



wwPDB EM Validation Summary Report ⓘ

Mar 14, 2026 – 07:20 AM UTC

PDB ID : 7ZUW / pdb_00007zuw
EMDB ID : EMD-14978
Title : Structure of RQT (C1) bound to the stalled ribosome in a disome unit from *S. cerevisiae*
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 : 2022-05-13
Resolution : 4.30 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

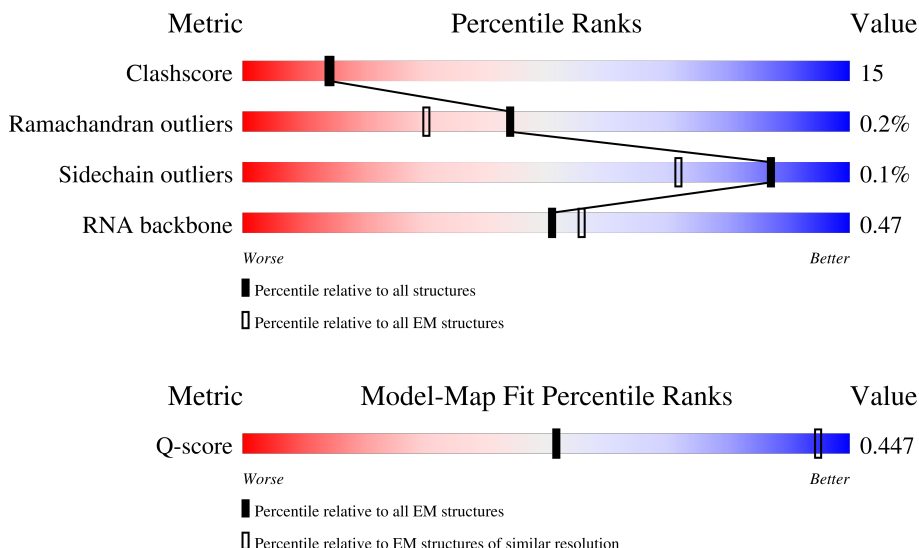
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 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	4585 (3.80 - 4.80)

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

Mol	Chain	Length	Quality of chain
1	2	1800	
2	3	158	
3	4	121	

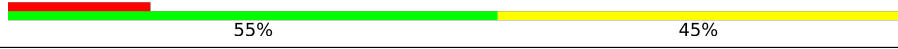
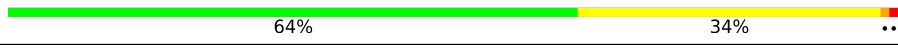
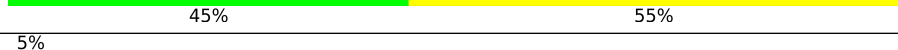
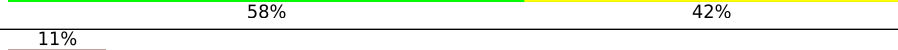
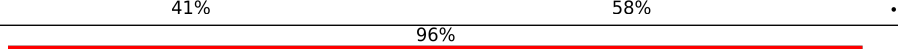
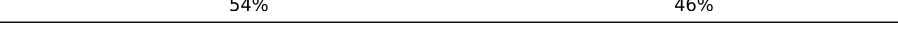
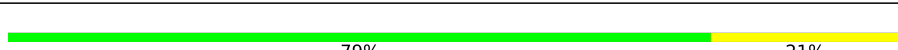
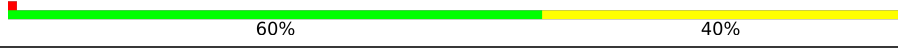
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Mol	Chain	Length	Quality of chain
4	5	3396	
5	6	76	
6	AA	206	
7	AB	255	
8	AC	216	
9	AD	222	
10	AE	258	
11	AF	206	
12	AG	228	
13	AH	184	
14	AI	200	
15	AJ	184	
16	AK	92	
17	AL	144	
18	AM	121	
19	AN	150	
20	AO	127	
21	AP	117	
22	AQ	141	
23	AR	136	
24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

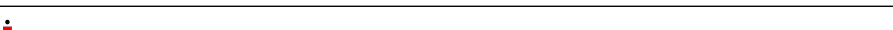
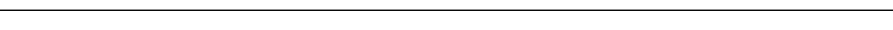
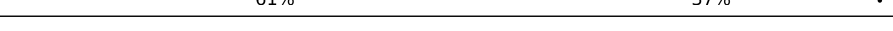
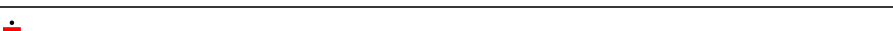
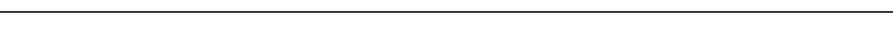
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Mol	Chain	Length	Quality of chain
29	AX	144	
30	AY	134	
31	AZ	82	
32	Aa	97	
33	Ab	81	
34	Ac	63	
35	Ad	53	
36	Ae	60	
37	Af	73	
38	Ag	312	
39	BA	251	
40	BB	386	
41	BC	361	
42	BD	294	
43	BE	176	
44	BF	222	
45	BG	233	
46	BH	191	
47	BI	218	
48	BJ	169	
49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

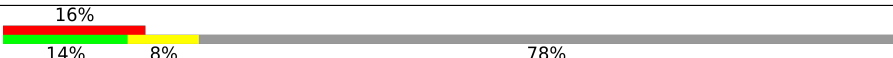
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Mol	Chain	Length	Quality of chain
54	BP	185	 69% 31%
55	BQ	188	 76% 24%
56	BR	171	 70% 30%
57	BS	159	 69% 31%
58	BT	100	 61% 39%
59	BU	136	 68% 32%
60	BV	126	 88% 12%
61	BW	121	 69% 31%
62	BX	125	 62% 38%
63	BY	135	 62% 38%
64	BZ	148	 61% 37%
65	Ba	58	 86% 14%
66	Bb	96	 66% 34%
67	Bc	109	 73% 27%
68	Bd	127	 77% 23%
69	Be	106	 77% 23%
70	Bf	112	 68% 32%
71	Bg	119	 68% 32%
72	Bh	99	 73% 27%
73	Bi	85	 72% 28%
74	Bj	77	 64% 36%
75	Bk	50	 66% 34%
76	Bl	52	 67% 33%
77	Bm	25	 80% 20%
78	Bn	103	 68% 32%

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Mol	Chain	Length	Quality of chain
79	Bo	91	 62% 38%
80	CA	1967	 50% 48% 41% 11%
81	CB	297	 100% 76% 24%
82	CC	530	 16% 14% 8% 78%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 218071 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	3163	Total	C	N	O	P	0	0
			67650	30218	12191	22078	3163		

- 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		

- 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-A.

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	0	0
			1473	946	263	264		

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

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

- 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	0	0
			1479	935	285	258	1		

- 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	0	0
			752	487	122	141	2		

- 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	0	0
			1159	742	219	195	3		

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

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

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

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

- 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-A.

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

- 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 40S ribosomal protein S26.

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 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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.

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 RPL9A isoform 1.

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 Ribosomal protein L15.

