	1.12
37:sj:228:ARG:NE	84:sh:266:PHE:CD1	2.20	1.09
84:sh:249:CYS:SG	84:sh:286:ALA:CA	2.39	1.09

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	LB	202/217 (93%)	158 (78%)	44 (22%)	0	100	100
4	sP	204/252 (81%)	189 (93%)	15 (7%)	0	100	100
5	sQ	222/255 (87%)	217 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	sE	115/142 (81%)	106 (92%)	9 (8%)	0	100	100
7	sR	214/254 (84%)	198 (92%)	16 (8%)	0	100	100
8	sA	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
9	sS	256/261 (98%)	239 (93%)	17 (7%)	0	100	100
10	sB	204/225 (91%)	198 (97%)	6 (3%)	0	100	100
11	sT	226/236 (96%)	212 (94%)	14 (6%)	0	100	100
12	sU	182/190 (96%)	172 (94%)	10 (6%)	0	100	100
13	sV	183/200 (92%)	172 (94%)	11 (6%)	0	100	100
14	sW	182/197 (92%)	170 (93%)	12 (7%)	0	100	100
15	sC	90/105 (86%)	75 (83%)	15 (17%)	0	100	100
16	sX	140/156 (90%)	131 (94%)	9 (6%)	0	100	100
17	sD	119/143 (83%)	90 (76%)	27 (23%)	2 (2%)	7	10
18	sY	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
19	sZ	125/137 (91%)	114 (91%)	11 (9%)	0	100	100
20	sF	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
21	sG	123/136 (90%)	122 (99%)	1 (1%)	0	100	100
22	sH	143/146 (98%)	135 (94%)	8 (6%)	0	100	100
23	sI	141/144 (98%)	136 (96%)	5 (4%)	0	100	100
24	sJ	98/121 (81%)	91 (93%)	7 (7%)	0	100	100
25	sa	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
26	sb	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
27	sc	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
28	sd	132/135 (98%)	126 (96%)	6 (4%)	0	100	100
29	sK	68/108 (63%)	63 (93%)	5 (7%)	0	100	100
30	se	95/119 (80%)	88 (93%)	7 (7%)	0	100	100
31	sf	79/82 (96%)	71 (90%)	8 (10%)	0	100	100
32	sM	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
33	sg	56/63 (89%)	53 (95%)	3 (5%)	0	100	100
34	sN	71/76 (93%)	48 (68%)	22 (31%)	1 (1%)	9	13
35	sO	310/319 (97%)	284 (92%)	26 (8%)	0	100	100
36	sL	61/67 (91%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	sj	133/235 (57%)	130 (98%)	3 (2%)	0	100	100
38	sk	112/114 (98%)	109 (97%)	3 (3%)	0	100	100
43	LE	249/254 (98%)	233 (94%)	16 (6%)	0	100	100
44	LF	384/387 (99%)	360 (94%)	24 (6%)	0	100	100
45	LG	359/362 (99%)	332 (92%)	26 (7%)	1 (0%)	36	50
46	LH	292/297 (98%)	282 (97%)	10 (3%)	0	100	100
47	LI	163/176 (93%)	156 (96%)	7 (4%)	0	100	100
48	LJ	220/244 (90%)	209 (95%)	11 (5%)	0	100	100
49	LK	231/256 (90%)	219 (95%)	12 (5%)	0	100	100
50	LL	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
51	LM	207/221 (94%)	198 (96%)	9 (4%)	0	100	100
52	LN	170/174 (98%)	166 (98%)	4 (2%)	0	100	100
53	LO	191/199 (96%)	172 (90%)	18 (9%)	1 (0%)	24	37
54	LP	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
55	LQ	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
56	LR	195/199 (98%)	190 (97%)	5 (3%)	0	100	100
57	LS	181/184 (98%)	169 (93%)	12 (7%)	0	100	100
58	LT	183/186 (98%)	173 (94%)	10 (6%)	0	100	100
59	LU	186/189 (98%)	182 (98%)	4 (2%)	0	100	100
60	LV	169/172 (98%)	164 (97%)	5 (3%)	0	100	100
61	LW	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
62	LX	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
63	LY	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
64	LZ	124/155 (80%)	123 (99%)	1 (1%)	0	100	100
65	La	119/142 (84%)	114 (96%)	5 (4%)	0	100	100
66	Lb	123/127 (97%)	119 (97%)	4 (3%)	0	100	100
67	Lc	133/136 (98%)	128 (96%)	4 (3%)	1 (1%)	16	25
68	Ld	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
69	Le	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	6	9
70	Lf	94/105 (90%)	94 (100%)	0	0	100	100
71	Lg	107/113 (95%)	98 (92%)	9 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	Lh	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
73	Li	104/107 (97%)	100 (96%)	4 (4%)	0	100	100
74	Lj	110/121 (91%)	108 (98%)	2 (2%)	0	100	100
75	Lk	117/120 (98%)	113 (97%)	4 (3%)	0	100	100
76	Ll	97/100 (97%)	94 (97%)	3 (3%)	0	100	100
77	Lm	79/88 (90%)	77 (98%)	2 (2%)	0	100	100
78	Ln	75/78 (96%)	75 (100%)	0	0	100	100
79	Lo	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
80	Lp	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
81	Lq	23/25 (92%)	23 (100%)	0	0	100	100
81	Lt	20/25 (80%)	20 (100%)	0	0	100	100
82	Lr	101/106 (95%)	95 (94%)	6 (6%)	0	100	100
83	Ls	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
84	sh	772/965 (80%)	748 (97%)	21 (3%)	3 (0%)	30	43
All	All	12203/13284 (92%)	11518 (94%)	675 (6%)	10 (0%)	49	64

