



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:37 PM UTC

PDB ID : 7ZPQ / pdb_00007zpq
EMDB ID : EMD-14861
Title : Structure of the RQT-bound 80S ribosome from *S. cerevisiae* (C1)
Authors : Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.
Deposited on : 2022-04-28
Resolution : 3.47 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

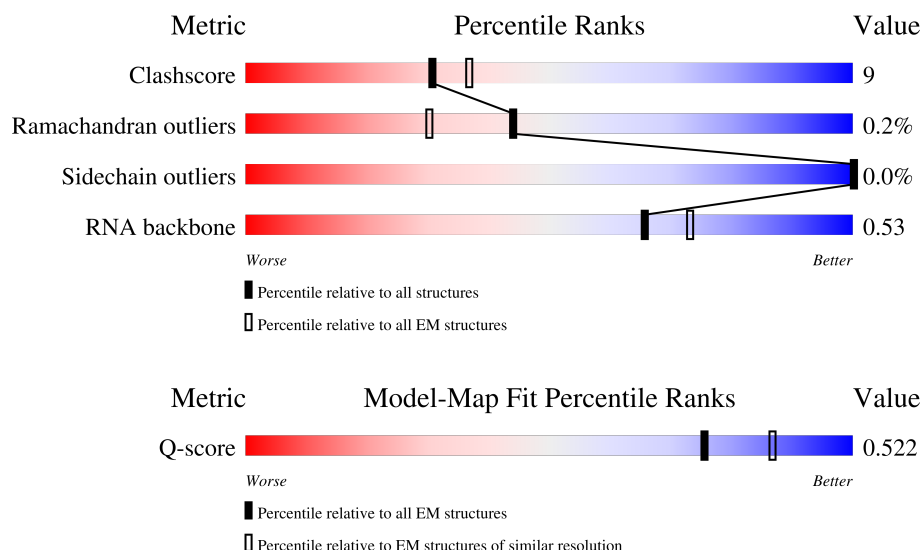
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.47 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13733 (2.97 - 3.97)

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

Mol	Chain	Length	Quality of chain
1	2	1798	
2	3	158	
3	4	121	

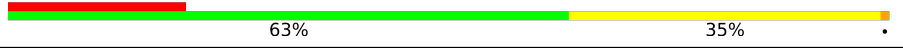
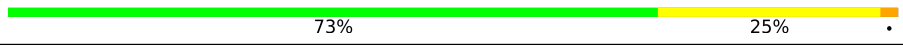
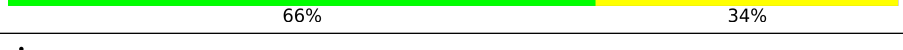
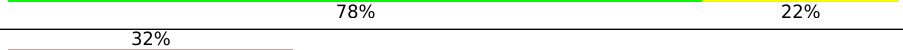
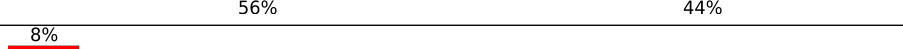
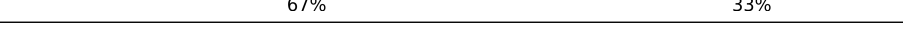
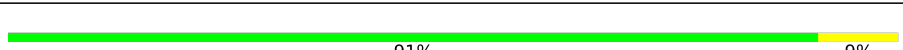
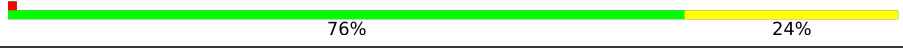
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Mol	Chain	Length	Quality of chain
4	5	3396	
5	6	76	
6	AA	206	
7	AB	255	
8	AC	216	
9	AD	222	
10	AE	258	
11	AF	206	
12	AG	228	
13	AH	184	
14	AI	200	
15	AJ	184	
16	AK	92	
17	AL	144	
18	AM	121	
19	AN	150	
20	AO	127	
21	AP	117	
22	AQ	141	
23	AR	136	
24	AS	145	
25	AT	143	
26	AU	100	
27	AV	87	
28	AW	129	

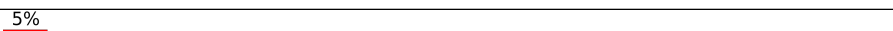
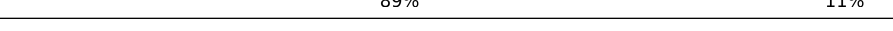
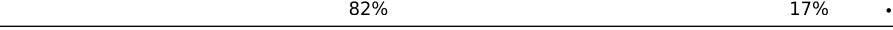
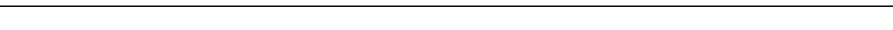
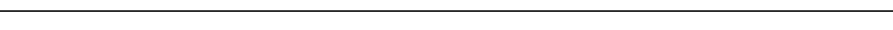
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Mol	Chain	Length	Quality of chain
29	AX	144	
30	AY	134	
31	AZ	82	
32	Aa	97	
33	Ab	81	
34	Ac	63	
35	Ad	53	
36	Ae	60	
37	Af	73	
38	Ag	312	
39	BA	251	
40	BB	386	
41	BC	361	
42	BD	294	
43	BE	176	
44	BF	222	
45	BG	233	
46	BH	191	
47	BI	218	
48	BJ	169	
49	BK	193	
50	BL	136	
51	BM	203	
52	BN	197	
53	BO	183	

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Mol	Chain	Length	Quality of chain
54	BP	185	 81% 19%
55	BQ	188	 78% 22%
56	BR	171	 80% 20%
57	BS	159	 81% 19%
58	BT	100	 71% 29%
59	BU	136	 82% 18%
60	BV	126	 5% 89% 11%
61	BW	121	 82% 17%
62	BX	125	 77% 23%
63	BY	135	 80% 20%
64	BZ	148	 70% 30%
65	Ba	58	 86% 14%
66	Bb	96	 76% 24%
67	Bc	109	 5% 84% 16%
68	Bd	127	 86% 14%
69	Be	106	 82% 18%
70	Bf	112	 87% 13%
71	Bg	119	 89% 11%
72	Bh	99	 92% 8%
73	Bi	85	 73% 27%
74	Bj	77	 74% 26%
75	Bk	50	 86% 14%
76	Bl	52	 77% 23%
77	Bm	25	 88% 12%
78	Bn	103	 85% 15%

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Mol	Chain	Length	Quality of chain
79	Bo	91	 85% 15%
80	CA	1967	 23% 60% 28% 11%
81	CB	297	 100% 27%
82	CC	530	 10% 17% 5% 78%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 218512 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

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

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	3184	Total	C	N	O	P	0	0
			68091	30415	12259	22233	3184		

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	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
6	34	U	G	conflict	GB 176436

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 7 is a protein called 40S ribosomal protein S1.

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

- Molecule 8 is a protein called RPS2 isoform 1.

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

- Molecule 9 is a protein called RPS3 isoform 1.

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

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 11 is a protein called Rps5p.

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

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S8.

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

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S12.

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

- Molecule 19 is a protein called 40S ribosomal protein S13.

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

- Molecule 20 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 21 is a protein called RPS15 isoform 1.

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

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 23 is a protein called 40S ribosomal protein S17-B.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	136	VAL	ASN	conflict	UNP P14127

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 26 is a protein called RPS20 isoform 1.

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

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 28 is a protein called RPS22A isoform 1.

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

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	AZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 32 is a protein called RPS26B isoform 1.

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

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 34 is a protein called RPS28A isoform 1.

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

- Molecule 35 is a protein called RPS29A isoform 1.

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

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 37 is a protein called RPS31 isoform 1.

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

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L3.

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

- Molecule 41 is a protein called RPL4A isoform 1.

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

- Molecule 42 is a protein called RPL5 isoform 1.

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

- Molecule 43 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BE	1	MET	-	initiating methionine	UNP P05739
BE	146	ILE	LEU	conflict	UNP P05739
BE	173	MET	LEU	conflict	UNP P05739

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 47 is a protein called RPL10 isoform 1.

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

- Molecule 48 is a protein called RPL11B isoform 1.

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

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 60 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BV	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BV	104	GLN	ASN	conflict	UNP A0A6A5PY83
BV	109	GLN	LEU	conflict	UNP A0A6A5PY83
BV	112	ASP	ASN	conflict	UNP A0A6A5PY83
BV	119	ALA	GLU	conflict	UNP A0A6A5PY83

- Molecule 61 is a protein called 60S ribosomal protein L25.

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

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 60S ribosomal protein L29.

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

- Molecule 66 is a protein called 60S ribosomal protein L30.

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

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 68 is a protein called RPL32 isoform 1.

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

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 74 is a protein called RPL38 isoform 1.

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

- Molecule 75 is a protein called 60S ribosomal protein L39.

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

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 77 is a protein called RPL41A isoform 1.

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

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 80 is a protein called SLH1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CA	1742	Total	C	N	O	S	0	0
			14008	8959	2378	2596	75		

- Molecule 81 is a protein called RQC trigger complex subunit CUE3.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CB	297	Total	C	N	O	S	0	0
			2415	1568	414	427	6		

- Molecule 82 is a protein called RQT4 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CC	114	Total	C	N	O	S	0	0
			886	539	167	172	8		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	2	84	Total	Mg	0
			84	84	
83	AQ	1	Total	Mg	0
			1	1	
83	AT	1	Total	Mg	0
			1	1	

- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Ad	1	Total	Zn	0
			1	1	
84	Af	1	Total	Zn	0
			1	1	
84	Bf	1	Total	Zn	0
			1	1	
84	Bi	1	Total	Zn	0
			1	1	
84	Bl	1	Total	Zn	0
			1	1	
84	Bn	1	Total	Zn	0
			1	1	
84	Bo	1	Total	Zn	0
			1	1	

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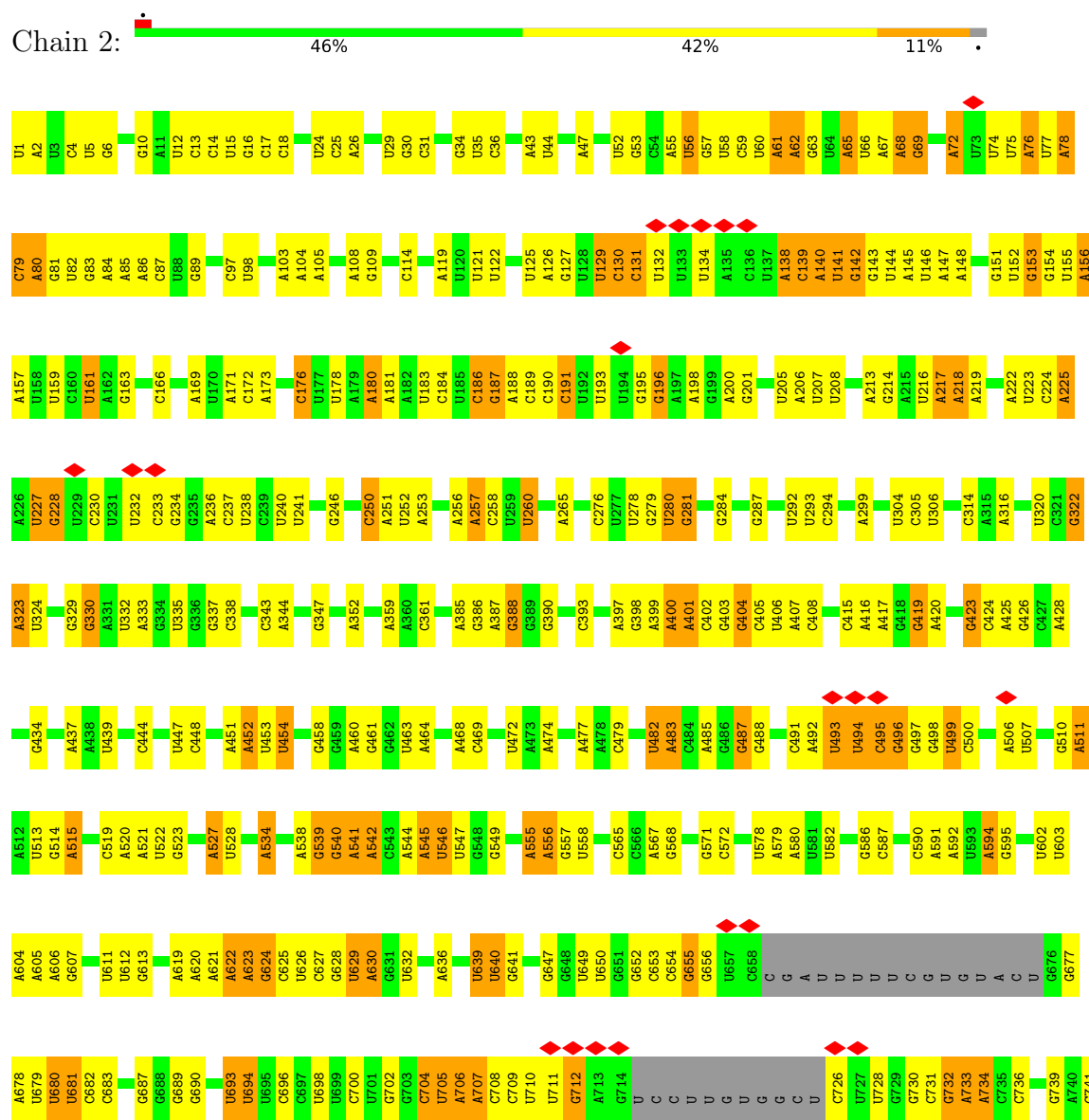
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Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
84	CC	2	2	2	0

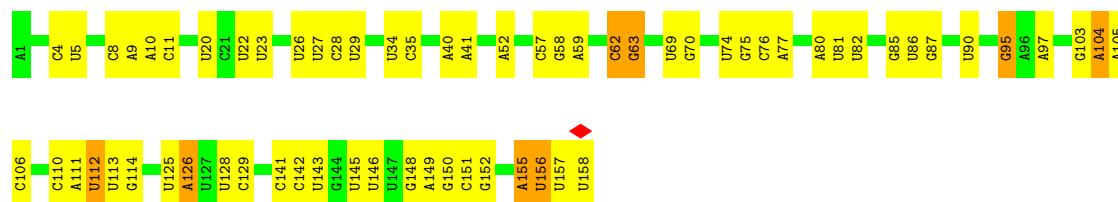
3 Residue-property plots

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

• Molecule 1: 18S ribosomal RNA

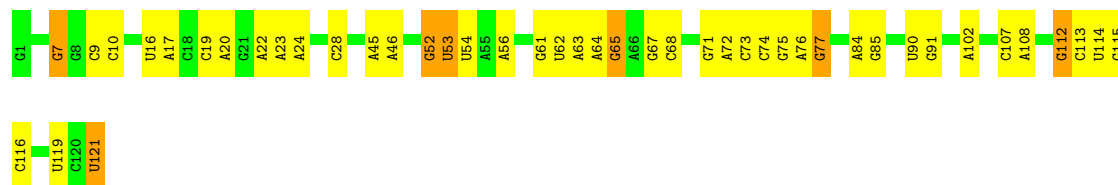






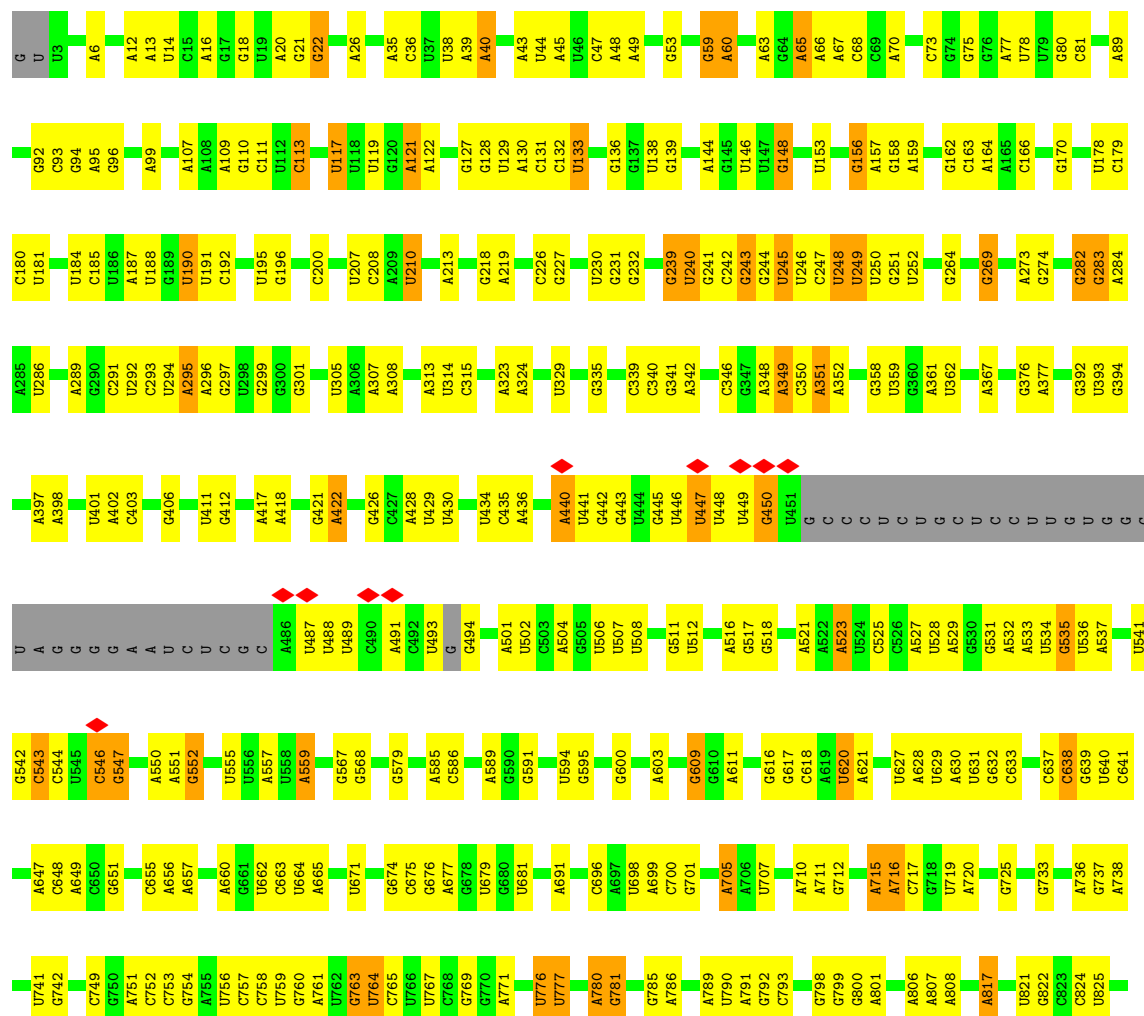
• Molecule 3: 5S ribosomal RNA

Chain 4: 63% 31% 6%



• Molecule 4: 25S ribosomal RNA

Chain 5: 53% 34% 6% 6%

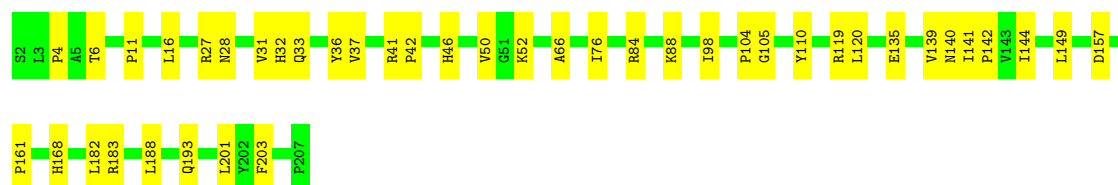
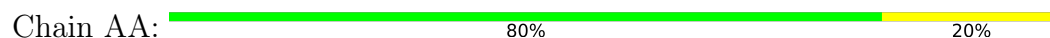