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	S	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 60S ribosomal protein L41.

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 RQC trigger complex helicase SLH1.

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 CUE3 isoform 1.

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 RQC trigger complex subunit RQT4.

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	AC	1	Total	Mg	0
			1	1	
83	AQ	1	Total	Mg	0
			1	1	

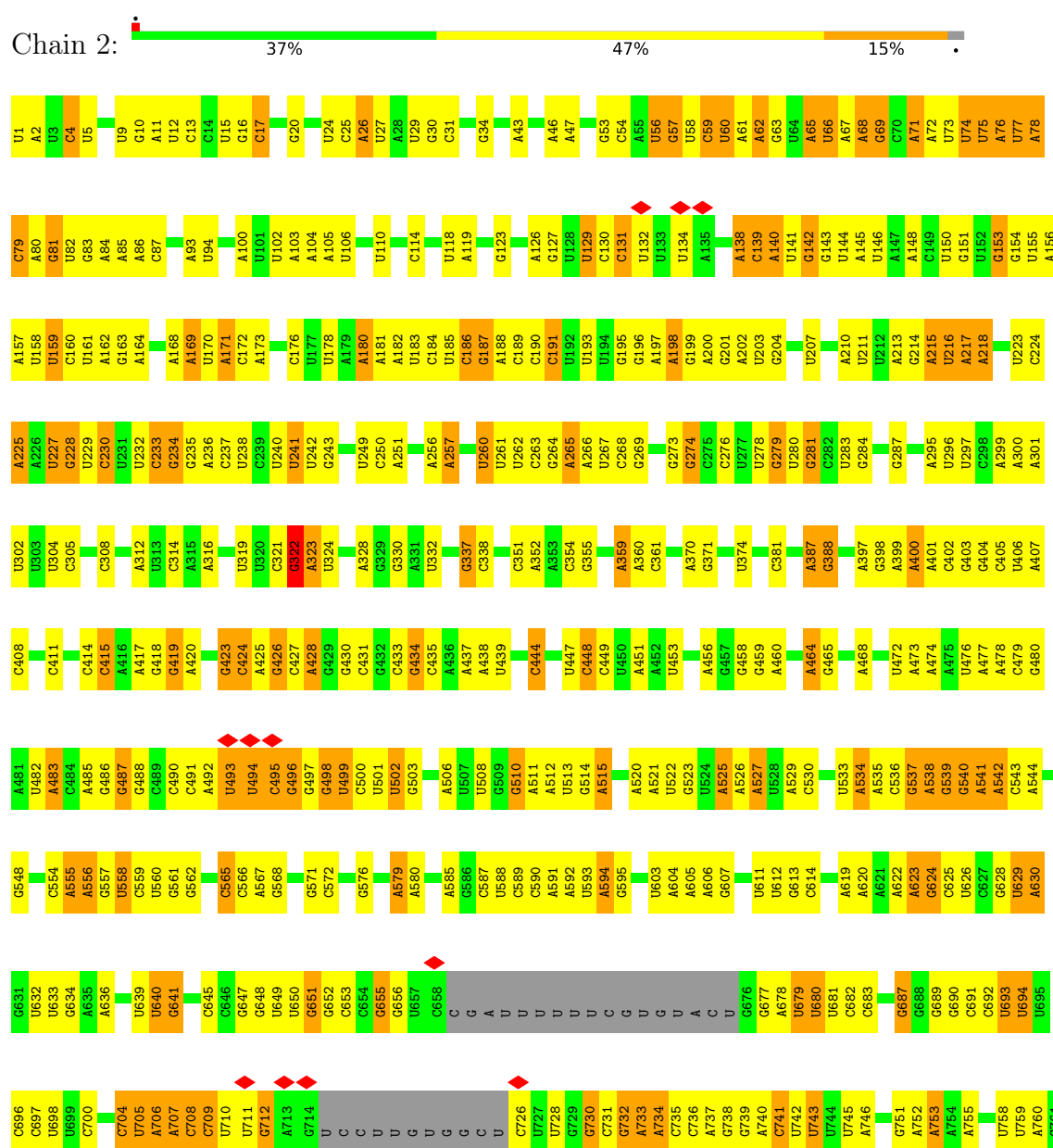
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

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	
84	CC	2	Total	Zn	0
			2	2	

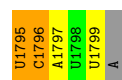
3 Residue-property plots

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.

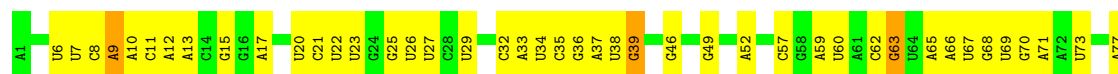
• Molecule 1: 18S ribosomal RNA



G1720	G1721	G1727	G1728	G1729	G1730	G1731	G1732	G1733	G1734	G1735	G1738	G1739	G1740	G1741	G1742	G1743	G1744	G1745	G1750	G1753	G1754	G1755	G1756	G1757	G1758	G1759	G1760	G1761	G1762	G1767	G1768	G1769	G1770	G1774	G1775	G1776	G1779	G1780	G1781	G1782	G1783	G1784	G1785	G1789	G1795	G1796	G802	G803	G804	G805	G806	G807	G808	G809	G810	G811	G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	U989	C1072	C1159	A1226	A1227	G1228	G1229	U1232	G1233	A1234	G1235	A1236	G1237	A1170	A1171	G1083	G1085	A1005	G1008	G925	A933	G913	G914	A915	A916	A1001	G1002	G1003	A918	A1004	A1005	G775	G776	G777	G778	A850	U779	U928	A929	A930	C931	A852	A853	U854	A855	A856	U857	A1023	U1024	A1025	G936	G937	G938	A861	A862	A940	A941	G942	A804	A805	G871	G872	A907	U946	C1037	U1038	A1039	G875	G876	A884	U885	A886	A887	G888	A889	C890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	U989	C1072	C1159	A1226	A1227	G1228	G1229	U1232	G1233	A1234	G1235	A1236	G1237	A1170	A1171	G1083	G1085	A1005	G1008	G925	A933	G913	G914	A915	A916	A1001	G1002	G1003	A918	A1004	A1005	G775	G776	G777	G778	A850	U779	U928	A929	A930	C931	A852	A853	U854	A855	A856	U857	A1023	U1024	A1025	G936	G937	G938	A861	A862	A940	A941	G942	A804	A805	G871	G872	A907	U946	C1037	U1038	A1039	G875	G876	A884	U885	A886	A887	G888	A889	C890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	U989	C1072	C1159	A1226	A1227	G1228	G1229	U1232	G1233	A1234	G1235	A1236	G1237	A1170	A1171	G1083	G1085	A1005	G1008	G925	A933	G913	G914	A915	A916	A1001	G1002	G1003	A918	A1004	A1005	G775	G776	G777	G778	A850	U779	U928	A929	A930	C931	A852	A853	U854	A855	A856	U857	A1023	U1024	A1025	G936	G937	G938	A861	A862	A940	A941	G942	A804	A805	G871	G872	A907	U946	C1037	U1038	A1039	G875	G876	A884	U885	A886	A887	G888	A889	C890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G984	G985	G986	G987	G988	G989	G990	G991	G992	G993	G994	G995	G996	G997	G998	G999	U989	C1072	C1159	A1226	A1227	G1228	G1229	U1232	G1233	A1234	G1235	A1236	G1237	A1170	A1171	G1083	G1085	A1005	G1008	G925	A933	G913	G914	A915	A916	A1001	G1002	G1003	A918	A1004	A1005	G775	G776	G777	G778	A850	U779	U928	A929	A930	C931	A852	A853	U854	A855	A856	U857	A1023	U1024	A1025	G936	G937	G938	A861	A862	A940	A941	G942	A804	A805	G871	G872	A907	U946	C1037	U1038	A1039	G875	G876	A884	U885	A886	A887	G888	A889	C890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964	G965	G966	G967	G968	G969	G970	G971	G972	G973	G974	G975	G976	G977	G978	G979	G980	G981	G982	G983	G9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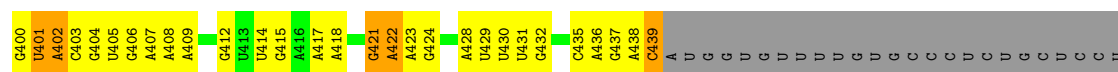
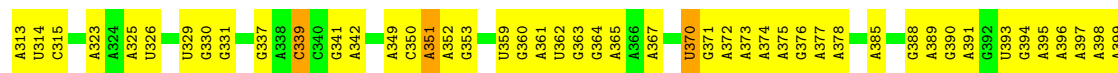
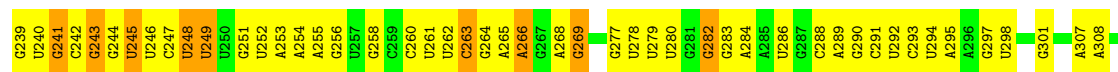
• Molecule 2: 5.8S ribosomal RNA



