



wwPDB EM Validation Summary Report ⓘ

Jul 15, 2024 – 03:18 pm BST

PDB ID : 7ZW0
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.dev92
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

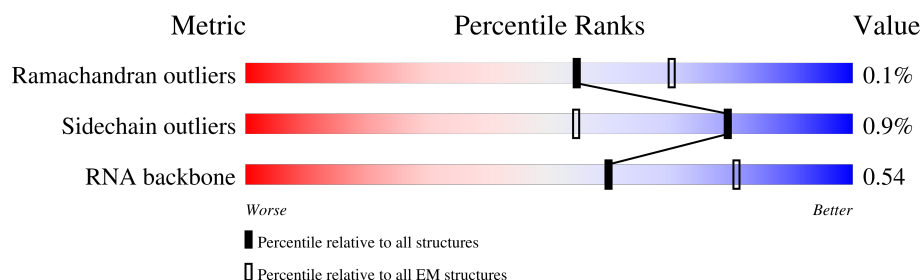
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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.



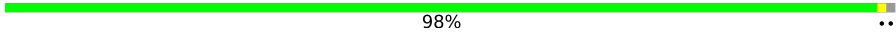

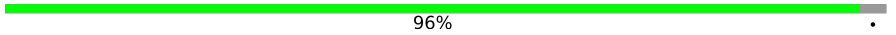
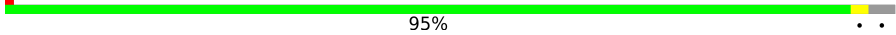
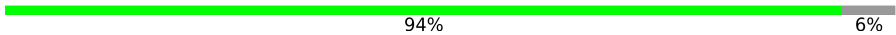
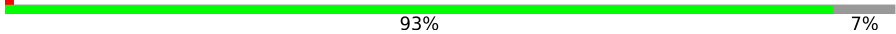



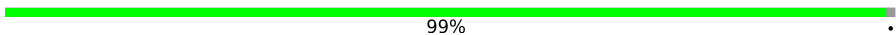

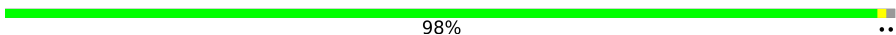


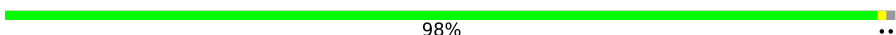

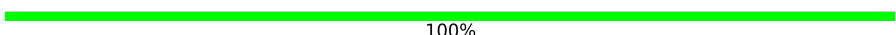
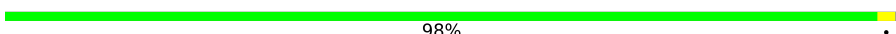
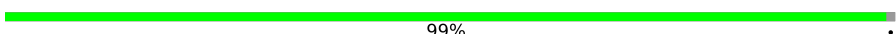
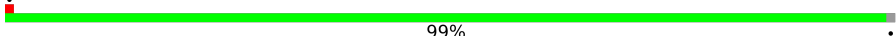


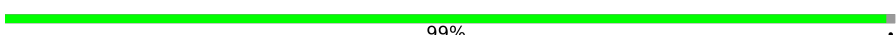


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	LA	3396	
2	LB	217	
3	2	1800	
4	sP	252	
5	sQ	255	
6	sE	142	
7	sR	254	
8	sA	240	

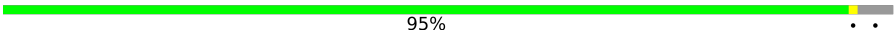
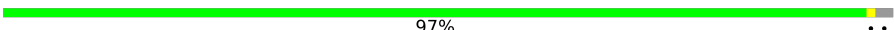


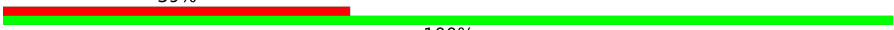
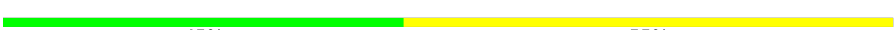




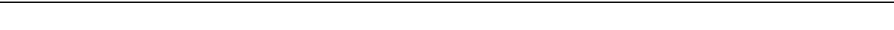

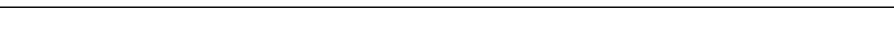
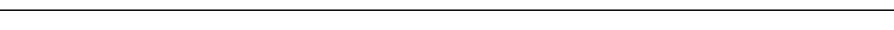
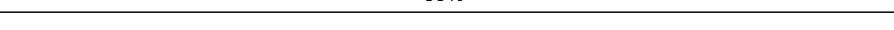
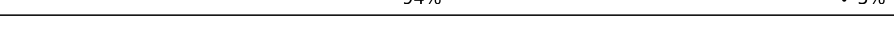


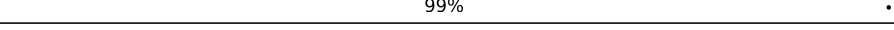
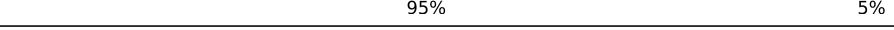
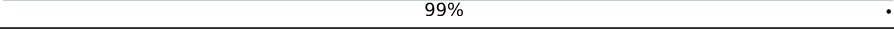
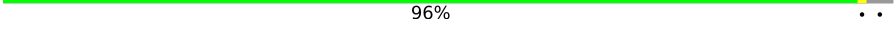
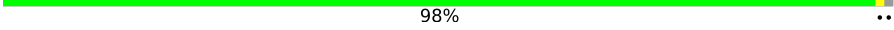
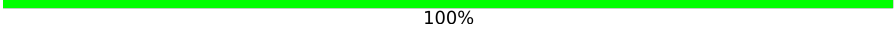
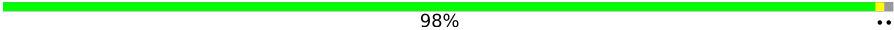
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Mol	Chain	Length	Quality of chain
9	sS	261	 98%
10	sB	225	 91%8%
11	sT	236	 96%
12	sU	190	 95%
13	sV	200	 94%6%
14	sW	197	 93%7%
15	sC	105	 87%12%
16	sX	156	 90%9%
17	sD	143	 81%15%
18	sY	151	 99%
19	sZ	137	 91%7%
20	sF	143	 98%
21	sG	136	 90%8%
22	sH	146	 99%
23	sI	144	 98%
24	sJ	121	 83%17%
25	sa	87	 100%
26	sb	130	 98%
27	sc	145	 99%
28	sd	135	 99%
29	sK	108	 65%35%
30	se	119	 82%18%
31	sf	82	 99%
32	sM	56	 93%5%
33	sg	63	 92%8%

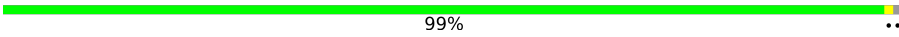
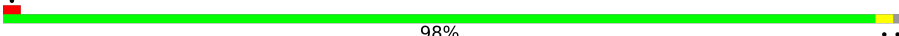
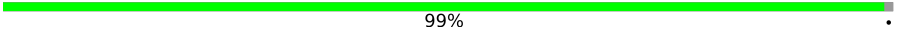
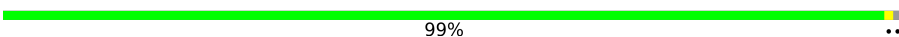


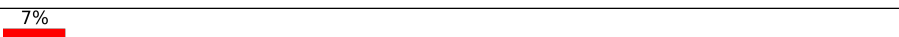
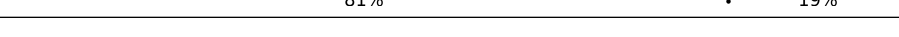
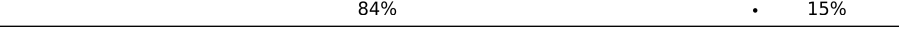
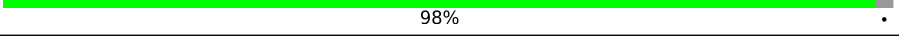
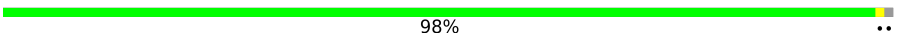
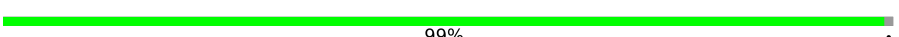



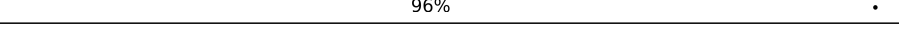
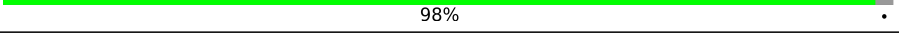
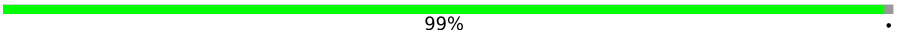
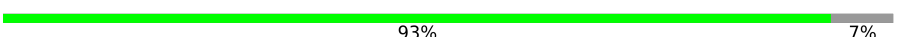
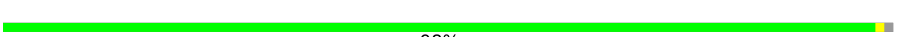

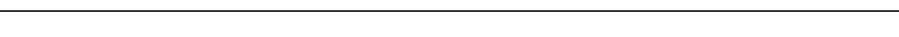
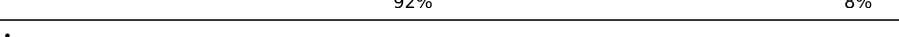
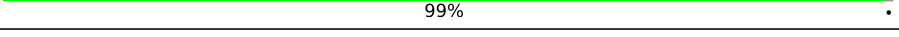
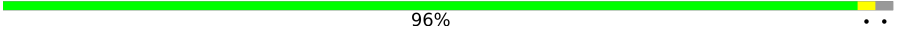
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Mol	Chain	Length	Quality of chain
34	sN	76	 95% . .
35	sO	319	 97% ..
36	sL	67	 94% 6%
37	sj	235	 57% 43%
38	sk	114	 39% 100%
39	sm	29	 45% 55%
40	sl	76	 68% 29% .
40	sn	76	 70% 29% .
41	LC	121	 88% 12%
42	LD	158	 82% 18% .
43	LE	254	 98% .
44	LF	387	 99% .
45	LG	362	 99% .
46	LH	297	 99% .
47	LI	176	 94% . 5%
48	LJ	244	 91% 9%
49	LK	256	 90% . 9%
50	LL	191	 99% .
51	LM	221	 95% 5%
52	LN	174	 99% .
53	LO	199	 96% . .
54	LP	138	 98% ..
55	LQ	204	 100%
56	LR	199	 98% ..
57	LS	184	 99% .

