



## wwPDB EM Validation Summary Report ⓘ

Nov 11, 2024 – 09:30 PM EST

PDB ID : 7RR5  
EMDB ID : EMD-24652  
Title : Structure of ribosomal complex bound with Rbg1/Tma46  
Authors : Zeng, F.; Li, X.; Pires-Alves, M.; Chen, X.; Hawk, C.W.; Jin, H.  
Deposited on : 2021-08-09  
Resolution : 3.23 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](mailto: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.dev113  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

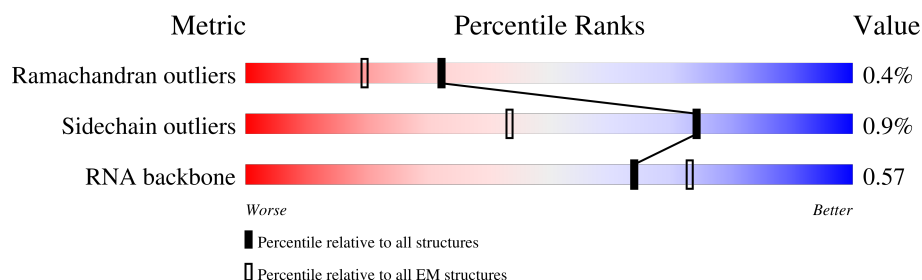
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.23 Å.

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





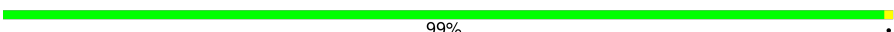

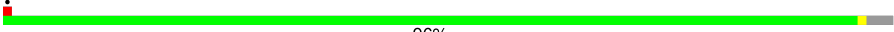







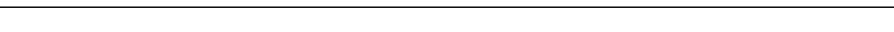

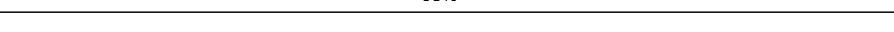

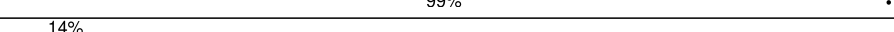


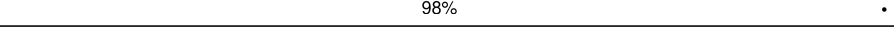
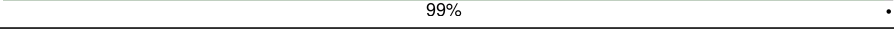
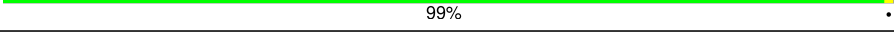
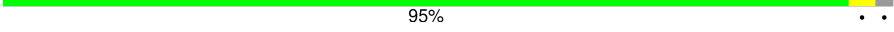

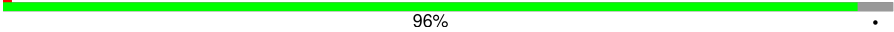
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	C1	3396	
2	C4	121	
3	C3	158	
4	LA	254	
5	LB	387	
6	LC	362	
7	LD	297	
8	LE	176	

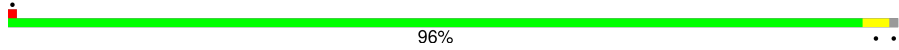
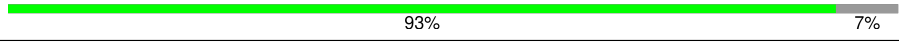
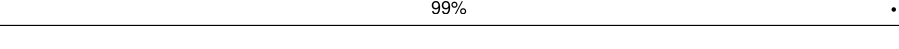
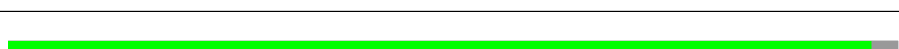
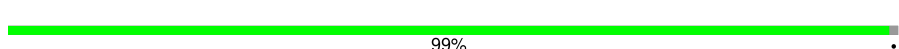
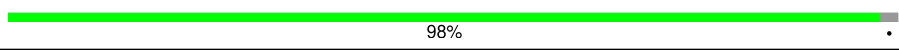
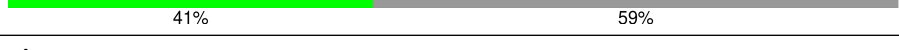
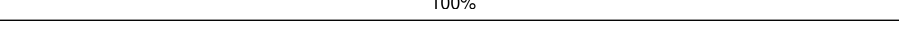



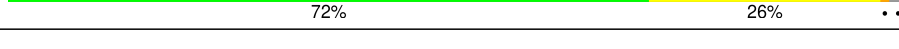

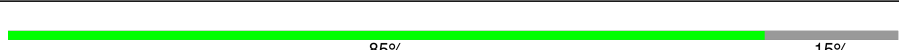
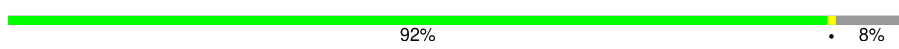
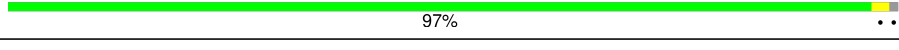
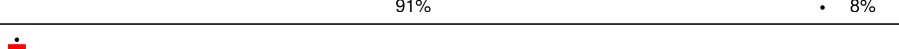


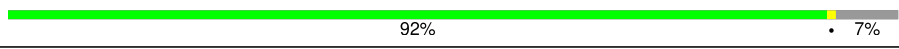




Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	LF	244	 91% 9%
10	LG	256	 90% 9%
11	LH	191	 99%
12	LI	221	 98% ..
13	LJ	174	 96% ..
14	LL	199	 96% ..
15	LM	138	 99% .
16	LN	204	 100%
17	LO	199	 98% ..
18	LP	184	 99% .
19	LQ	186	 98% ..
20	LR	189	 98% ..
21	LS	172	 99% ..
22	LT	160	 98% ..
23	LU	121	 83% 17%
24	LV	137	 99% .
25	LW	155	 14% 81% 19%
26	LX	142	 84% 15%
27	LY	127	 98% .
28	LZ	136	 99% .
29	La	149	 99% ..
30	Lb	59	 95% ..
31	Lc	105	 91% 9%
32	Ld	113	 96% .
33	Le	130	 98% .



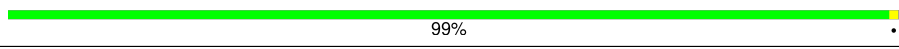
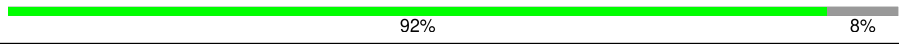

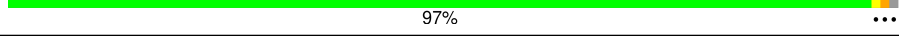
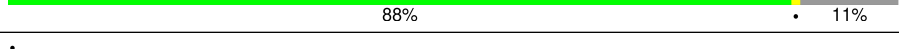
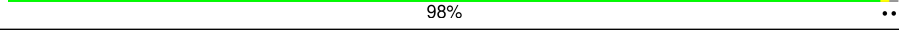
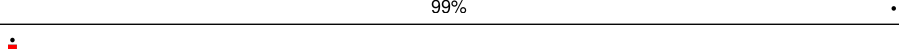
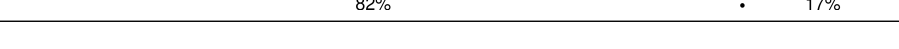
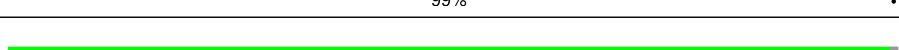
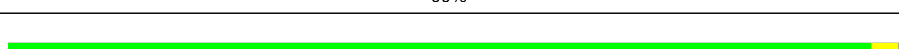
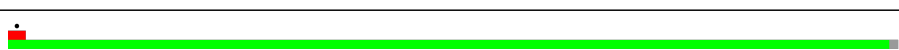

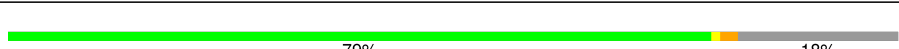
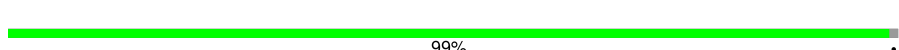
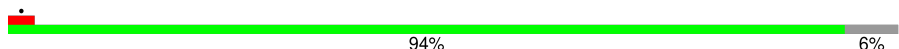
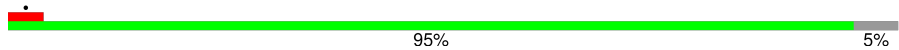
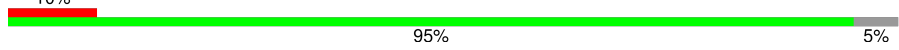

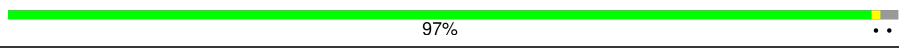
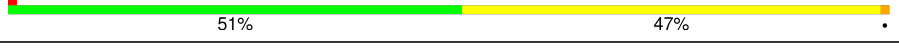



Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Lf	107	
35	Lg	121	
36	Lh	120	
37	Li	100	
38	Lj	88	
39	Lk	78	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	P0	312	
46	P2	165	
47	C2	1800	
48	SA	252	
49	SB	255	
50	SC	254	
51	SD	240	
52	SE	261	
53	SF	225	
54	SG	236	
55	SH	190	
56	SI	200	
57	SJ	197	
58	SK	105	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	SL	156	
60	SM	143	
61	SN	151	
62	SO	138	
63	SP	142	
64	SQ	143	
65	SR	136	
66	SS	146	
67	ST	144	
68	SU	121	
69	SV	87	
70	SW	130	
71	SX	145	
72	SY	135	
73	SZ	108	
74	Sa	119	
75	Sb	82	
76	Sc	67	
77	Sd	56	
78	Se	63	
79	Sf	152	
80	Sg	319	
81	A	76	
82	P	76	
83	m	16	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
84	5	157	<div><div></div><div>10%</div><div>92%</div><div></div><div></div></div>
85	R	410	<div><div></div><div>12%</div><div>85%</div><div></div><div>13%</div></div>
86	T	345	<div><div></div><div>15%</div><div>45%</div><div></div><div>53%</div></div>
87	L1	210	<div><div></div><div>6%</div><div>95%</div><div></div><div>5%</div></div>

## 2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 212517 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C1	3221	Total	C	N	O	P	0	0
			68888	30771	12409	22487	3221		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-B.

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

- Molecule 5 is a protein called RPL3 isoform 1.

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

- Molecule 6 is a protein called RPL4A isoform 1.

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

- Molecule 7 is a protein called RPL5 isoform 1.

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

- Molecule 8 is a protein called 60S ribosomal protein L6.

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

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 12 is a protein called RPL10 isoform 1.

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

- Molecule 13 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 14 is a protein called 60S ribosomal protein L13.



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

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L18-B.

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

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LU	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 24 is a protein called 60S ribosomal protein L23-B.

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

- Molecule 25 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LW	126	Total	C	N	O	S	0	0
			849	532	167	149	1		

- Molecule 26 is a protein called 60S ribosomal protein L25.

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

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LY	125	Total	C	N	O	S	0	0
			984	620	191	173			

- Molecule 28 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	LZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 30 is a protein called RPL29 isoform 1.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 33 is a protein called RPL32 isoform 1.

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

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 38 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 39 is a protein called RPL38 isoform 1.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 45 is a protein called RPP0 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	P0	189	Total	C	N	O	S	0	0
			1473	942	257	270	4		

- Molecule 46 is a protein called RPL12A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P2	94	Total	C	N	O	S	0	0
			723	448	138	135	2		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	C2	1771	Total	C	N	O	P	0	0
			37604	16807	6624	12402	1771		

- Molecule 48 is a protein called 40S ribosomal protein S0.

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

- Molecule 49 is a protein called RPS1A isoform 1.