• Molecule 3: 5S ribosomal RNA

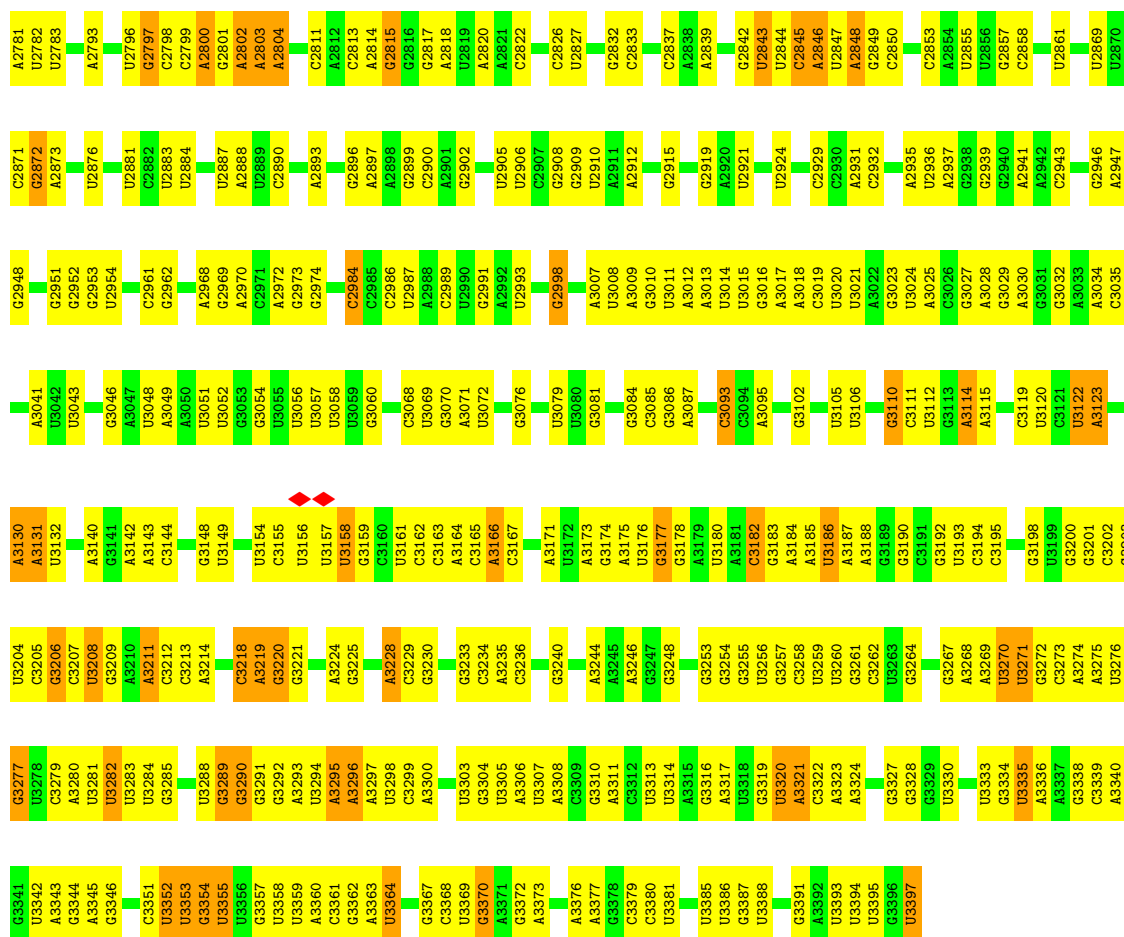


• Molecule 4: 25S ribosomal RNA

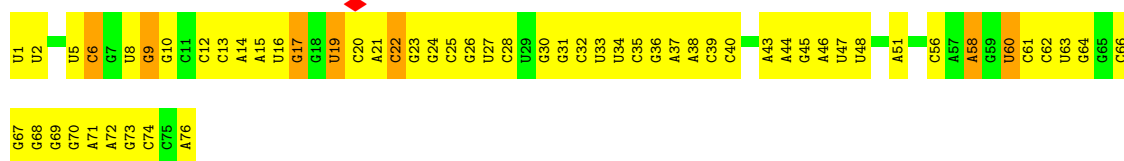


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A1558	U1357	C1276	G1117	U1215	G1117	U1042	U961	U873	A772	G686	A602	G536	U
A1559	G1358	U1277	G1118	U1216	C1119	C1044	C962	C874	A777	G687	A603	U537	G
A1559	C1359	C1278	C1119	C1217	C1119	A1048	A963	U875	U777	A692	A604	U541	G
U1459	A1279	A1278	C1120	A1218	A1120	A1048	G964	U880	U778	A692	G605	U542	U
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U1568	U1379	A1288	G1132	G1227	C976	A1063	U977	A889	G788	A709	U617	U550	U
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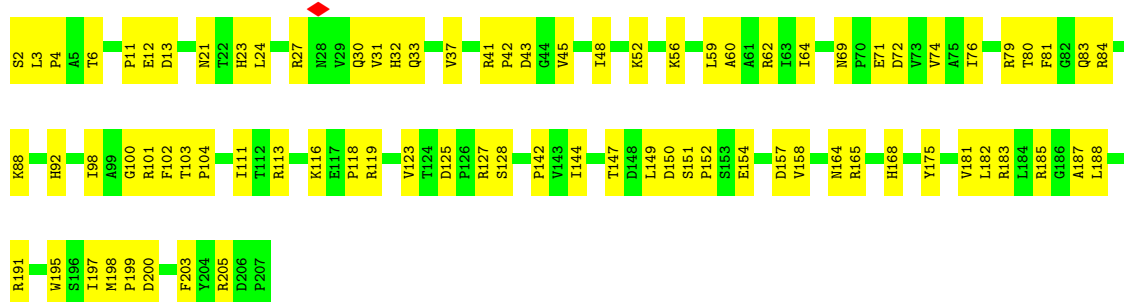
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G2096	A2097	U2098	C2099	G2100	A2101	C2102	U2103	U2104	A2105	A2108	U2113	A2114	C2115	G2116	C2119	A2120	A2121	G2122	G2123	A2127	A2132	C2133	C2137	