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	sD	85	LYS
34	sN	145	HIS
84	sh	309	PRO
67	Lc	59	ALA
84	sh	366	SER

5.3.2 Protein sidechains ⓘ

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	LB	185/198 (93%)	185 (100%)	0	100	100
4	sP	170/210 (81%)	170 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	sQ	200/224 (89%)	200 (100%)	0	100	100
6	sE	95/118 (80%)	95 (100%)	0	100	100
7	sR	175/205 (85%)	174 (99%)	1 (1%)	78	89
8	sA	182/195 (93%)	182 (100%)	0	100	100
9	sS	220/222 (99%)	220 (100%)	0	100	100
10	sB	172/191 (90%)	172 (100%)	0	100	100
11	sT	189/201 (94%)	189 (100%)	0	100	100
12	sU	163/170 (96%)	163 (100%)	0	100	100
13	sV	148/161 (92%)	148 (100%)	0	100	100
14	sW	156/166 (94%)	156 (100%)	0	100	100
15	sC	77/98 (79%)	77 (100%)	0	100	100
16	sX	126/137 (92%)	125 (99%)	1 (1%)	73	86
17	sD	88/119 (74%)	88 (100%)	0	100	100
18	sY	127/128 (99%)	127 (100%)	0	100	100
19	sZ	90/105 (86%)	90 (100%)	0	100	100
20	sF	117/119 (98%)	117 (100%)	0	100	100
21	sG	105/124 (85%)	102 (97%)	3 (3%)	37	60
22	sH	127/129 (98%)	127 (100%)	0	100	100
23	sI	115/116 (99%)	115 (100%)	0	100	100
24	sJ	93/114 (82%)	93 (100%)	0	100	100
25	sa	71/74 (96%)	71 (100%)	0	100	100
26	sb	110/111 (99%)	110 (100%)	0	100	100
27	sc	119/120 (99%)	119 (100%)	0	100	100
28	sd	112/113 (99%)	112 (100%)	0	100	100
29	sK	61/89 (68%)	61 (100%)	0	100	100
30	se	82/101 (81%)	82 (100%)	0	100	100
31	sf	70/71 (99%)	70 (100%)	0	100	100
32	sM	47/49 (96%)	47 (100%)	0	100	100
33	sg	47/54 (87%)	47 (100%)	0	100	100
34	sN	56/66 (85%)	56 (100%)	0	100	100
35	sO	250/262 (95%)	250 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	sL	55/60 (92%)	55 (100%)	0	100	100
37	sj	128/213 (60%)	128 (100%)	0	100	100
38	sk	95/95 (100%)	94 (99%)	1 (1%)	65	82
43	LE	190/196 (97%)	190 (100%)	0	100	100
44	LF	319/323 (99%)	319 (100%)	0	100	100
45	LG	288/289 (100%)	288 (100%)	0	100	100
46	LH	241/245 (98%)	241 (100%)	0	100	100
47	LI	139/155 (90%)	139 (100%)	0	100	100
48	LJ	186/205 (91%)	186 (100%)	0	100	100
49	LK	187/208 (90%)	187 (100%)	0	100	100
50	LL	168/171 (98%)	168 (100%)	0	100	100
51	LM	181/187 (97%)	181 (100%)	0	100	100
52	LN	146/150 (97%)	146 (100%)	0	100	100
53	LO	154/159 (97%)	154 (100%)	0	100	100
54	LP	107/109 (98%)	107 (100%)	0	100	100
55	LQ	175/176 (99%)	175 (100%)	0	100	100
56	LR	160/162 (99%)	160 (100%)	0	100	100
57	LS	138/146 (94%)	138 (100%)	0	100	100
58	LT	150/151 (99%)	150 (100%)	0	100	100
59	LU	153/154 (99%)	152 (99%)	1 (1%)	76	88
60	LV	155/156 (99%)	155 (100%)	0	100	100
61	LW	135/137 (98%)	135 (100%)	0	100	100
62	LX	87/107 (81%)	87 (100%)	0	100	100
63	LY	104/105 (99%)	104 (100%)	0	100	100
64	LZ	65/129 (50%)	64 (98%)	1 (2%)	57	77
65	La	104/118 (88%)	102 (98%)	2 (2%)	50	71
66	Lb	108/110 (98%)	108 (100%)	0	100	100
67	Lc	112/116 (97%)	111 (99%)	1 (1%)	70	85
68	Ld	117/119 (98%)	117 (100%)	0	100	100
69	Le	46/47 (98%)	46 (100%)	0	100	100
70	Lf	81/88 (92%)	81 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	Lg	92/97 (95%)	92 (100%)	0	100	100
72	Lh	107/111 (96%)	107 (100%)	0	100	100
73	Li	90/91 (99%)	90 (100%)	0	100	100
74	Lj	95/103 (92%)	95 (100%)	0	100	100
75	Lk	104/105 (99%)	104 (100%)	0	100	100
76	Ll	80/82 (98%)	80 (100%)	0	100	100
77	Lm	67/71 (94%)	67 (100%)	0	100	100
78	Ln	68/69 (99%)	68 (100%)	0	100	100
79	Lo	45/46 (98%)	45 (100%)	0	100	100
80	Lp	45/47 (96%)	45 (100%)	0	100	100
81	Lq	22/23 (96%)	22 (100%)	0	100	100
81	Lt	20/23 (87%)	20 (100%)	0	100	100
82	Lr	87/91 (96%)	87 (100%)	0	100	100
83	Ls	71/72 (99%)	71 (100%)	0	100	100
84	sh	709/879 (81%)	646 (91%)	63 (9%)	9	15
All	All	10321/11256 (92%)	10247 (99%)	74 (1%)	73	88