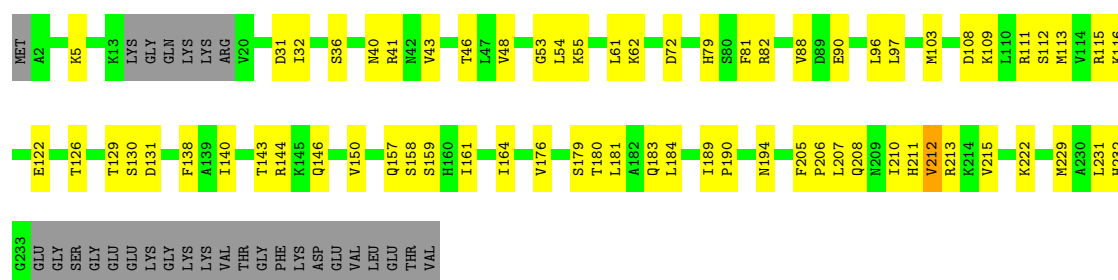




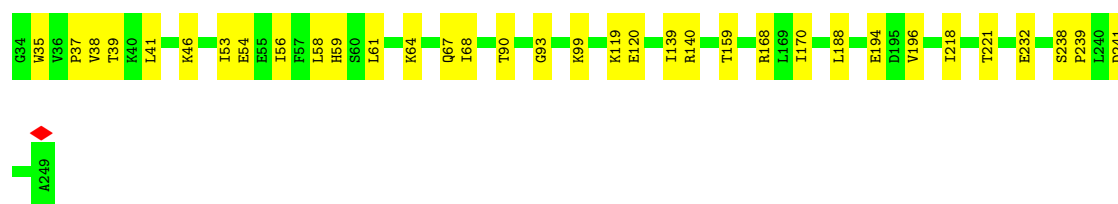
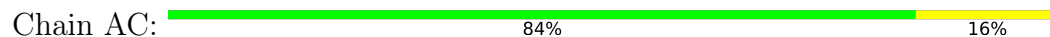
- Molecule 6: 40S ribosomal protein S0-A



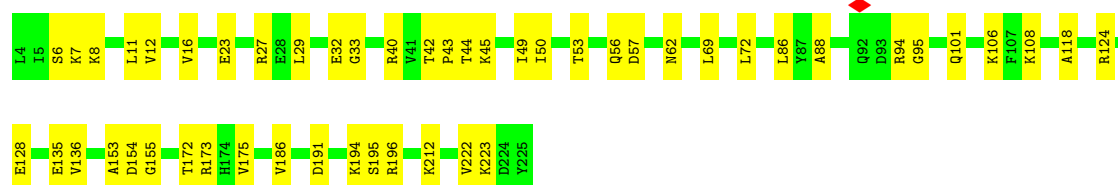
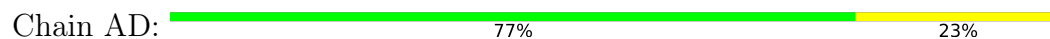
- Molecule 7: 40S ribosomal protein S1



- Molecule 8: RPS2 isoform 1

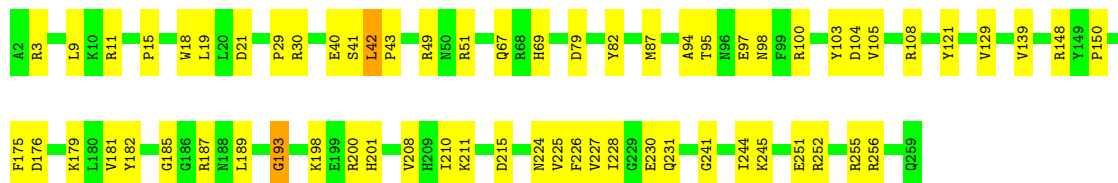


- Molecule 9: RPS3 isoform 1



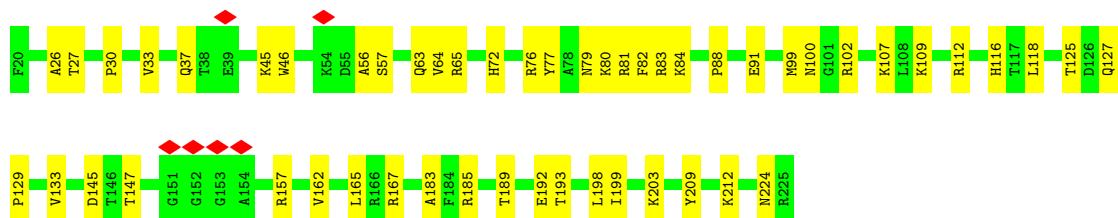
- Molecule 10: 40S ribosomal protein S4-A

Chain AE:  75% 24%



- Molecule 11: Rps5p

Chain AF:  75% 25%



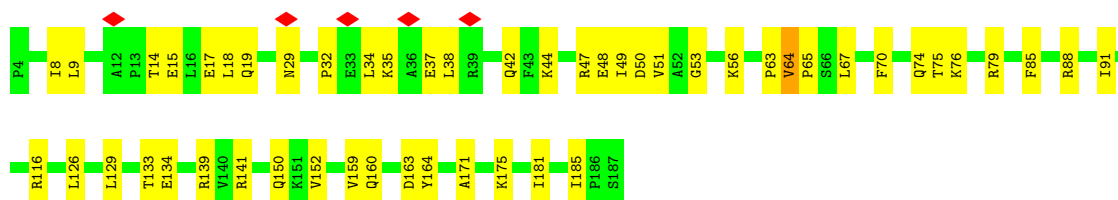
- Molecule 12: 40S ribosomal protein S6-A

Chain AG:  67% 32%



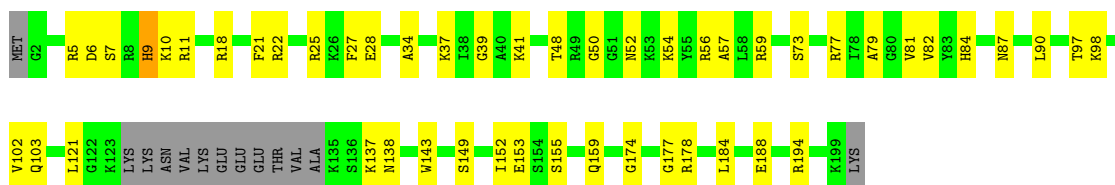
- Molecule 13: 40S ribosomal protein S7-A

Chain AH:  72% 28%

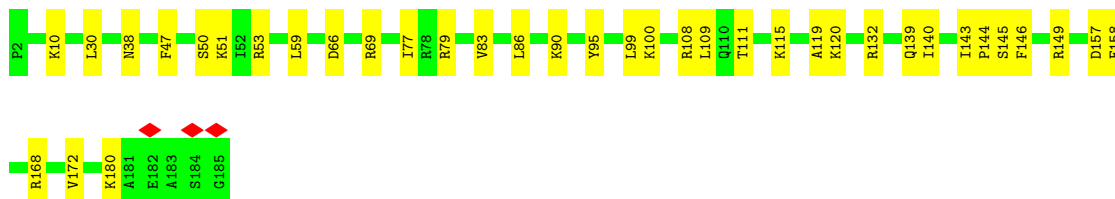
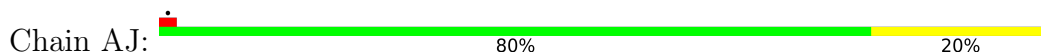


- Molecule 14: 40S ribosomal protein S8

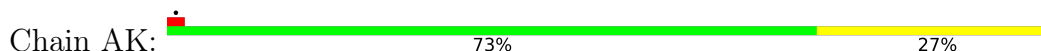
Chain AI:  68% 24% 6%



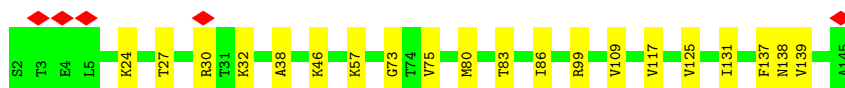
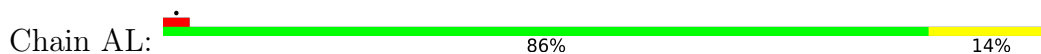
- Molecule 15: 40S ribosomal protein S9-A



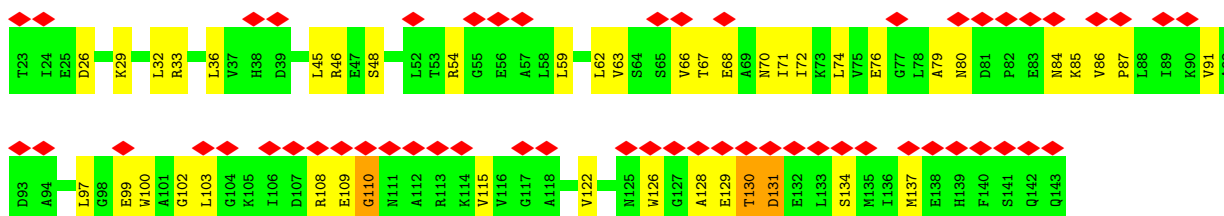
- Molecule 16: 40S ribosomal protein S10-A



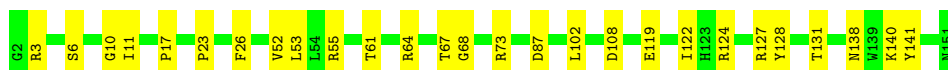
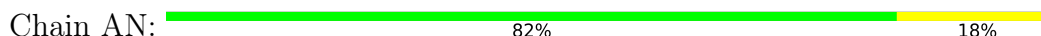
- Molecule 17: 40S ribosomal protein S11-A



- Molecule 18: 40S ribosomal protein S12

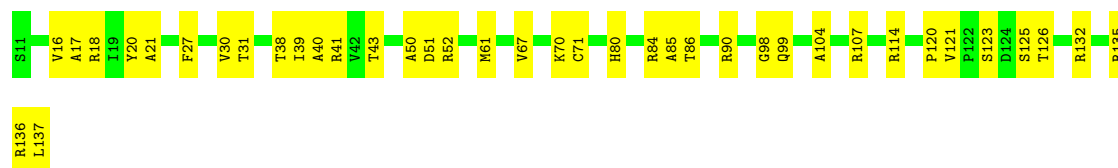


- Molecule 19: 40S ribosomal protein S13



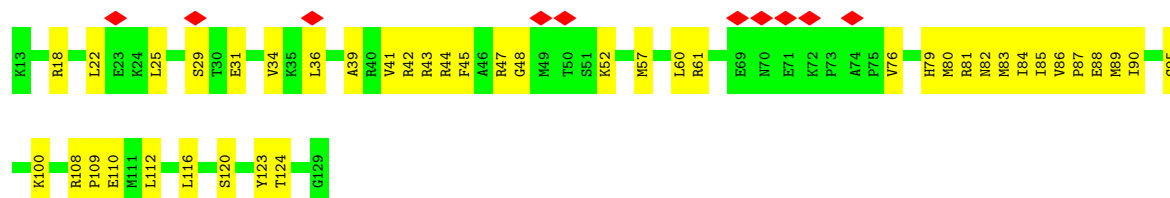
- Molecule 20: 40S ribosomal protein S14-B

Chain AO:  69% 31%



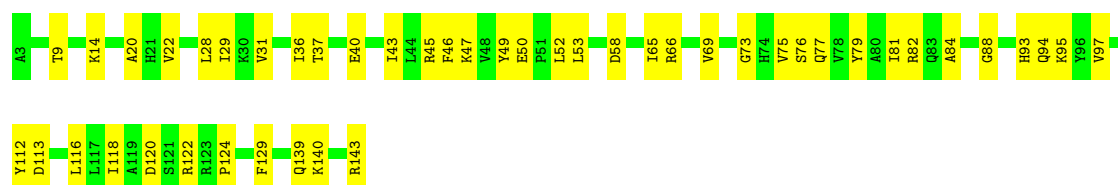
- Molecule 21: RPS15 isoform 1

Chain AP:  9% 64% 36%



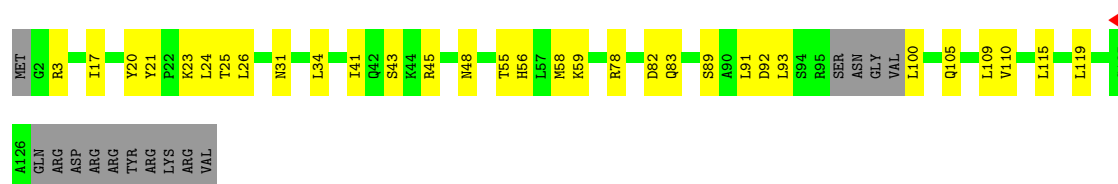
- Molecule 22: 40S ribosomal protein S16-A

Chain AQ:  67% 33%



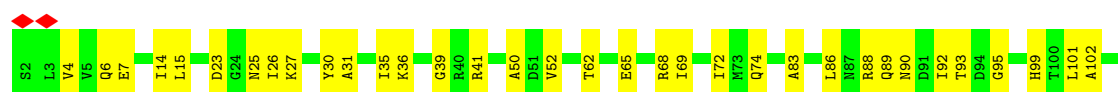
- Molecule 23: 40S ribosomal protein S17-B

Chain AR:  66% 23% 11%



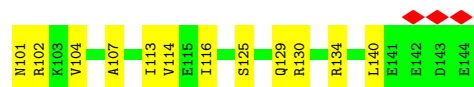
- Molecule 24: 40S ribosomal protein S18-A

Chain AS:  66% 34%

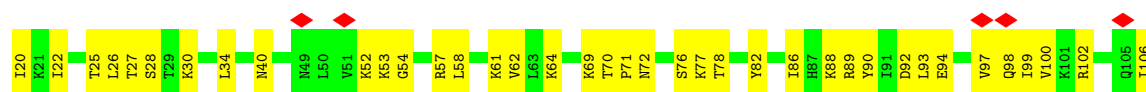




- Molecule 25: 40S ribosomal protein S19-A



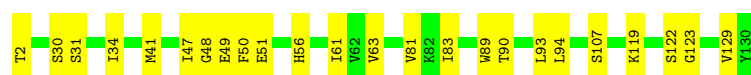
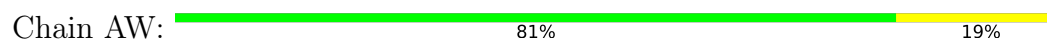
- Molecule 26: RPS20 isoform 1



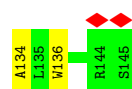
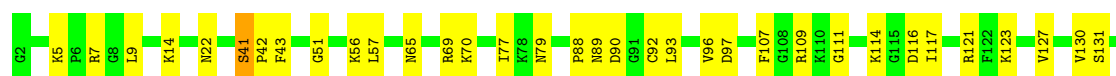
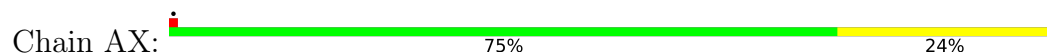
- Molecule 27: 40S ribosomal protein S21-A