U2138	A2139	U2140	U2141	U2142	A2143	A2144	U2145	A2146	U2149	A2150	A2153	U2154	U2155	G2156	C2157	G2158	A2159	U2160	G2161	G2162	A2167	A2168	A2169	U2170	U2171	G2172						
G	G	G	C	A	C	C	U	C	U	U	G	A	G	A	G	U	U	U	U	A	G	U	U	C	U	U	U	G	U	A	G	C	C	U	G	C	U	U	C	C	A	C	C	A	U	A	C2094	C2095								
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U1718	G1719	U1720	U1721	U1722	U1723	U1724	U1725	C1726	A1730	G1731	G1734	G1735	U1741	A1742	U1743	G1744	G1745	U1746	U1747	G1748	G1749	A1750	A1751	G1752	A1758	G1759	C1760	U1765	U1766	G1767	C1768	G1771	G1776	G1779	C1780	G1781	G1785	U1786	G1787	A1788	G1795	U1796	G1797	A1798	U1799	A1800	A1801	U1802								
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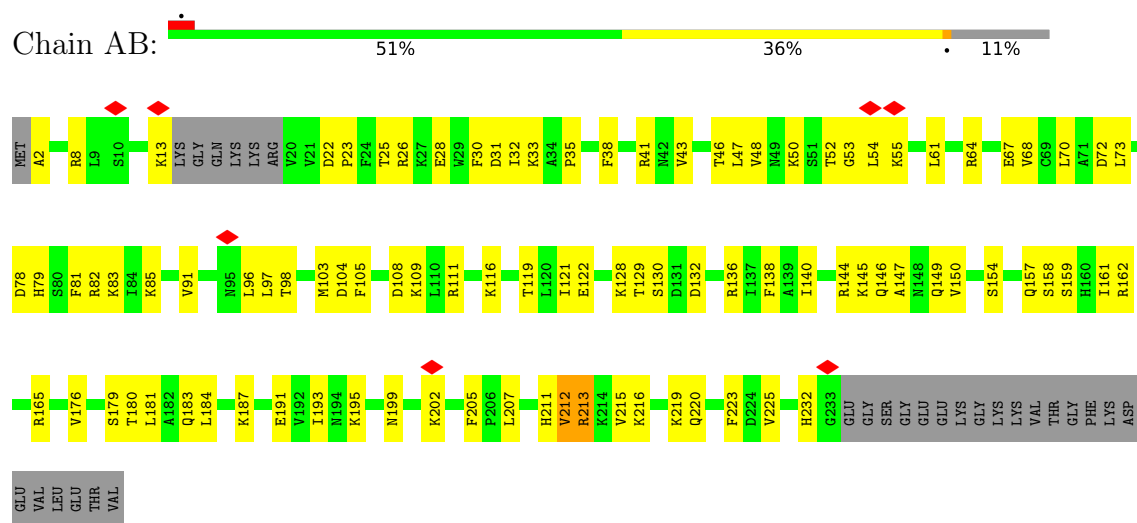
• Molecule 5: tRNA



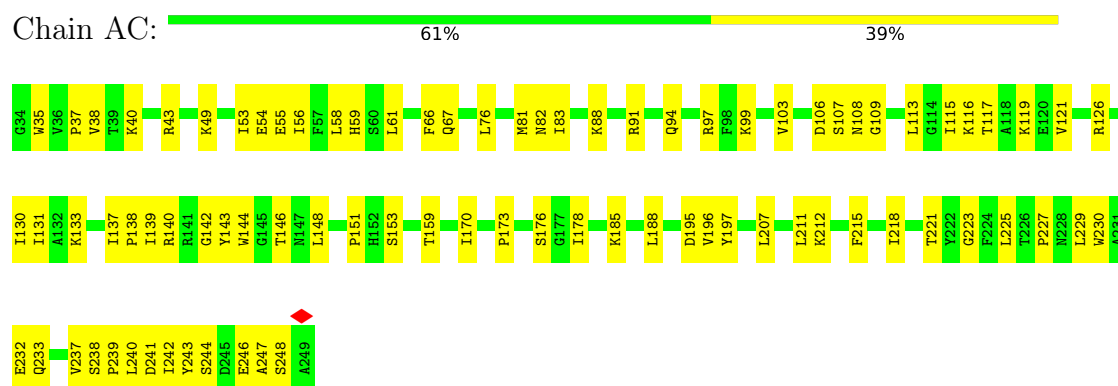
• Molecule 6: 40S ribosomal protein S0-A



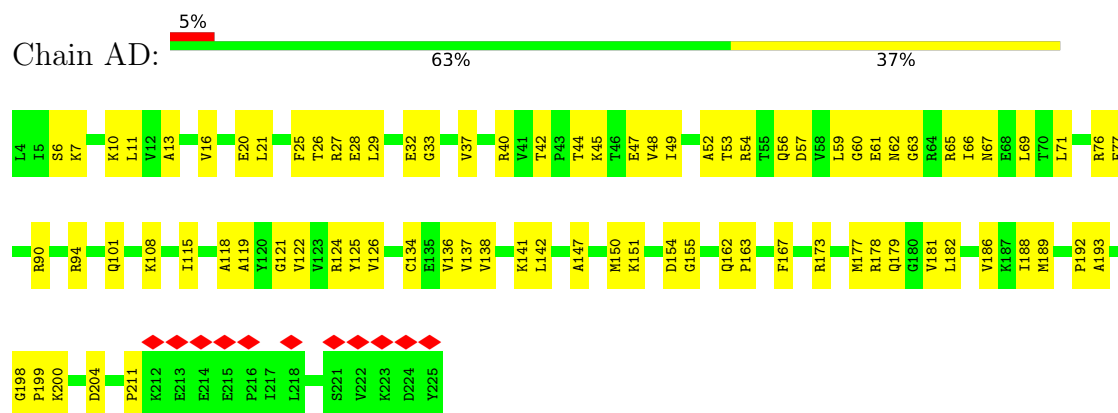
- Molecule 7: 40S ribosomal protein S1-A