5 of 74 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
84	sh	573	VAL
84	sh	733	GLU
84	sh	586	CYS
84	sh	651	VAL
84	sh	168	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 110 such sidechains are listed below:

Mol	Chain	Res	Type
49	LK	61	GLN
57	LS	45	GLN
84	sh	610	GLN
79	Lo	33	ASN
50	LL	58	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3213/3396 (94%)	562 (17%)	39 (1%)
3	2	1761/1800 (97%)	436 (24%)	37 (2%)
39	sm	28/29 (96%)	16 (57%)	0
40	sl	75/76 (98%)	20 (26%)	0
40	sn	75/76 (98%)	19 (25%)	0
41	LC	120/121 (99%)	11 (9%)	1 (0%)
42	LD	157/158 (99%)	27 (17%)	1 (0%)
All	All	5429/5656 (95%)	1091 (20%)	78 (1%)

5 of 1091 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	LA	6	A
1	LA	13	A
1	LA	14	U
1	LA	26	A
1	LA	40	A

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	863	A
3	2	1534	G
3	2	928	U
3	2	1273	G
3	2	1791	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 359 ligands modelled in this entry, 358 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	$\# Z > 2$
86	SPD	LA	3618	-	9,9,9	0.40	0	8,8,8	1.00	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	SPD	LA	3618	-	-	5/7/7/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
86	LA	3618	SPD	N6-C7-C8-C9
86	LA	3618	SPD	C3-C4-C5-N6
86	LA	3618	SPD	C2-C3-C4-C5
86	LA	3618	SPD	C4-C5-N6-C7
86	LA	3618	SPD	C8-C7-N6-C5

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

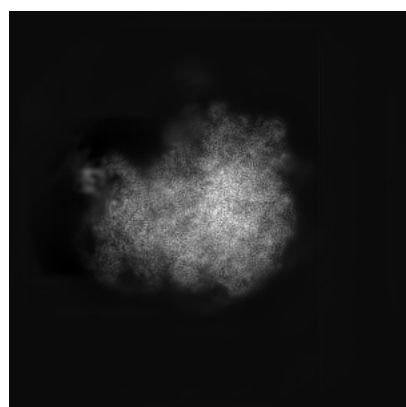
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14990. These allow visual inspection of the internal detail of the map and identification of artifacts.

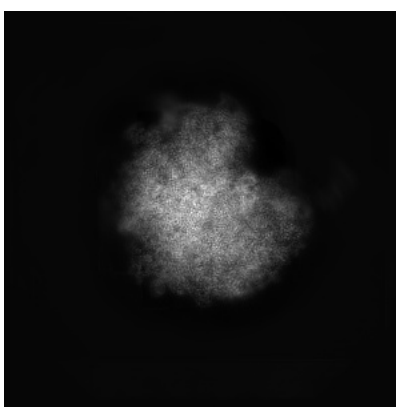
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

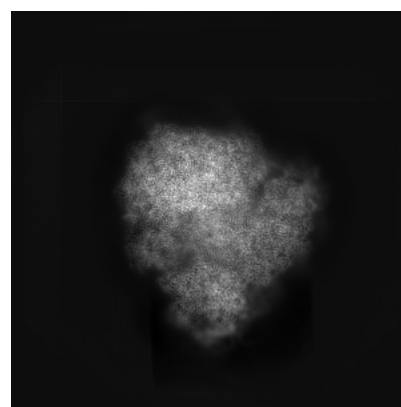
6.1.1 Primary map



X



Y

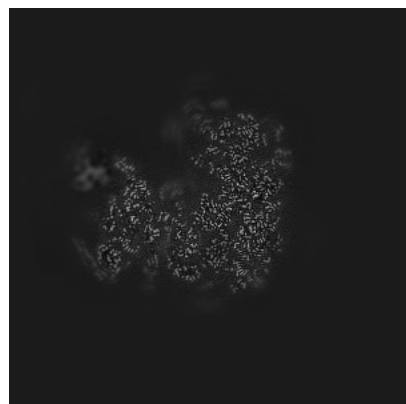


Z

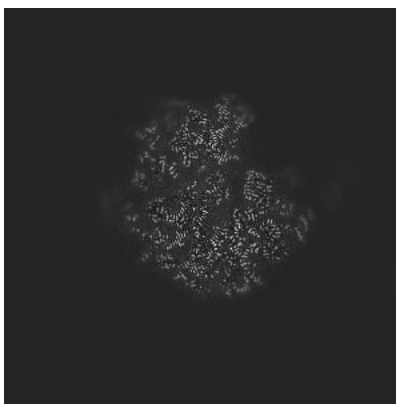
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

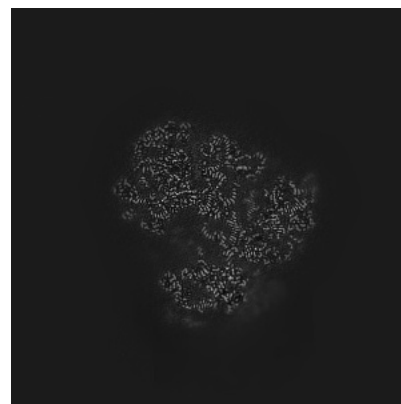
6.2.1 Primary map



X Index: 240



Y Index: 240

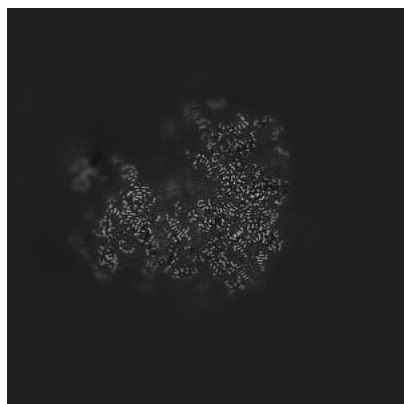


Z Index: 240

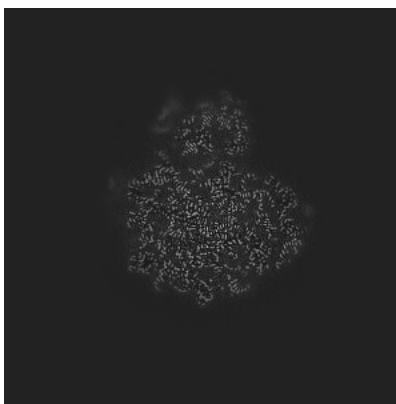
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 236