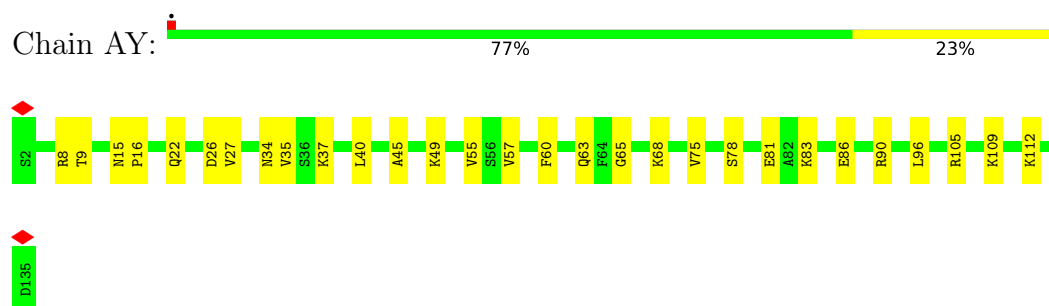
- Molecule 28: RPS22A isoform 1



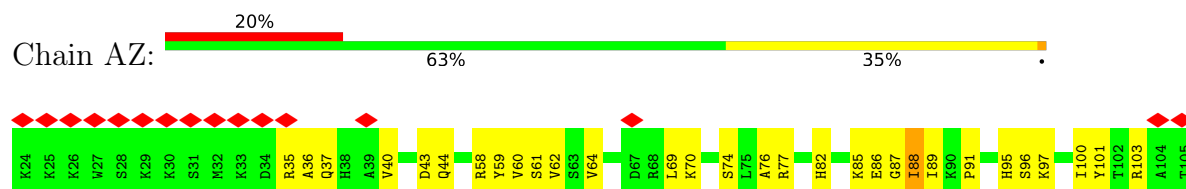
- Molecule 29: 40S ribosomal protein S23-A



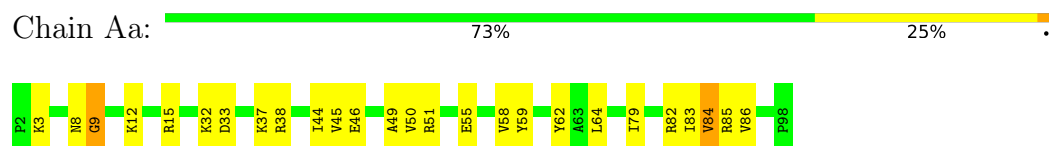
- Molecule 30: 40S ribosomal protein S24-A



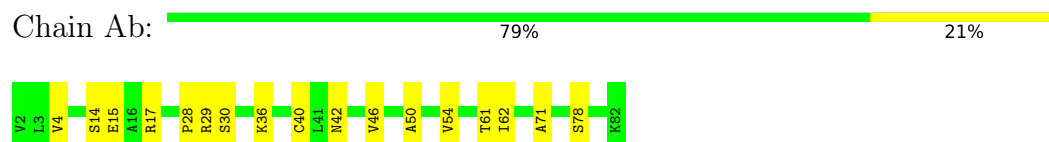
- Molecule 31: 40S ribosomal protein S25



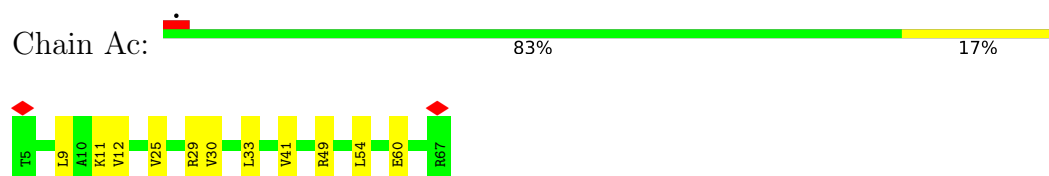
- Molecule 32: RPS26B isoform 1



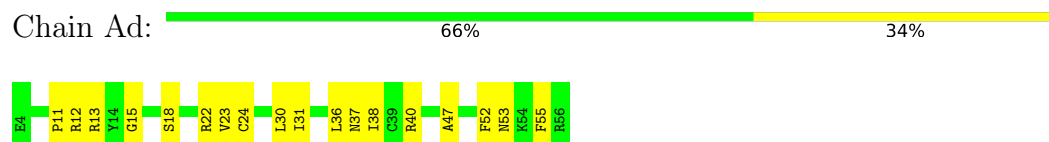
- Molecule 33: 40S ribosomal protein S27-A



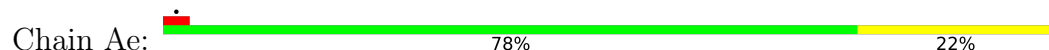
- Molecule 34: RPS28A isoform 1

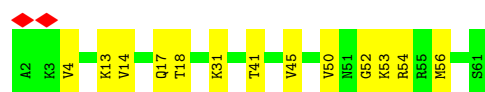


- Molecule 35: RPS29A isoform 1

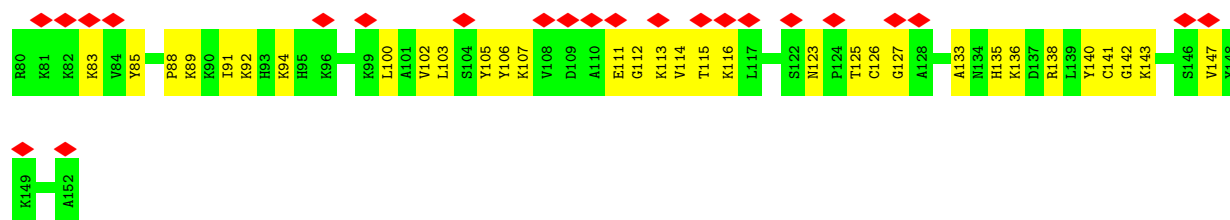


- Molecule 36: 40S ribosomal protein S30-A

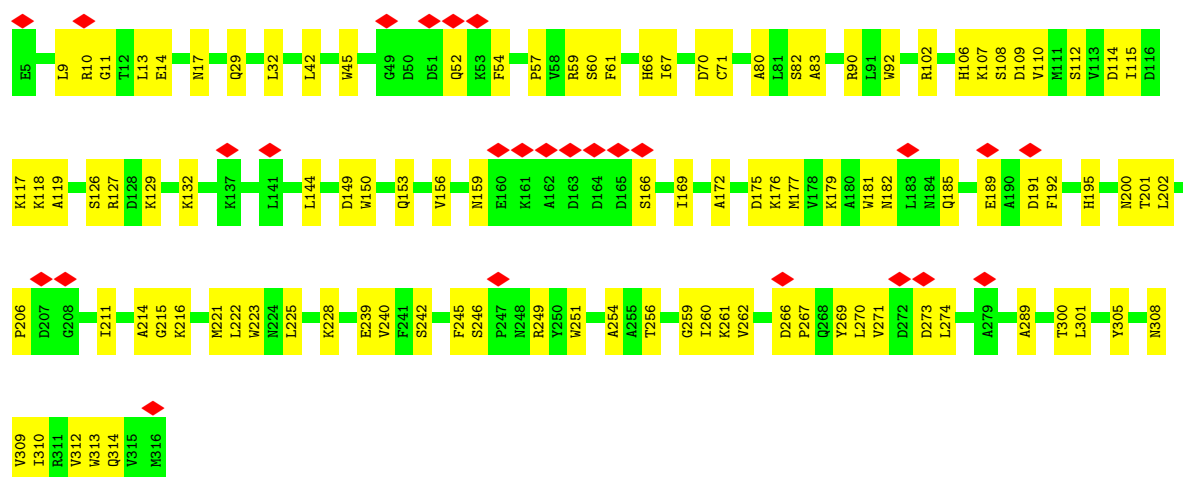




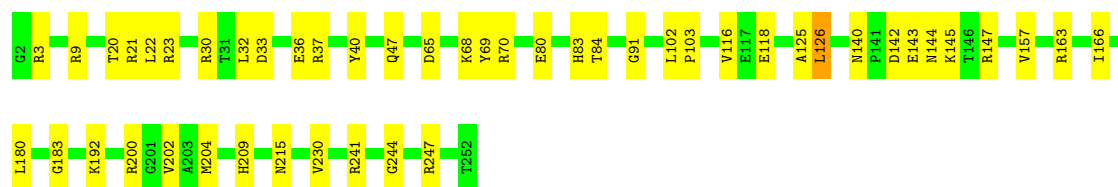
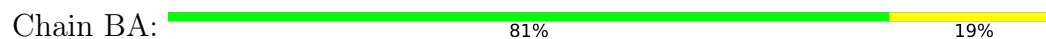
- Molecule 37: RPS31 isoform 1



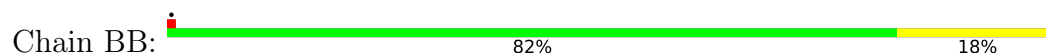
- Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein

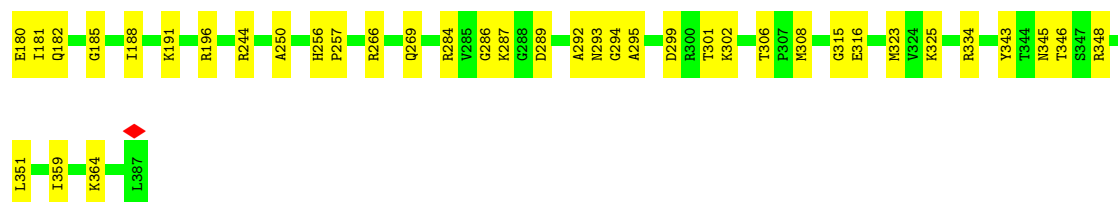


- Molecule 39: 60S ribosomal protein L2-A



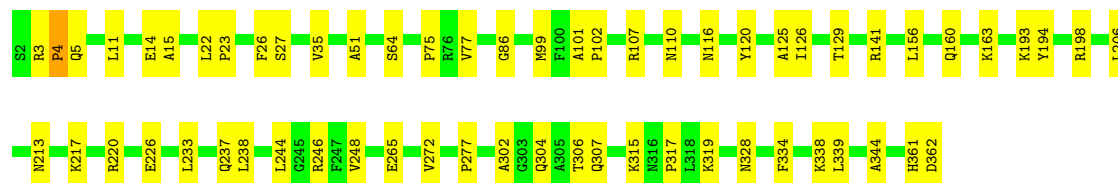
- Molecule 40: 60S ribosomal protein L3





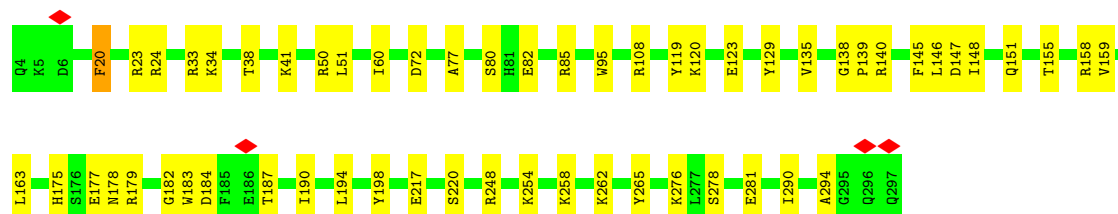
- Molecule 41: RPL4A isoform 1

Chain BC: 83% 17%



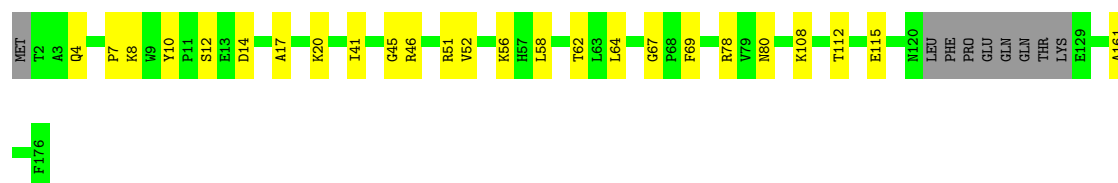
- Molecule 42: RPL5 isoform 1

Chain BD: 81% 19%



- Molecule 43: 60S ribosomal protein L6-B

Chain BE: 81% 14% 5%



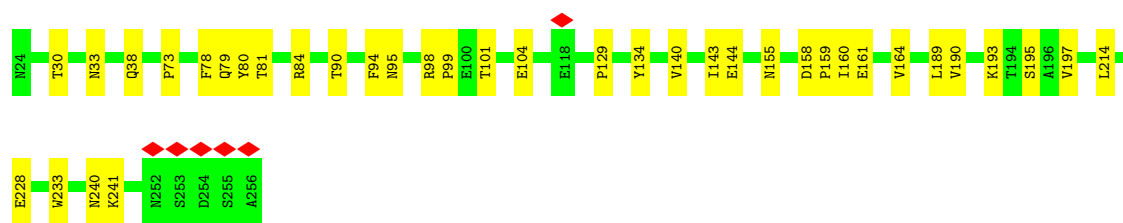
- Molecule 44: 60S ribosomal protein L7-A

Chain BF: 91% 9%



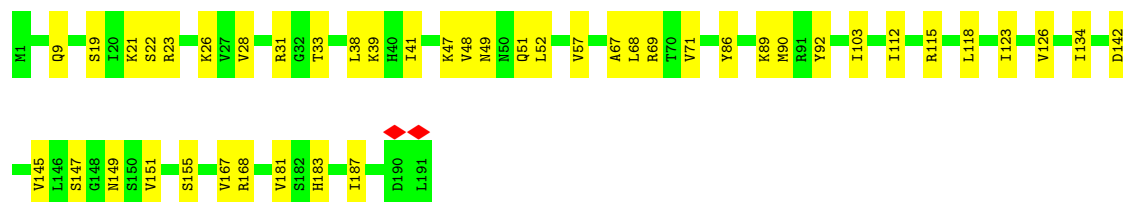
- Molecule 45: 60S ribosomal protein L8-A

Chain BG: 84% 16%



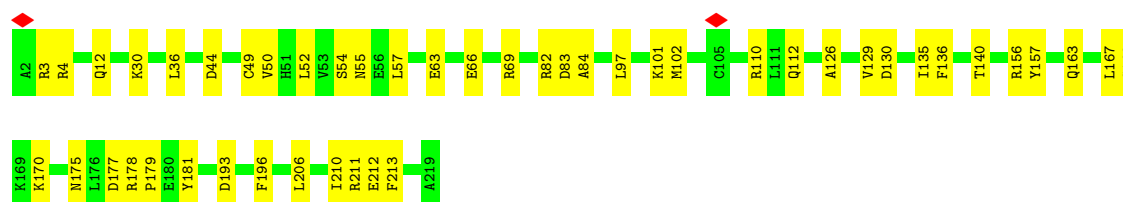
- Molecule 46: 60S ribosomal protein L9-A

Chain BH: 77% 23%



- Molecule 47: RPL10 isoform 1

Chain BI: 78% 22%



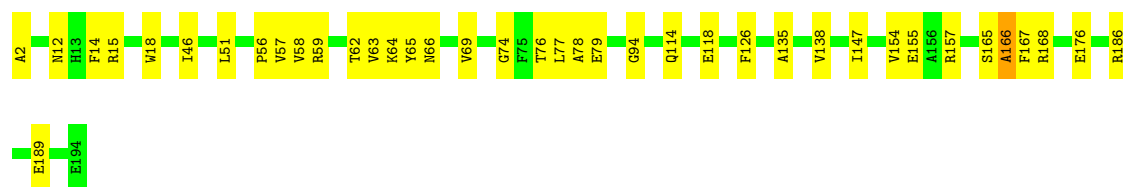
- Molecule 48: RPL11B isoform 1

Chain BJ: 72% 28%



- Molecule 49: 60S ribosomal protein L13-A

Chain BK: 80% 20%



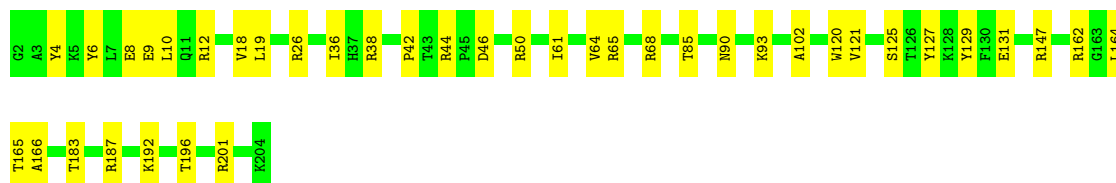
- Molecule 50: 60S ribosomal protein L14-A

Chain BL:  76% 24%



- Molecule 51: 60S ribosomal protein L15-A

Chain BM:  81% 19%



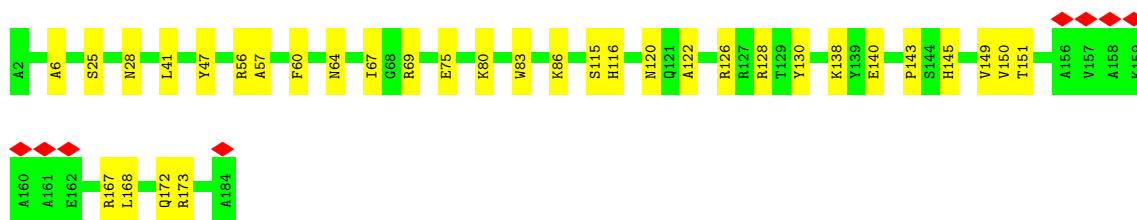
- Molecule 52: 60S ribosomal protein L16-A

Chain BN:  85% 15%



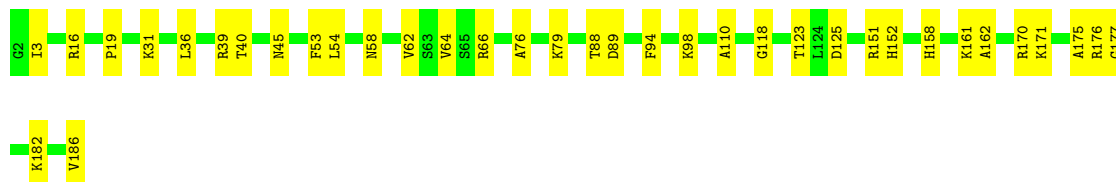
- Molecule 53: 60S ribosomal protein L17-A