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

- Molecule 50 is a protein called RPS2 isoform 1.

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

- Molecule 51 is a protein called RPS3 isoform 1.

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

- Molecule 52 is a protein called 40S ribosomal protein S4.

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

- Molecule 53 is a protein called Rps5p.

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

- Molecule 54 is a protein called 40S ribosomal protein S6.

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

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called RPS8A isoform 1.

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

- Molecule 57 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 58 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 59 is a protein called 40S ribosomal protein S11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	144	Total	C	N	O	S	0	0
			1159	742	219	195	3		

- Molecule 60 is a protein called 40S ribosomal protein S12.

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

- Molecule 61 is a protein called 40S ribosomal protein S13.

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

- Molecule 62 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 63 is a protein called RPS15 isoform 1.

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

- Molecule 64 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 65 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 66 is a protein called 40S ribosomal protein S18-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 67 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 68 is a protein called RPS20 isoform 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 70 is a protein called RPS22A isoform 1.



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

- Molecule 71 is a protein called 40S ribosomal protein S23.

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

- Molecule 72 is a protein called 40S ribosomal protein S24.

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

- Molecule 73 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SZ	100	Total	C	N	O		0	0
			771	491	147	133			

- Molecule 74 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 75 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 76 is a protein called RPS28A isoform 1.

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

- Molecule 77 is a protein called RPS29A isoform 1.

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

- Molecule 78 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Se	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S31.

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

- Molecule 80 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
81	A	76	Total	C	N	O	P	0	0
			1609	720	278	536	75		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
82	P	76	Total	C	N	O	P	0	0
			1619	722	288	533	76		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	34	U	G	conflict	GB 176436

- Molecule 83 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	m	16	Total	C	N	O	P	0	0
			351	157	72	106	16		

- Molecule 84 is a protein called Eukaryotic translation initiation factor 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	5	154	Total	C	N	O	S	0	0
			1143	709	195	230	9		

- Molecule 85 is a protein called Ribosome-interacting GTPase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	R	355	Total	C	N	O	S	0	0
			2738	1733	483	513	9		

There are 41 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	370	LYS	-	expression tag	UNP A0A6A5PWT7
R	371	ARG	-	expression tag	UNP A0A6A5PWT7
R	372	ARG	-	expression tag	UNP A0A6A5PWT7
R	373	TRP	-	expression tag	UNP A0A6A5PWT7
R	374	LYS	-	expression tag	UNP A0A6A5PWT7
R	375	LYS	-	expression tag	UNP A0A6A5PWT7
R	376	ASN	-	expression tag	UNP A0A6A5PWT7
R	377	PHE	-	expression tag	UNP A0A6A5PWT7
R	378	ILE	-	expression tag	UNP A0A6A5PWT7
R	379	ALA	-	expression tag	UNP A0A6A5PWT7
R	380	VAL	-	expression tag	UNP A0A6A5PWT7
R	381	SER	-	expression tag	UNP A0A6A5PWT7
R	382	ALA	-	expression tag	UNP A0A6A5PWT7
R	383	ALA	-	expression tag	UNP A0A6A5PWT7
R	384	ASN	-	expression tag	UNP A0A6A5PWT7
R	385	ARG	-	expression tag	UNP A0A6A5PWT7
R	386	PHE	-	expression tag	UNP A0A6A5PWT7
R	387	LYS	-	expression tag	UNP A0A6A5PWT7
R	388	LYS	-	expression tag	UNP A0A6A5PWT7
R	389	ILE	-	expression tag	UNP A0A6A5PWT7
R	390	SER	-	expression tag	UNP A0A6A5PWT7
R	391	SER	-	expression tag	UNP A0A6A5PWT7
R	392	SER	-	expression tag	UNP A0A6A5PWT7
R	393	GLY	-	expression tag	UNP A0A6A5PWT7
R	394	ALA	-	expression tag	UNP A0A6A5PWT7

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
R	395	LEU	-	expression tag	UNP A0A6A5PWT7
R	396	ASP	-	expression tag	UNP A0A6A5PWT7
R	397	TYR	-	expression tag	UNP A0A6A5PWT7
R	398	ASP	-	expression tag	UNP A0A6A5PWT7
R	399	ILE	-	expression tag	UNP A0A6A5PWT7
R	400	PRO	-	expression tag	UNP A0A6A5PWT7
R	401	THR	-	expression tag	UNP A0A6A5PWT7
R	402	THR	-	expression tag	UNP A0A6A5PWT7
R	403	ALA	-	expression tag	UNP A0A6A5PWT7
R	404	SER	-	expression tag	UNP A0A6A5PWT7
R	405	GLU	-	expression tag	UNP A0A6A5PWT7
R	406	ASN	-	expression tag	UNP A0A6A5PWT7
R	407	LEU	-	expression tag	UNP A0A6A5PWT7
R	408	TYR	-	expression tag	UNP A0A6A5PWT7
R	409	PHE	-	expression tag	UNP A0A6A5PWT7
R	410	GLN	-	expression tag	UNP A0A6A5PWT7

- Molecule 86 is a protein called Translation machinery-associated protein 46.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	T	162	Total	C	N	O	S	0	0
			1276	810	221	240	5		

- Molecule 87 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms				AltConf	Trace
87	L1	200	Total	C	N	O	0	0
			1000	600	200	200		

- Molecule 88 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

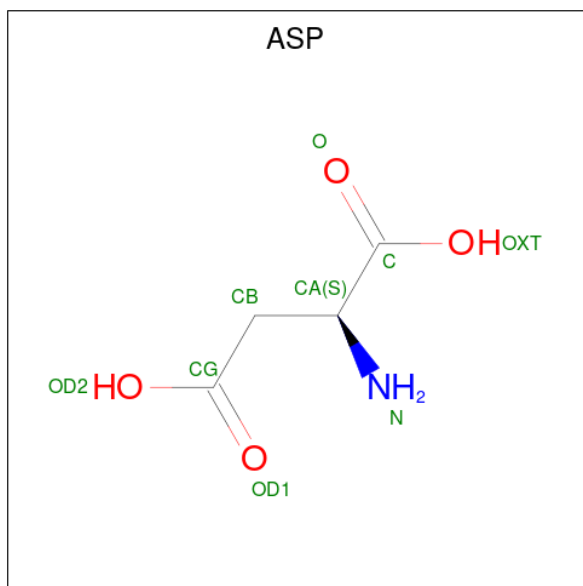
Mol	Chain	Residues	Atoms		AltConf
88	C1	192	Total	Mg	0
			192	192	
88	C4	1	Total	Mg	0
			1	1	
88	LA	2	Total	Mg	0
			2	2	
88	LB	1	Total	Mg	0
			1	1	

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
88	LN	1	Total	Mg	0
			1	1	
88	LP	1	Total	Mg	0
			1	1	
88	LV	1	Total	Mg	0
			1	1	
88	Le	1	Total	Mg	0
			1	1	
88	C2	82	Total	Mg	0
			82	82	
88	SC	1	Total	Mg	0
			1	1	
88	SX	1	Total	Mg	0
			1	1	
88	Sa	1	Total	Mg	0
			1	1	
88	P	1	Total	Mg	0
			1	1	

- Molecule 89 is ASPARTIC ACID (three-letter code: ASP) (formula:  $C_4H_7NO_4$ ).



Mol	Chain	Residues	Atoms				AltConf
89	C1	1	Total	C	N	O	0
			5	3	1	1	

- Molecule 90 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
90	Lg	1	Total 1	Zn 1	0
90	Lj	1	Total 1	Zn 1	0
90	Lm	1	Total 1	Zn 1	0
90	Lo	1	Total 1	Zn 1	0
90	Lp	1	Total 1	Zn 1	0
90	Sd	1	Total 1	Zn 1	0
90	Sf	1	Total 1	Zn 1	0
90	T	1	Total 1	Zn 1	0



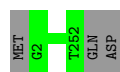






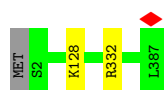
- Molecule 4: 60S ribosomal protein L2-B

Chain LA: 99%



- Molecule 5: RPL3 isoform 1

Chain LB: 99%



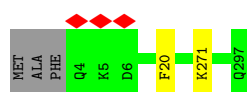
- Molecule 6: RPL4A isoform 1

Chain LC: 99%



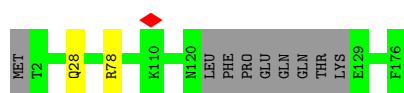
- Molecule 7: RPL5 isoform 1

Chain LD: 98%



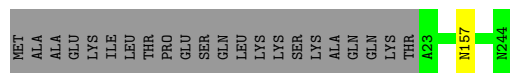
- Molecule 8: 60S ribosomal protein L6

Chain LE: 94% 5%



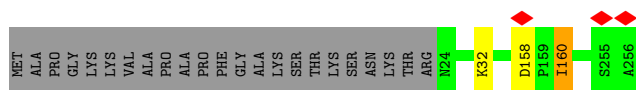
- Molecule 9: 60S ribosomal protein L7-A

Chain LF: 91% 9%



- Molecule 10: 60S ribosomal protein L8-A

Chain LG: 90% 9%



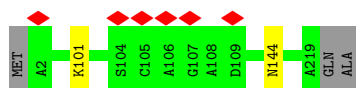
- Molecule 11: 60S ribosomal protein L9-A

Chain LH: 99%



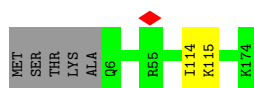
- Molecule 12: RPL10 isoform 1

Chain LI: 98%



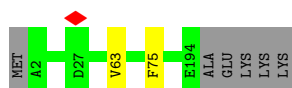
- Molecule 13: RPL11B isoform 1

Chain LJ: 96%



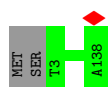
- Molecule 14: 60S ribosomal protein L13

Chain LL: 96%



- Molecule 15: 60S ribosomal protein L14-A

Chain LM: 99%



- Molecule 16: 60S ribosomal protein L15-A

Chain LN: 100%



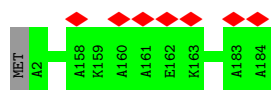
- Molecule 17: 60S ribosomal protein L16-A

Chain LO:  98% ..



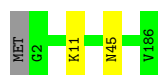
- Molecule 18: 60S ribosomal protein L17-A

Chain LP:  99% ..



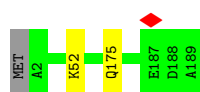
- Molecule 19: 60S ribosomal protein L18-B

Chain LQ:  98% ..



- Molecule 20: 60S ribosomal protein L19-A

Chain LR:  98% ..



- Molecule 21: 60S ribosomal protein L20-A

Chain LS:  99% ..




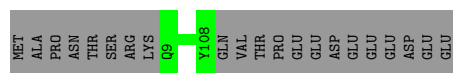
- Molecule 22: 60S ribosomal protein L21-A

Chain LT:  98% ..