Y Index: 260

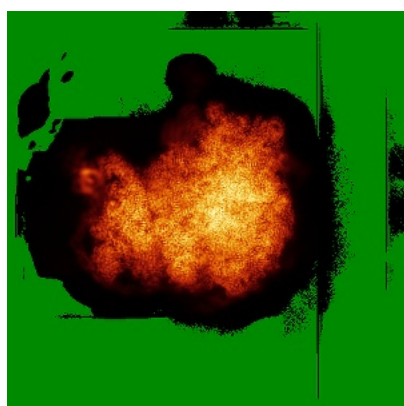


Z Index: 253

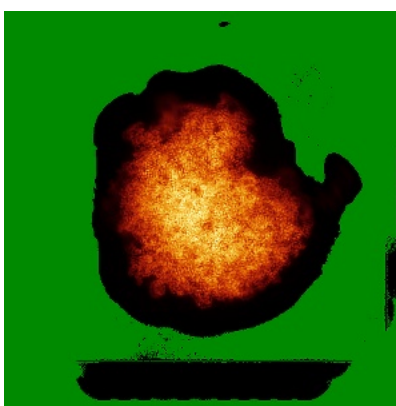
The images above show the largest variance slices of the map in three orthogonal directions.

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

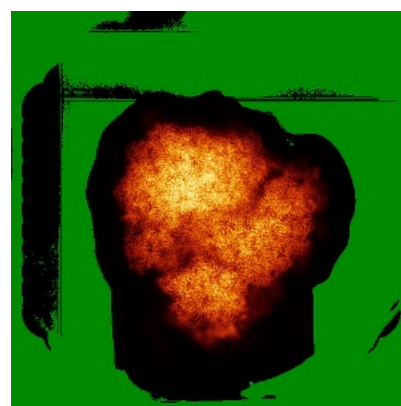
6.4.1 Primary map



X



Y

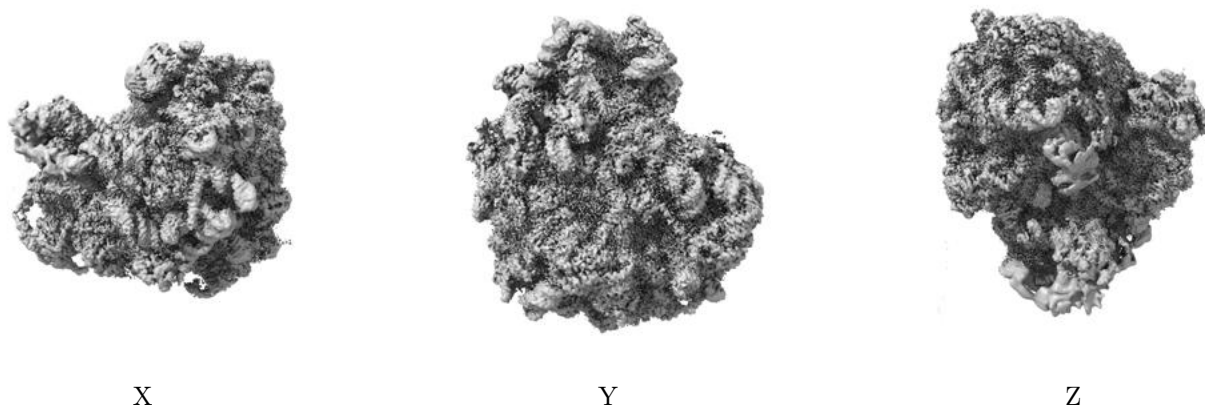


Z

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



The images above show the 3D surface view of the map at the recommended contour level 2.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