Chain BO:  82% 18%



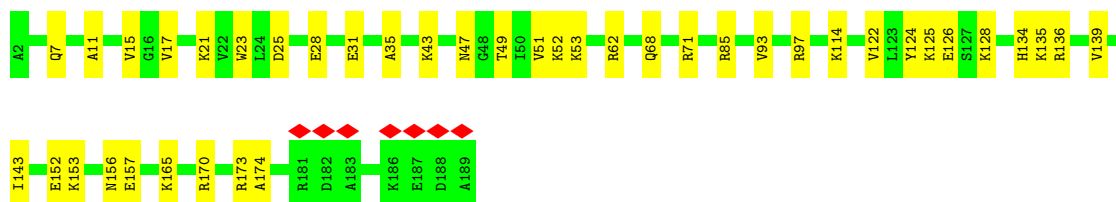
- Molecule 54: 60S ribosomal protein L18-A

Chain BP:  81% 19%



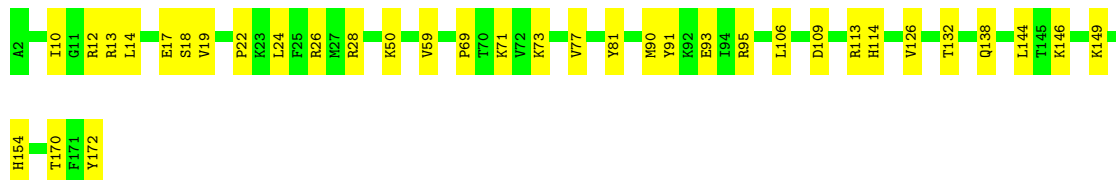
- Molecule 55: 60S ribosomal protein L19-A

Chain BQ:  78% 22%



- Molecule 56: 60S ribosomal protein L20-A

Chain BR: 80% 20%



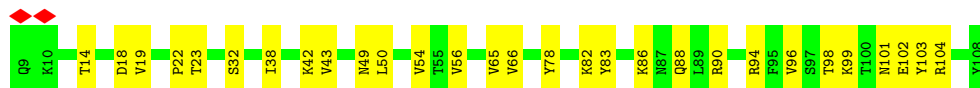
- Molecule 57: 60S ribosomal protein L21-A

Chain BS: 81% 19%



- Molecule 58: 60S ribosomal protein L22-A

Chain BT: 71% 29%



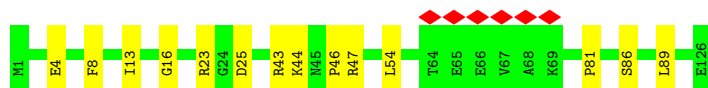
- Molecule 59: 60S ribosomal protein L23-A

Chain BU: 82% 18%



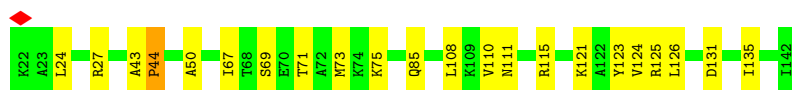
- Molecule 60: RPL24A isoform 1

Chain BV: 5% 89% 11%



- Molecule 61: 60S ribosomal protein L25

Chain BW: 82% 17%



- Molecule 62: 60S ribosomal protein L26-A

Chain BX: 77% 23%



- Molecule 63: 60S ribosomal protein L27-A

Chain BY: 80% 20%



- Molecule 64: 60S ribosomal protein L28

Chain BZ: 70% 30%



- Molecule 65: 60S ribosomal protein L29

Chain Ba: 86% 14%



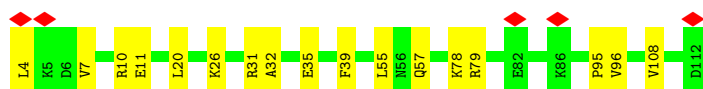
- Molecule 66: 60S ribosomal protein L30

Chain Bb: 76% 24%



- Molecule 67: 60S ribosomal protein L31-A

Chain Bc: 5% 84% 16%



● Molecule 68: RPL32 isoform 1

Chain Bd:  86% 14%

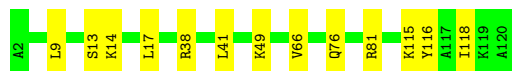
● Molecule 69: 60S ribosomal protein L33-A

Chain Be:  82% 18%

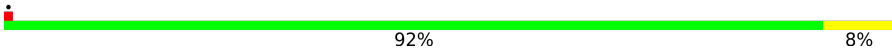
● Molecule 70: 60S ribosomal protein L34-A

Chain Bf:  87% 13%

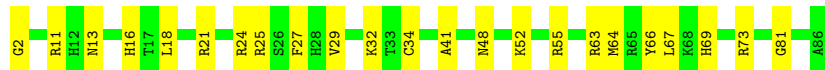
● Molecule 71: 60S ribosomal protein L35-A

Chain Bg:  89% 11%

● Molecule 72: 60S ribosomal protein L36-A

Chain Bh:  92% 8%

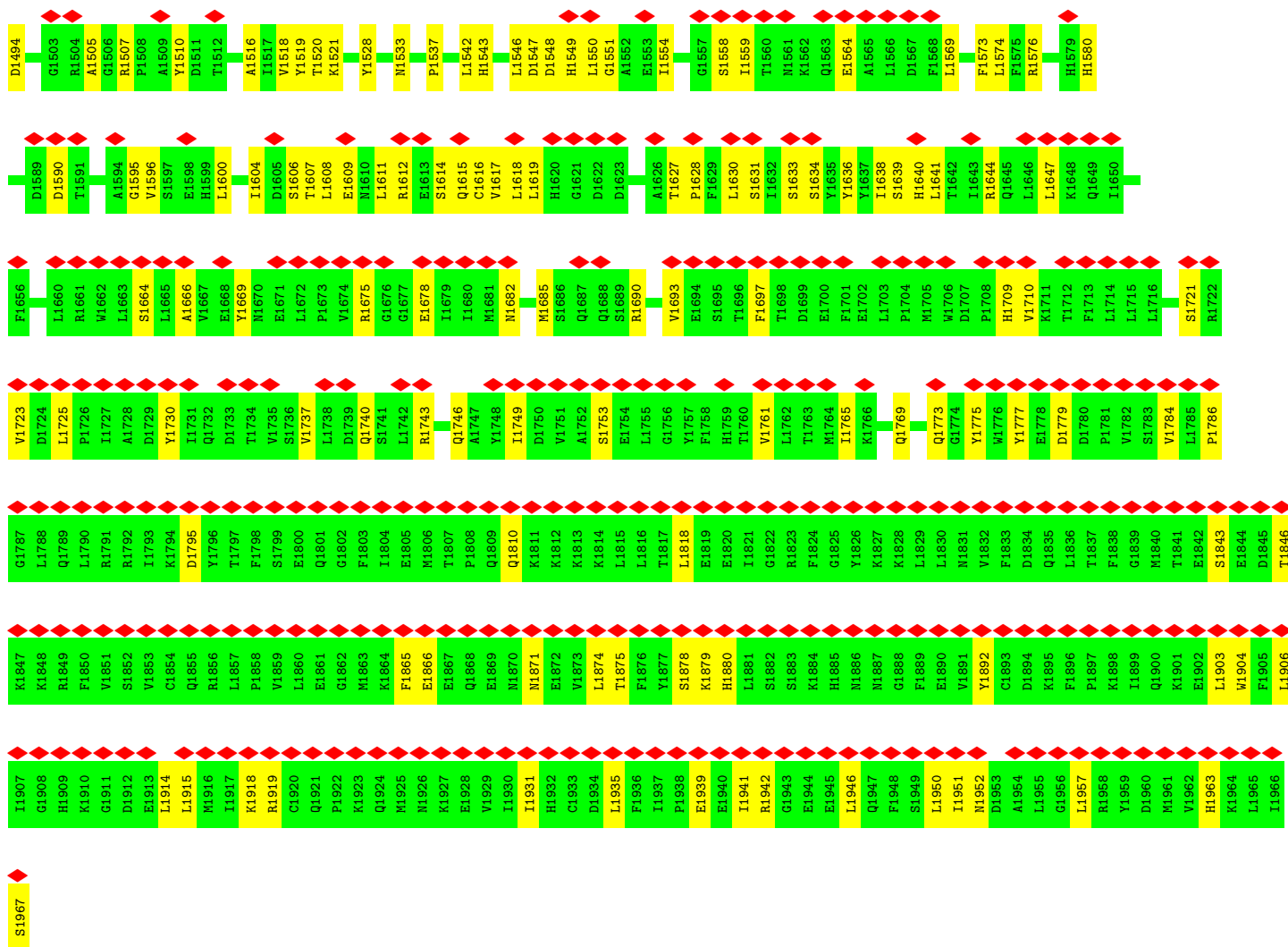
● Molecule 73: 60S ribosomal protein L37-A

Chain Bi:  73% 27%

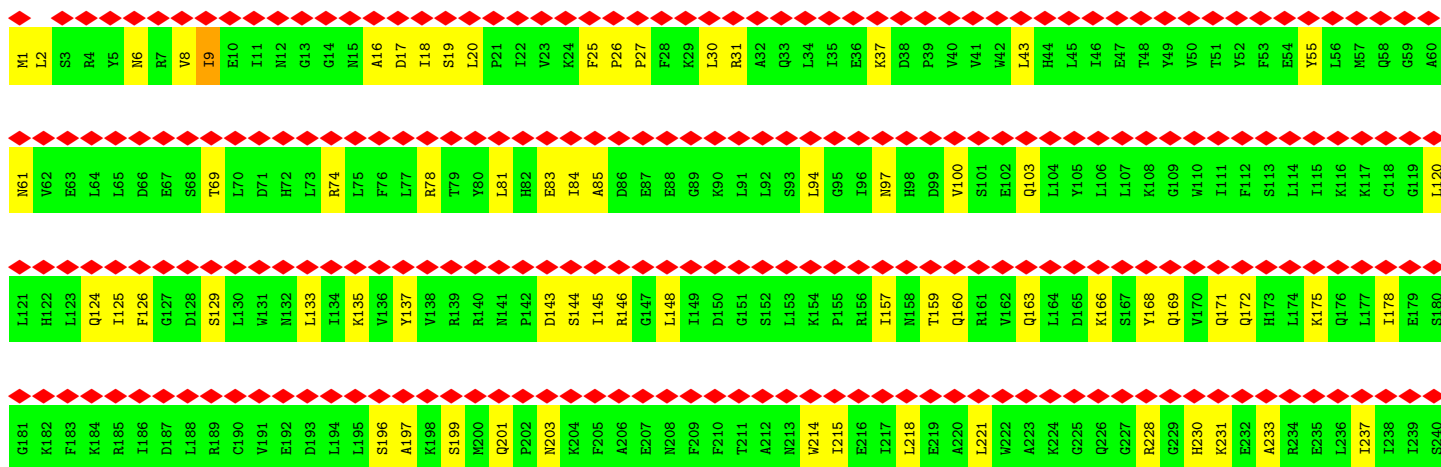
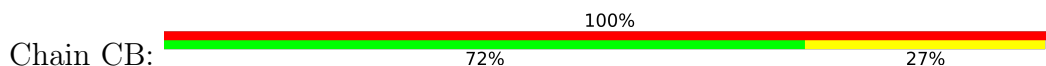
● Molecule 74: RPL38 isoform 1

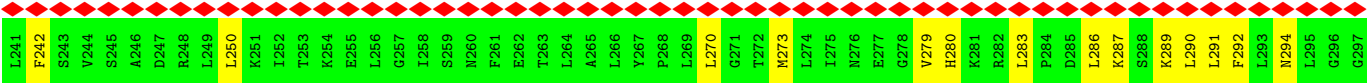
Chain Bj:  74% 26%

Y1414	H1321	K1243	Q1079	S963	N809	T685	G601	G509	H433	P354	T252	PHE
L1415	Y1324	F1244	K1083	L967	E810	S686	R602	S510	E434	L355	T253	LEU
S1416	Q1417	D1245	V1084	L968	E813	R689	A603	Q512	R436	K356	P254	THR
Q1417	R1331	G1246	L1174	E969	Q817	L690	R604	S513	G437	D257	GLN	
T1422	L1335	I1247	I1090	E971	M818	V693	S605	K514	S438	Q258	ASP	
L1423	K1336	S1248	T1095	K983	E825	V694	D606	V520	V439	Q259	ILE	
K1424	M1337	R1249	I1104	R987	F838	L696	R607	D523	T442	N261	ARG	
L1425	Y1338	N1250	P1105	R987	F838	L696	N608	K524	R446	N262	ARG	
Q1428	D1339	M1251	F1106	K990	R844	T698	L609	L525	F373	N263	GLN	
I1431	G1341	Q1252	F1107	K990	R844	Q699	K612	R531	T447	Y264	LEU	
H1434	F1342	T1253	M1108	R994	E846	Q700	D616	G532	L448	L265	LYS	
H1434	P1343	R1254	K1114	E946	E846	R706	D616	G532	E452	Y266	ALA	
H1435	L1344	K1255	L1115	R853	R853	L711	L619	Y533	S453	T267	GLU	
A1436	N1345	F1256	L1116	N998	L711	L734	K620	Q534	S454	K268	ASP	
G1437	L1346	V1257	K1117	I1000	S858	G735	V621	Y535	Q455	T381	ALA	
L1438	A1347	Q1258	L1118	E1001	S858	V718	L622	M536	S456	K271	LYS	
V1439	F1348	R1259	L1119	I1004	A880	W719	G623	F537	D383	L272	ASN	
Q1440	C1349	V1260	R1119	I1004	Y881	S720	C624	F538	M457	S273	LYS	
P1350	P1350	S1261	R1119	I1004	Y881	L721	T625	V539	I460	Y274	LEU	
L1351	L1351	I1262	P1122	I1007	F888	G722	V632	H540	G462	H277	ASN	
M1352	M1352	T1263	T1123	T1008	D889	S723	N633	S541	L463	F278	PRO	
H1447	K1357	I1263	S1124	T1009	L892	L734	G637	E544	S464	C279	ALA	
Q1448	L1449	M1264	Q1127	V1011	L892	G735	D637	T545	A393	K280	THR	
P1358	P1358	M1265	N1128	M1012	V898	V736	C638	V546	T394	V282	LYS	
Q1451	M1361	F1267	P1128	R1013	V899	V737	V639	K547	Q395	T381	THR	
K1452	A1362	I1268	P1129	I1014	N902	Y738	T640	A549	V396	E286	LYS	
L1453	I1363	L1269	S1133	A1017	N902	R742	L641	R550	V398	T287	TRP	
K1454	D1369	L1270	Y1139	I1018	R908	R742	T644	D472	T399	L288	PRO	
L1457	L1373	G1276	F1140	D1021	A909	P747	Q645	T553	K403	Q292	VAL	
L1458	I1374	L1279	F1141	F1022	L910	F748	Q645	D563	V404	V298	PHE	
L1459	R1379	I1282	P1142	V1023	F911	D753	K651	Y575	T408	A299	ARG	
L1464	Q1381	R1285	M1143	R1027	L912	W754	T655	K572	T408	Y300	S223	
G1467	T1382	M1286	Q1144	I1028	R917	I757	L657	Y575	M412	K301	T224	
V1468	R1383	M1286	T1147	V1037	K921	L763	G658	S976	G413	T302	Q232	
N1469	L1384	I1289	F1148	E1041	F922	V764	S660	R577	D414	T323	K233	
V1475	T1386	I1289	L1151	S1042	N924	E765	D661	S578	M415	F331	F234	
K1478	L1387	Q1292	Y1152	S1045	V925	R766	Q664	K581	D416	SER	T235	
G1479	L1388	T1293	N1153	L1048	N926	M770	T665	R583	L417	VAL	L236	
T1480	L1389	K1294	T1154	L1048	N928	L777	F666	K582	S419	VAL	P237	
Q1481	Q1295	F1296	N1155	L1055	N928	L778	P666	R583	V418	GLY	V238	
F1482	P1296	E1156	E1156	L1056	N928	L778	P666	R583	V418	GLY	G239	
F1483	V1297	A1158	A1158	R1057	N928	L778	P666	R583	V418	GLY	T240	
D1484	R1298	L1225	A1158	R1057	N928	L778	P666	R583	V418	GLY	R242	
L1485	L1299	P1226	F1159	R1058	N928	L778	P666	R583	V418	GLY	N246	
K1486	L1300	D1227	V1160	R1058	N928	L778	P666	R583	V418	GLY	T247	
D1487	G1301	P1228	G1161	L1055	N928	L778	P666	R583	V418	GLY	D341	
E1488	M1302	P1228	S1162	M1066	N928	L778	P666	R583	V418	GLY	T247	
G1489	L1303	K1229	P1163	M1066	N928	L778	P666	R583	V418	GLY	D341	
Y1490	W1315	D1230	G1164	M1066	N928	L778	P666	R583	V418	GLY	D341	
R1491	L1316	H1231	G1165	M1066	N928	L778	P666	R583	V418	GLY	D341	
D1492	K1319	D1233	T1169	P1077	D948	A795	L682	H598	V428	D346	E249	
M1493	D1320	D1233	T1169	P1078	P962	A795	L683	I597	H430	F347	E250	
		I1236	V1237	P1078	P962	A795	L683	I597	H430	F347	E250	
		I1238					C684		L432	V349	I251	