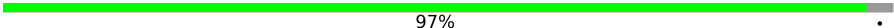
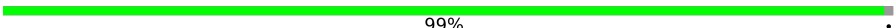

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Mol	Chain	Length	Quality of chain
58	LT	186	 99% ..
59	LU	189	 98% ..
60	LV	172	 99% .
61	LW	160	 99% ..
62	LX	121	 82% . 17%
63	LY	137	 99% .
64	LZ	155	 7% 81% . 19%
65	La	142	 84% . 15%
66	Lb	127	 98% .
67	Lc	136	 98% ..
68	Ld	149	 99% .
69	Le	59	 92% 7% .
70	Lf	105	 91% 9%
71	Lg	113	 96% .
72	Lh	130	 98% .
73	Li	107	 99% .
74	Lj	121	 93% 7%
75	Lk	120	 98% ..
76	Ll	100	 99% .
77	Lm	88	 92% 8%
78	Ln	78	 99% .
79	Lo	51	 96% ..
80	Lp	52	 100%
81	Lq	25	 100%
81	Lt	25	 88% 12%

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Mol	Chain	Length	Quality of chain
82	Lr	106	 97%
83	Ls	92	 99%
84	sh	965	 17% 73% 7% 20%

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		

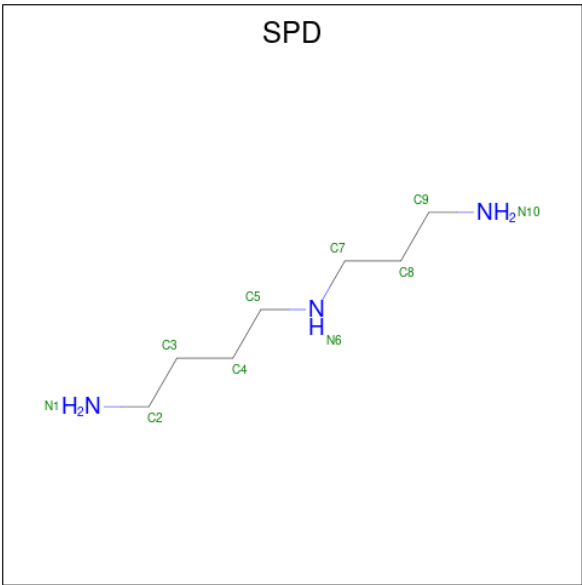
- Molecule 84 is a protein called FAP1 isoform 1.

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 (three-letter code: 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 (three-letter code: SPD) (formula: C₇H₁₉N₃).



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

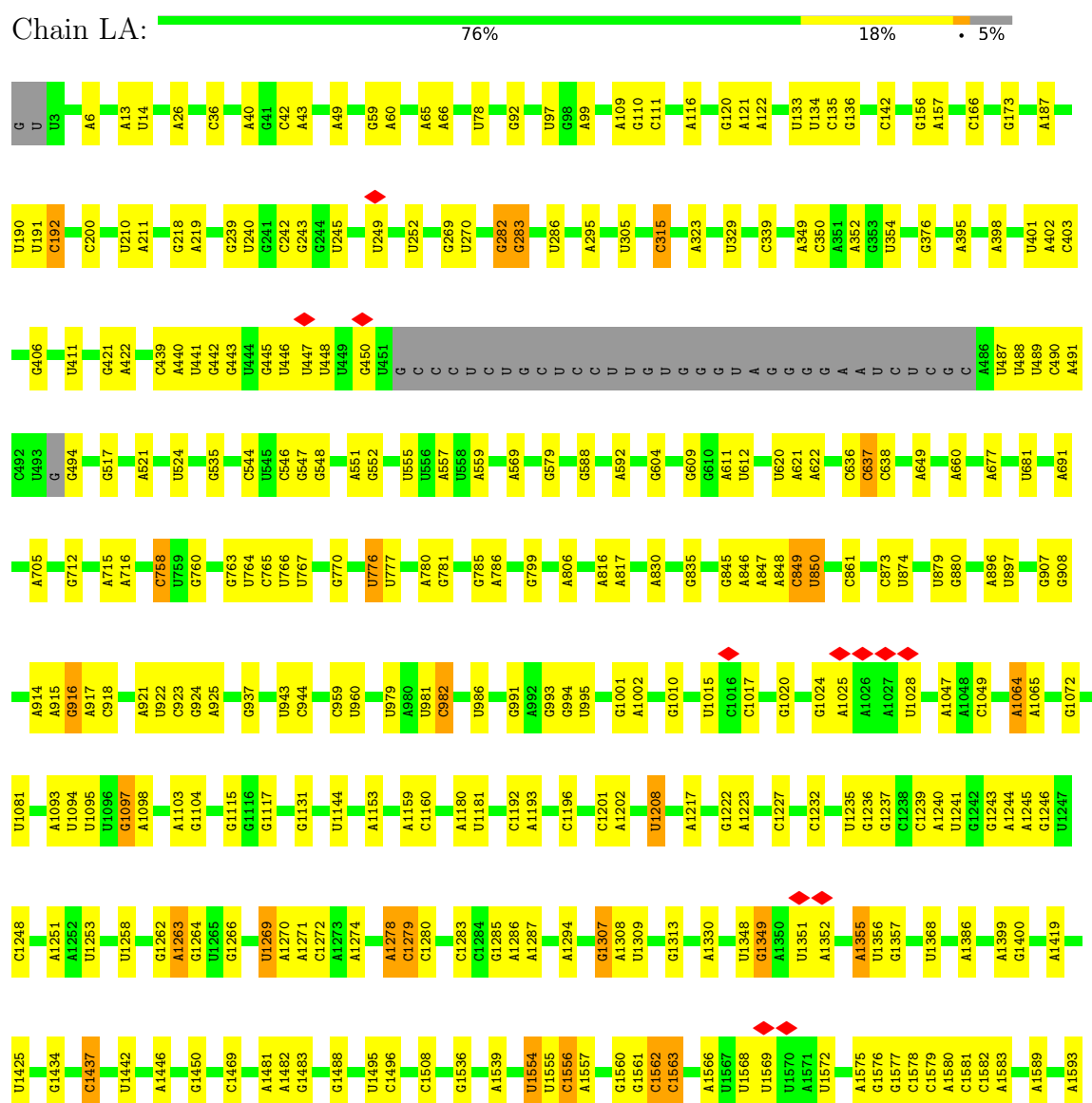
- Molecule 87 is ZINC ION (three-letter code: ZN) (formula: Zn).

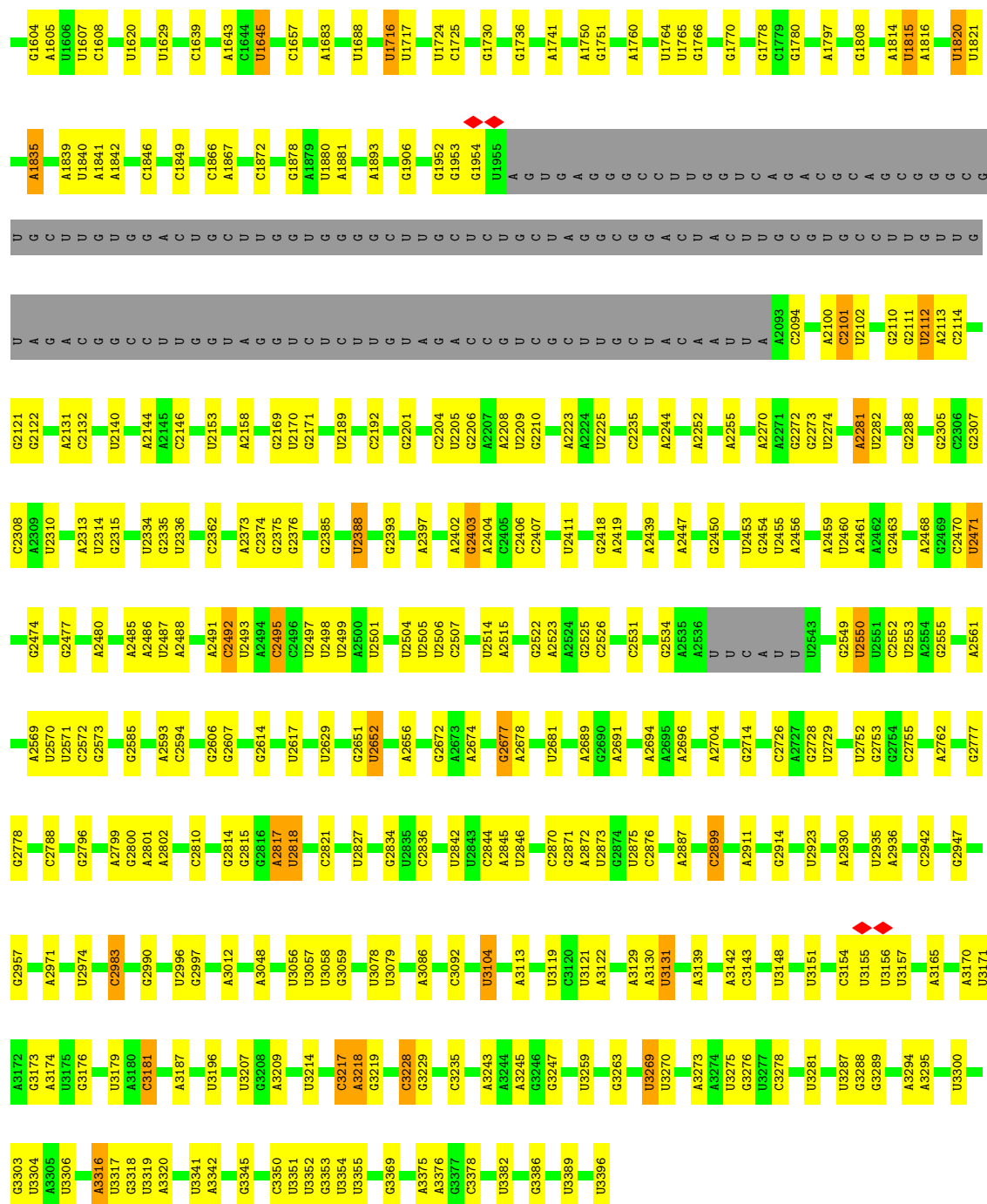
Mol	Chain	Residues	Atoms		AltConf
87	sM	1	Total	Zn	0
			1	1	
87	sN	1	Total	Zn	0
			1	1	
87	Lj	1	Total	Zn	0
			1	1	
87	Lm	1	Total	Zn	0
			1	1	
87	Lp	1	Total	Zn	0
			1	1	
87	Lr	1	Total	Zn	0
			1	1	
87	Ls	1	Total	Zn	0
			1	1	
87	sh	27	Total	Zn	0
			27	27	