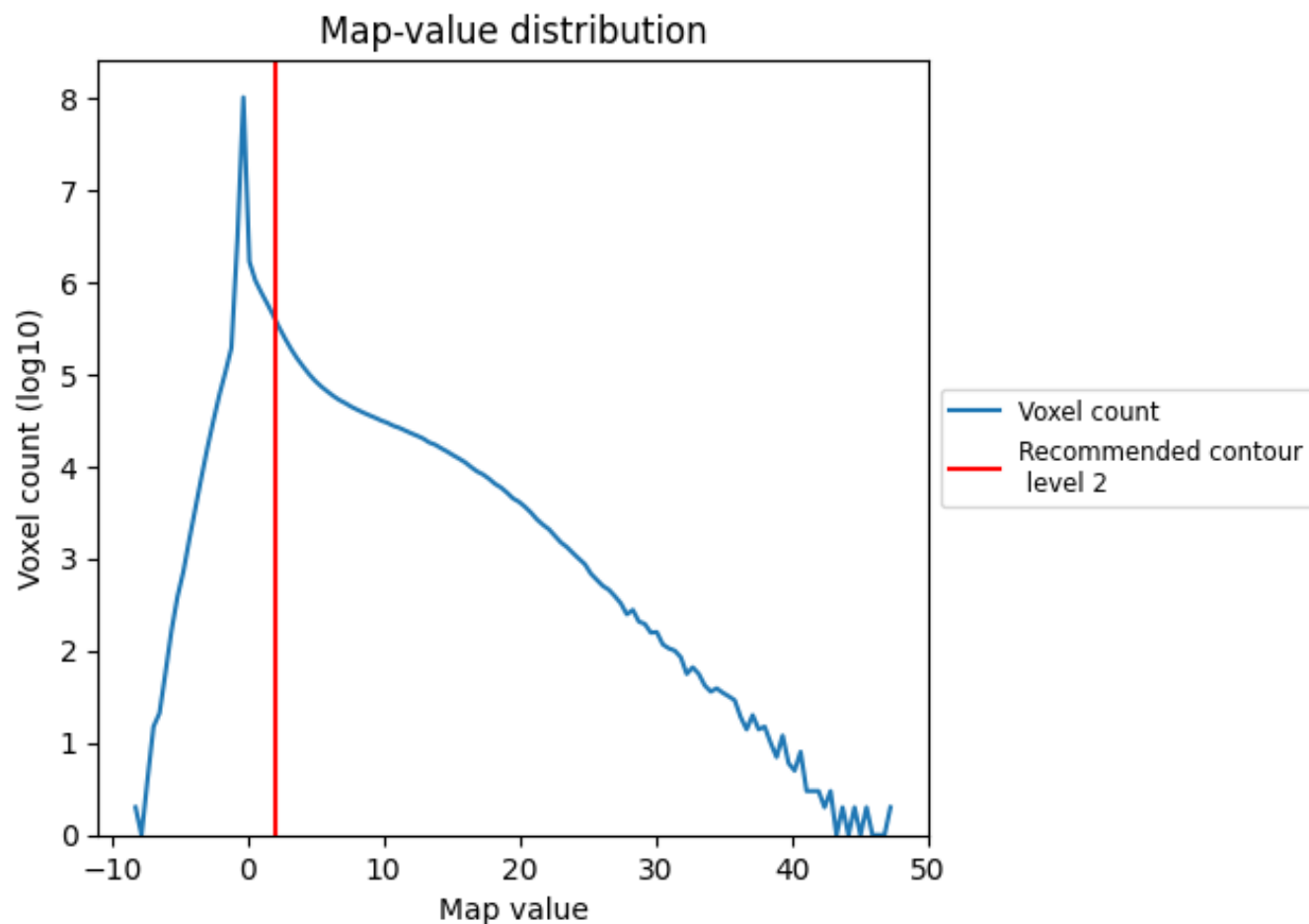
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

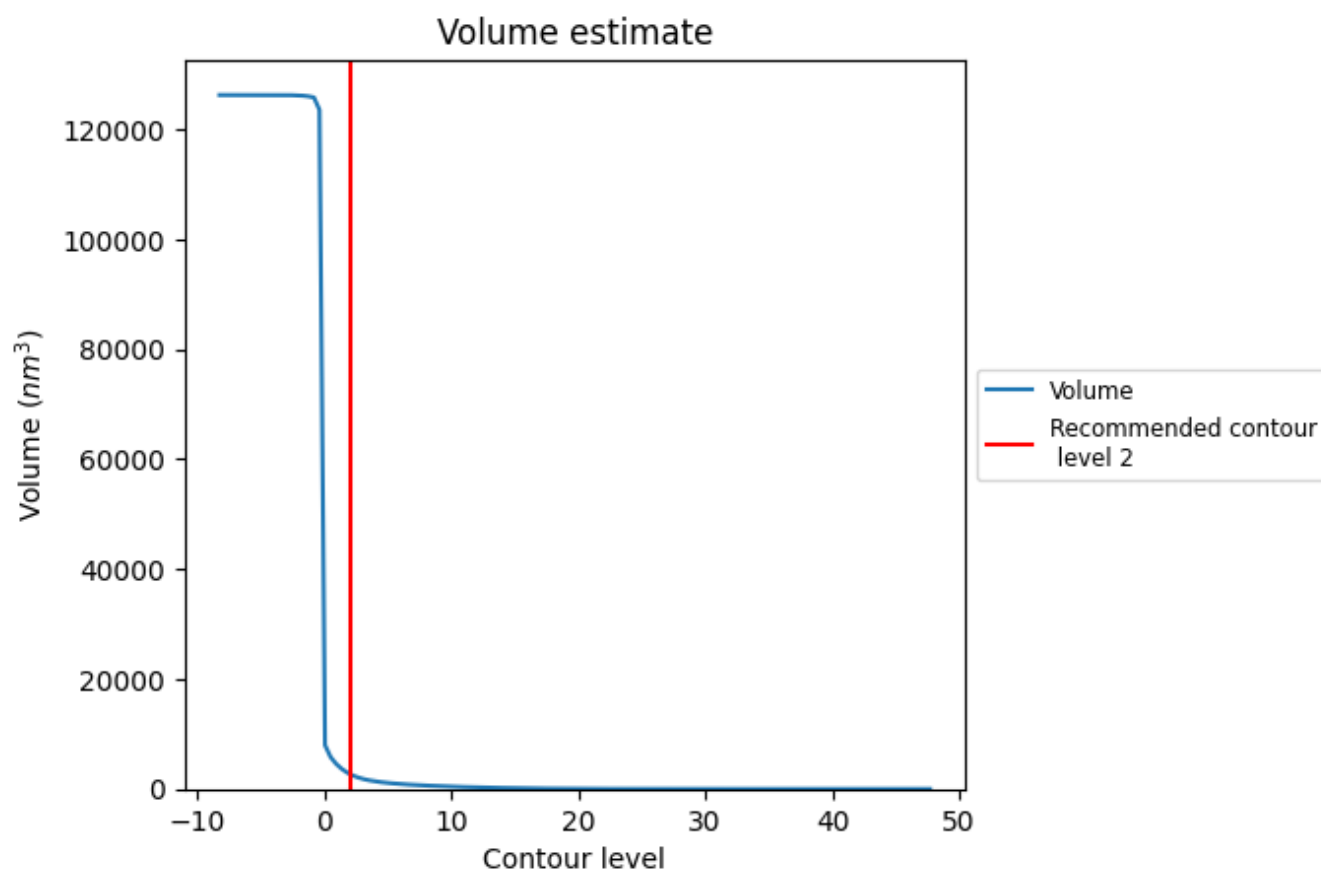
This section contains the results of statistical analysis of the map.