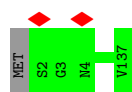
- Molecule 23: 60S ribosomal protein L22-A

Chain LU:  83% 17%




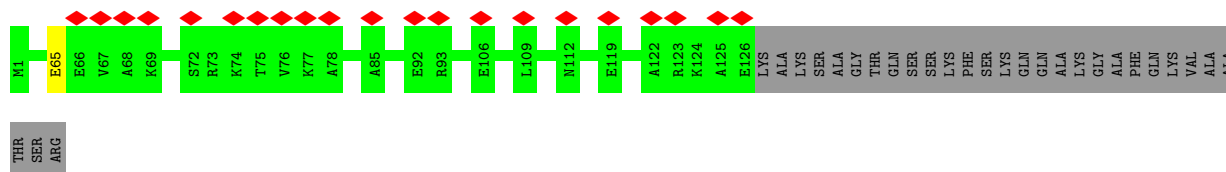
- Molecule 24: 60S ribosomal protein L23-B

Chain LV:  99%




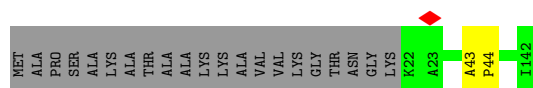
- Molecule 25: RPL24A isoform 1

Chain LW:  14% 81% 19%



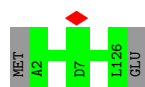
- Molecule 26: 60S ribosomal protein L25

Chain LX:  84% 15%



- Molecule 27: 60S ribosomal protein L26-A

Chain LY:  98%



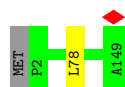
- Molecule 28: 60S ribosomal protein L27

Chain LZ:  99%



- Molecule 29: 60S ribosomal protein L28

Chain La:  99%

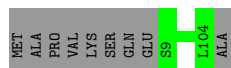


- Molecule 30: RPL29 isoform 1

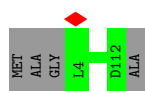
Chain Lb:  95%



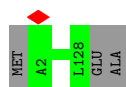
- Molecule 31: 60S ribosomal protein L30



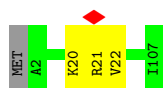
- Molecule 32: 60S ribosomal protein L31-A



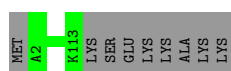
- Molecule 33: RPL32 isoform 1



- Molecule 34: 60S ribosomal protein L33-A



- Molecule 35: 60S ribosomal protein L34-A



- Molecule 36: 60S ribosomal protein L35-A



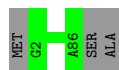
- Molecule 37: 60S ribosomal protein L36-A





- Molecule 38: Ribosomal protein L37

Chain Lj: 97%



- Molecule 39: RPL38 isoform 1

Chain Lk: 99%



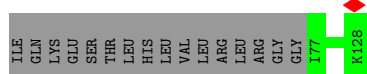
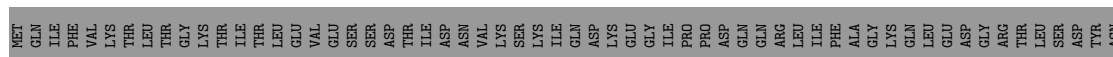
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 98%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 41%



- Molecule 42: 60S ribosomal protein L41-A

Chain Ln: 100%

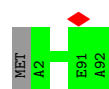


- Molecule 43: 60S ribosomal protein L42-A

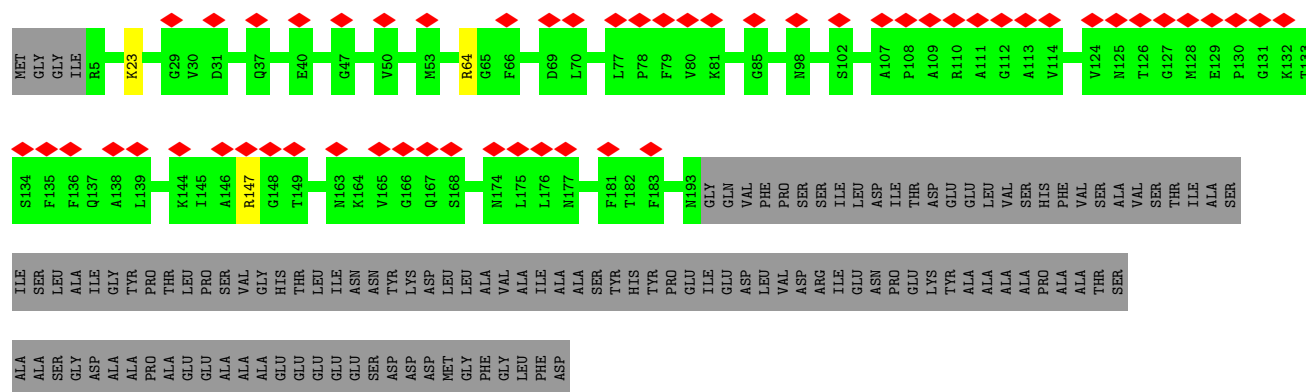
Chain Lo: 96%



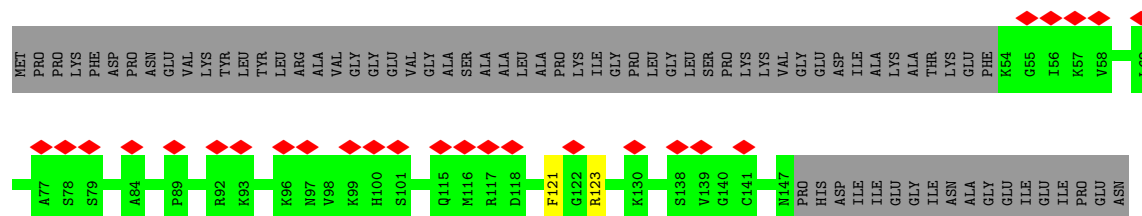
- Molecule 44: 60S ribosomal protein L43-A




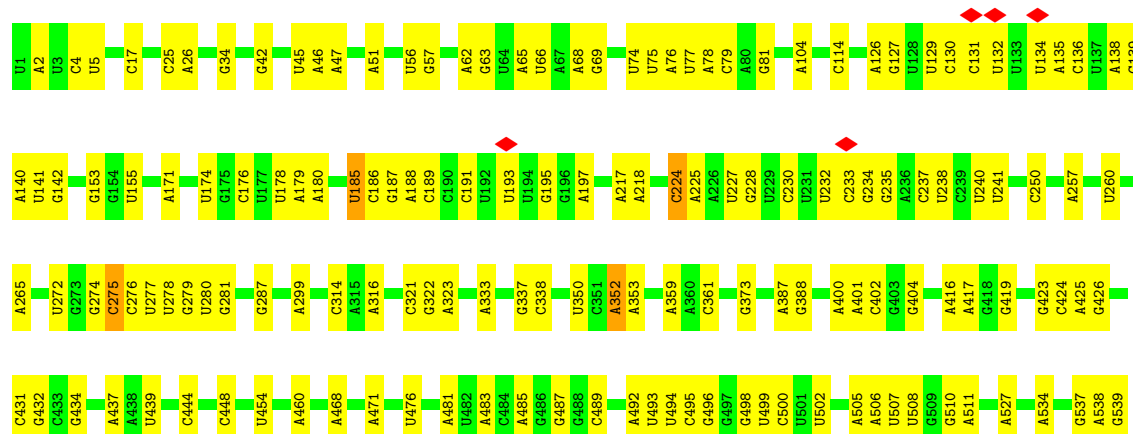
- Chain P0: 

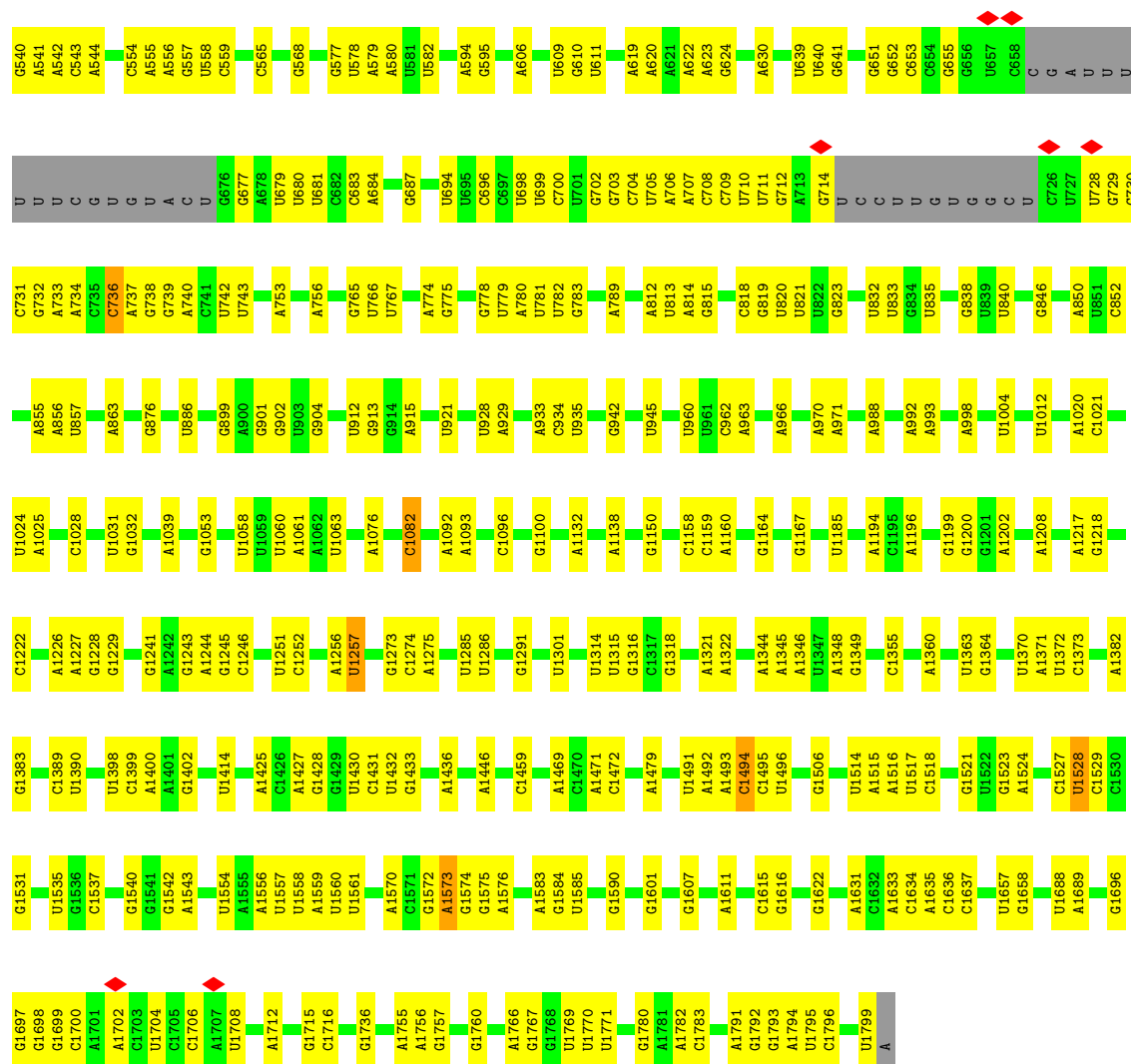


- Chain P2: 



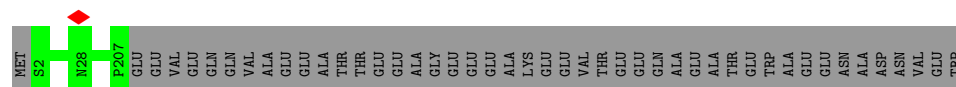
- Chain C2:  72% 26%





• Molecule 48: 40S ribosomal protein S0

Chain SA:



• Molecule 49: RPS1A isoform 1

Chain SB:

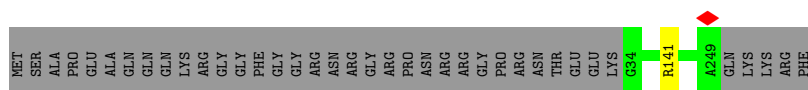


• Molecule 50: RPS2 isoform 1

Chain SC:







- Molecule 51: RPS3 isoform 1

Chain SD: 92% 8%



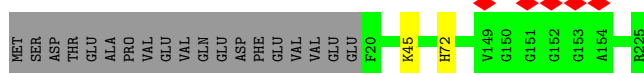
- Molecule 52: 40S ribosomal protein S4

Chain SE: 97% ..



- Molecule 53: Rps5p

Chain SF: 91% 8%



- Molecule 54: 40S ribosomal protein S6

Chain SG: 95% ..



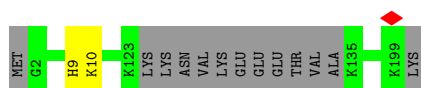
- Molecule 55: 40S ribosomal protein S7

Chain SH: 95% ..