- Molecule 8: RPS2 isoform 1

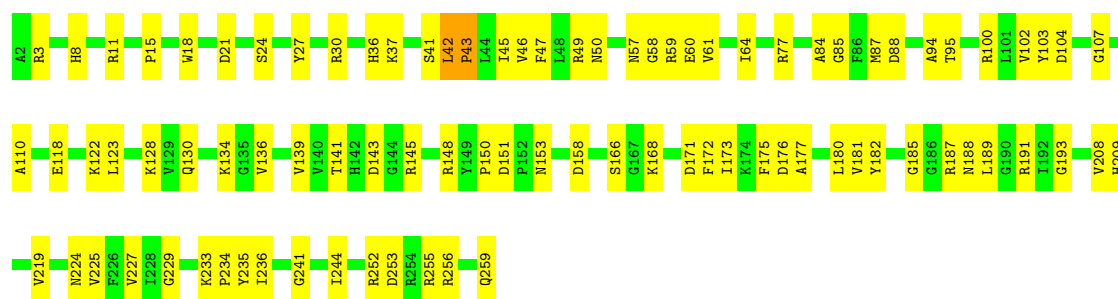


- Molecule 9: RPS3 isoform 1



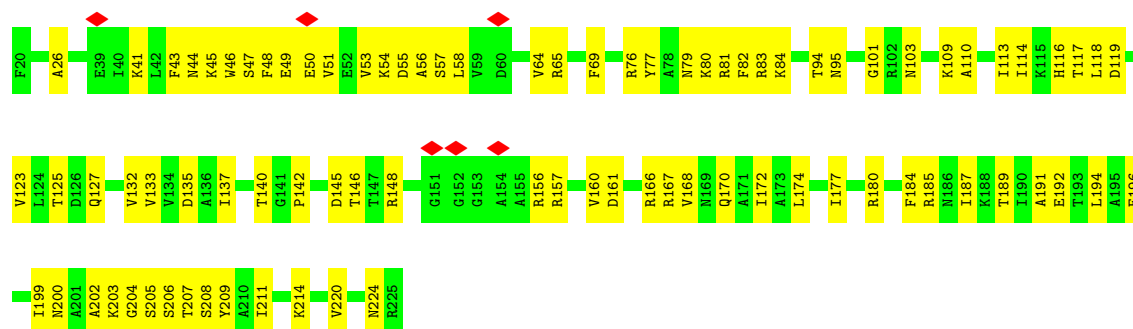
- Molecule 10: 40S ribosomal protein S4-A





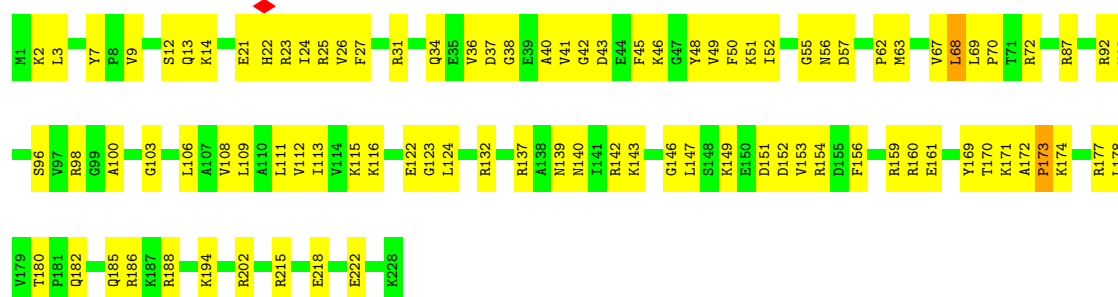
• Molecule 11: Rps5p

Chain AF: 58% 42%



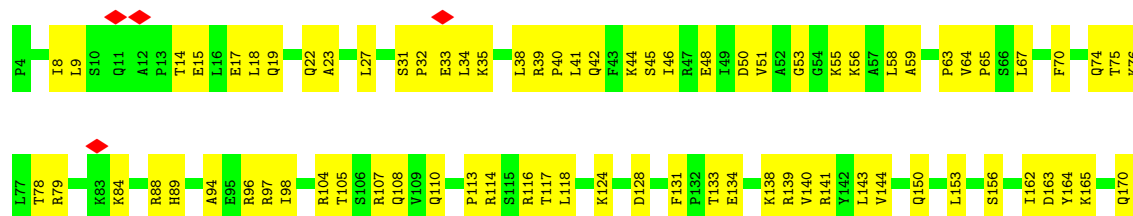
• Molecule 12: 40S ribosomal protein S6-A

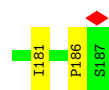
Chain AG: 59% 40%



• Molecule 13: 40S ribosomal protein S7-A

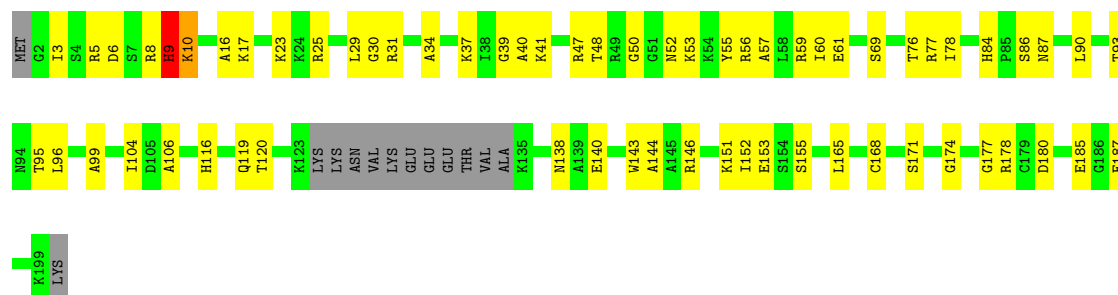
Chain AH: 57% 43%





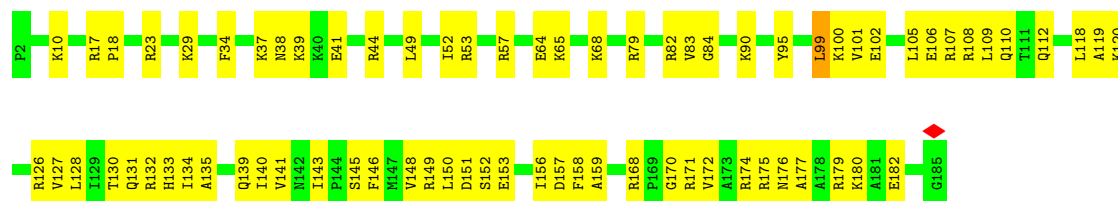
• Molecule 14: 40S ribosomal protein S8-B

Chain AI: 62% 31% 6%



• Molecule 15: 40S ribosomal protein S9-A

Chain AJ: 60% 40%



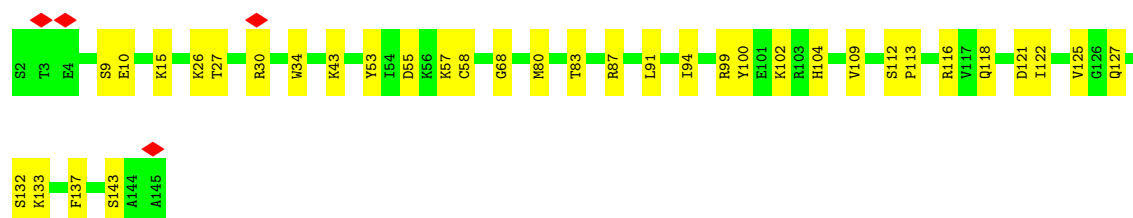
• Molecule 16: 40S ribosomal protein S10-A