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.

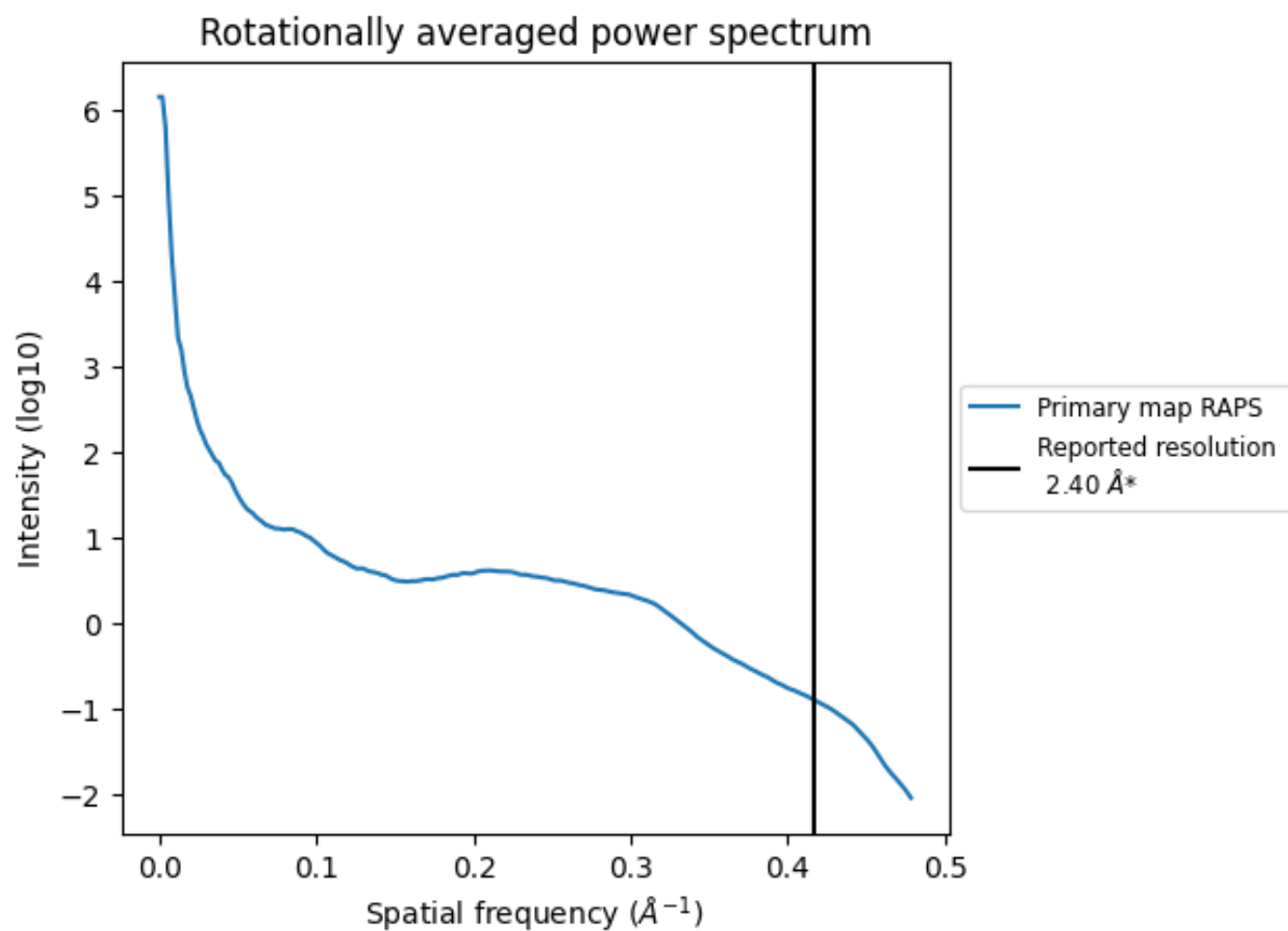
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2756 nm^3 ; this corresponds to an approximate mass of 2490 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

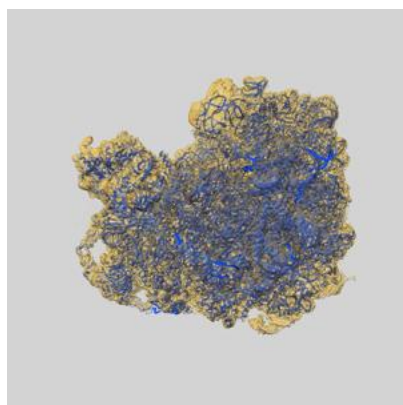
8 Fourier-Shell correlation

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

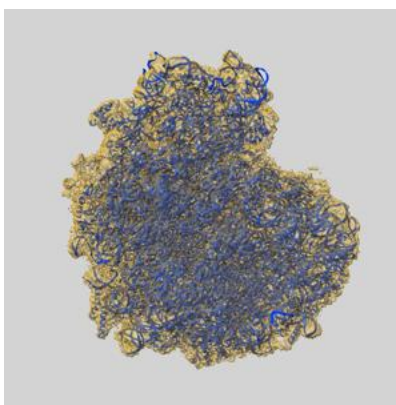
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14990 and PDB model 7ZW0. Per-residue inclusion information can be found in section 3 on page 21.