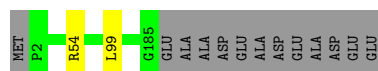
- Molecule 56: RPS8A isoform 1

Chain SI: 92% 6%



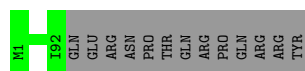
- Molecule 57: 40S ribosomal protein S9-A

Chain SJ:  92% 7%



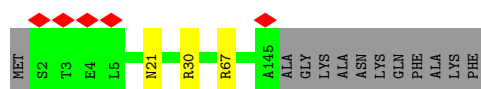
- Molecule 58: 40S ribosomal protein S10-A

Chain SK:  88% 12%




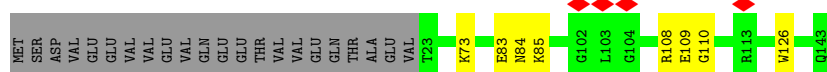
- Molecule 59: 40S ribosomal protein S11-B

Chain SL:  90% 8%



- Molecule 60: 40S ribosomal protein S12

Chain SM:  79% 6% 15%



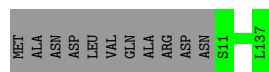
- Molecule 61: 40S ribosomal protein S13

Chain SN:  99%




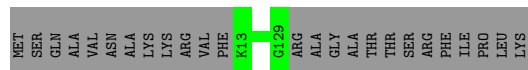
- Molecule 62: 40S ribosomal protein S14-B

Chain SO:  92% 8%



- Molecule 63: RPS15 isoform 1

Chain SP:  82% 18%




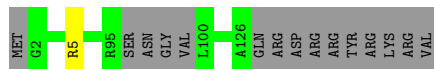
- Molecule 64: 40S ribosomal protein S16-A

Chain SQ:  97% ...



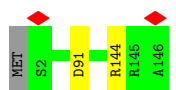
- Molecule 65: 40S ribosomal protein S17-A

Chain SR:  88% 11%



- Molecule 66: 40S ribosomal protein S18-B

Chain SS:  98% ..




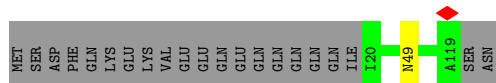
- Molecule 67: 40S ribosomal protein S19-A

Chain ST:  99% .



- Molecule 68: RPS20 isoform 1

Chain SU:  82% 17%



- Molecule 69: 40S ribosomal protein S21-A

Chain SV:  99% .



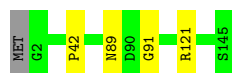
- Molecule 70: RPS22A isoform 1

Chain SW:  99% .



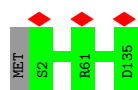
- Molecule 71: 40S ribosomal protein S23

Chain SX:  97%




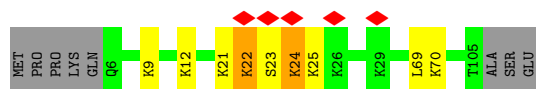
- Molecule 72: 40S ribosomal protein S24

Chain SY:  99%




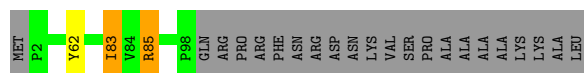
- Molecule 73: RPS25A isoform 1

Chain SZ:  84%



- Molecule 74: RPS26B isoform 1

Chain Sa:  79%



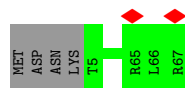
- Molecule 75: 40S ribosomal protein S27-A

Chain Sb:  99%



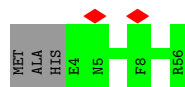
- Molecule 76: RPS28A isoform 1

Chain Sc:  94%



- Molecule 77: RPS29A isoform 1

Chain Sd:  95%



- Molecule 78: 40S ribosomal protein S30





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	95380	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 ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.029	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.08, 1.08, 1.08	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, 5CT, 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	C1	0.20	0/77108	0.81	37/120216 (0.0%)
2	C4	0.16	0/2883	0.75	0/4491
3	C3	0.18	0/3746	0.80	2/5832 (0.0%)
4	LA	0.25	0/1933	0.50	0/2598
5	LB	0.24	0/3146	0.47	0/4228
6	LC	0.25	0/2800	0.46	0/3790
7	LD	0.26	0/2400	0.48	0/3239
8	LE	0.25	0/1329	0.48	0/1794
9	LF	0.26	0/1821	0.43	0/2451
10	LG	0.27	0/1836	0.48	0/2481
11	LH	0.26	0/1529	0.51	0/2060
12	LI	0.25	0/1801	0.47	0/2416
13	LJ	0.26	0/1371	0.54	0/1838
14	LL	0.26	0/1568	0.52	0/2106
15	LM	0.25	0/1068	0.46	0/1438
16	LN	0.24	0/1757	0.46	0/2354
17	LO	0.28	0/1585	0.49	0/2128
18	LP	0.25	0/1439	0.48	0/1938
19	LQ	0.25	0/1465	0.46	0/1965
20	LR	0.26	0/1532	0.48	0/2043
21	LS	0.27	0/1473	0.50	0/1980
22	LT	0.25	0/1300	0.46	0/1743
23	LU	0.27	0/812	0.54	0/1099
24	LV	0.26	0/1018	0.47	0/1369
25	LW	0.25	0/863	0.49	0/1169
26	LX	0.27	0/979	0.52	0/1321
27	LY	0.25	0/995	0.47	0/1329
28	LZ	0.25	0/1118	0.46	0/1497
29	La	0.24	0/1204	0.45	0/1612
30	Lb	0.24	0/473	0.45	0/629
31	Lc	0.26	0/745	0.49	0/1001
32	Ld	0.24	0/890	0.46	0/1196



Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	Le	0.24	0/1038	0.46	0/1390
34	Lf	0.25	0/868	0.47	0/1168
35	Lg	0.25	0/890	0.48	0/1189
36	Lh	0.26	0/978	0.48	0/1301
37	Li	0.26	0/772	0.48	0/1026
38	Lj	0.25	0/685	0.51	0/908
39	Lk	0.26	0/618	0.54	0/826
40	Ll	0.23	0/443	0.45	0/588
41	Lm	0.29	0/423	0.53	0/562
42	Ln	0.22	0/230	0.38	0/296
43	Lo	0.26	0/836	0.48	0/1104
44	Lp	0.25	0/701	0.49	0/934
45	P0	0.25	0/1498	0.52	0/2025
46	P2	0.24	0/728	0.51	0/975
47	C2	0.20	0/42053	0.83	27/65522 (0.0%)
48	SA	0.25	0/1644	0.49	0/2249
49	SB	0.25	0/1823	0.54	0/2447
50	SC	0.26	0/1656	0.51	0/2251
51	SD	0.26	0/1754	0.50	0/2361
52	SE	0.25	0/2097	0.50	0/2823
53	SF	0.26	0/1625	0.51	0/2197
54	SG	0.26	0/1839	0.51	1/2460 (0.0%)
55	SH	0.27	0/1498	0.55	0/2019
56	SI	0.25	0/1501	0.48	0/2006
57	SJ	0.25	0/1504	0.48	0/2016
58	SK	0.28	0/769	0.55	0/1039
59	SL	0.25	0/1185	0.47	0/1598
60	SM	0.27	0/883	0.77	3/1199 (0.3%)
61	SN	0.26	0/1215	0.50	0/1638
62	SO	0.25	0/937	0.52	0/1261
63	SP	0.26	0/936	0.53	0/1259
64	SQ	0.27	0/1125	0.54	0/1510
65	SR	0.27	0/957	0.54	0/1283
66	SS	0.25	0/1211	0.52	0/1628
67	ST	0.26	0/1130	0.52	0/1517
68	SU	0.26	0/807	0.59	0/1091
69	SV	0.25	0/682	0.56	0/921
70	SW	0.26	0/1038	0.50	0/1395
71	SX	0.26	0/1139	0.56	0/1518
72	SY	0.26	0/1087	0.52	0/1449
73	SZ	0.26	0/781	0.62	0/1045
74	Sa	0.25	0/782	0.54	0/1047
75	Sb	0.23	0/620	0.54	0/838

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	Sc	0.24	0/493	0.55	0/663
77	Sd	0.25	0/452	0.48	0/600
78	Se	0.26	0/480	0.49	0/639
79	Sf	0.27	0/567	0.62	0/764
80	Sg	0.25	0/2436	0.55	0/3318
81	A	0.27	0/1796	0.96	1/2796 (0.0%)
82	P	0.20	0/1808	0.83	0/2816
83	m	0.18	0/395	0.71	0/615
84	5	0.26	0/1142	0.62	0/1537
85	R	0.25	0/2777	0.51	0/3754
86	T	0.26	0/1301	0.53	0/1745
All	All	0.22	0/226620	0.71	71/332477 (0.0%)

There are no bond length outliers.

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C1	1569	U	O4'-C1'-N1	9.26	115.61	108.20
1	C1	1243	G	N1-C6-O6	-7.46	115.42	119.90
1	C1	260	C	N3-C2-O2	-7.32	116.78	121.90
47	C2	276	C	C2-N1-C1'	7.17	126.69	118.80
47	C2	1389	C	C2-N1-C1'	7.10	126.61	118.80

There are no chirality outliers.

There are no planarity outliers.

## 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	
4	LA	249/254 (98%)	230 (92%)	19 (8%)	0	100	100
5	LB	384/387 (99%)	354 (92%)	30 (8%)	0	100	100
6	LC	359/362 (99%)	330 (92%)	27 (8%)	2 (1%)	22	54
7	LD	292/297 (98%)	274 (94%)	17 (6%)	1 (0%)	37	67
8	LE	163/176 (93%)	146 (90%)	17 (10%)	0	100	100
9	LF	220/244 (90%)	208 (94%)	12 (6%)	0	100	100
10	LG	231/256 (90%)	214 (93%)	16 (7%)	1 (0%)	30	62
11	LH	189/191 (99%)	173 (92%)	16 (8%)	0	100	100
12	LI	216/221 (98%)	205 (95%)	11 (5%)	0	100	100
13	LJ	167/174 (96%)	146 (87%)	21 (13%)	0	100	100
14	LL	191/199 (96%)	171 (90%)	19 (10%)	1 (0%)	25	58
15	LM	134/138 (97%)	124 (92%)	10 (8%)	0	100	100
16	LN	201/204 (98%)	186 (92%)	15 (8%)	0	100	100
17	LO	195/199 (98%)	189 (97%)	4 (2%)	2 (1%)	13	44
18	LP	181/184 (98%)	168 (93%)	13 (7%)	0	100	100
19	LQ	183/186 (98%)	171 (93%)	12 (7%)	0	100	100
20	LR	186/189 (98%)	179 (96%)	6 (3%)	1 (0%)	25	58
21	LS	169/172 (98%)	161 (95%)	8 (5%)	0	100	100
22	LT	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
23	LU	98/121 (81%)	90 (92%)	8 (8%)	0	100	100
24	LV	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
25	LW	124/155 (80%)	108 (87%)	15 (12%)	1 (1%)	16	48
26	LX	119/142 (84%)	111 (93%)	6 (5%)	2 (2%)	7	33
27	LY	123/127 (97%)	117 (95%)	6 (5%)	0	100	100
28	LZ	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
29	La	146/149 (98%)	130 (89%)	15 (10%)	1 (1%)	19	51
30	Lb	56/59 (95%)	50 (89%)	4 (7%)	2 (4%)	3	17
31	Lc	94/105 (90%)	90 (96%)	4 (4%)	0	100	100
32	Ld	107/113 (95%)	96 (90%)	11 (10%)	0	100	100
33	Le	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
34	Lf	104/107 (97%)	97 (93%)	7 (7%)	0	100	100
35	Lg	110/121 (91%)	106 (96%)	4 (4%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lh	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
37	Li	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
38	Lj	83/88 (94%)	76 (92%)	7 (8%)	0	100	100
39	Lk	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
40	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
41	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
42	Ln	23/25 (92%)	23 (100%)	0	0	100	100
43	Lo	101/106 (95%)	94 (93%)	7 (7%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	P0	187/312 (60%)	160 (86%)	27 (14%)	0	100	100
46	P2	92/165 (56%)	74 (80%)	18 (20%)	0	100	100
48	SA	204/252 (81%)	180 (88%)	24 (12%)	0	100	100
49	SB	222/255 (87%)	192 (86%)	28 (13%)	2 (1%)	14	46
50	SC	214/254 (84%)	198 (92%)	16 (8%)	0	100	100
51	SD	220/240 (92%)	212 (96%)	8 (4%)	0	100	100
52	SE	256/261 (98%)	232 (91%)	24 (9%)	0	100	100
53	SF	204/225 (91%)	188 (92%)	16 (8%)	0	100	100
54	SG	226/236 (96%)	197 (87%)	27 (12%)	2 (1%)	14	46
55	SH	182/190 (96%)	167 (92%)	14 (8%)	1 (0%)	25	58
56	SI	183/200 (92%)	163 (89%)	18 (10%)	2 (1%)	12	41
57	SJ	182/197 (92%)	162 (89%)	19 (10%)	1 (0%)	25	58
58	SK	90/105 (86%)	76 (84%)	14 (16%)	0	100	100
59	SL	142/156 (91%)	126 (89%)	16 (11%)	0	100	100
60	SM	119/143 (83%)	81 (68%)	36 (30%)	2 (2%)	7	33
61	SN	148/151 (98%)	133 (90%)	15 (10%)	0	100	100
62	SO	125/138 (91%)	110 (88%)	15 (12%)	0	100	100
63	SP	115/142 (81%)	106 (92%)	9 (8%)	0	100	100
64	SQ	139/143 (97%)	128 (92%)	10 (7%)	1 (1%)	19	51
65	SR	117/136 (86%)	105 (90%)	12 (10%)	0	100	100
66	SS	143/146 (98%)	130 (91%)	12 (8%)	1 (1%)	19	51
67	ST	141/144 (98%)	124 (88%)	17 (12%)	0	100	100