3 Residue-property plots

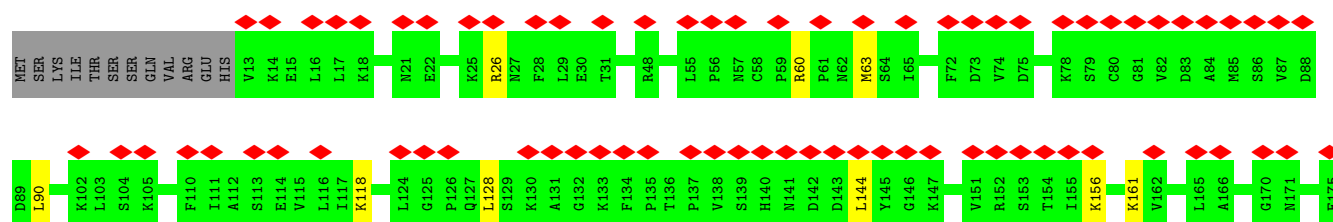
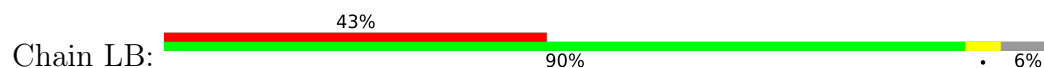
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

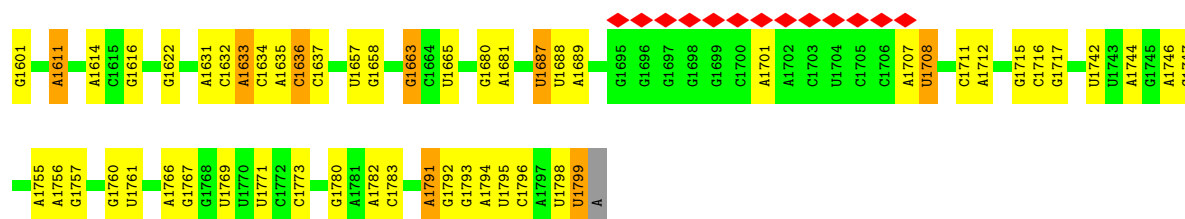
• Molecule 1: 25S ribosomal RNA (RDN25-1)





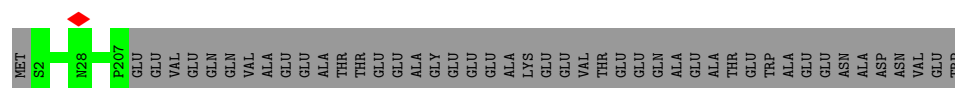
• Molecule 2: 60S ribosomal protein L1-A





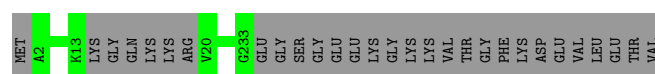
- Molecule 4: 40S ribosomal protein S0-A

Chain sP: 82% 18%



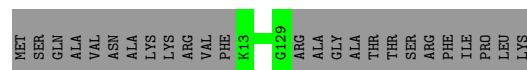
- Molecule 5: 40S ribosomal protein S1-A

Chain sQ: 89% 11%



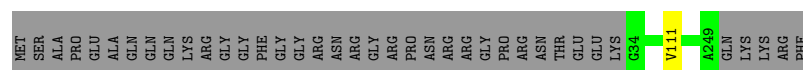
- Molecule 6: RPS15 isoform 1

Chain sE: 82% 18%



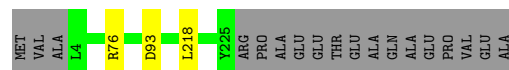
- Molecule 7: 40S ribosomal protein S2

Chain sR: 85% 15%



- Molecule 8: 40S ribosomal protein S3

Chain sA: 91% 8%



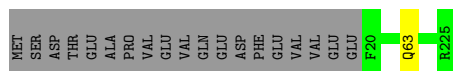
- Molecule 9: 40S ribosomal protein S4-B

Chain sS: 98% 2%



- Molecule 10: 40S ribosomal protein S5

Chain sB:  91% 8%



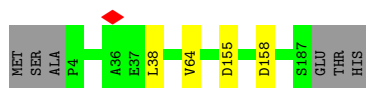
- Molecule 11: 40S ribosomal protein S6-B

Chain sT:  96% .



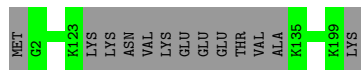
- Molecule 12: 40S ribosomal protein S7-A

Chain sU:  95% . .



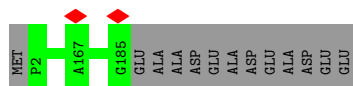
- Molecule 13: 40S ribosomal protein S8-A

Chain sV:  94% 6%



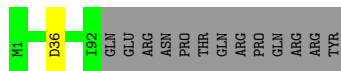
- Molecule 14: 40S ribosomal protein S9-A

Chain sW:  93% 7%



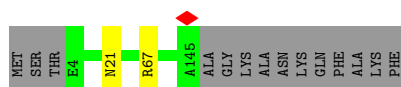
- Molecule 15: 40S ribosomal protein S10-A

Chain sC:  87% . 12%




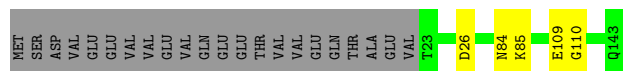
- Molecule 16: 40S ribosomal protein S11-A

Chain sX:  90% . 9%



- Molecule 17: 40S ribosomal protein S12

Chain sD:  81% 15%



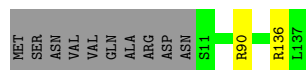
- Molecule 18: 40S ribosomal protein S13

Chain sY:  99%



- Molecule 19: 40S ribosomal protein S14-A

Chain sZ:  91% 7%



- Molecule 20: 40S ribosomal protein S16-A

Chain sF:  98%



- Molecule 21: 40S ribosomal protein S17-A

Chain sG:  90% 8%



- Molecule 22: 40S ribosomal protein S18-A

Chain sH:  99%




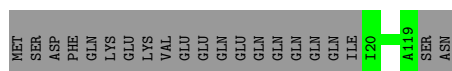
- Molecule 23: 40S ribosomal protein S19-A

Chain sI:  98%



- Molecule 24: 40S ribosomal protein S20

Chain sJ:  83% 17%



- Molecule 25: 40S ribosomal protein S21-A

Chain sa:  100%

There are no outlier residues recorded for this chain.

- Molecule 26: 40S ribosomal protein S22-A

Chain sb:  98% ..



- Molecule 27: 40S ribosomal protein S23-A

Chain sc:  99% .



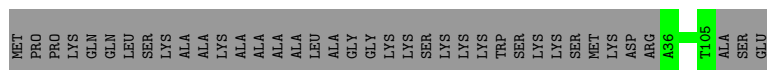
- Molecule 28: 40S ribosomal protein S24-A

Chain sd:  99% .




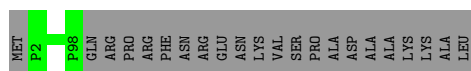
- Molecule 29: 40S ribosomal protein S25-A

Chain sK:  65% 35%



- Molecule 30: 40S ribosomal protein S26-A

Chain se:  82% 18%



- Molecule 31: 40S ribosomal protein S27-A

Chain sf:  99% .



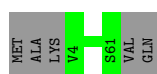
- Molecule 32: RPS29A isoform 1

Chain sM: 93% 5%



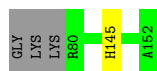
- Molecule 33: 40S ribosomal protein S30-A

Chain sg: 92% 8%



- Molecule 34: 40S ribosomal protein S31

Chain sN: 95% ..



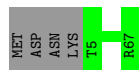
- Molecule 35: Guanine nucleotide-binding protein subunit beta-like protein

Chain sO: 97% ..