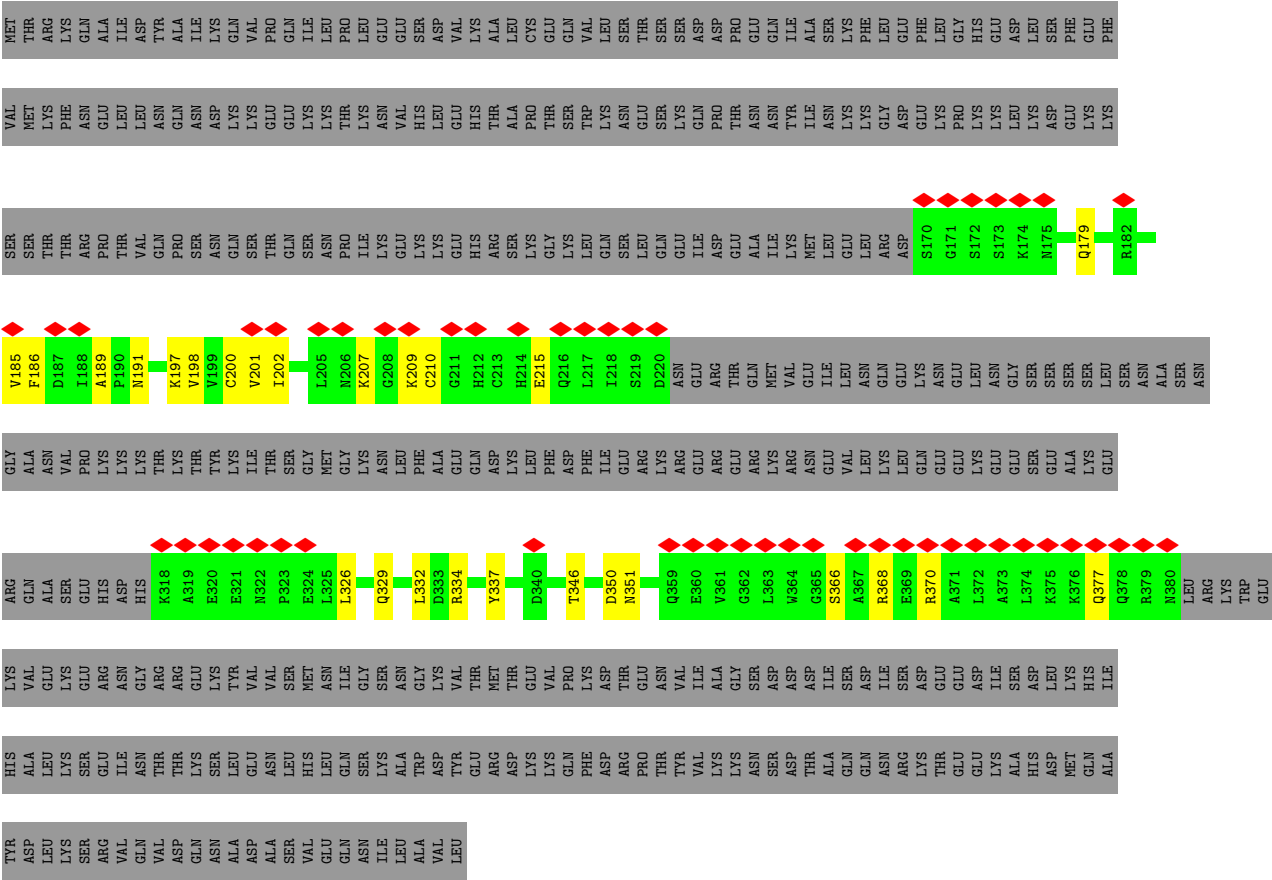


● Molecule 81: RQC trigger complex subunit CUE3





• Molecule 82: RQT4 isoform 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	194186	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 ($e^-/\text{\AA}^2$)	43.6	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	7.920	Depositor
Minimum map value	-1.030	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.145	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	2	0.14	0/42211	0.28	0/65773
2	3	0.17	0/3746	0.28	0/5832
3	4	0.15	0/2883	0.23	0/4491
4	5	0.17	0/76214	0.28	0/118821
5	6	0.08	0/1808	0.20	0/2816
6	AA	0.13	0/1644	0.34	0/2249
7	AB	0.16	0/1823	0.44	0/2447
8	AC	0.15	0/1656	0.31	0/2251
9	AD	0.11	0/1754	0.28	0/2361
10	AE	0.16	0/2097	0.38	1/2823 (0.0%)
11	AF	0.13	0/1625	0.35	0/2197
12	AG	0.14	0/1839	0.38	0/2460
13	AH	0.14	0/1498	0.40	0/2019
14	AI	0.15	0/1501	0.41	0/2006
15	AJ	0.14	0/1504	0.36	0/2016
16	AK	0.11	0/769	0.33	0/1039
17	AL	0.16	0/1185	0.34	0/1598
18	AM	0.14	0/883	0.53	0/1199
19	AN	0.15	0/1215	0.39	0/1638
20	AO	0.16	0/937	0.38	0/1261
21	AP	0.13	0/936	0.37	0/1259
22	AQ	0.13	0/1125	0.38	1/1510 (0.1%)
23	AR	0.14	0/957	0.40	0/1283
24	AS	0.11	0/1211	0.36	0/1628
25	AT	0.14	0/1130	0.37	0/1517
26	AU	0.14	0/807	0.36	0/1091
27	AV	0.18	0/682	0.34	0/921
28	AW	0.17	0/1038	0.36	0/1395
29	AX	0.17	0/1139	0.44	0/1518
30	AY	0.13	0/1087	0.33	0/1449
31	AZ	0.13	0/661	0.45	1/888 (0.1%)
32	Aa	0.18	0/782	0.60	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.14	0/620	0.38	0/838
34	Ac	0.12	0/493	0.30	0/663
35	Ad	0.12	0/452	0.30	0/600
36	Ae	0.17	0/480	0.40	0/639
37	Af	0.19	0/567	0.65	0/764
38	Ag	0.12	0/2436	0.36	0/3318
39	BA	0.18	0/1933	0.37	0/2598
40	BB	0.16	0/3146	0.34	0/4228
41	BC	0.16	0/2800	0.36	0/3790
42	BD	0.14	0/2400	0.33	0/3239
43	BE	0.14	0/1327	0.33	0/1790
44	BF	0.15	0/1821	0.29	0/2451
45	BG	0.16	0/1836	0.36	0/2481
46	BH	0.13	0/1529	0.29	0/2060
47	BI	0.14	0/1801	0.31	0/2416
48	BJ	0.12	0/1371	0.33	0/1838
49	BK	0.16	0/1568	0.38	0/2106
50	BL	0.13	0/1068	0.31	0/1438
51	BM	0.16	0/1757	0.33	0/2354
52	BN	0.15	0/1585	0.31	0/2128
53	BO	0.15	0/1439	0.33	0/1938
54	BP	0.15	0/1465	0.31	0/1965
55	BQ	0.14	0/1532	0.32	0/2043
56	BR	0.16	0/1473	0.30	0/1980
57	BS	0.17	0/1300	0.33	0/1743
58	BT	0.13	0/812	0.36	0/1099
59	BU	0.14	0/1018	0.27	0/1369
60	BV	0.13	0/850	0.32	0/1152
61	BW	0.15	0/979	0.32	0/1321
62	BX	0.15	0/995	0.28	0/1329
63	BY	0.15	0/1118	0.35	0/1497
64	BZ	0.19	0/1204	0.42	0/1612
65	Ba	0.14	0/473	0.33	0/629
66	Bb	0.15	0/745	0.28	0/1001
67	Bc	0.14	0/890	0.29	0/1196
68	Bd	0.15	0/1038	0.32	0/1390
69	Be	0.16	0/868	0.29	0/1168
70	Bf	0.16	0/890	0.30	0/1189
71	Bg	0.13	0/978	0.29	0/1301
72	Bh	0.13	0/772	0.27	0/1026
73	Bi	0.17	0/685	0.33	0/908
74	Bj	0.13	0/618	0.29	0/826
75	Bk	0.15	0/443	0.27	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bl	0.14	0/423	0.32	0/562
77	Bm	0.13	0/230	0.25	0/296
78	Bn	0.15	0/836	0.33	0/1104
79	Bo	0.15	0/701	0.31	0/934
80	CA	0.11	0/14309	0.34	1/19348 (0.0%)
81	CB	0.08	0/2463	0.25	0/3324
82	CC	0.09	0/897	0.33	0/1203
All	All	0.15	0/233781	0.31	4/341583 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
7	AB	0	2
10	AE	0	1
12	AG	0	1
13	AH	0	1
18	AM	0	2
22	AQ	0	1
29	AX	0	2
31	AZ	0	1
32	Aa	0	1
40	BB	0	1
45	BG	0	1
52	BN	0	1
61	BW	0	1
65	Ba	0	2
All	All	0	18

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	AZ	88	ILE	N-CA-C	-5.92	106.95	111.62
80	CA	1117	LYS	N-CA-C	-5.34	104.03	110.44
10	AE	193	GLY	N-CA-C	5.29	125.71	113.18
22	AQ	43	ILE	N-CA-C	-5.21	108.76	113.71

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	AB	211	HIS	Peptide
7	AB	81	PHE	Peptide
10	AE	42	LEU	Peptide
12	AG	68	LEU	Peptide
13	AH	64	VAL	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	37739	0	18988	658	0
2	3	3353	0	1695	50	0
3	4	2579	0	1304	32	0
4	5	68091	0	34217	828	0
5	6	1619	0	821	19	0
6	AA	1603	0	1610	36	0
7	AB	1798	0	1890	51	0
8	AC	1626	0	1715	26	0
9	AD	1729	0	1812	39	0
10	AE	2056	0	2140	42	0
11	AF	1605	0	1669	42	0
12	AG	1815	0	1894	66	0
13	AH	1473	0	1555	39	0
14	AI	1476	0	1501	41	0
15	AJ	1479	0	1556	28	0
16	AK	752	0	719	18	0
17	AL	1159	0	1225	15	0
18	AM	875	0	878	34	0
19	AN	1192	0	1255	24	0
20	AO	926	0	950	32	0
21	AP	916	0	941	35	0
22	AQ	1105	0	1166	44	0
23	AR	948	0	990	29	0
24	AS	1192	0	1222	32	0
25	AT	1112	0	1124	36	0
26	AU	797	0	863	45	0
27	AV	673	0	662	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
28	AW	1021	0	1060	19	0
29	AX	1121	0	1196	25	0
30	AY	1073	0	1132	24	0
31	AZ	651	0	682	19	0
32	Aa	769	0	818	28	0
33	Ab	610	0	633	10	0
34	Ac	491	0	524	8	0
35	Ad	442	0	428	17	0
36	Ae	472	0	521	9	0
37	Af	556	0	547	32	0
38	Ag	2383	0	2332	72	0
39	BA	1899	0	1957	39	0
40	BB	3075	0	3142	50	0
41	BC	2748	0	2859	45	0
42	BD	2351	0	2294	44	0
43	BE	1305	0	1370	18	0
44	BF	1784	0	1862	15	0
45	BG	1804	0	1877	26	0
46	BH	1508	0	1572	30	0
47	BI	1764	0	1804	33	0
48	BJ	1350	0	1381	36	0
49	BK	1543	0	1608	30	0
50	BL	1053	0	1149	23	0
51	BM	1720	0	1779	32	0
52	BN	1555	0	1659	19	0
53	BO	1416	0	1433	21	0
54	BP	1441	0	1543	27	0
55	BQ	1515	0	1606	32	0
56	BR	1437	0	1475	29	0
57	BS	1276	0	1323	24	0
58	BT	796	0	812	22	0
59	BU	1003	0	1048	14	0
60	BV	836	0	709	12	0
61	BW	964	0	1025	14	0
62	BX	984	0	1075	22	0
63	BY	1092	0	1155	23	0
64	BZ	1173	0	1215	46	0
65	Ba	462	0	491	6	0
66	Bb	737	0	792	18	0
67	Bc	876	0	912	10	0
68	Bd	1017	0	1081	14	0
69	Be	850	0	880	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
70	Bf	880	0	941	14	0
71	Bg	969	0	1078	10	0
72	Bh	766	0	844	8	0
73	Bi	670	0	673	17	0
74	Bj	612	0	682	13	0
75	Bk	436	0	475	6	0
76	Bl	417	0	455	9	0
77	Bm	229	0	273	3	0
78	Bn	824	0	888	12	0
79	Bo	694	0	735	11	0
80	CA	14008	0	14058	395	0
81	CB	2415	0	2508	55	0
82	CC	886	0	857	21	0
83	2	84	0	0	0	0
83	AQ	1	0	0	0	0
83	AT	1	0	0	0	0
84	Ad	1	0	0	0	0
84	Af	1	0	0	0	0
84	Bf	1	0	0	0	0
84	Bi	1	0	0	0	0
84	Bl	1	0	0	0	0
84	Bn	1	0	0	0	0
84	Bo	1	0	0	0	0
84	CC	2	0	0	0	0
All	All	218512	0	165590	3384	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 3384 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:6:5:U:H3	5:6:68:G:H1	0.99	0.96
1:2:1588:G:H1	1:2:1608:U:H3	1.18	0.91
4:5:1018:G:H1	4:5:1034:U:H3	0.95	0.91
12:AG:23:ARG:NH1	12:AG:40:ALA:O	2.07	0.88
1:2:555:A:N7	1:2:590:C:O2'	2.08	0.86

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AA	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
7	AB	222/255 (87%)	211 (95%)	10 (4%)	1 (0%)	24	58
8	AC	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
9	AD	220/222 (99%)	218 (99%)	2 (1%)	0	100	100
10	AE	256/258 (99%)	245 (96%)	10 (4%)	1 (0%)	30	62
11	AF	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
12	AG	226/228 (99%)	211 (93%)	14 (6%)	1 (0%)	30	62
13	AH	182/184 (99%)	172 (94%)	10 (6%)	0	100	100
14	AI	183/200 (92%)	173 (94%)	8 (4%)	2 (1%)	11	42
15	AJ	182/184 (99%)	173 (95%)	9 (5%)	0	100	100
16	AK	90/92 (98%)	85 (94%)	5 (6%)	0	100	100
17	AL	142/144 (99%)	136 (96%)	6 (4%)	0	100	100
18	AM	119/121 (98%)	95 (80%)	22 (18%)	2 (2%)	7	34
19	AN	148/150 (99%)	141 (95%)	7 (5%)	0	100	100
20	AO	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
21	AP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
22	AQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
23	AR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
24	AS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
25	AT	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
26	AU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
27	AV	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
28	AW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
29	AX	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
30	AY	132/134 (98%)	125 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	AZ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
32	Aa	95/97 (98%)	81 (85%)	11 (12%)	3 (3%)	3	24
33	Ab	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
34	Ac	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
35	Ad	51/53 (96%)	51 (100%)	0	0	100	100
36	Ae	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
37	Af	71/73 (97%)	63 (89%)	8 (11%)	0	100	100
38	Ag	310/312 (99%)	302 (97%)	8 (3%)	0	100	100
39	BA	249/251 (99%)	238 (96%)	10 (4%)	1 (0%)	30	62
40	BB	384/386 (100%)	371 (97%)	12 (3%)	1 (0%)	36	67
41	BC	359/361 (99%)	347 (97%)	11 (3%)	1 (0%)	36	67
42	BD	292/294 (99%)	283 (97%)	8 (3%)	1 (0%)	36	67
43	BE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
44	BF	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
45	BG	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
46	BH	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
47	BI	216/218 (99%)	214 (99%)	2 (1%)	0	100	100
48	BJ	167/169 (99%)	158 (95%)	9 (5%)	0	100	100
49	BK	191/193 (99%)	178 (93%)	10 (5%)	3 (2%)	7	36
50	BL	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
51	BM	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
52	BN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	12	44
53	BO	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
54	BP	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
55	BQ	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
56	BR	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
57	BS	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
58	BT	98/100 (98%)	98 (100%)	0	0	100	100
59	BU	134/136 (98%)	134 (100%)	0	0	100	100
60	BV	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
61	BW	119/121 (98%)	117 (98%)	1 (1%)	1 (1%)	16	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	BX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
63	BY	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
64	BZ	146/148 (99%)	136 (93%)	8 (6%)	2 (1%)	9	38
65	Ba	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Bb	94/96 (98%)	94 (100%)	0	0	100	100
67	Bc	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
68	Bd	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Be	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
70	Bf	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
71	Bg	117/119 (98%)	115 (98%)	2 (2%)	0	100	100
72	Bh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
73	Bi	83/85 (98%)	83 (100%)	0	0	100	100
74	Bj	75/77 (97%)	75 (100%)	0	0	100	100
75	Bk	48/50 (96%)	48 (100%)	0	0	100	100
76	Bl	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
77	Bm	23/25 (92%)	23 (100%)	0	0	100	100
78	Bn	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
79	Bo	89/91 (98%)	89 (100%)	0	0	100	100
80	CA	1738/1967 (88%)	1664 (96%)	69 (4%)	5 (0%)	36	67
81	CB	295/297 (99%)	292 (99%)	2 (1%)	1 (0%)	36	67
82	CC	110/530 (21%)	106 (96%)	4 (4%)	0	100	100
All	All	13127/14000 (94%)	12615 (96%)	484 (4%)	28 (0%)	44	74

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	AI	10	LYS
32	Aa	84	VAL
52	BN	111[A]	PRO
80	CA	224	THR
80	CA	621	VAL