Chain AK: 46% 54%

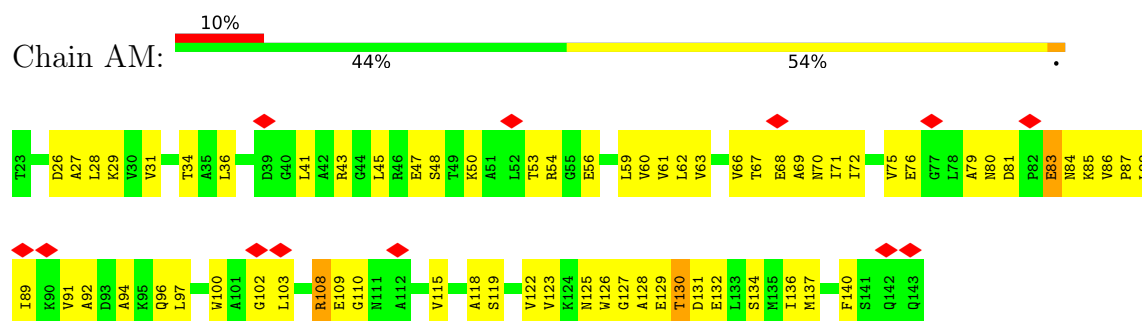


• Molecule 17: 40S ribosomal protein S11-A

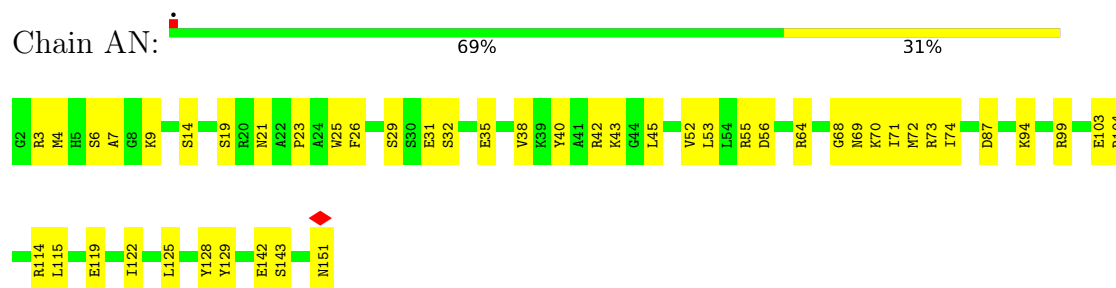
Chain AL: 76% 24%



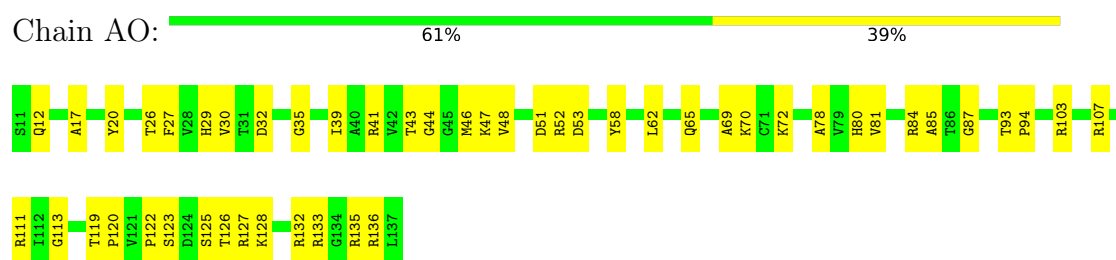
- Molecule 18: 40S ribosomal protein S12



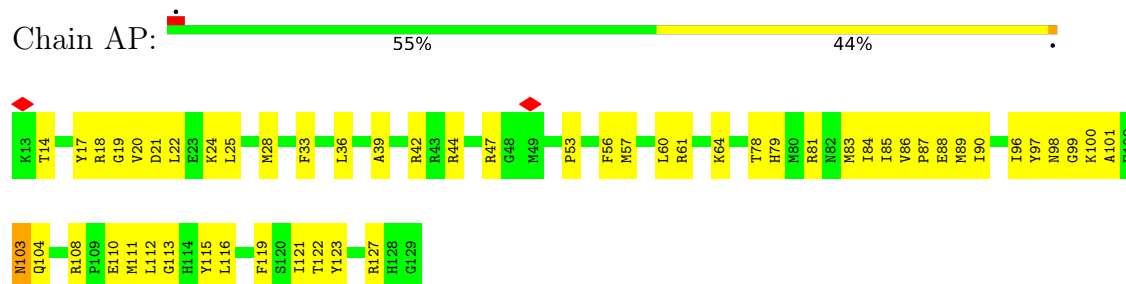
- Molecule 19: 40S ribosomal protein S13



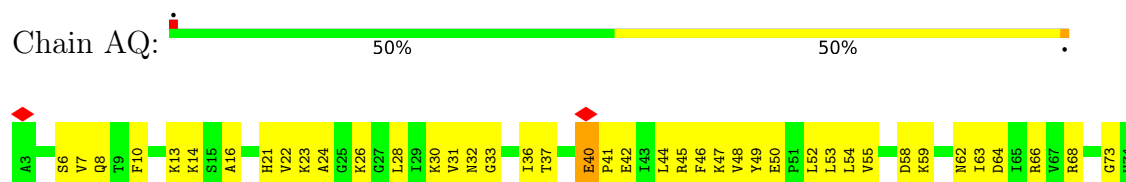
- Molecule 20: 40S ribosomal protein S14-B

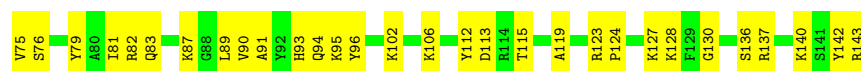


- Molecule 21: RPS15 isoform 1

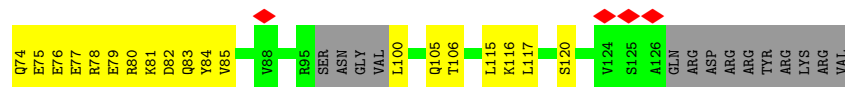
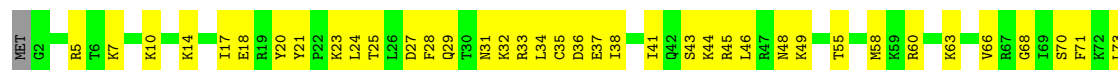


- Molecule 22: 40S ribosomal protein S16-A

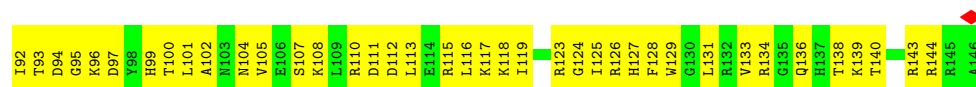
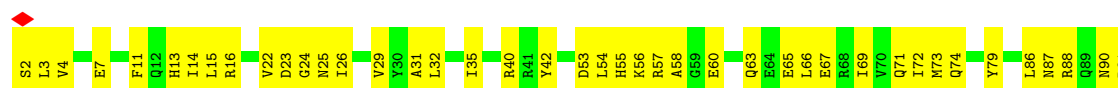