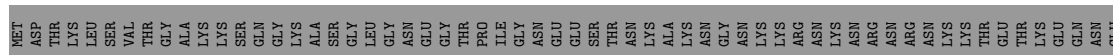
- Molecule 36: 40S ribosomal protein S28-A

Chain sL: 94% 6%

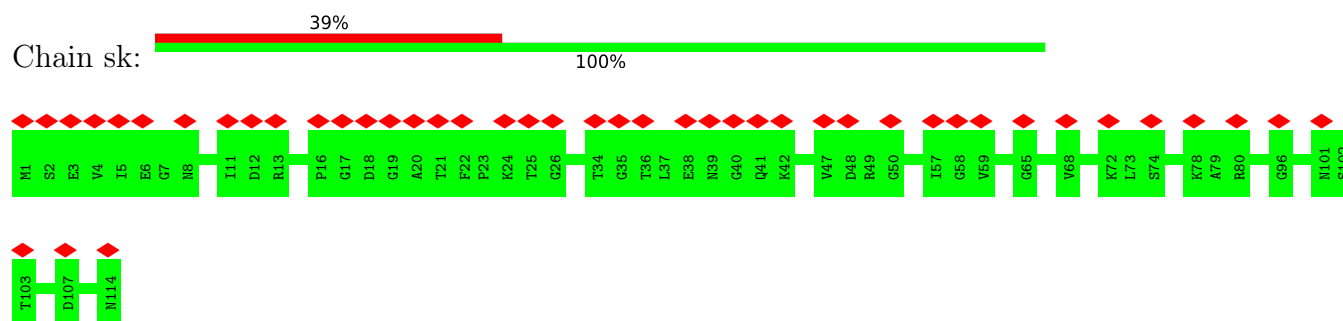


- Molecule 37: Uncharacterized protein YIL161W

Chain sj: 57% 43%



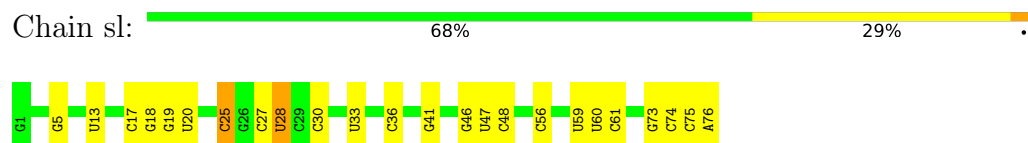
- Molecule 38: FK506-binding protein 1



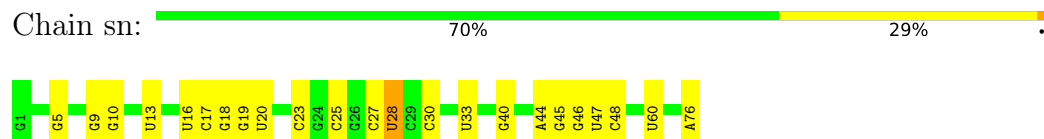
- Molecule 39: mRNA



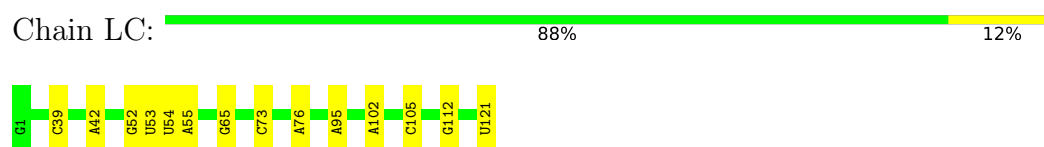
- Molecule 40: tRNA



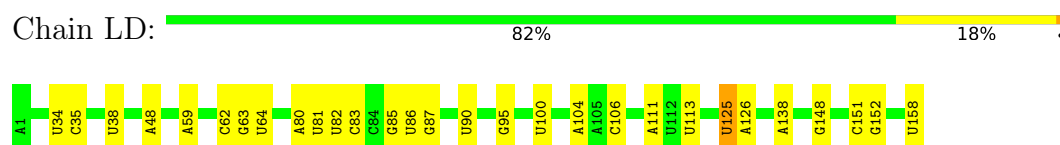
- Molecule 40: tRNA



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



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



- Molecule 43: 60S ribosomal protein L2-A





- Molecule 44: 60S ribosomal protein L3

Chain LF: 99%



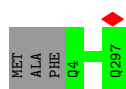
- Molecule 45: 60S ribosomal protein L4-A

Chain LG: 99%



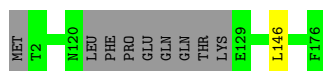
- Molecule 46: 60S ribosomal protein L5

Chain LH: 99%



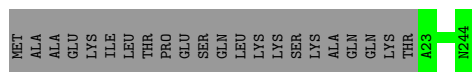
- Molecule 47: 60S ribosomal protein L6-B

Chain LI: 94% 5%



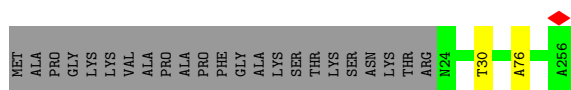
- Molecule 48: 60S ribosomal protein L7-A

Chain LJ: 91% 9%



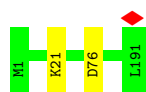
- Molecule 49: 60S ribosomal protein L8-A

Chain LK: 90% 9%



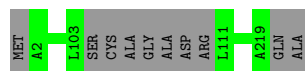
- Molecule 50: 60S ribosomal protein L9-A

Chain LL: 99%



- Molecule 51: 60S ribosomal protein L10

Chain LM: 95% 5%



- Molecule 52: 60S ribosomal protein L11-A

Chain LN: 99% .



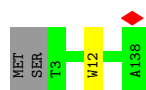
- Molecule 53: 60S ribosomal protein L13-A

Chain LO: 96% ..



- Molecule 54: 60S ribosomal protein L14-A

Chain LP: 98% ..



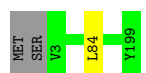
- Molecule 55: 60S ribosomal protein L15-A

Chain LQ: 100%



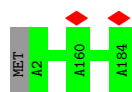
- Molecule 56: 60S ribosomal protein L16-A

Chain LR: 98% ..



- Molecule 57: 60S ribosomal protein L17-A

Chain LS: 99% .



- Molecule 58: 60S ribosomal protein L18-A

Chain LT: 99% ..



- Molecule 59: 60S ribosomal protein L19-A

Chain LU: 98% ..



- Molecule 60: 60S ribosomal protein L20-A

Chain LV: 99% .



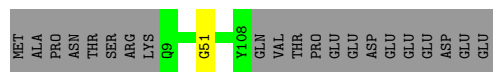
- Molecule 61: 60S ribosomal protein L21-A

Chain LW: 99% ..



- Molecule 62: 60S ribosomal protein L22-A

Chain LX: 82% . 17%



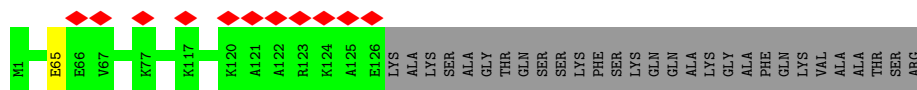
- Molecule 63: 60S ribosomal protein L23-A

Chain LY: 99% .



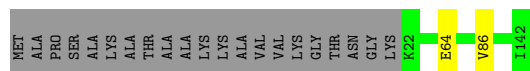
- Molecule 64: 60S ribosomal protein L24-A

Chain LZ: 7% 81% . 19%



- Molecule 65: 60S ribosomal protein L25

Chain La: 84% 15%



- Molecule 66: 60S ribosomal protein L26-A

Chain Lb: 98% .



- Molecule 67: 60S ribosomal protein L27-A

Chain Lc: 98% ..



- Molecule 68: 60S ribosomal protein L28

Chain Ld: 99% .



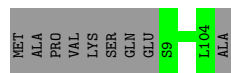
- Molecule 69: 60S ribosomal protein L29

Chain Le: 92% 7% .



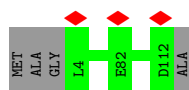
- Molecule 70: 60S ribosomal protein L30

Chain Lf: 91% 9%



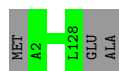
- Molecule 71: 60S ribosomal protein L31-A

Chain Lg: 96% .



- Molecule 72: 60S ribosomal protein L32

Chain Lh: 98%



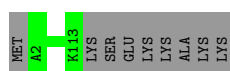
- Molecule 73: 60S ribosomal protein L33-A

Chain Li: 99%



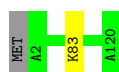
- Molecule 74: 60S ribosomal protein L34-A

Chain Lj: 93% 7%



- Molecule 75: 60S ribosomal protein L35-A

Chain Lk: 98% ..



- Molecule 76: 60S ribosomal protein L36-A

Chain Ll: 99%



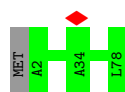
- Molecule 77: 60S ribosomal protein L37-A

Chain Lm: 92% 8%



- Molecule 78: 60S ribosomal protein L38

Chain Ln: 99%



- Molecule 79: 60S ribosomal protein L39

Chain Lo: 96%



- Molecule 80: 60S ribosomal protein L40-A

Chain Lp: 100%

There are no outlier residues recorded for this chain.

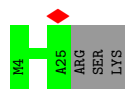
- Molecule 81: 60S ribosomal protein L41-A

Chain Lq: 100%

There are no outlier residues recorded for this chain.