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	
6	AA	170/173 (98%)	170 (100%)	0	100	100
7	AB	200/224 (89%)	200 (100%)	0	100	100
8	AC	175/175 (100%)	175 (100%)	0	100	100
9	AD	182/182 (100%)	182 (100%)	0	100	100
10	AE	220/220 (100%)	220 (100%)	0	100	100
11	AF	172/173 (99%)	172 (100%)	0	100	100
12	AG	189/195 (97%)	189 (100%)	0	100	100
13	AH	163/165 (99%)	163 (100%)	0	100	100
14	AI	148/161 (92%)	148 (100%)	0	100	100
15	AJ	156/157 (99%)	156 (100%)	0	100	100
16	AK	77/85 (91%)	77 (100%)	0	100	100
17	AL	129/129 (100%)	129 (100%)	0	100	100
18	AM	88/98 (90%)	88 (100%)	0	100	100
19	AN	127/127 (100%)	127 (100%)	0	100	100
20	AO	91/96 (95%)	91 (100%)	0	100	100
21	AP	95/98 (97%)	95 (100%)	0	100	100
22	AQ	117/117 (100%)	117 (100%)	0	100	100
23	AR	101/124 (82%)	101 (100%)	0	100	100
24	AS	128/128 (100%)	128 (100%)	0	100	100
25	AT	115/115 (100%)	115 (100%)	0	100	100
26	AU	93/93 (100%)	93 (100%)	0	100	100
27	AV	71/74 (96%)	71 (100%)	0	100	100
28	AW	110/110 (100%)	110 (100%)	0	100	100
29	AX	119/119 (100%)	119 (100%)	0	100	100
30	AY	112/112 (100%)	112 (100%)	0	100	100
31	AZ	67/73 (92%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	Aa	83/83 (100%)	83 (100%)	0	100	100
33	Ab	70/70 (100%)	70 (100%)	0	100	100
34	Ac	55/56 (98%)	55 (100%)	0	100	100
35	Ad	47/47 (100%)	47 (100%)	0	100	100
36	Ae	50/51 (98%)	50 (100%)	0	100	100
37	Af	56/64 (88%)	56 (100%)	0	100	100
38	Ag	250/257 (97%)	250 (100%)	0	100	100
39	BA	190/193 (98%)	190 (100%)	0	100	100
40	BB	321/322 (100%)	319 (99%)	2 (1%)	78	79
41	BC	288/288 (100%)	288 (100%)	0	100	100
42	BD	241/243 (99%)	241 (100%)	0	100	100
43	BE	138/155 (89%)	138 (100%)	0	100	100
44	BF	186/186 (100%)	186 (100%)	0	100	100
45	BG	187/191 (98%)	187 (100%)	0	100	100
46	BH	168/171 (98%)	168 (100%)	0	100	100
47	BI	185/185 (100%)	184 (100%)	1 (0%)	81	80
48	BJ	146/147 (99%)	146 (100%)	0	100	100
49	BK	154/154 (100%)	154 (100%)	0	100	100
50	BL	107/107 (100%)	107 (100%)	0	100	100
51	BM	175/175 (100%)	175 (100%)	0	100	100
52	BN	160/160 (100%)	160 (100%)	0	100	100
53	BO	138/145 (95%)	138 (100%)	0	100	100
54	BP	150/150 (100%)	150 (100%)	0	100	100
55	BQ	152/153 (99%)	152 (100%)	0	100	100
56	BR	155/155 (100%)	155 (100%)	0	100	100
57	BS	136/136 (100%)	136 (100%)	0	100	100
58	BT	87/87 (100%)	87 (100%)	0	100	100
59	BU	104/104 (100%)	104 (100%)	0	100	100
60	BV	56/107 (52%)	56 (100%)	0	100	100
61	BW	104/105 (99%)	104 (100%)	0	100	100
62	BX	108/108 (100%)	108 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	BY	115/115 (100%)	115 (100%)	0	100	100
64	BZ	118/118 (100%)	118 (100%)	0	100	100
65	Ba	46/46 (100%)	46 (100%)	0	100	100
66	Bb	81/81 (100%)	81 (100%)	0	100	100
67	Bc	92/96 (96%)	92 (100%)	0	100	100
68	Bd	108/109 (99%)	108 (100%)	0	100	100
69	Be	90/90 (100%)	90 (100%)	0	100	100
70	Bf	95/95 (100%)	95 (100%)	0	100	100
71	Bg	104/104 (100%)	104 (100%)	0	100	100
72	Bh	80/81 (99%)	80 (100%)	0	100	100
73	Bi	69/69 (100%)	69 (100%)	0	100	100
74	Bj	68/68 (100%)	68 (100%)	0	100	100
75	Bk	45/45 (100%)	45 (100%)	0	100	100
76	Bl	47/47 (100%)	47 (100%)	0	100	100
77	Bm	22/23 (96%)	22 (100%)	0	100	100
78	Bn	87/88 (99%)	87 (100%)	0	100	100
79	Bo	71/71 (100%)	71 (100%)	0	100	100
80	CA	1560/1770 (88%)	1560 (100%)	0	100	100
81	CB	266/266 (100%)	266 (100%)	0	100	100
82	CC	97/482 (20%)	97 (100%)	0	100	100
All	All	11123/11942 (93%)	11120 (100%)	3 (0%)	100	100

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
40	BB	89	VAL
40	BB	90	VAL
47	BI	55	ASN

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

Mol	Chain	Res	Type
47	BI	162	GLN
63	BY	103	GLN

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Mol	Chain	Res	Type
82	CC	377	GLN
80	CA	1412	GLN
51	BM	182	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1798 (98%)	413 (23%)	36 (2%)
2	3	157/158 (99%)	27 (17%)	1 (0%)
3	4	120/121 (99%)	9 (7%)	1 (0%)
4	5	3180/3396 (93%)	530 (16%)	30 (0%)
5	6	75/76 (98%)	12 (16%)	0
All	All	5300/5549 (95%)	991 (18%)	68 (1%)

5 of 991 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	34	G

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	2500	A
4	5	2541	U
4	5	3350	C
1	2	1226	A
1	2	1216	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 95 ligands modelled in this entry, 95 are monoatomic - leaving 0 for Mogul analysis.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

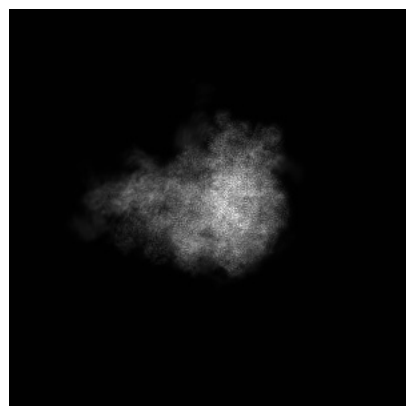
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14861. These allow visual inspection of the internal detail of the map and identification of artifacts.

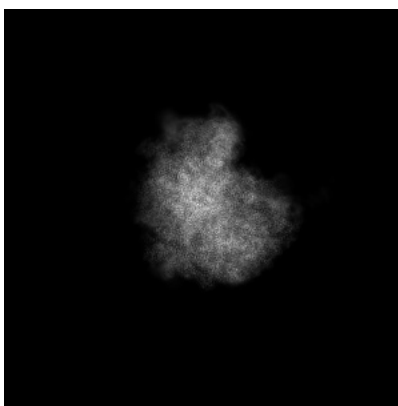
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

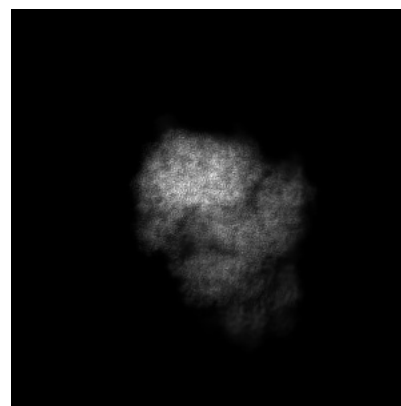
6.1.1 Primary map



X

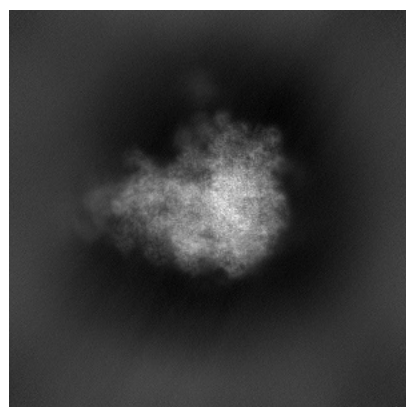


Y

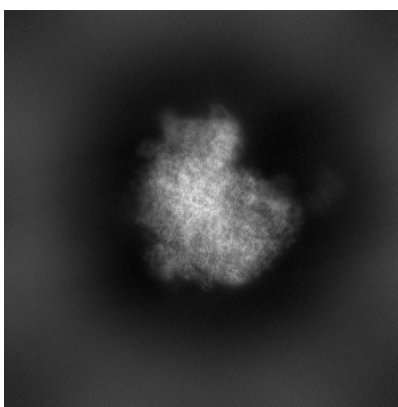


Z

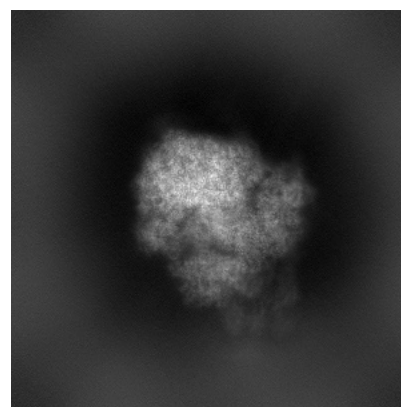
6.1.2 Raw map



X



Y

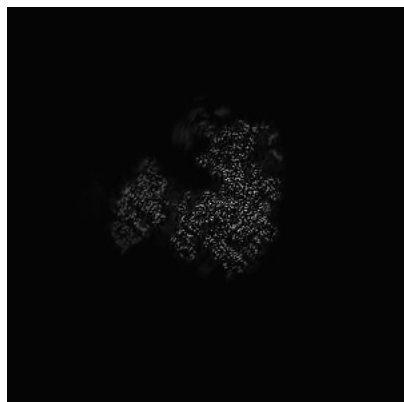


Z

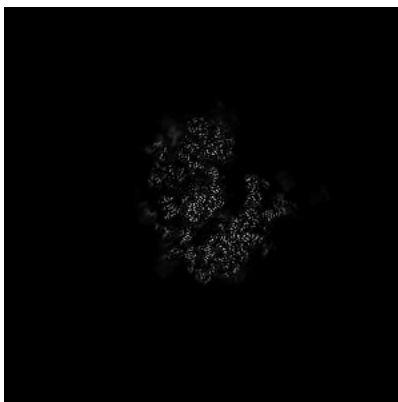
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

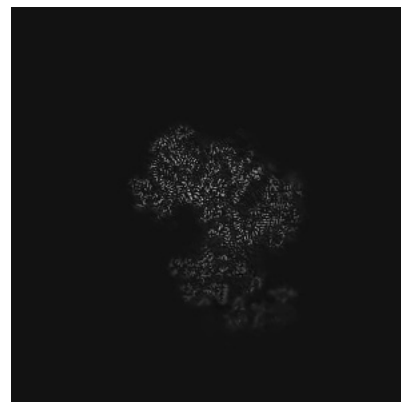
6.2.1 Primary map



X Index: 280

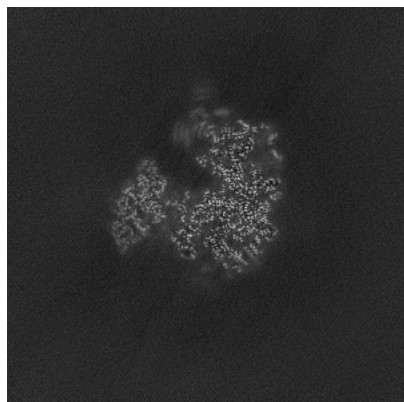


Y Index: 280

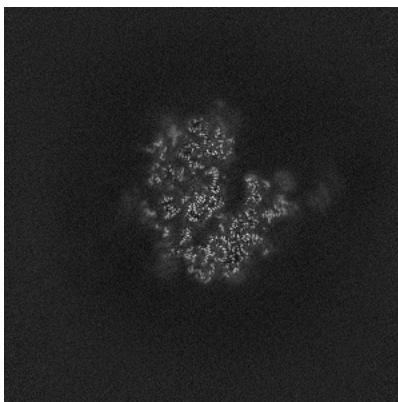


Z Index: 280

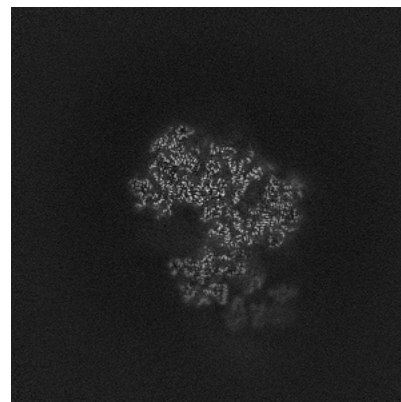
6.2.2 Raw map



X Index: 280



Y Index: 280

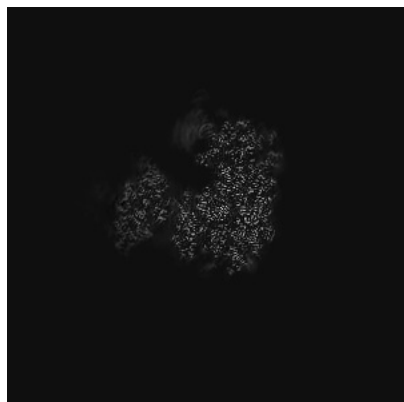


Z Index: 280

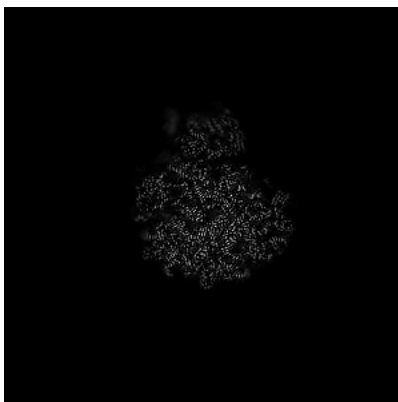
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

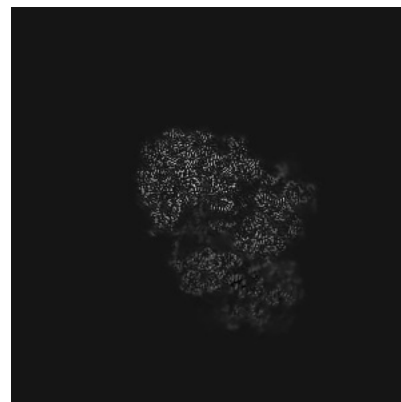
6.3.1 Primary map



X Index: 285

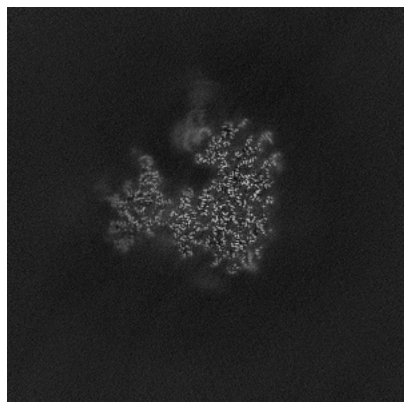


Y Index: 314

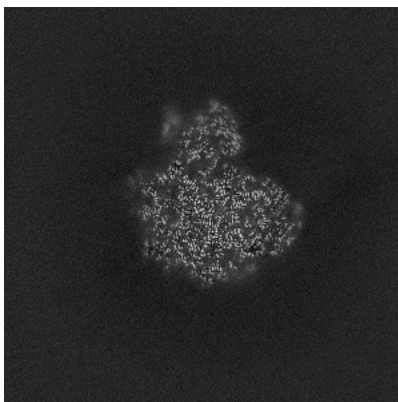


Z Index: 300

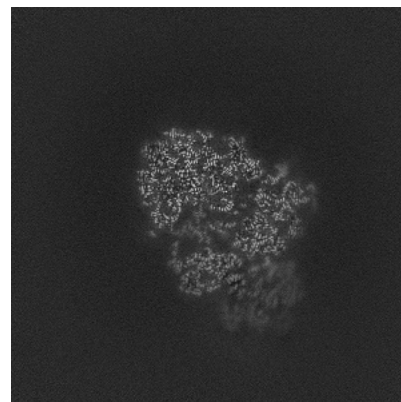
6.3.2 Raw map



X Index: 290



Y Index: 305

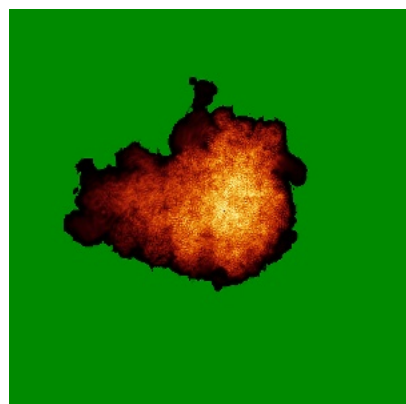


Z Index: 300

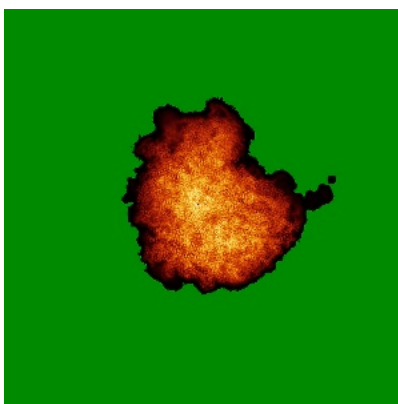
The images above show the largest variance slices of the map in three orthogonal directions.