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	SU	98/121 (81%)	92 (94%)	6 (6%)	0	100	100
69	SV	85/87 (98%)	74 (87%)	10 (12%)	1 (1%)	11	40
70	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
71	SX	142/145 (98%)	122 (86%)	17 (12%)	3 (2%)	5	28
72	SY	132/135 (98%)	122 (92%)	10 (8%)	0	100	100
73	SZ	98/108 (91%)	85 (87%)	10 (10%)	3 (3%)	3	20
74	Sa	95/119 (80%)	78 (82%)	14 (15%)	3 (3%)	3	19
75	Sb	79/82 (96%)	70 (89%)	9 (11%)	0	100	100
76	Sc	61/67 (91%)	55 (90%)	6 (10%)	0	100	100
77	Sd	51/56 (91%)	49 (96%)	2 (4%)	0	100	100
78	Se	58/63 (92%)	46 (79%)	12 (21%)	0	100	100
79	Sf	71/152 (47%)	44 (62%)	24 (34%)	3 (4%)	2	14
80	Sg	310/319 (97%)	280 (90%)	29 (9%)	1 (0%)	37	67
84	5	151/157 (96%)	125 (83%)	22 (15%)	4 (3%)	4	24
85	R	351/410 (86%)	330 (94%)	18 (5%)	3 (1%)	14	46
86	T	158/345 (46%)	138 (87%)	19 (12%)	1 (1%)	22	54
All	All	11941/13270 (90%)	10875 (91%)	1018 (8%)	48 (0%)	32	62

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	LO	111[A]	PRO
26	LX	44	PRO
56	SI	10	LYS
60	SM	109	GLU
66	SS	91	ASP

### 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	
4	LA	190/196 (97%)	190 (100%)	0	100	100
5	LB	319/323 (99%)	317 (99%)	2 (1%)	84	91
6	LC	288/289 (100%)	288 (100%)	0	100	100
7	LD	241/245 (98%)	240 (100%)	1 (0%)	89	93
8	LE	139/155 (90%)	137 (99%)	2 (1%)	62	80
9	LF	186/205 (91%)	185 (100%)	1 (0%)	86	92
10	LG	187/208 (90%)	184 (98%)	3 (2%)	58	77
11	LH	168/171 (98%)	167 (99%)	1 (1%)	84	91
12	LI	185/187 (99%)	183 (99%)	2 (1%)	70	84
13	LJ	146/151 (97%)	144 (99%)	2 (1%)	62	80
14	LL	154/159 (97%)	153 (99%)	1 (1%)	84	91
15	LM	107/109 (98%)	107 (100%)	0	100	100
16	LN	175/176 (99%)	175 (100%)	0	100	100
17	LO	160/162 (99%)	160 (100%)	0	100	100
18	LP	138/146 (94%)	138 (100%)	0	100	100
19	LQ	150/151 (99%)	148 (99%)	2 (1%)	65	81
20	LR	152/154 (99%)	151 (99%)	1 (1%)	81	90
21	LS	155/156 (99%)	154 (99%)	1 (1%)	84	91
22	LT	136/137 (99%)	134 (98%)	2 (2%)	60	78
23	LU	87/107 (81%)	87 (100%)	0	100	100
24	LV	104/105 (99%)	104 (100%)	0	100	100
25	LW	60/129 (46%)	60 (100%)	0	100	100
26	LX	104/118 (88%)	104 (100%)	0	100	100
27	LY	108/110 (98%)	108 (100%)	0	100	100
28	LZ	115/116 (99%)	115 (100%)	0	100	100
29	La	118/119 (99%)	118 (100%)	0	100	100
30	Lb	46/47 (98%)	46 (100%)	0	100	100
31	Lc	81/88 (92%)	81 (100%)	0	100	100
32	Ld	92/97 (95%)	92 (100%)	0	100	100
33	Le	108/111 (97%)	108 (100%)	0	100	100
34	Lf	90/91 (99%)	87 (97%)	3 (3%)	33	61
35	Lg	95/103 (92%)	95 (100%)	0	100	100

Continued on next page...

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	Lh	104/105 (99%)	104 (100%)	0	100	100
37	Li	80/82 (98%)	80 (100%)	0	100	100
38	Lj	69/71 (97%)	69 (100%)	0	100	100
39	Lk	68/69 (99%)	68 (100%)	0	100	100
40	Ll	45/46 (98%)	45 (100%)	0	100	100
41	Lm	47/116 (40%)	47 (100%)	0	100	100
42	Ln	22/23 (96%)	22 (100%)	0	100	100
43	Lo	87/91 (96%)	86 (99%)	1 (1%)	70	84
44	Lp	71/72 (99%)	71 (100%)	0	100	100
45	P0	160/254 (63%)	157 (98%)	3 (2%)	52	74
46	P2	81/136 (60%)	79 (98%)	2 (2%)	42	68
48	SA	170/210 (81%)	170 (100%)	0	100	100
49	SB	200/224 (89%)	200 (100%)	0	100	100
50	SC	175/205 (85%)	174 (99%)	1 (1%)	84	91
51	SD	182/195 (93%)	180 (99%)	2 (1%)	70	84
52	SE	220/222 (99%)	216 (98%)	4 (2%)	54	75
53	SF	172/191 (90%)	170 (99%)	2 (1%)	67	83
54	SG	189/201 (94%)	187 (99%)	2 (1%)	70	84
55	SH	163/170 (96%)	160 (98%)	3 (2%)	54	75
56	SI	148/161 (92%)	148 (100%)	0	100	100
57	SJ	156/166 (94%)	155 (99%)	1 (1%)	84	91
58	SK	77/98 (79%)	77 (100%)	0	100	100
59	SL	129/137 (94%)	126 (98%)	3 (2%)	45	69
60	SM	88/119 (74%)	84 (96%)	4 (4%)	23	54
61	SN	127/128 (99%)	126 (99%)	1 (1%)	79	88
62	SO	91/105 (87%)	91 (100%)	0	100	100
63	SP	95/118 (80%)	95 (100%)	0	100	100
64	SQ	117/119 (98%)	115 (98%)	2 (2%)	56	76
65	SR	101/124 (82%)	100 (99%)	1 (1%)	73	85
66	SS	128/129 (99%)	127 (99%)	1 (1%)	79	88
67	ST	115/116 (99%)	115 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	SU	93/114 (82%)	92 (99%)	1 (1%)	70	84
69	SV	71/74 (96%)	71 (100%)	0	100	100
70	SW	110/111 (99%)	110 (100%)	0	100	100
71	SX	119/120 (99%)	118 (99%)	1 (1%)	79	88
72	SY	112/113 (99%)	112 (100%)	0	100	100
73	SZ	77/89 (86%)	69 (90%)	8 (10%)	5	23
74	Sa	83/100 (83%)	81 (98%)	2 (2%)	44	68
75	Sb	70/71 (99%)	70 (100%)	0	100	100
76	Sc	55/60 (92%)	55 (100%)	0	100	100
77	Sd	47/49 (96%)	47 (100%)	0	100	100
78	Se	50/54 (93%)	50 (100%)	0	100	100
79	Sf	56/135 (42%)	53 (95%)	3 (5%)	18	49
80	Sg	250/262 (95%)	249 (100%)	1 (0%)	89	93
84	5	118/132 (89%)	111 (94%)	7 (6%)	16	45
85	R	299/353 (85%)	294 (98%)	5 (2%)	56	76
86	T	134/302 (44%)	128 (96%)	6 (4%)	23	54
All	All	10005/11163 (90%)	9914 (99%)	91 (1%)	74	87

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
68	SU	49	ASN
79	Sf	143	LYS
73	SZ	9	LYS
73	SZ	69	LEU
84	5	49	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
69	SV	7	GLN
85	R	174	ASN
71	SX	63	GLN
76	Sc	43	ASN
38	Lj	48	ASN



### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C1	3217/3396 (94%)	565 (17%)	36 (1%)
2	C4	120/121 (99%)	11 (9%)	1 (0%)
3	C3	157/158 (99%)	25 (15%)	1 (0%)
47	C2	1768/1800 (98%)	456 (25%)	45 (2%)
81	A	75/76 (98%)	36 (48%)	3 (4%)
82	P	75/76 (98%)	20 (26%)	0
83	m	15/16 (93%)	5 (33%)	0
All	All	5427/5643 (96%)	1118 (20%)	86 (1%)

5 of 1118 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C1	13	A
1	C1	14	U
1	C1	18	G
1	C1	26	A
1	C1	40	A

5 of 86 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
47	C2	765	G
47	C2	1471	A
47	C2	819	G
47	C2	1273	G
47	C2	1557	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
84	5CT	5	51	84	13,14,15	0.68	0	8,15,17	0.87	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
84	5CT	5	51	84	-	8/13/14/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
84	5	51	5CT	C2-C1-NZ-CE
84	5	51	5CT	NZ-C1-C2-C3
84	5	51	5CT	NZ-C1-C2-O1
84	5	51	5CT	C-CA-CB-CG
84	5	51	5CT	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 295 ligands modelled in this entry, 294 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	$\# Z  > 2$
89	ASP	C1	3593	88	3,4,8	1.01	0	2,4,10	0.97	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
89	ASP	C1	3593	88	-	0/1/2/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

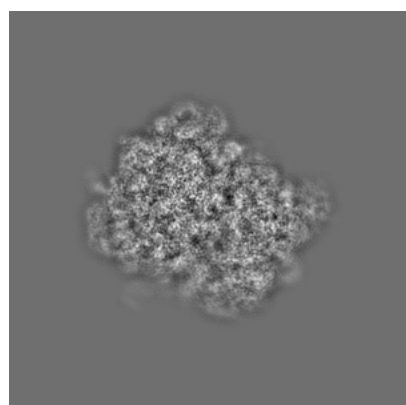
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24652. These allow visual inspection of the internal detail of the map and identification of artifacts.