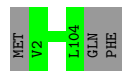
- Molecule 81: 60S ribosomal protein L41-A

Chain Lt: 88% 12%



- Molecule 82: 60S ribosomal protein L42-A

Chain Lr: 97%



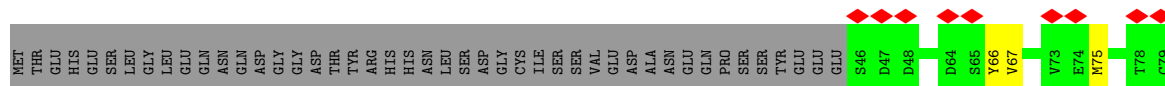
- Molecule 83: 60S ribosomal protein L43-A

Chain Ls: 99%



- Molecule 84: FAP1 isoform 1

Chain sh: 17% 73% 7% 20%





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	2.0	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: ZN, MG, SPD

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	0.75	0/77021	0.99	229/120082 (0.2%)
2	LB	0.30	0/1634	0.74	4/2195 (0.2%)
3	2	0.78	0/42071	1.03	165/65553 (0.3%)
4	sP	0.36	0/1644	0.59	0/2249
5	sQ	0.35	0/1823	0.61	0/2447
6	sE	0.41	0/936	0.71	0/1259
7	sR	0.40	0/1656	0.65	0/2251
8	sA	0.38	0/1754	0.65	2/2361 (0.1%)
9	sS	0.42	0/2097	0.70	3/2823 (0.1%)
10	sB	0.38	0/1625	0.60	0/2197
11	sT	0.34	0/1839	0.63	0/2460
12	sU	0.35	0/1498	0.71	3/2019 (0.1%)
13	sV	0.39	0/1501	0.65	0/2006
14	sW	0.36	0/1504	0.64	0/2016
15	sC	0.43	0/769	0.72	1/1039 (0.1%)
16	sX	0.42	0/1168	0.60	0/1575
17	sD	0.35	0/883	0.88	1/1199 (0.1%)
18	sY	0.41	0/1215	0.68	0/1638
19	sZ	0.39	0/934	0.68	0/1257
20	sF	0.40	0/1125	0.62	0/1510
21	sG	0.38	0/989	0.68	0/1327
22	sH	0.42	0/1207	0.68	0/1623
23	sI	0.43	0/1130	0.73	2/1517 (0.1%)
24	sJ	0.40	0/807	0.67	0/1091
25	sa	0.41	0/682	0.68	0/921
26	sb	0.41	0/1038	0.67	1/1395 (0.1%)
27	sc	0.39	0/1139	0.59	0/1518
28	sd	0.38	0/1087	0.61	0/1449
29	sK	0.39	0/571	0.67	0/768
30	se	0.41	0/778	0.74	0/1042
31	sf	0.36	0/620	0.60	0/838
32	sM	0.45	0/452	0.66	0/600

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	sg	0.36	0/458	0.69	0/610
34	sN	0.34	0/567	0.72	0/764
35	sO	0.36	0/2436	0.65	0/3318
36	sL	0.40	0/493	0.71	0/663
37	sj	0.26	0/1149	0.57	0/1541
38	sk	0.27	0/878	0.56	0/1192
39	sm	0.47	0/714	0.87	0/1111
40	sl	0.37	0/1810	1.06	8/2821 (0.3%)
40	sn	0.52	0/1810	1.09	8/2821 (0.3%)
41	LC	0.69	0/2883	0.91	2/4491 (0.0%)
42	LD	0.78	0/3746	0.93	3/5832 (0.1%)
43	LE	0.41	0/1933	0.67	1/2598 (0.0%)
44	LF	0.39	0/3146	0.62	0/4228
45	LG	0.40	0/2800	0.63	1/3790 (0.0%)
46	LH	0.36	0/2400	0.61	0/3239
47	LI	0.35	0/1329	0.63	1/1794 (0.1%)
48	LJ	0.40	0/1821	0.59	0/2451
49	LK	0.36	0/1836	0.58	0/2481
50	LL	0.37	0/1529	0.61	1/2060 (0.0%)
51	LM	0.41	0/1755	0.62	0/2353
52	LN	0.33	0/1386	0.61	0/1859
53	LO	0.36	0/1568	0.65	0/2106
54	LP	0.39	0/1068	0.61	0/1438
55	LQ	0.41	0/1757	0.66	0/2354
56	LR	0.41	0/1585	0.62	1/2128 (0.0%)
57	LS	0.39	0/1439	0.65	0/1938
58	LT	0.38	0/1465	0.63	0/1965
59	LU	0.38	0/1538	0.62	0/2050
60	LV	0.46	0/1473	0.62	0/1980
61	LW	0.40	0/1296	0.60	0/1739
62	LX	0.37	0/812	0.60	1/1099 (0.1%)
63	LY	0.38	0/1018	0.63	0/1369
64	LZ	0.34	0/883	0.57	0/1193
65	La	0.44	0/979	0.60	0/1321
66	Lb	0.36	0/995	0.62	0/1329
67	Lc	0.38	0/1106	0.56	0/1485
68	Ld	0.41	0/1200	0.59	0/1607
69	Le	0.32	0/473	0.59	0/629
70	Lf	0.35	0/745	0.51	0/1001
71	Lg	0.39	0/890	0.63	0/1196
72	Lh	0.36	0/1034	0.59	0/1385
73	Li	0.43	0/868	0.64	0/1168
74	Lj	0.38	0/890	0.64	0/1189

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Lk	0.36	0/978	0.60	0/1301
76	Ll	0.34	0/772	0.63	0/1026
77	Lm	0.40	0/660	0.69	0/875
78	Ln	0.36	0/618	0.62	0/826
79	Lo	0.36	0/443	0.73	1/588 (0.2%)
80	Lp	0.34	0/416	0.65	0/553
81	Lq	0.34	0/230	0.75	0/296
81	Lt	0.24	0/208	0.71	0/267
82	Lr	0.37	0/836	0.65	0/1104
83	Ls	0.34	0/701	0.62	0/934
84	sh	0.34	0/6154	0.59	1/8290 (0.0%)
All	All	0.62	0/229174	0.88	440/335971 (0.1%)

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 440 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	LA	3217	C	N1-C2-O2	12.18	126.21	118.90
1	LA	3217	C	C2-N1-C1'	10.79	130.67	118.80
3	2	453	U	C2-N1-C1'	10.52	130.33	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	453	U	N1-C2-O2	10.43	130.10	122.80
3	2	1560	U	N3-C2-O2	-10.26	115.02	122.20

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](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	9	11
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%)	11	15
35	sO	310/319 (97%)	284 (92%)	26 (8%)	0	100	100
36	sL	61/67 (91%)	59 (97%)	2 (3%)	0	100	100
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%)	41	55
46	LH	292/297 (98%)	282 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	29	41
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%)	19	29
68	Ld	146/149 (98%)	132 (90%)	14 (10%)	0	100	100
69	Le	56/59 (95%)	53 (95%)	2 (4%)	1 (2%)	8	10
70	Lf	94/105 (90%)	94 (100%)	0	0	100	100
71	Lg	107/113 (95%)	98 (92%)	9 (8%)	0	100	100
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	34	48
All	All	12203/13284 (92%)	11518 (94%)	675 (6%)	10 (0%)	54	68

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%)	180 (97%)	5 (3%)	44	65
4	sP	170/210 (81%)	170 (100%)	0	100	100
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%)	86	94
8	sA	182/195 (93%)	181 (100%)	1 (0%)	88	95
9	sS	220/222 (99%)	220 (100%)	0	100	100
10	sB	172/191 (90%)	171 (99%)	1 (1%)	86	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	sT	189/201 (94%)	188 (100%)	1 (0%)	88	95
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%)	124 (98%)	2 (2%)	62	79
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%)	89 (99%)	1 (1%)	73	87
20	sF	117/119 (98%)	117 (100%)	0	100	100
21	sG	105/124 (85%)	103 (98%)	2 (2%)	57	75
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%)	46 (98%)	1 (2%)	53	72
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%)	249 (100%)	1 (0%)	91	96
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%)	95 (100%)	0	100	100
43	LE	190/196 (97%)	190 (100%)	0	100	100
44	LF	319/323 (99%)	318 (100%)	1 (0%)	92	97
45	LG	288/289 (100%)	288 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	153 (99%)	1 (1%)	86	94
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%)	149 (99%)	1 (1%)	84	92
59	LU	153/154 (99%)	150 (98%)	3 (2%)	55	74
60	LV	155/156 (99%)	155 (100%)	0	100	100
61	LW	135/137 (98%)	134 (99%)	1 (1%)	84	92
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%)	65 (100%)	0	100	100
65	La	104/118 (88%)	102 (98%)	2 (2%)	57	75
66	Lb	108/110 (98%)	108 (100%)	0	100	100
67	Lc	112/116 (97%)	111 (99%)	1 (1%)	78	90
68	Ld	117/119 (98%)	117 (100%)	0	100	100
69	Le	46/47 (98%)	44 (96%)	2 (4%)	29	46
70	Lf	81/88 (92%)	81 (100%)	0	100	100
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	645 (91%)	64 (9%)	9	14
All	All	10321/11256 (92%)	10229 (99%)	92 (1%)	79	90

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
84	sh	328	CYS
84	sh	534	MET
84	sh	339	THR
84	sh	370	THR
84	sh	573	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
84	sh	184	HIS
84	sh	365	HIS
84	sh	610	GLN
84	sh	601	GLN
50	LL	100	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	LA	3213/3396 (94%)	561 (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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
41	LC	120/121 (99%)	11 (9%)	1 (0%)
42	LD	157/158 (99%)	27 (17%)	1 (0%)
All	All	5429/5656 (95%)	1090 (20%)	78 (1%)

5 of 1090 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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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	C8-C7-N6-C5
86	LA	3618	SPD	C4-C5-N6-C7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

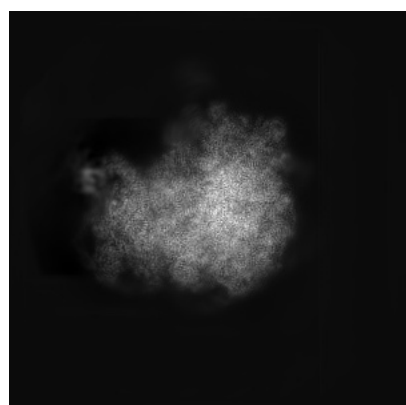
6 Map visualisation [i](#)

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.