- Molecule 23: 40S ribosomal protein S17-A



- Molecule 24: 40S ribosomal protein S18-A



- Molecule 25: 40S ribosomal protein S19-A



- Molecule 26: RPS20 isoform 1



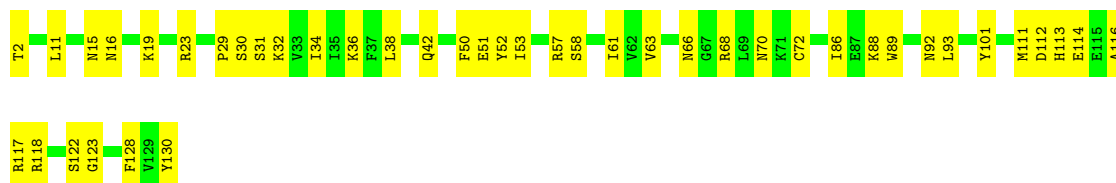
- Molecule 27: 40S ribosomal protein S21-A





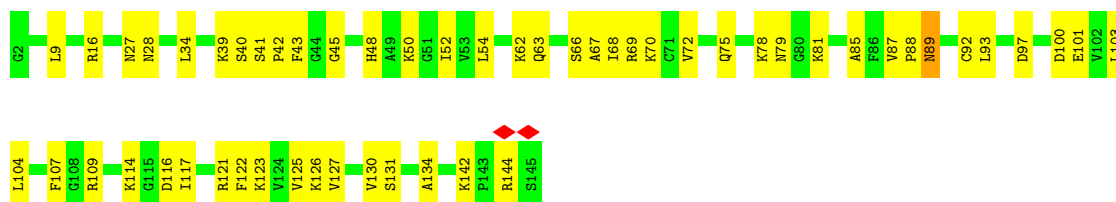
- Molecule 28: RPS22A isoform 1

Chain AW: 67% 33%



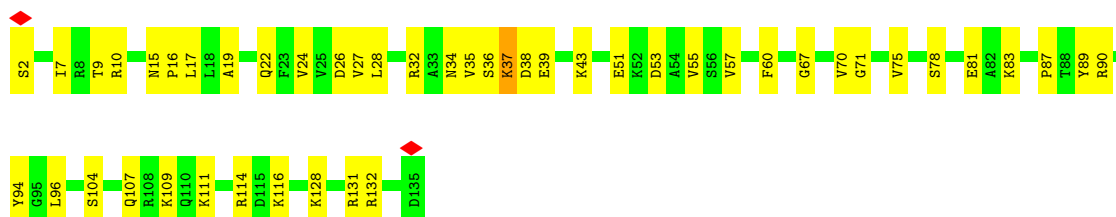
- Molecule 29: 40S ribosomal protein S23-A

Chain AX: 62% 37%



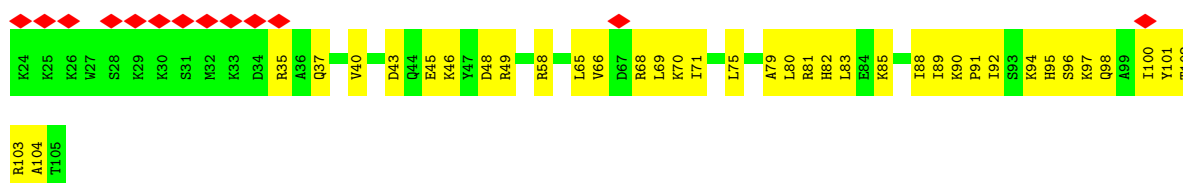
- Molecule 30: 40S ribosomal protein S24-A

Chain AY: 65% 34%



- Molecule 31: 40S ribosomal protein S25

Chain AZ: 16% 55% 45%



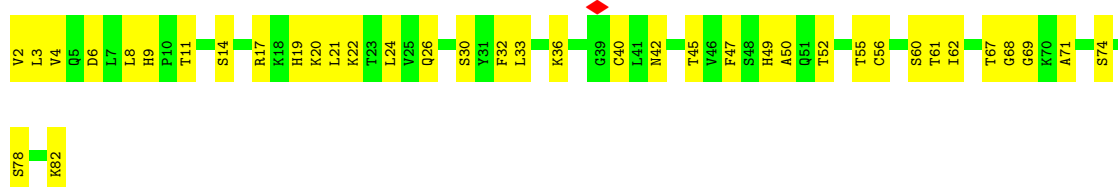
- Molecule 32: 40S ribosomal protein S26

Chain Aa: 64% 34%





- Molecule 33: 40S ribosomal protein S27-A



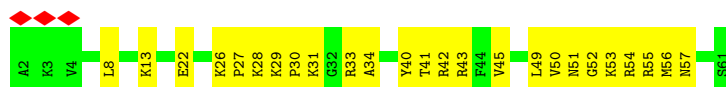
- Molecule 34: RPS28A isoform 1



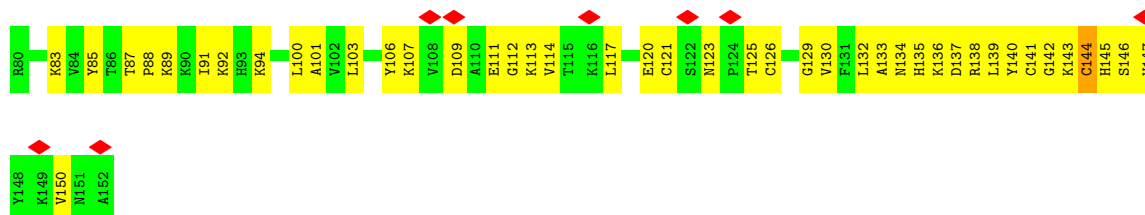
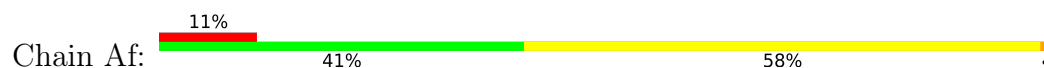
- Molecule 35: RPS29A isoform 1