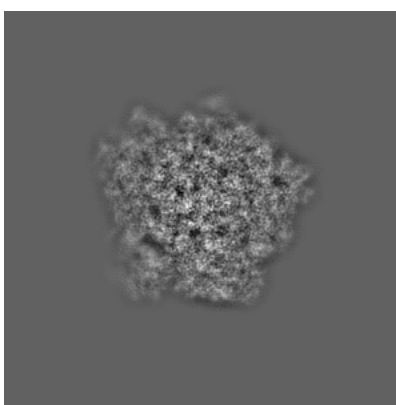
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

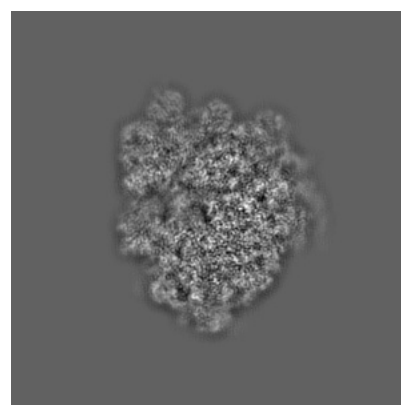
#### 6.1.1 Primary map



X



Y

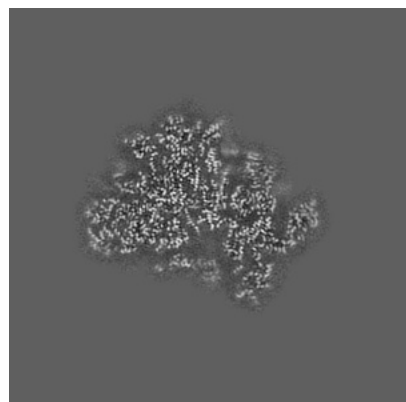


Z

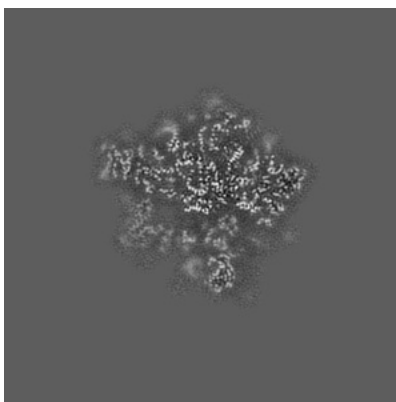
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

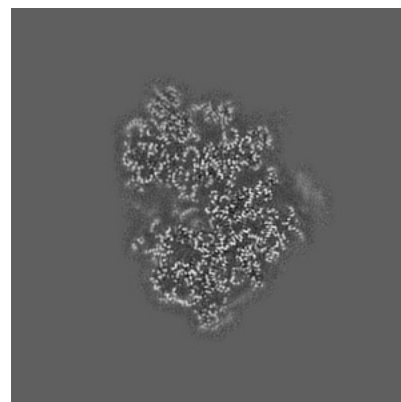
#### 6.2.1 Primary map



X Index: 224



Y Index: 224

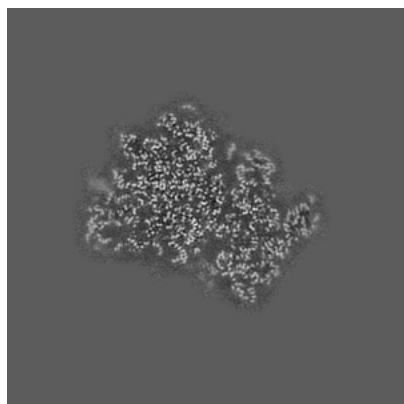


Z Index: 224

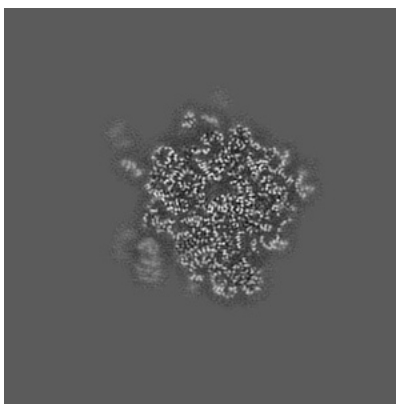
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

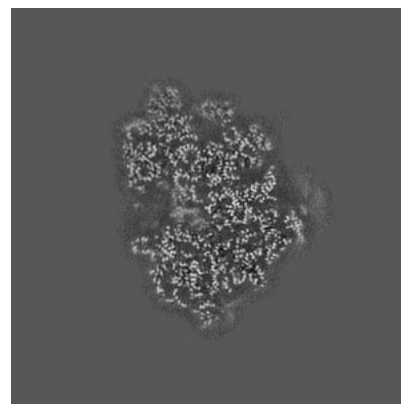
### 6.3.1 Primary map



X Index: 232



Y Index: 192

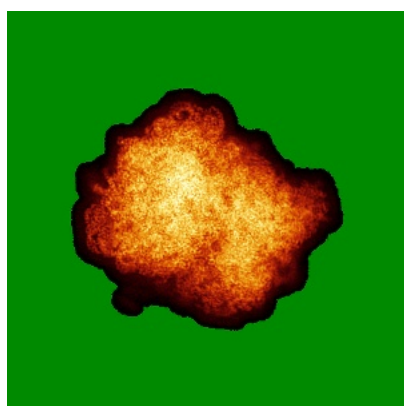


Z Index: 227

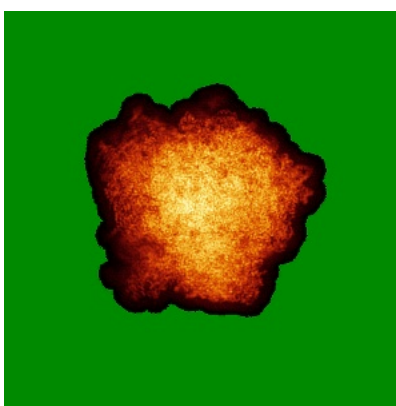
The images above show the largest variance slices of the map in three orthogonal directions.

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

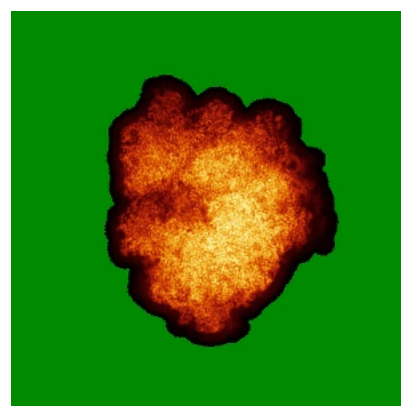
### 6.4.1 Primary map



X



Y

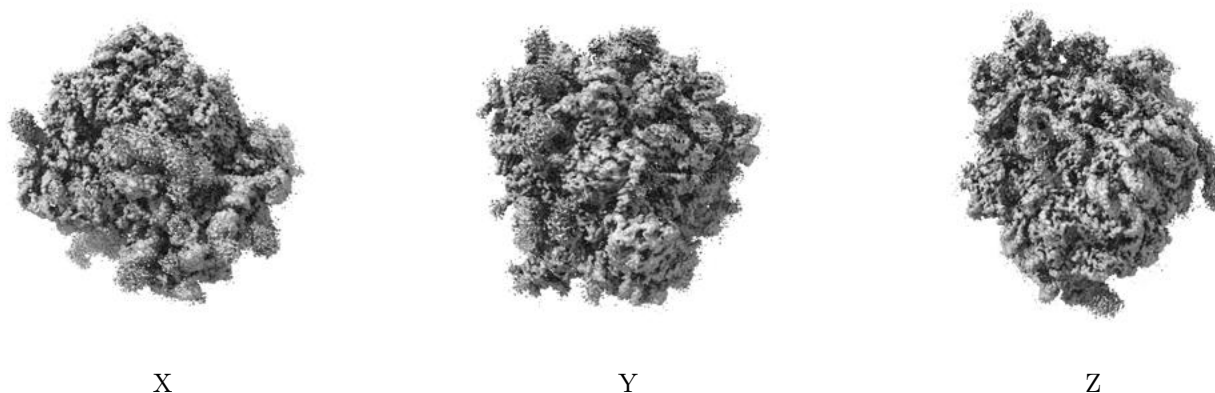


Z

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 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

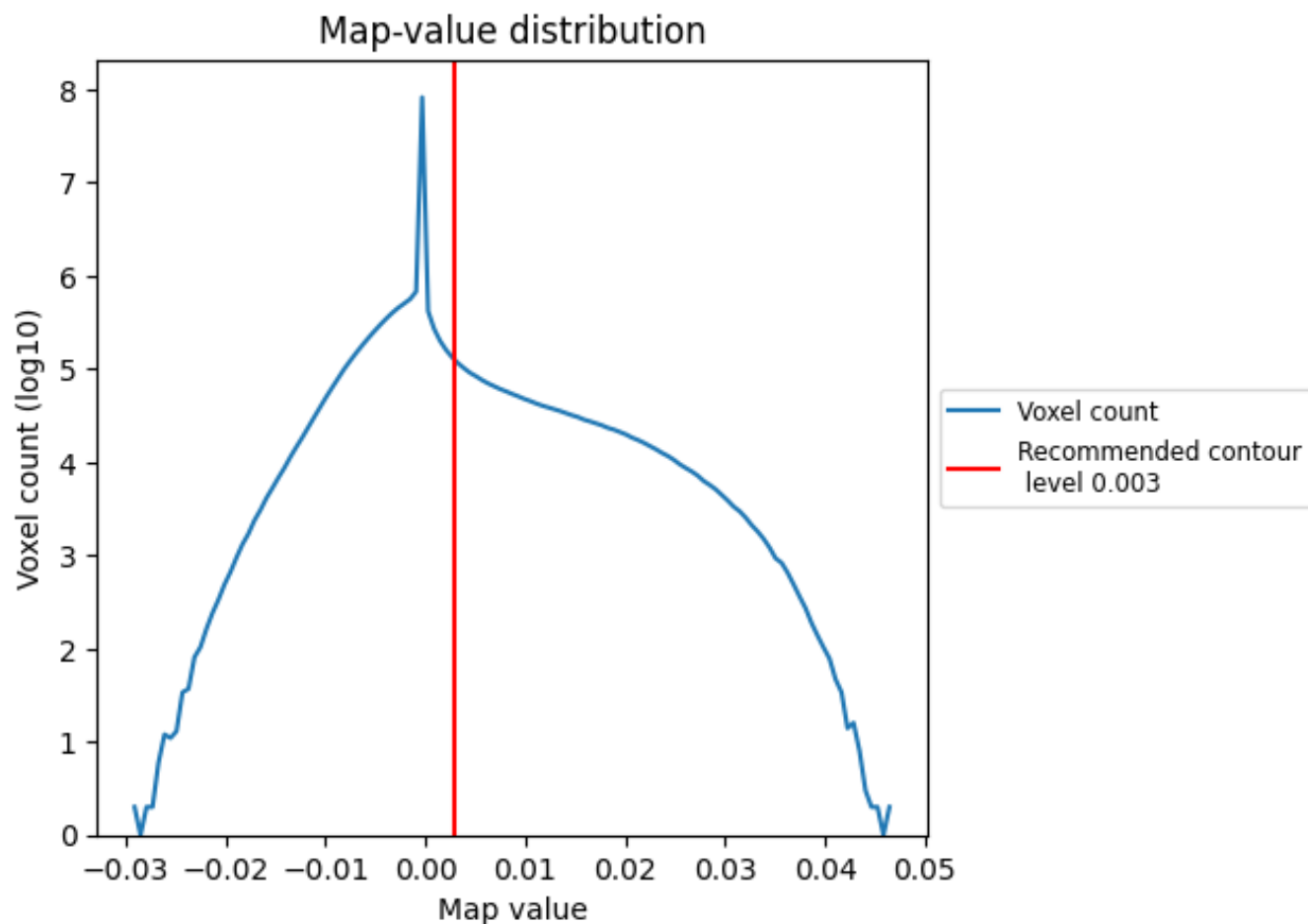
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