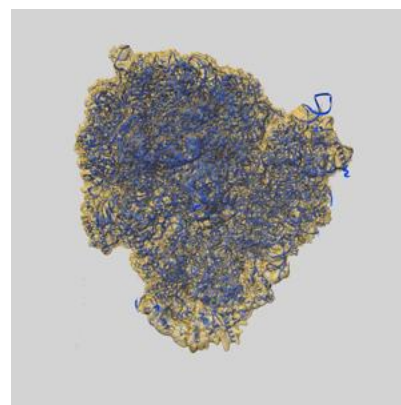
9.1 Map-model overlay [i](#)



X



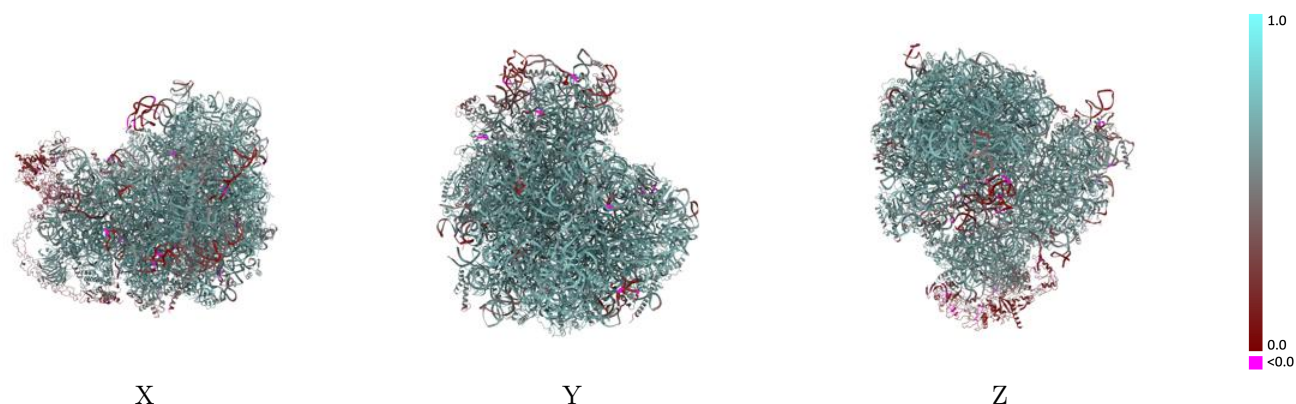
Y



Z

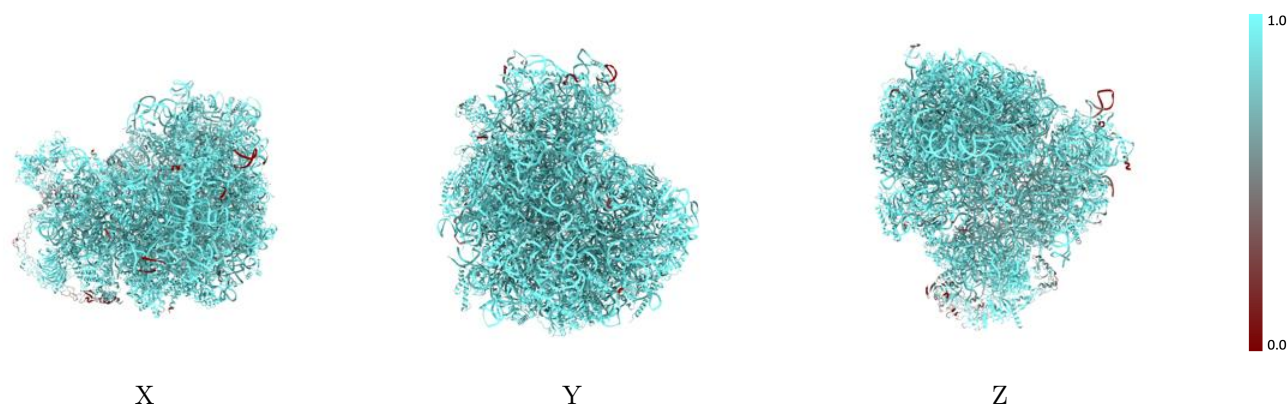
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