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

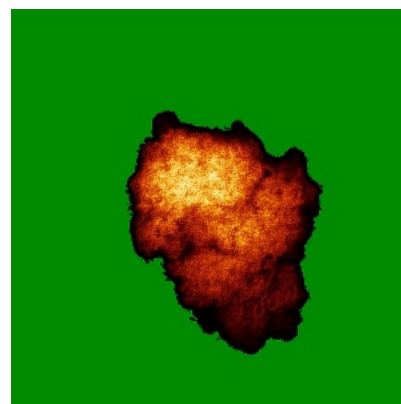
6.4.1 Primary map



X

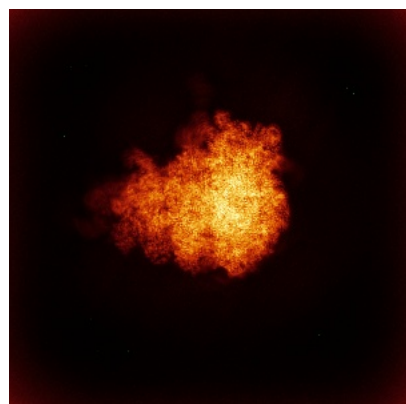


Y

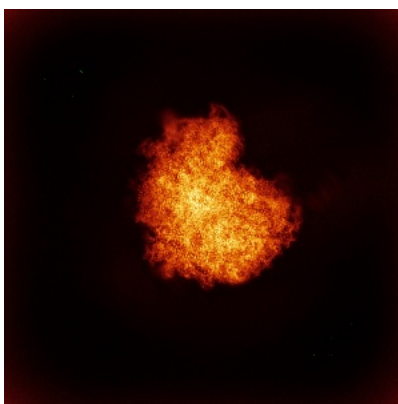


Z

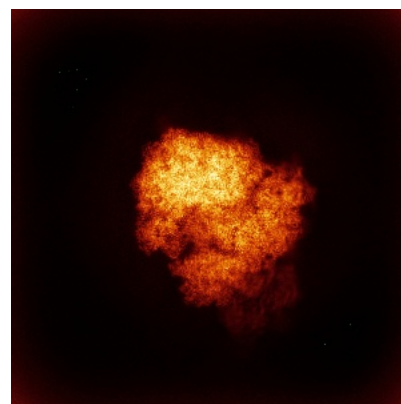
6.4.2 Raw map



X



Y

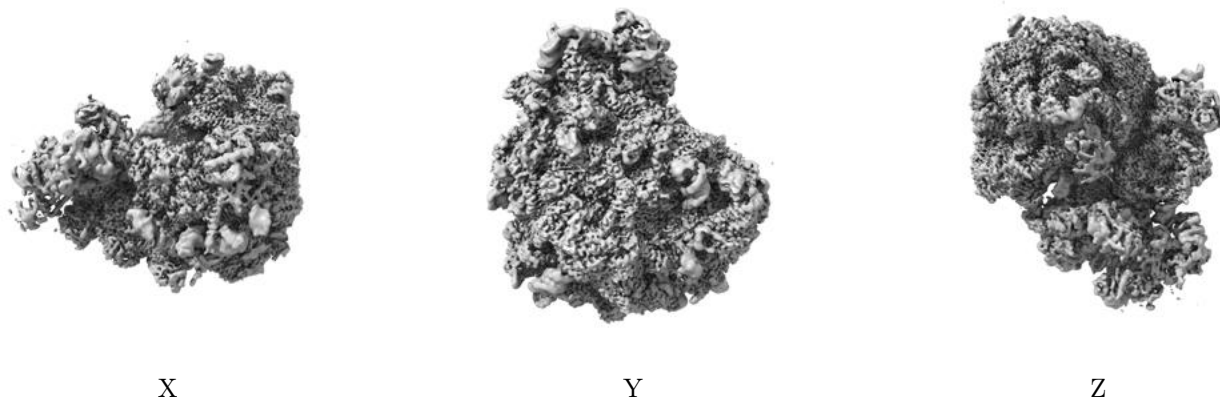


Z

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.

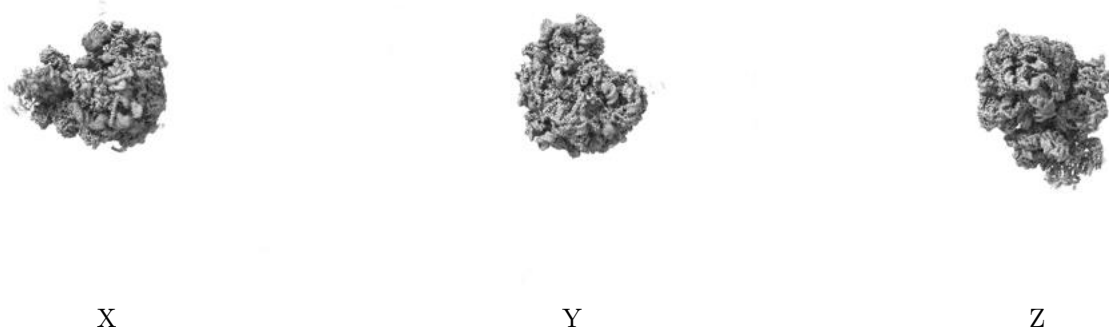
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

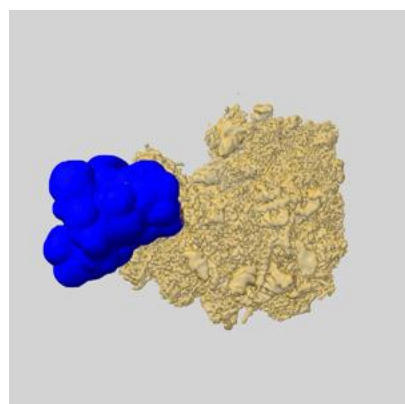
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

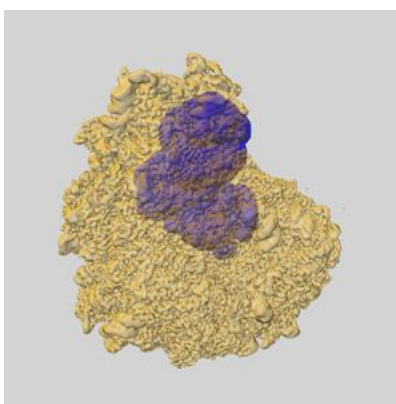
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

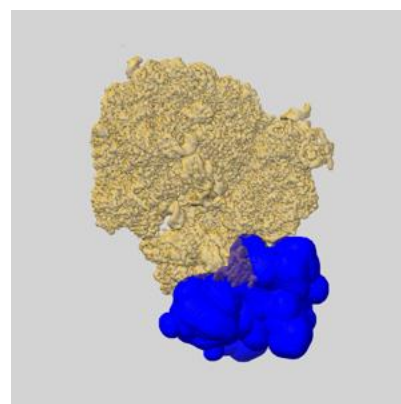
6.6.1 emd_14861_msk_2.map [i](#)



X

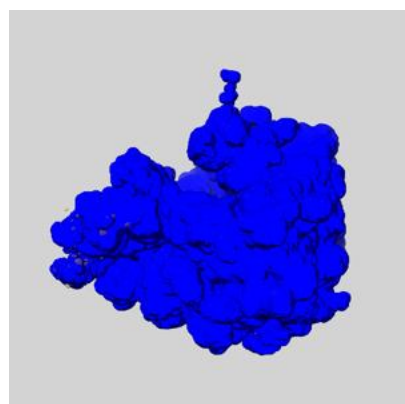


Y

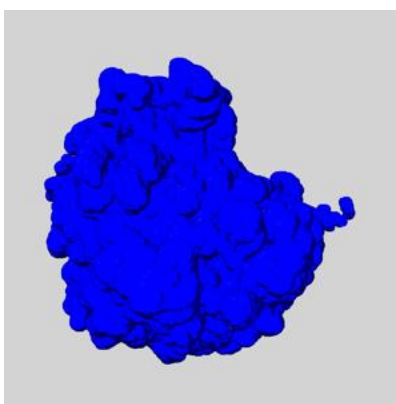


Z

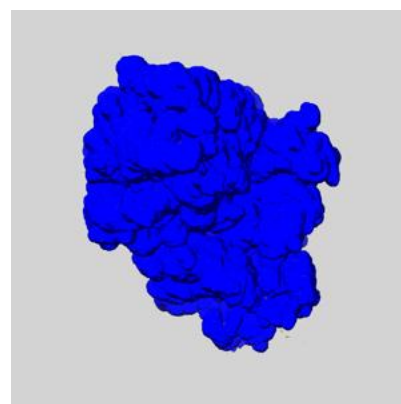
6.6.2 emd_14861_msk_1.map [i](#)



X



Y

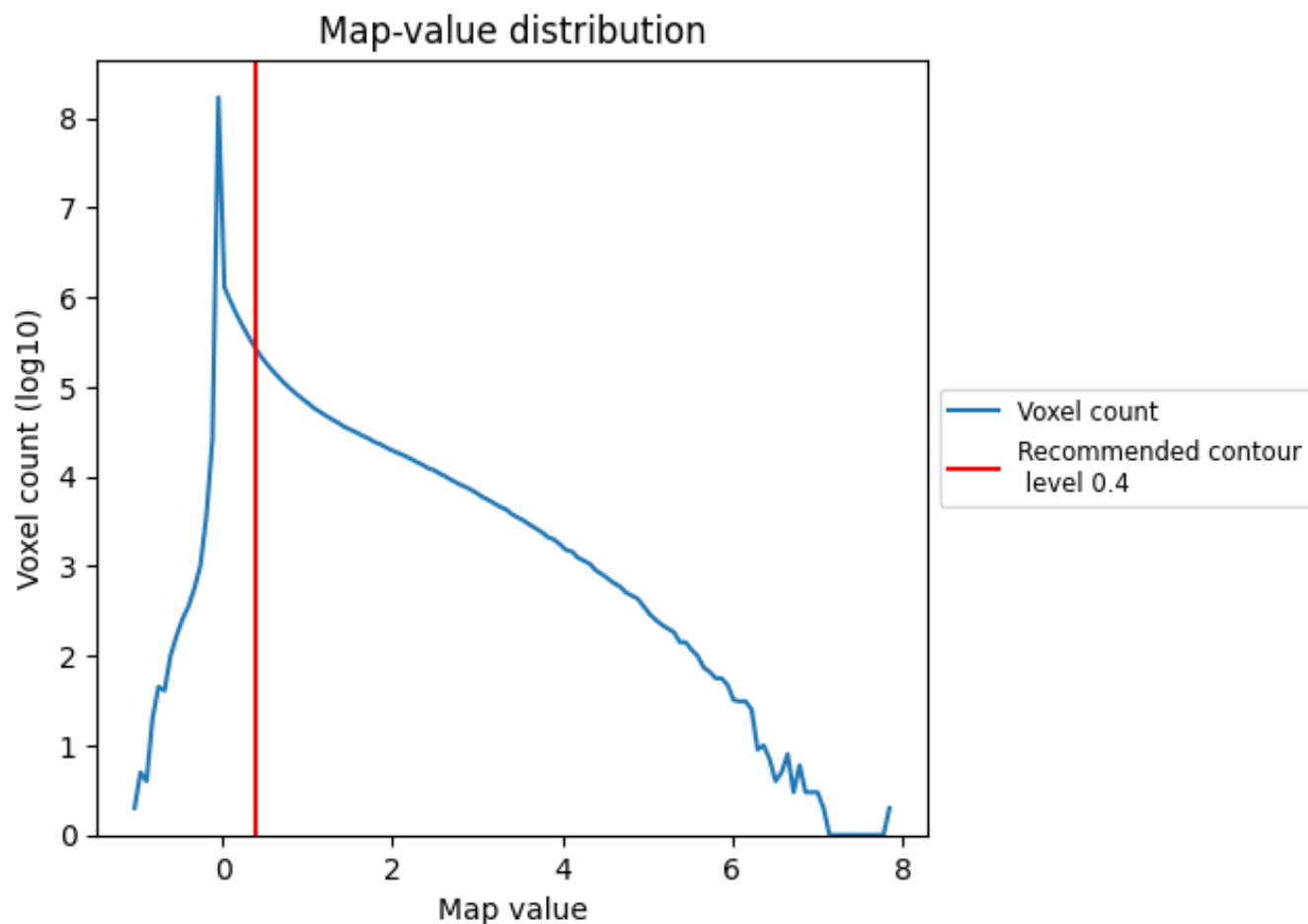


Z

7 Map analysis [i](#)

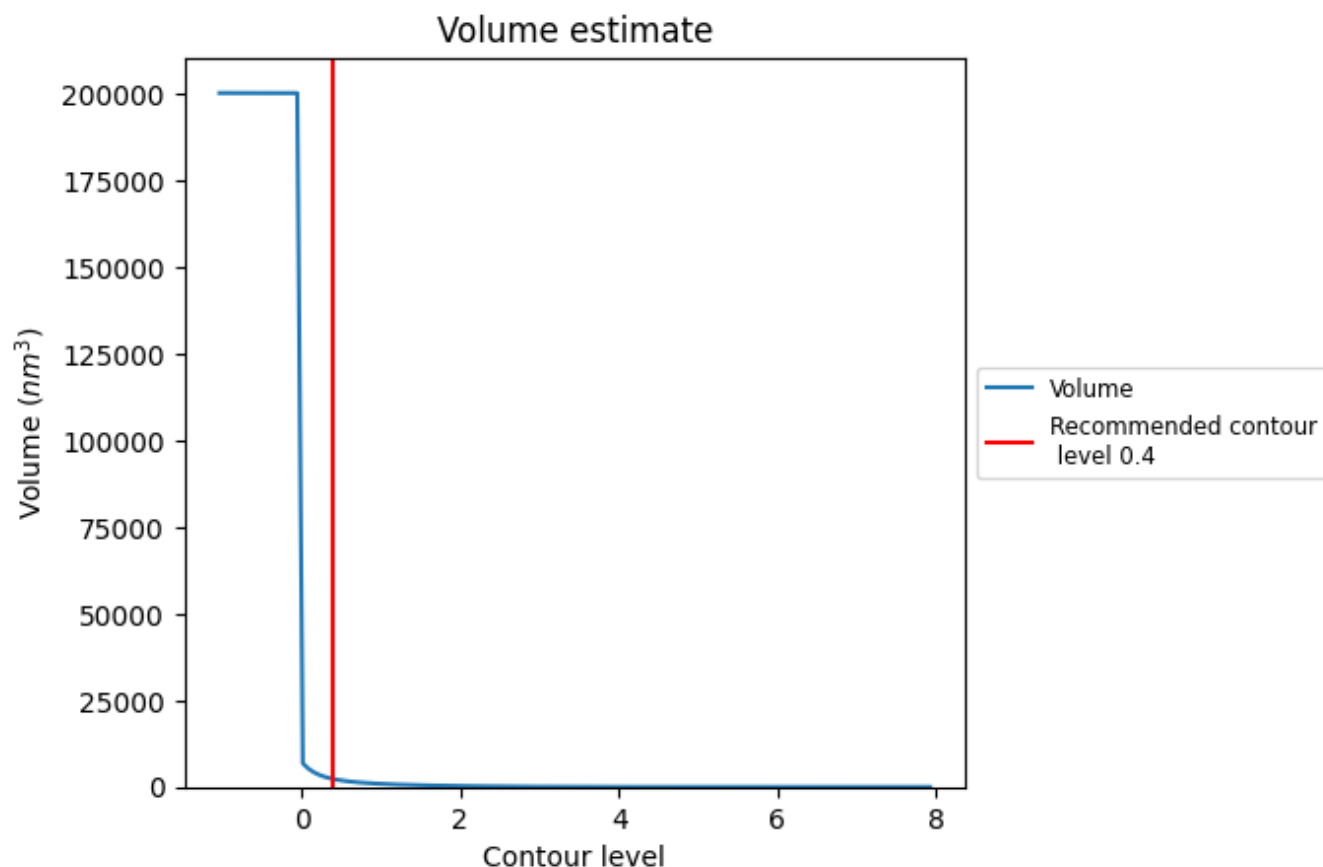
This section contains the results of statistical analysis of the map.

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.