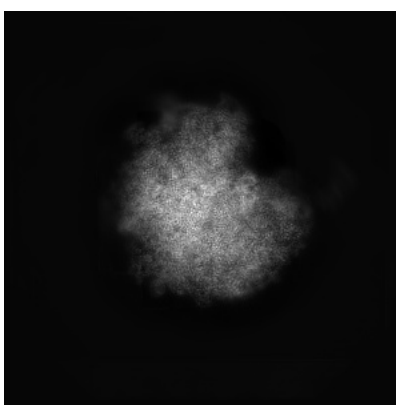
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

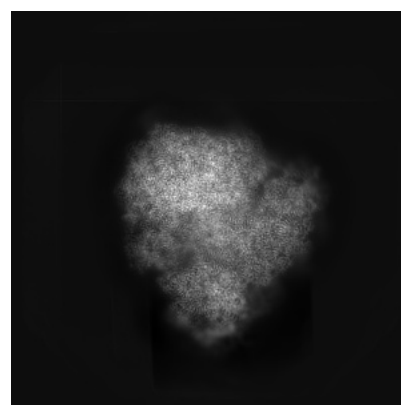
6.1.1 Primary map



X



Y

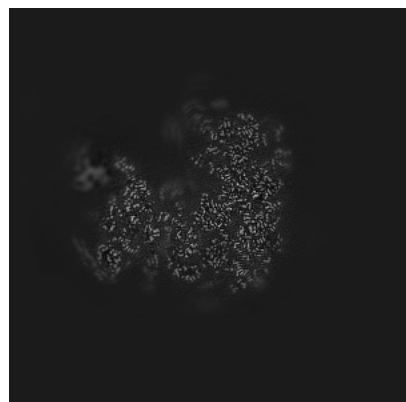


Z

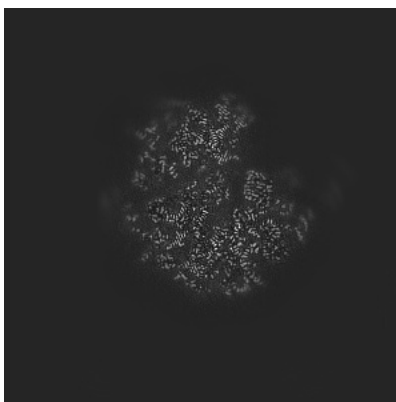
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

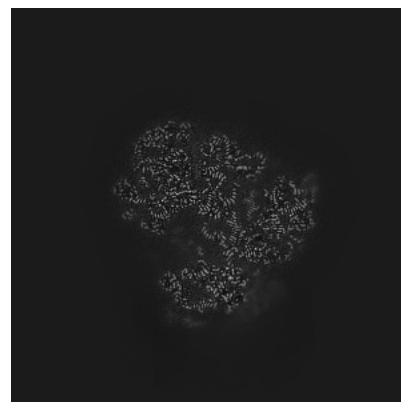
6.2.1 Primary map



X Index: 240



Y Index: 240

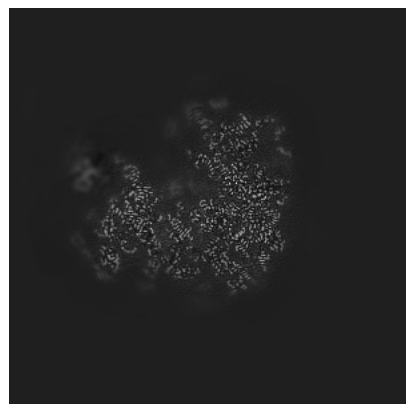


Z Index: 240

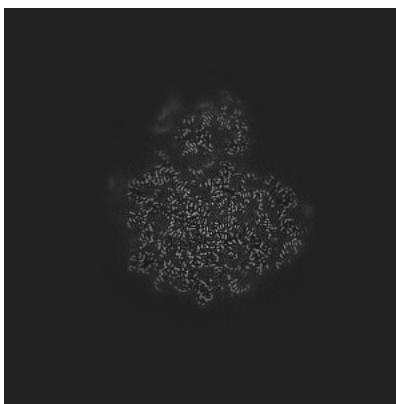
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

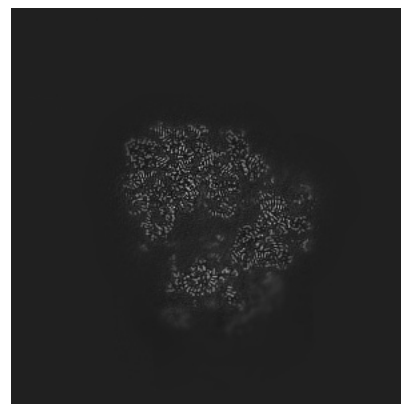
6.3.1 Primary map



X Index: 236



Y Index: 260

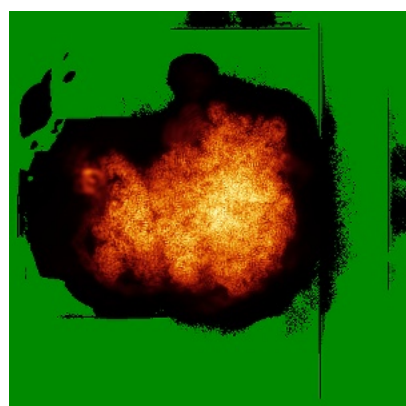


Z Index: 253

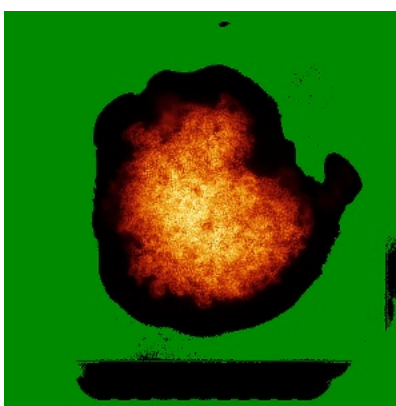
The images above show the largest variance slices of the map in three orthogonal directions.

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

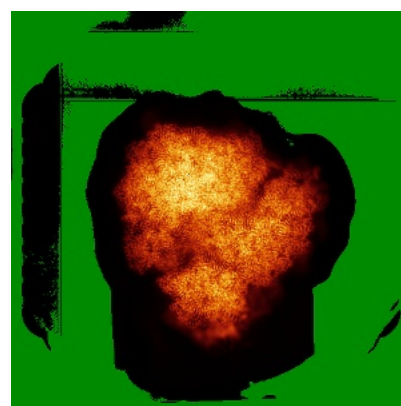
6.4.1 Primary map



X



Y

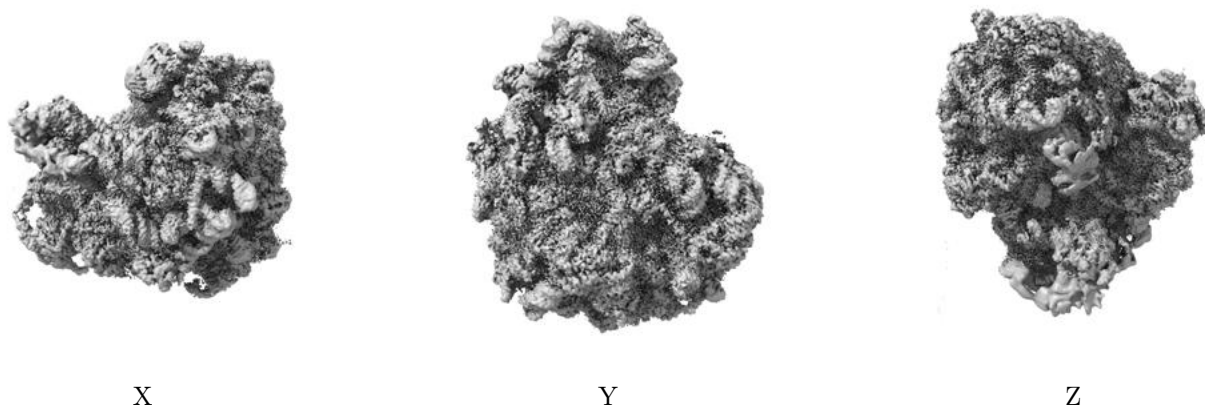


Z

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.