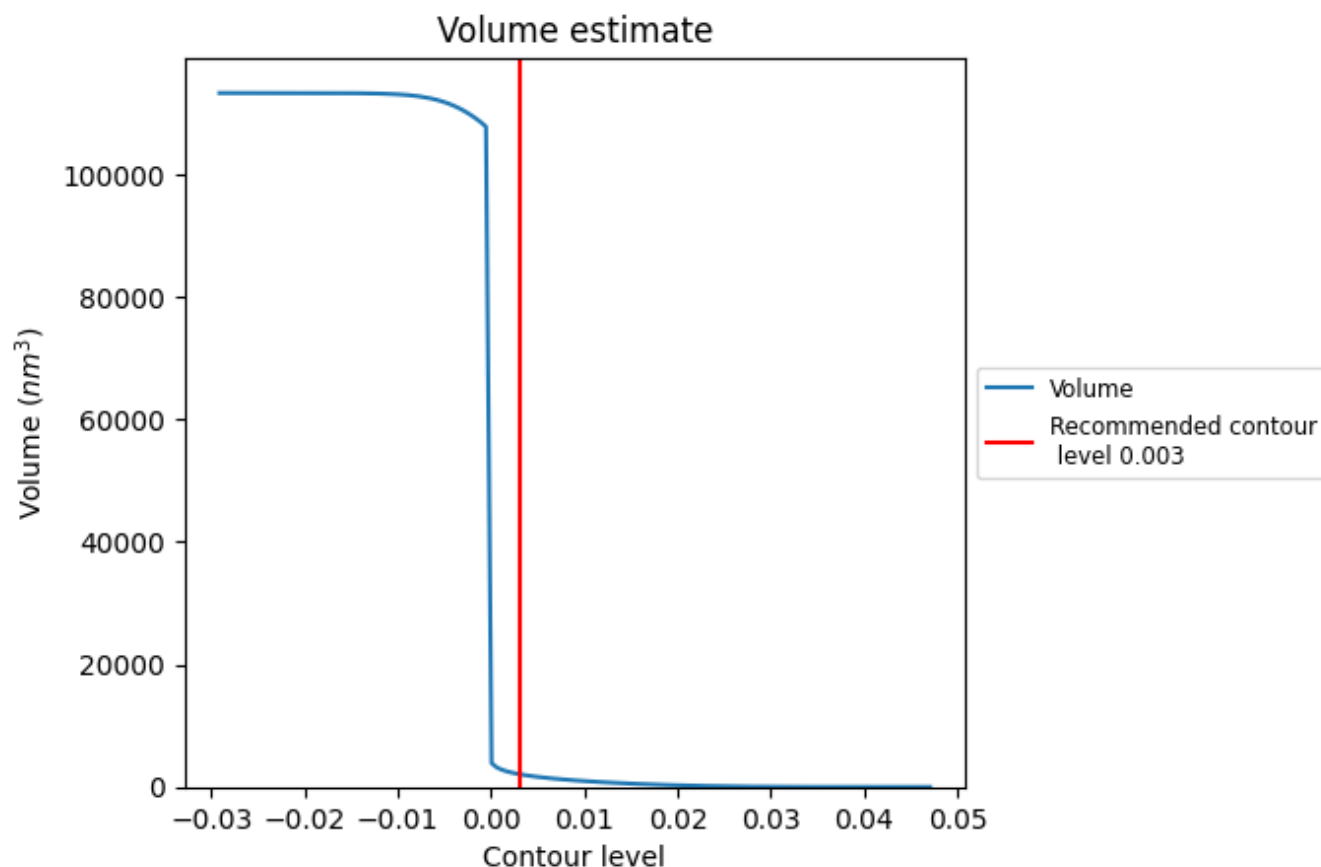
This section contains the results of statistical analysis of the map.

### 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](#)

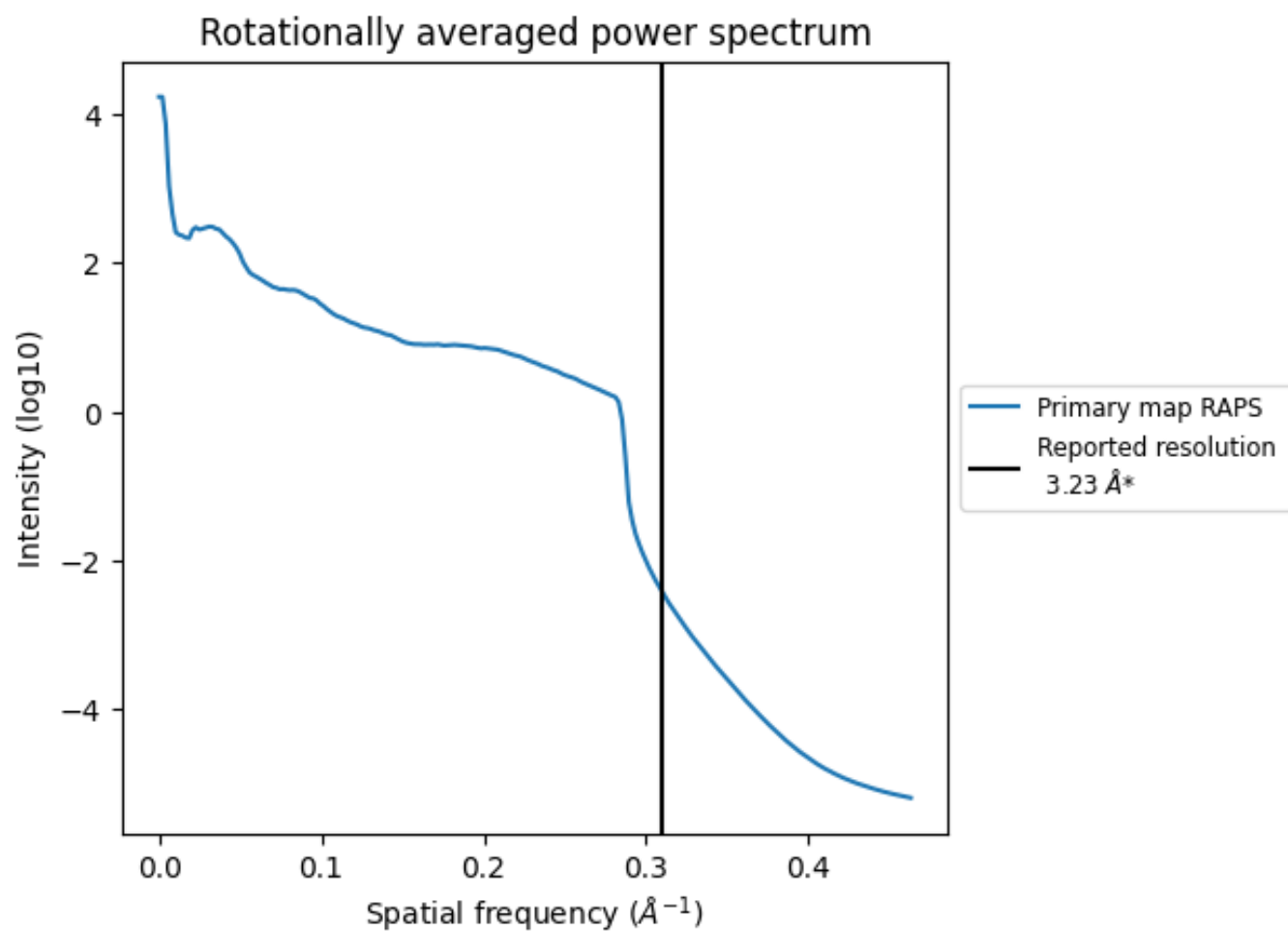


The volume at the recommended contour level is 2093 nm<sup>3</sup>; this corresponds to an approximate mass of 1891 kDa.

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 ⓘ

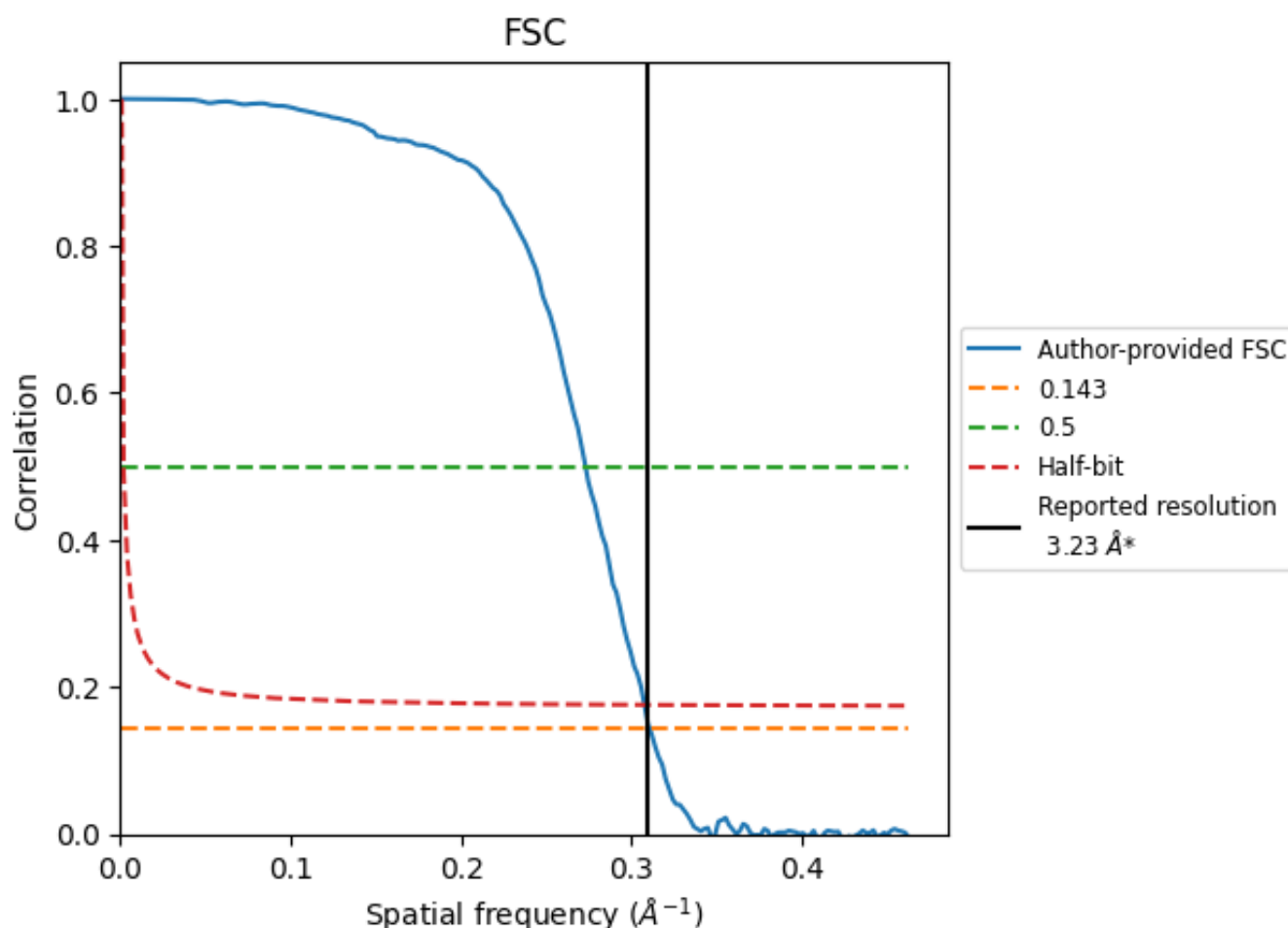


\*Reported resolution corresponds to spatial frequency of 0.310 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.310  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