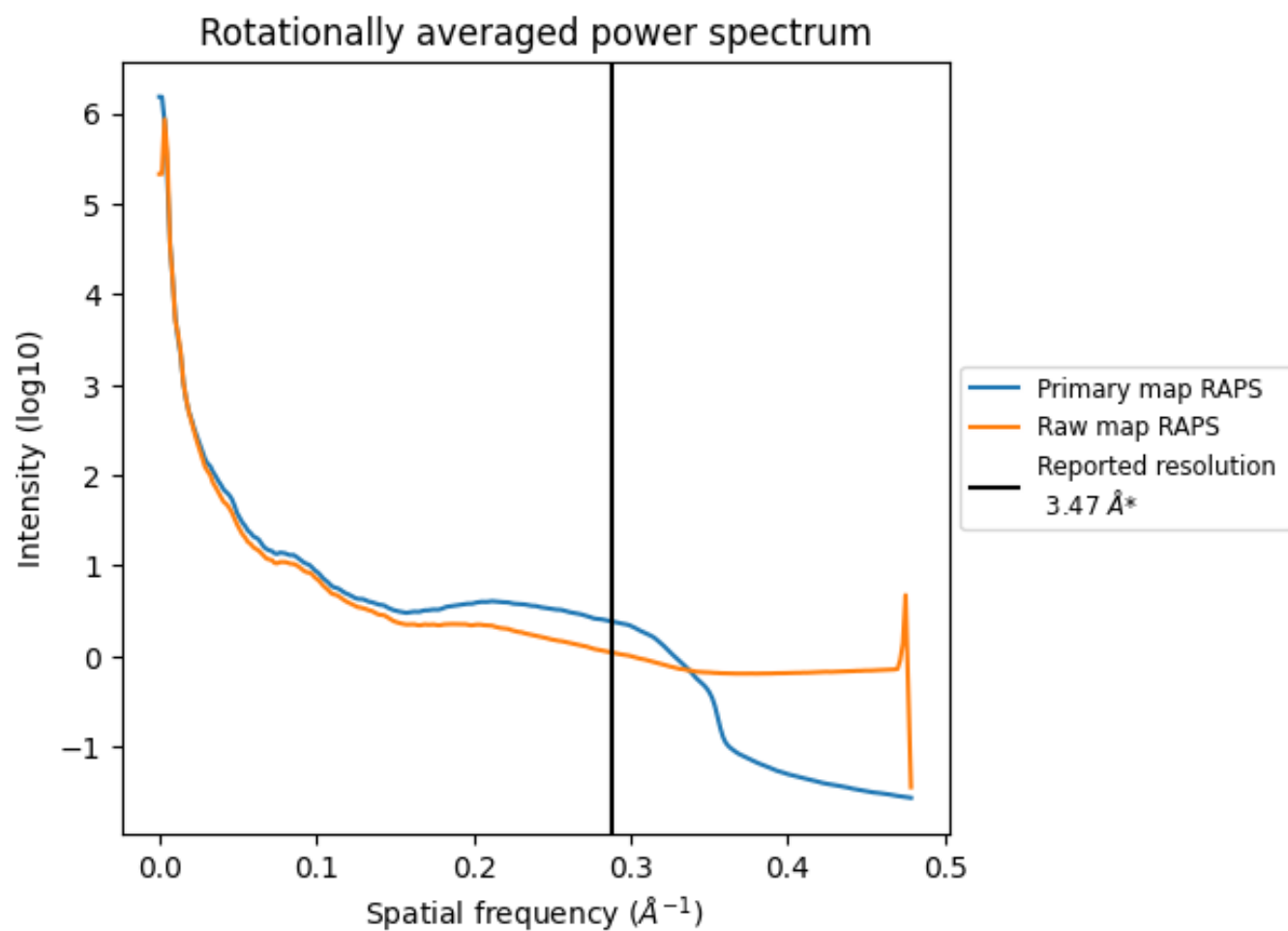
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2315 nm^3 ; this corresponds to an approximate mass of 2091 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 ⓘ

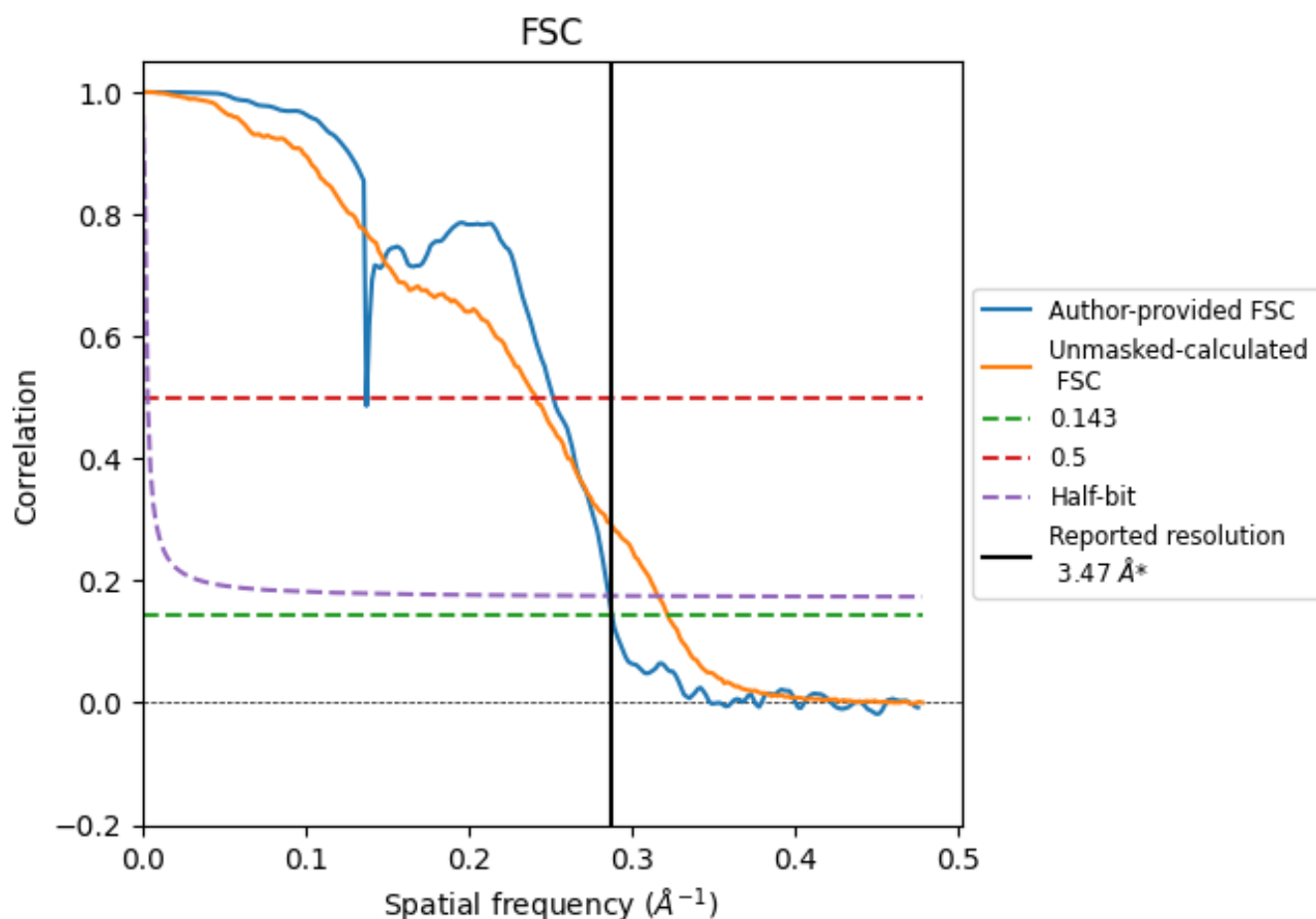


*Reported resolution corresponds to spatial frequency of 0.288 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.288 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

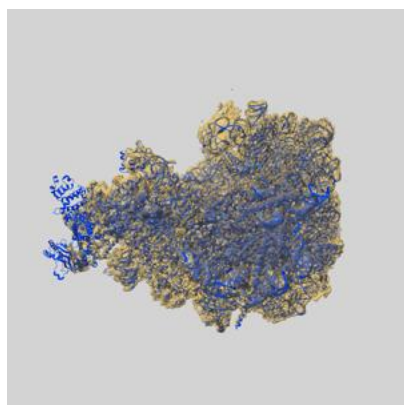
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.47	7.27	3.49
Unmasked-calculated*	3.10	4.14	3.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.10 differs from the reported value 3.47 by more than 10 %

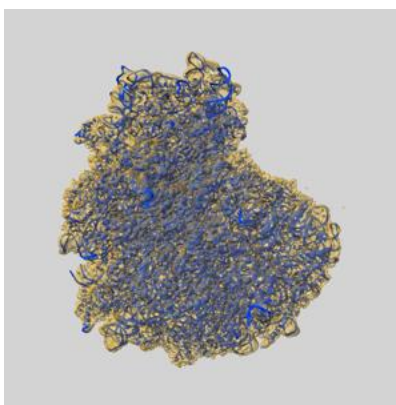
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-14861 and PDB model 7ZPQ. Per-residue inclusion information can be found in section [3](#) on page [21](#).

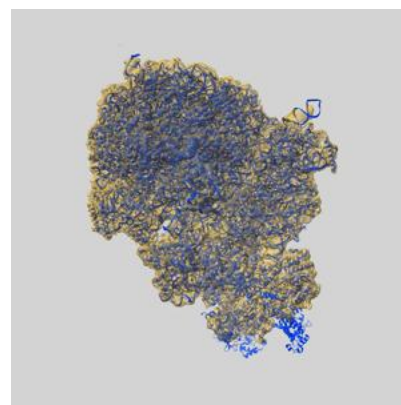
9.1 Map-model overlay [i](#)



X



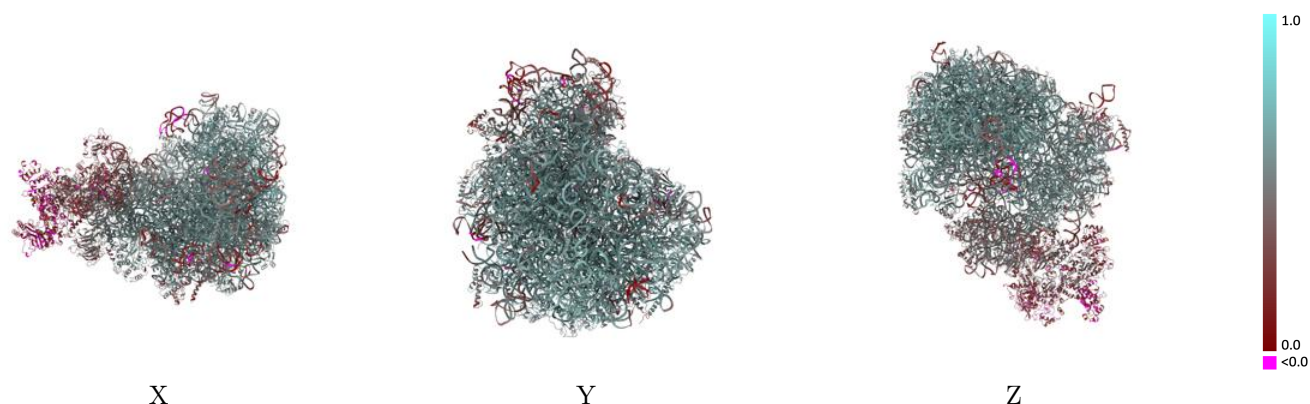
Y



Z

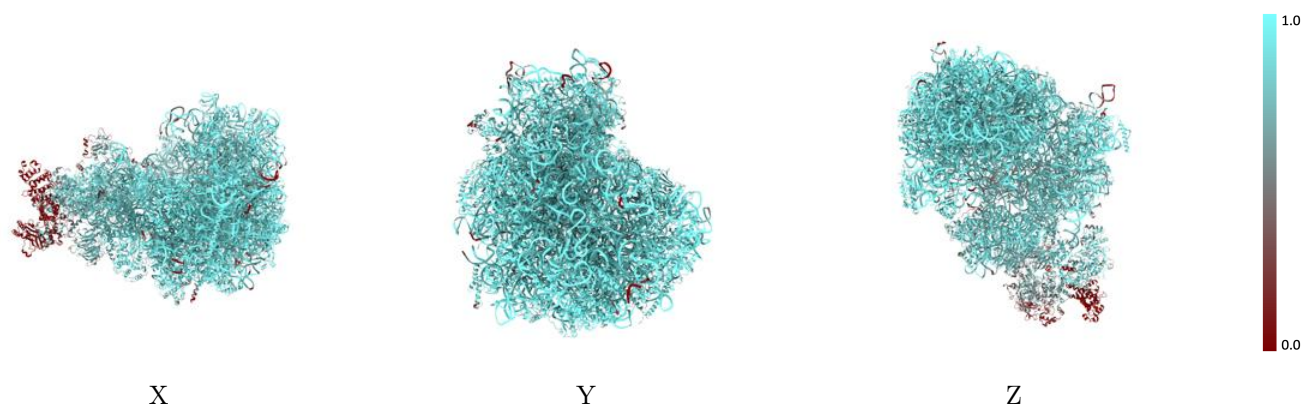
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



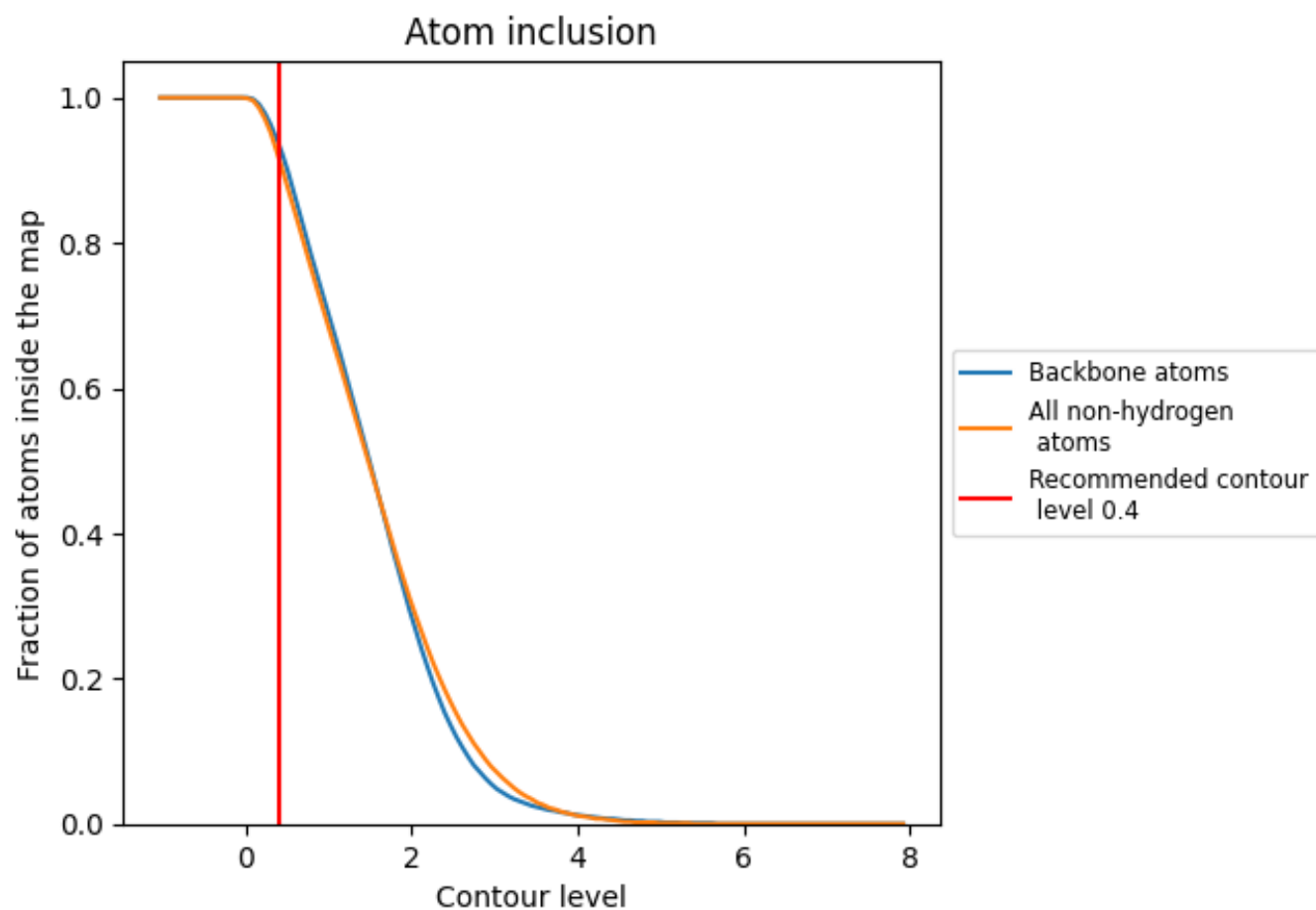
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9160	 0.5220
2	 0.9550	 0.5070
3	 0.9840	 0.6030
4	 0.9940	 0.5830
5	 0.9730	 0.5810
6	 0.7800	 0.3420
AA	 0.9560	 0.5340
AB	 0.9370	 0.5280
AC	 0.9800	 0.5800
AD	 0.9130	 0.4710
AE	 0.9690	 0.5590
AF	 0.8620	 0.4420
AG	 0.8810	 0.4570
AH	 0.8740	 0.4690
AI	 0.9620	 0.5670
AJ	 0.9360	 0.5350
AK	 0.8360	 0.3770
AL	 0.9500	 0.5850
AM	 0.4240	 0.2170
AN	 0.9510	 0.5690
AO	 0.9750	 0.5550
AP	 0.8030	 0.3460
AQ	 0.8910	 0.4500
AR	 0.9090	 0.4860
AS	 0.8430	 0.3680
AT	 0.8540	 0.3900
AU	 0.8400	 0.4140
AV	 0.9510	 0.5510
AW	 0.9900	 0.6070
AX	 0.9610	 0.5750
AY	 0.9120	 0.4900
AZ	 0.7100	 0.3240
Aa	 0.9530	 0.5480
Ab	 0.9470	 0.5290
Ac	 0.8880	 0.4940



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Chain	Atom inclusion	Q-score
Ad	 0.9600	 0.5120
Ae	 0.9030	 0.5010
Af	 0.5810	 0.2000
Ag	 0.7310	 0.3670
BA	 0.9880	 0.6380
BB	 0.9770	 0.6060
BC	 0.9770	 0.6100
BD	 0.9310	 0.5350
BE	 0.9480	 0.5500
BF	 0.9770	 0.6100
BG	 0.9370	 0.5430
BH	 0.9520	 0.5660
BI	 0.9600	 0.5730
BJ	 0.9170	 0.4780
BK	 0.9600	 0.5890
BL	 0.9700	 0.5780
BM	 0.9960	 0.6420
BN	 0.9820	 0.6130
BO	 0.9580	 0.6080
BP	 0.9890	 0.6210
BQ	 0.9270	 0.5640
BR	 0.9830	 0.6130
BS	 0.9700	 0.5930
BT	 0.9270	 0.5100
BU	 0.9630	 0.6130
BV	 0.9340	 0.5150
BW	 0.9650	 0.5820
BX	 0.9780	 0.5910
BY	 0.9400	 0.5550
BZ	 0.9780	 0.6210
Ba	 0.9450	 0.5620
Bb	 0.9810	 0.5840
Bc	 0.9340	 0.5730
Bd	 0.9860	 0.6270
Be	 0.9930	 0.6410
Bf	 0.9610	 0.5970
Bg	 0.9640	 0.5820
Bh	 0.9600	 0.5670
Bi	 0.9940	 0.6460
Bj	 0.9130	 0.5180
Bk	 0.9880	 0.6270
Bl	 0.9480	 0.5850

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Chain	Atom inclusion	Q-score
Bm	 0.9950	 0.6340
Bn	 0.9720	 0.5940
Bo	 0.9840	 0.6190
CA	 0.6130	 0.2420
CB	 0.0080	 0.1040
CC	 0.3930	 0.1640