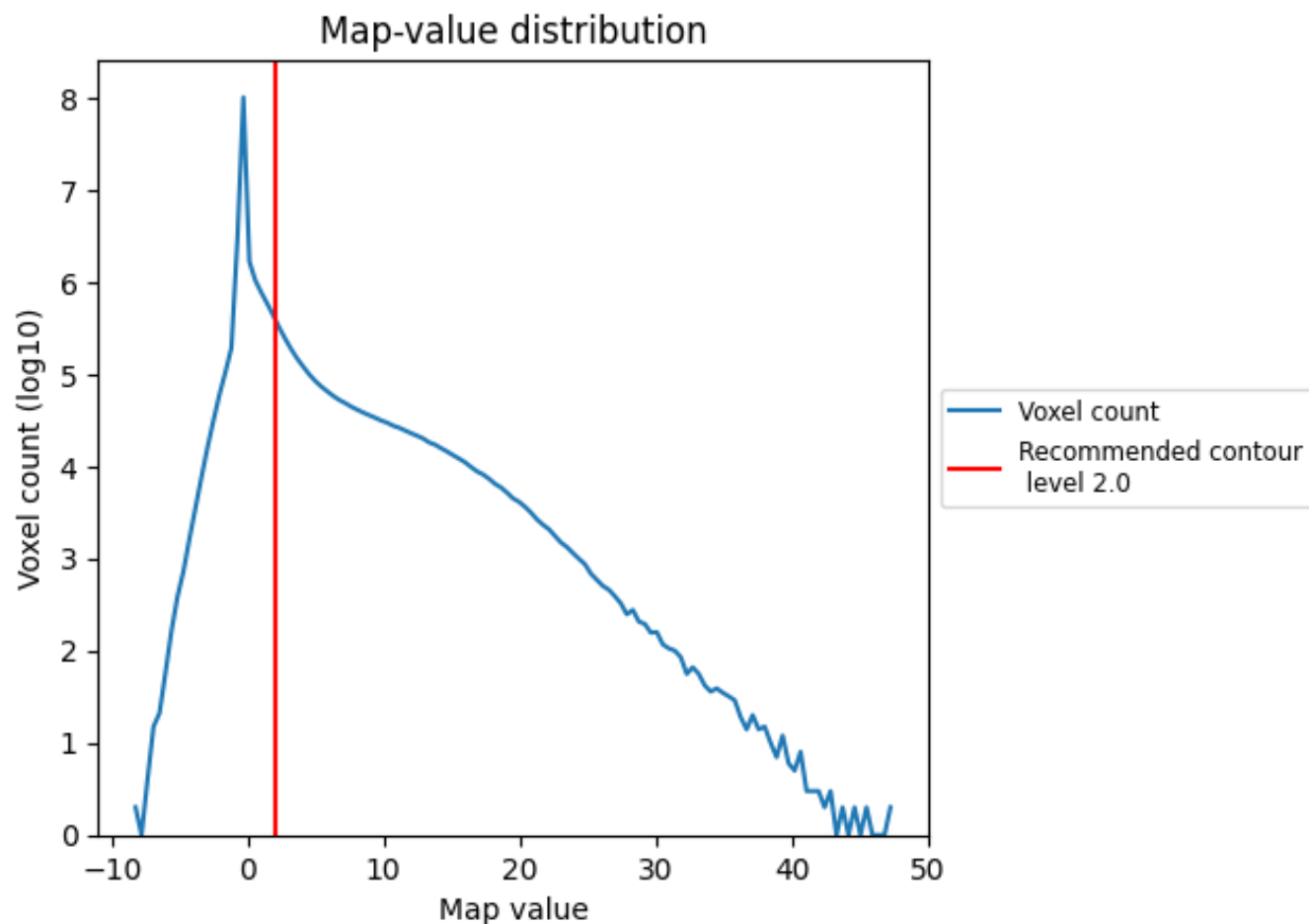
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

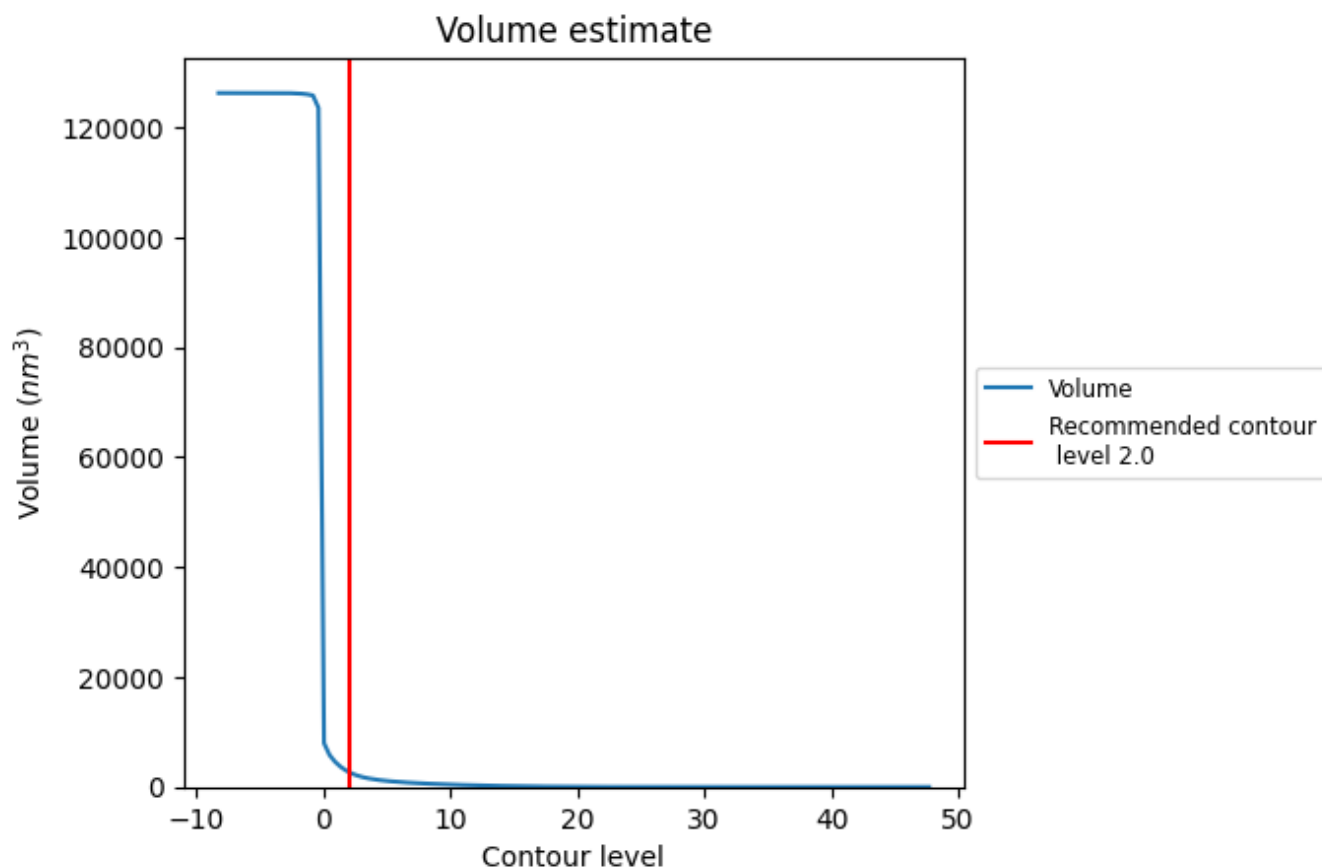
This section contains the results of statistical analysis of the map.

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.

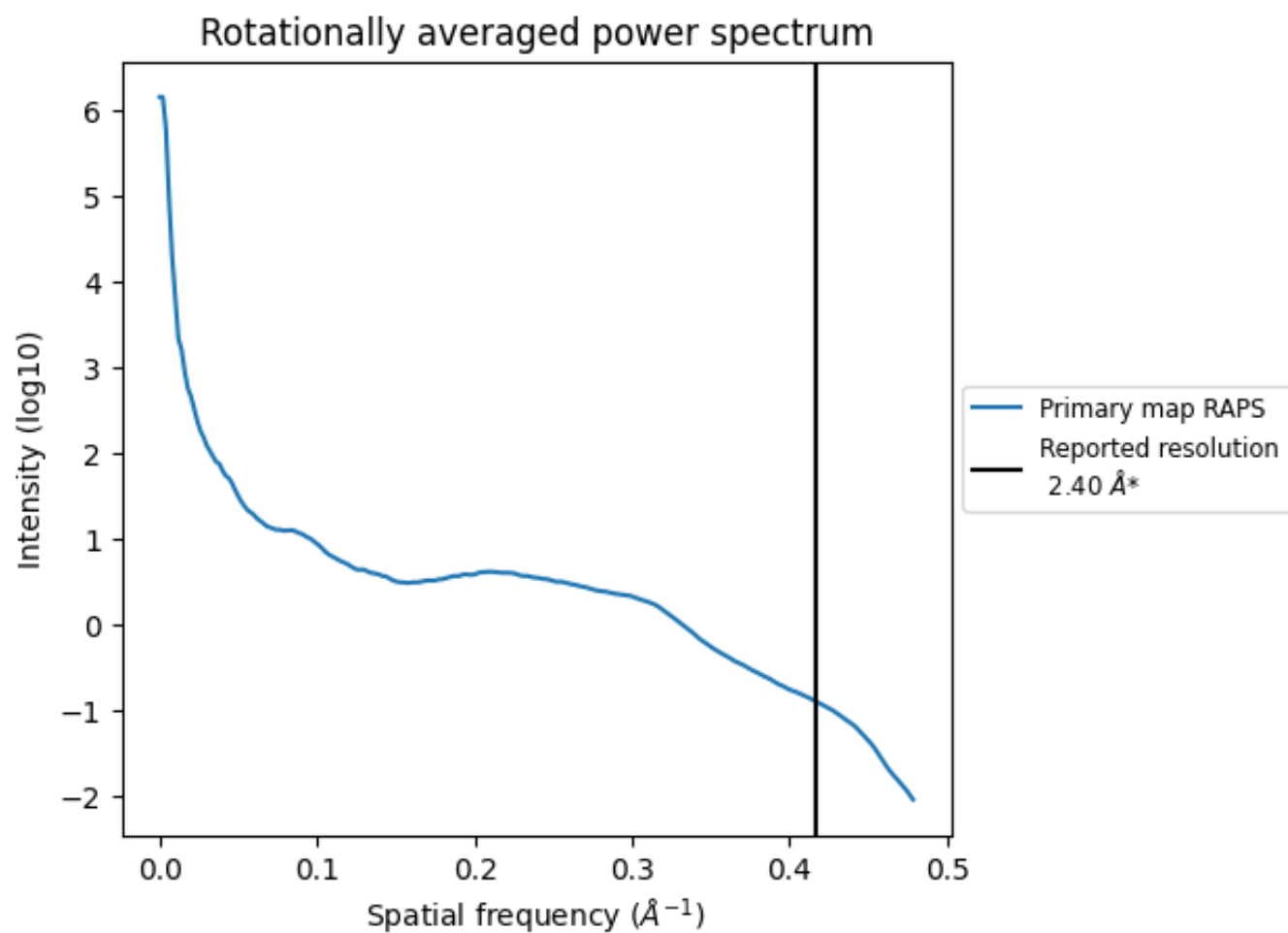
7.2 Volume estimate [i](#)