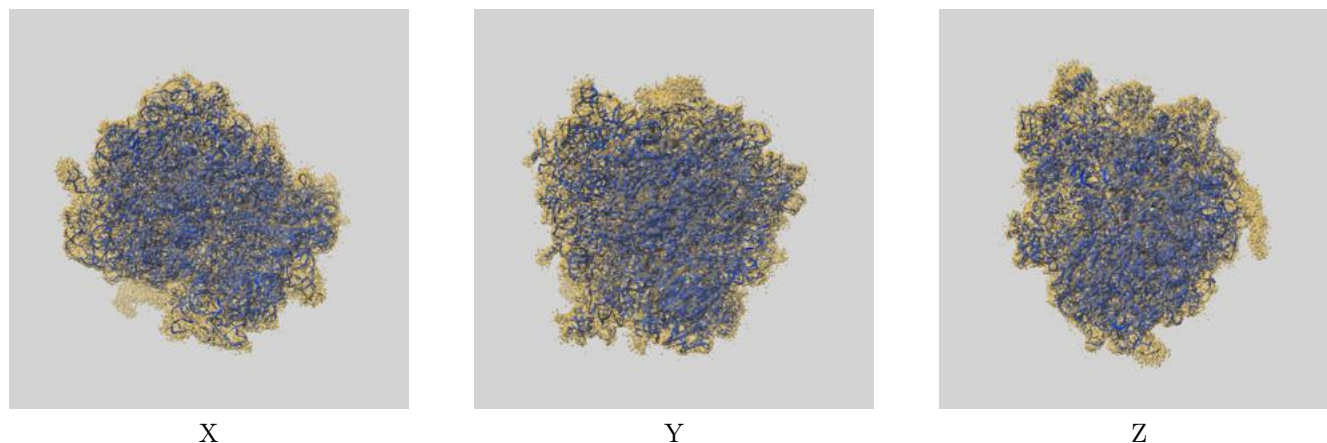
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.23	-	-
Author-provided FSC curve	3.22	3.66	3.25
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

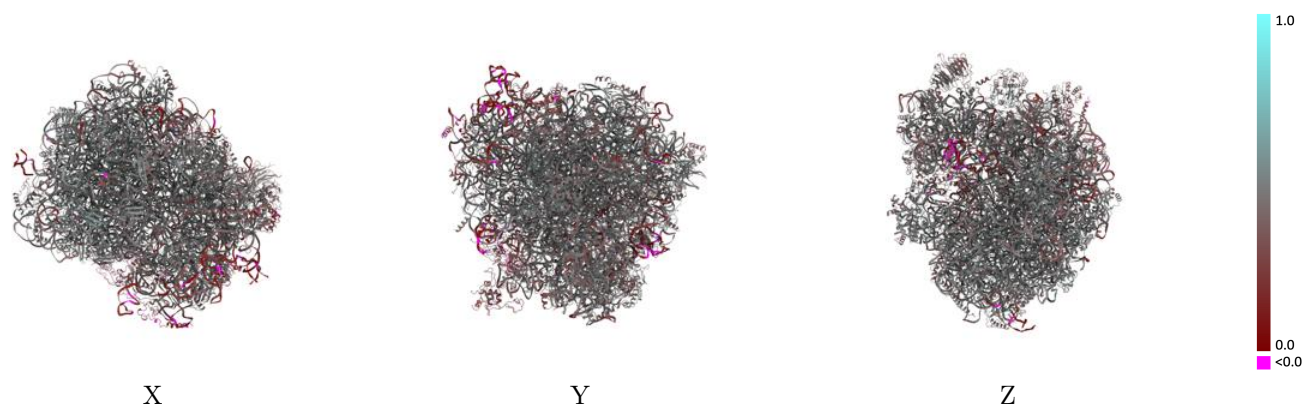
This section contains information regarding the fit between EMDB map EMD-24652 and PDB model 7RR5. Per-residue inclusion information can be found in [section 3](#) on [page 23](#).

### 9.1 Map-model overlay [i](#)



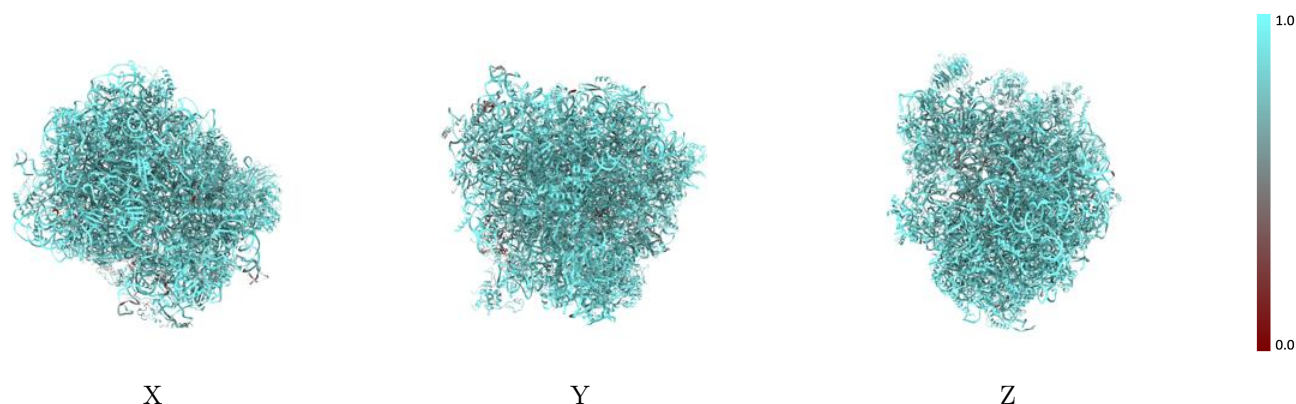
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



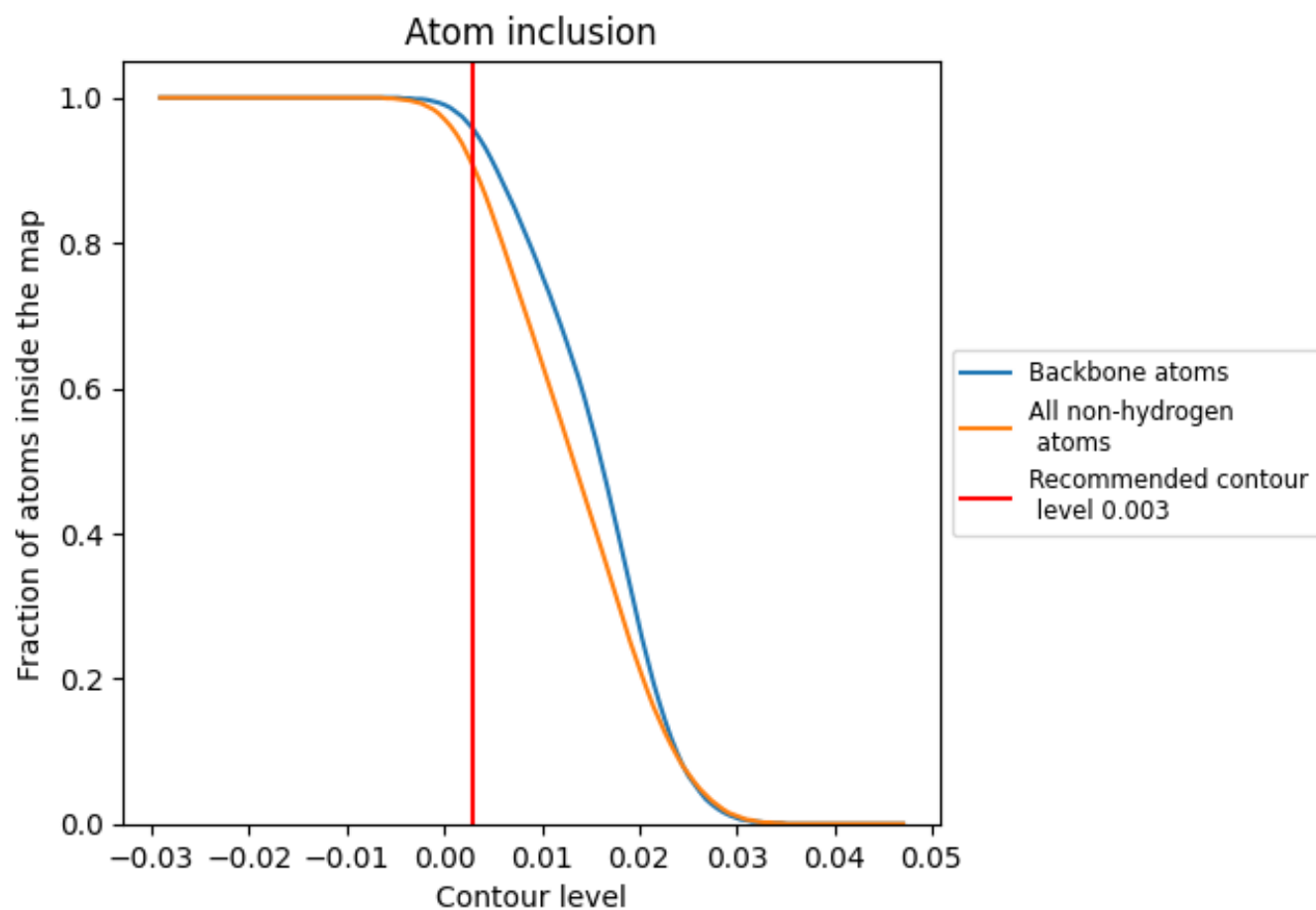
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.003).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.4370
5	 0.7240	 0.3570
A	 0.9130	 0.3670
C1	 0.9420	 0.4440
C2	 0.9290	 0.4180
C3	 0.9570	 0.4650
C4	 0.9730	 0.4790
L1	 0.8580	 0.3200
LA	 0.8770	 0.5050
LB	 0.9190	 0.5110
LC	 0.9070	 0.4810
LD	 0.9050	 0.4590
LE	 0.8980	 0.4520
LF	 0.8880	 0.4740
LG	 0.9000	 0.4540
LH	 0.9100	 0.4720
LI	 0.8900	 0.4840
LJ	 0.8800	 0.4470
LL	 0.9020	 0.4560
LM	 0.9180	 0.4880
LN	 0.8760	 0.5060
LO	 0.8960	 0.4920
LP	 0.8770	 0.4680
LQ	 0.8810	 0.4830
LR	 0.8950	 0.4390
LS	 0.8890	 0.4880
LT	 0.8890	 0.4960
LU	 0.9390	 0.4610
LV	 0.8840	 0.5050
LW	 0.7500	 0.3550
LX	 0.8580	 0.4600
LY	 0.9230	 0.5030
LZ	 0.8860	 0.4490
La	 0.9120	 0.4960
Lb	 0.8410	 0.4450



*Continued on next page...*























*Continued from previous page...*

Chain	Atom inclusion	Q-score
Lc	 0.9320	 0.4680
Ld	 0.8930	 0.4850
Le	 0.8840	 0.5040
Lf	 0.8990	 0.5160
Lg	 0.8530	 0.4700
Lh	 0.9050	 0.4640
Li	 0.8930	 0.4550
Lj	 0.8870	 0.4940
Lk	 0.8980	 0.4450
Ll	 0.8840	 0.5020
Lm	 0.8610	 0.4730
Ln	 0.8510	 0.4700
Lo	 0.8930	 0.4940
Lp	 0.8820	 0.4820
P	 0.9070	 0.3590
P0	 0.5840	 0.1510
P2	 0.6260	 0.0780
R	 0.6920	 0.3460
SA	 0.9080	 0.4490
SB	 0.8530	 0.4130
SC	 0.8930	 0.4760
SD	 0.8540	 0.4290
SE	 0.8710	 0.4560
SF	 0.8670	 0.4290
SG	 0.8650	 0.3990
SH	 0.8590	 0.3560
SI	 0.8920	 0.4690
SJ	 0.8750	 0.4590
SK	 0.8920	 0.4210
SL	 0.8720	 0.4750
SM	 0.8050	 0.2760
SN	 0.8700	 0.4510
SO	 0.8680	 0.4580
SP	 0.9100	 0.4390
SQ	 0.8600	 0.4710
SR	 0.8880	 0.4300
SS	 0.8940	 0.4340
ST	 0.8840	 0.4500
SU	 0.8350	 0.4280
SV	 0.9160	 0.4540
SW	 0.8760	 0.4840
SX	 0.8570	 0.4800

*Continued on next page...*



*Continued from previous page...*

Chain	Atom inclusion	Q-score
SY	 0.8690	 0.4350
SZ	 0.8420	 0.3920
Sa	 0.8720	 0.4590
Sb	 0.8980	 0.4120
Sc	 0.8560	 0.4340
Sd	 0.8260	 0.4800
Se	 0.8050	 0.4260
Sf	 0.8240	 0.2690
Sg	 0.8900	 0.4080
T	 0.5870	 0.2400
m	 0.7120	 0.3330