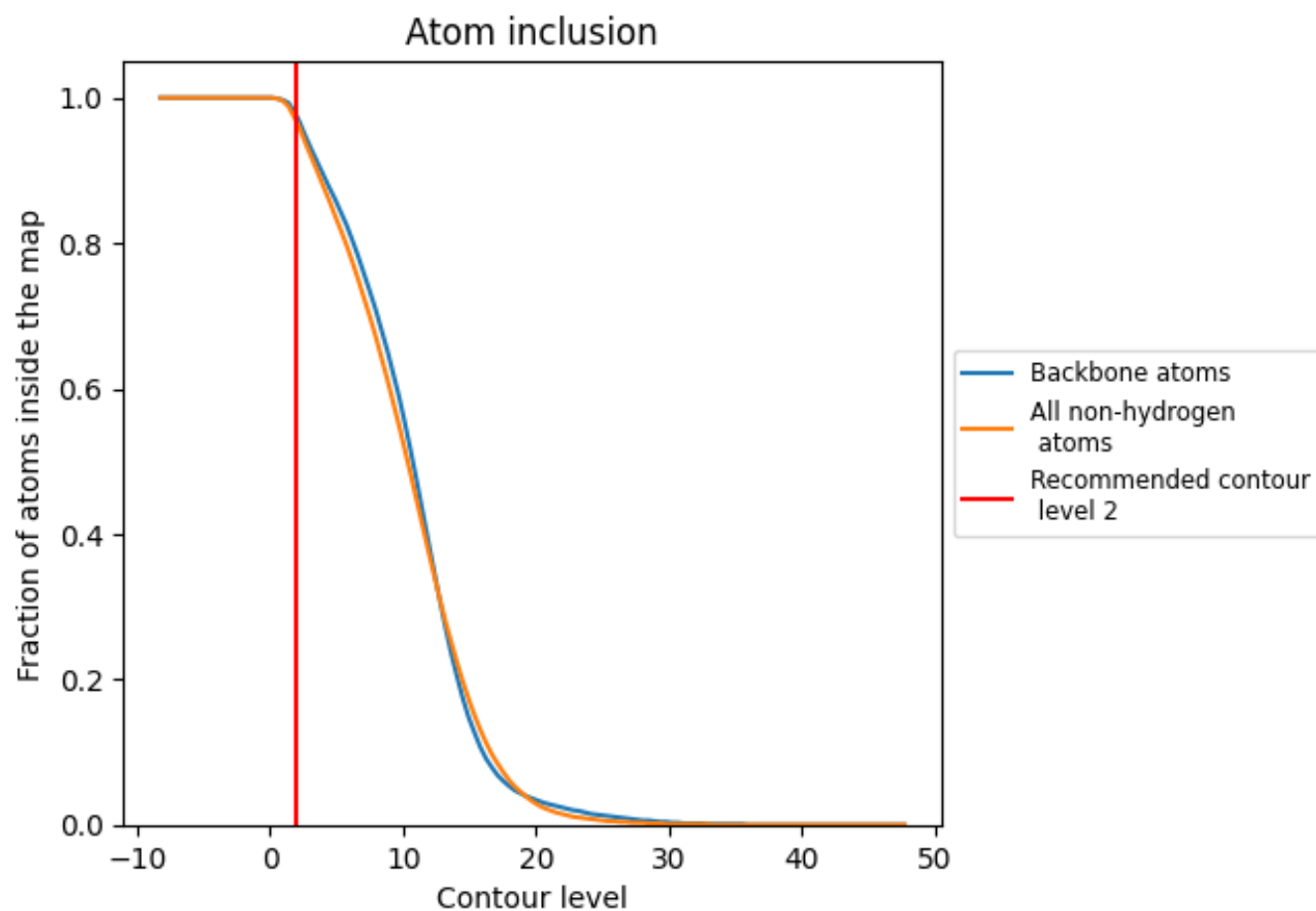
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 97% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.6030
2	 0.9700	 0.6030
LA	 0.9870	 0.6360
LB	 0.4740	 0.1140
LC	 0.9980	 0.6570
LD	 0.9950	 0.6700
LE	 0.9940	 0.6940
LF	 0.9890	 0.6680
LG	 0.9870	 0.6630
LH	 0.9650	 0.5970
LI	 0.9780	 0.6140
LJ	 0.9870	 0.6590
LK	 0.9700	 0.6010
LL	 0.9870	 0.6360
LM	 0.9850	 0.6560
LN	 0.9740	 0.5860
LO	 0.9760	 0.6420
LP	 0.9830	 0.6480
LQ	 0.9990	 0.7010
LR	 0.9890	 0.6830
LS	 0.9850	 0.6810
LT	 0.9890	 0.6700
LU	 0.9600	 0.5990
LV	 0.9910	 0.6790
LW	 0.9880	 0.6430
LX	 0.9670	 0.5570
LY	 0.9890	 0.6700
LZ	 0.9140	 0.5770
La	 0.9890	 0.6660
Lb	 0.9890	 0.6460
Lc	 0.9870	 0.6280
Ld	 0.9870	 0.6840
Le	 0.9740	 0.6170
Lf	 0.9950	 0.6300
Lg	 0.9590	 0.6270



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Chain	Atom inclusion	Q-score
Lh	 0.9980	 0.7010
Li	 0.9960	 0.7090
Lj	 0.9910	 0.6620
Lk	 0.9880	 0.6450
Ll	 0.9800	 0.6170
Lm	 0.9980	 0.7120
Ln	 0.9570	 0.5920
Lo	 0.9950	 0.6940
Lp	 0.9850	 0.6650
Lq	 1.0000	 0.6730
Lr	 0.9830	 0.6600
Ls	 0.9960	 0.6740
Lt	 0.8460	 0.5180
sA	 0.9850	 0.5740
sB	 0.9940	 0.6390
sC	 0.9860	 0.5550
sD	 0.9670	 0.3550
sE	 0.9840	 0.5990
sF	 0.9950	 0.6590
sG	 0.9720	 0.5770
sH	 0.9890	 0.6200
sI	 0.9820	 0.6300
sJ	 0.9800	 0.5640
sK	 0.9870	 0.5950
sL	 0.9890	 0.6140
sM	 0.9980	 0.6630
sN	 0.9360	 0.3470
sO	 0.9850	 0.5620
sP	 0.9860	 0.5990
sQ	 0.9930	 0.6270
sR	 0.9930	 0.6500
sS	 0.9940	 0.6240
sT	 0.9730	 0.5500
sU	 0.9460	 0.5260
sV	 0.9900	 0.6220
sW	 0.9710	 0.5680
sX	 0.9780	 0.6410
sY	 0.9910	 0.6320
sZ	 0.9910	 0.6410
sa	 0.9890	 0.6260
sb	 0.9930	 0.6760
sc	 0.9900	 0.6810

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Chain	Atom inclusion	Q-score
sd	 0.9650	 0.5890
se	 0.9930	 0.6690
sf	 0.9750	 0.6210
sg	 0.9890	 0.5770
sh	 0.6700	 0.2320
sj	 0.9450	 0.1420
sk	 0.5530	 0.1880
sl	 0.9240	 0.2800
sm	 0.9810	 0.3350
sn	 0.9900	 0.5100