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

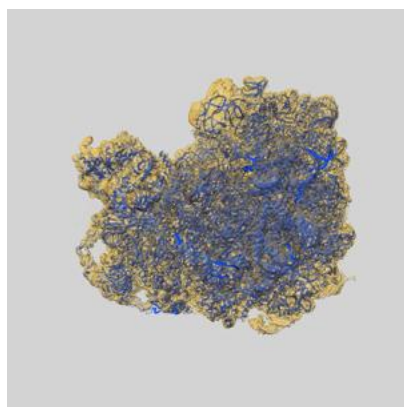
8 Fourier-Shell correlation

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

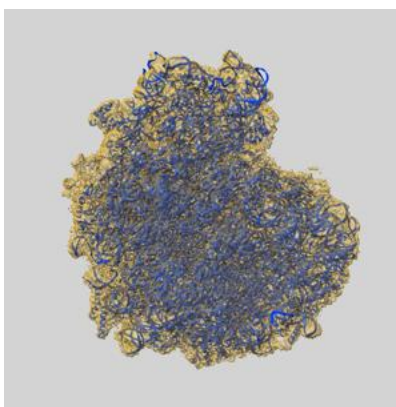
9 Map-model fit [i](#)

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.

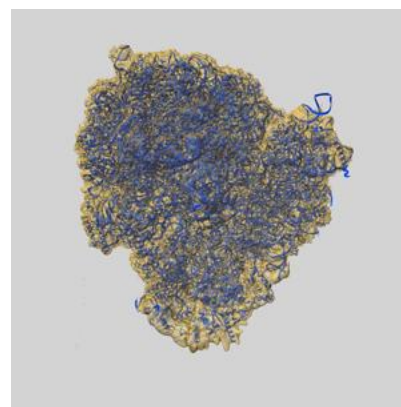
9.1 Map-model overlay [i](#)



X



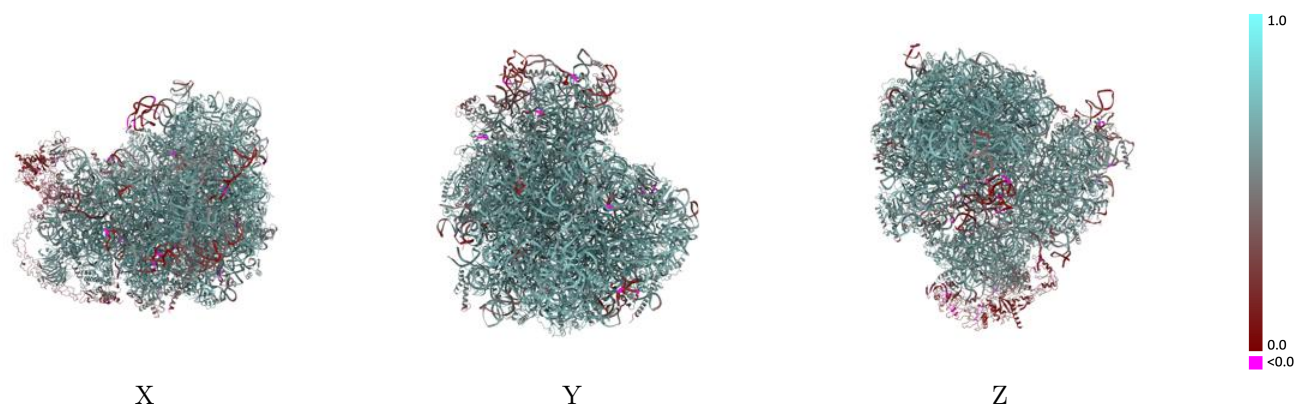
Y



Z

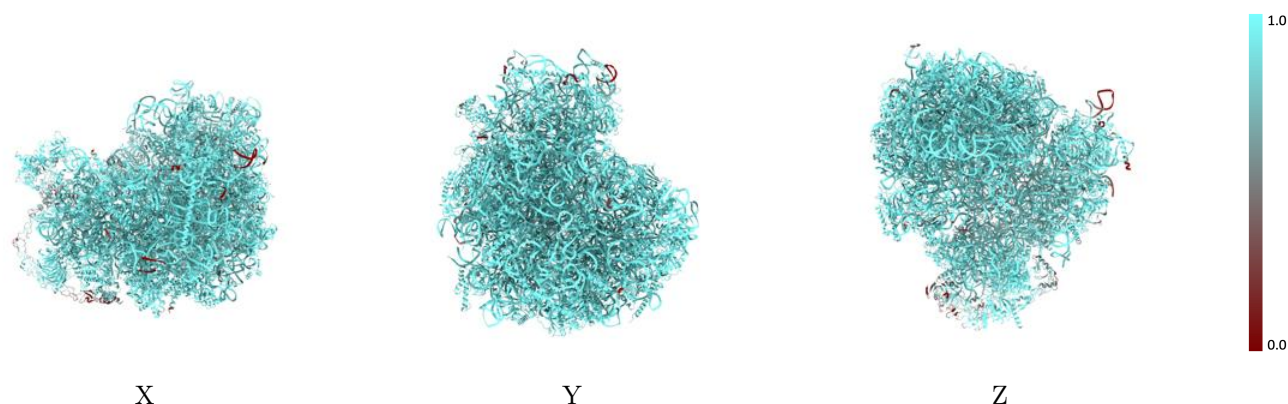
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



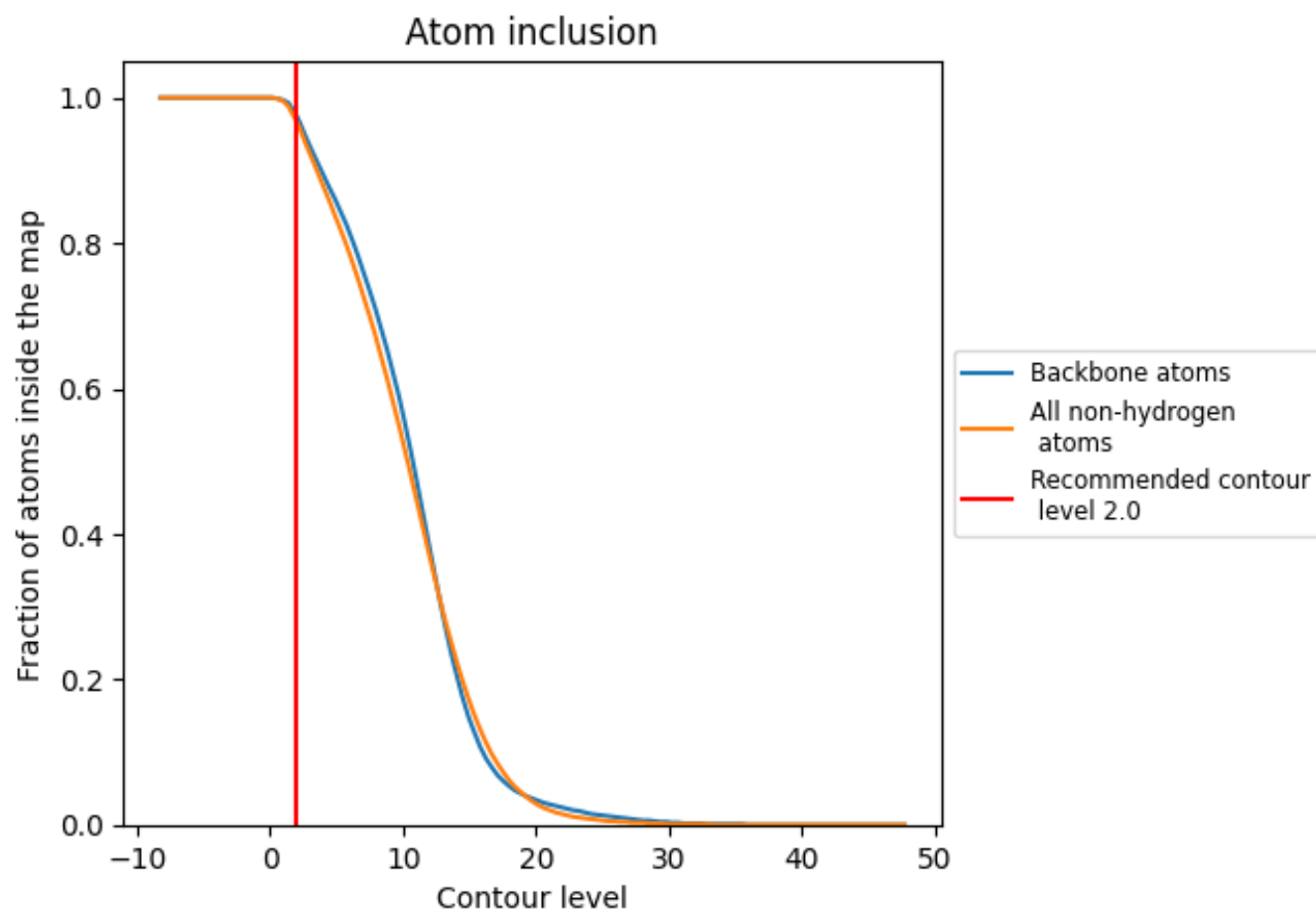
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.0).







































































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 (2.0) 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