- Molecule 36: 40S ribosomal protein S30-A

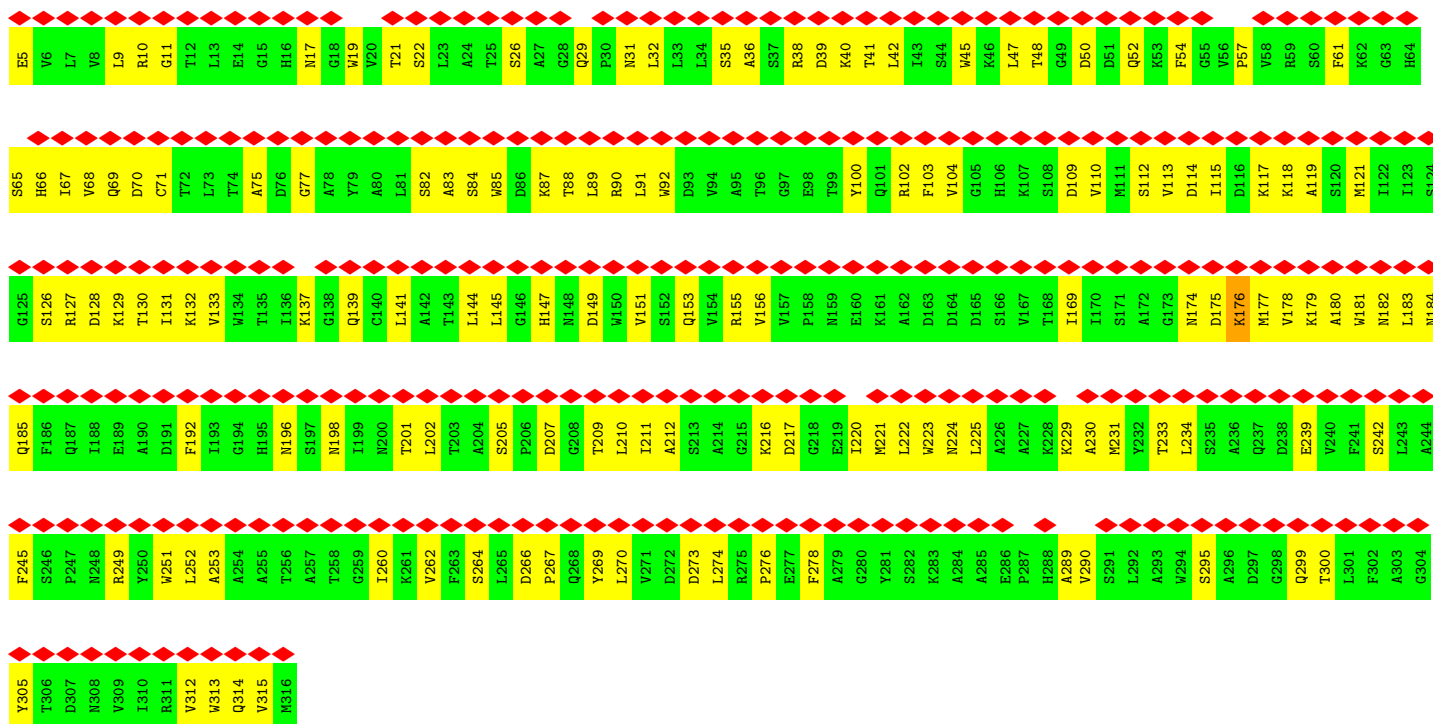


- Molecule 37: RPS31 isoform 1



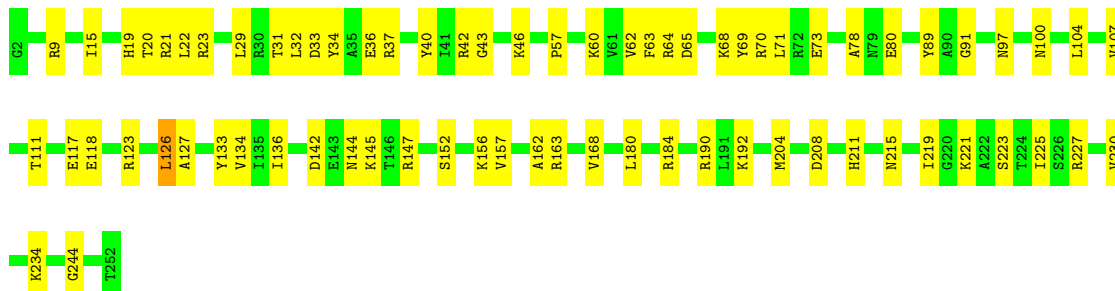
- Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein





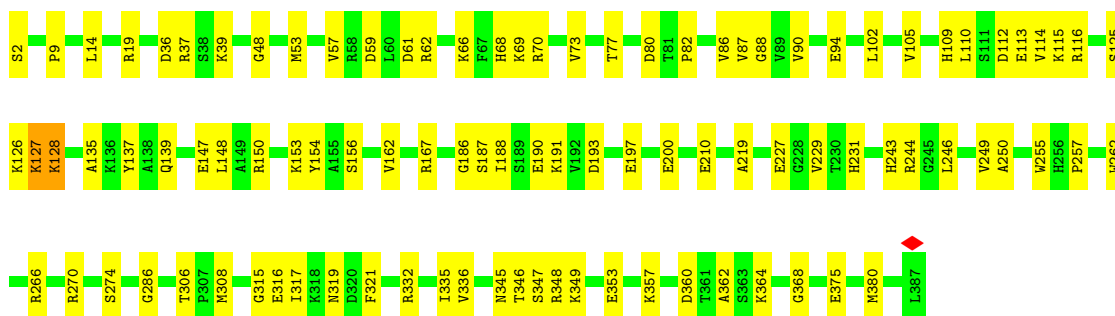
• Molecule 39: 60S ribosomal protein L2-A

Chain BA: 71% 28%



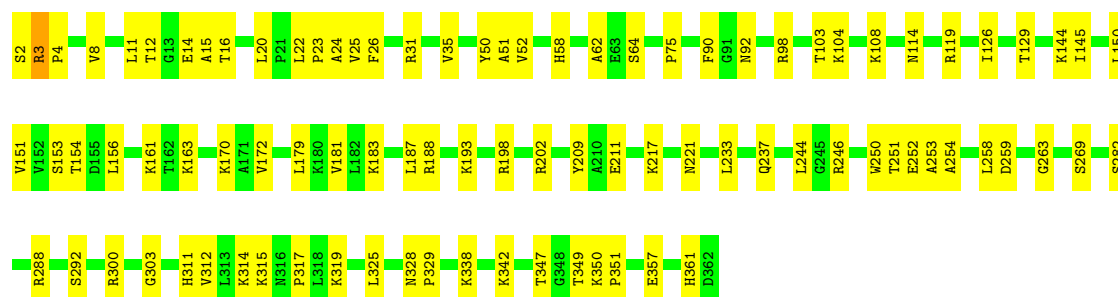
• Molecule 40: 60S ribosomal protein L3

Chain BB: 75% 25%



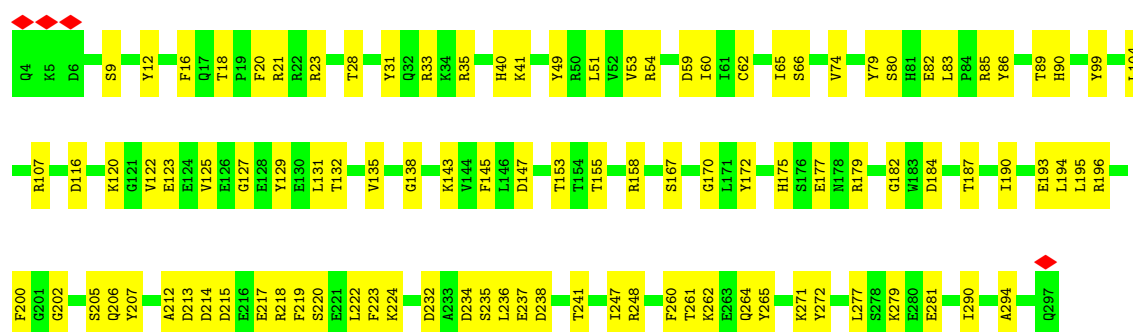
• Molecule 41: RPL4A isoform 1

Chain BC:  75% 25%



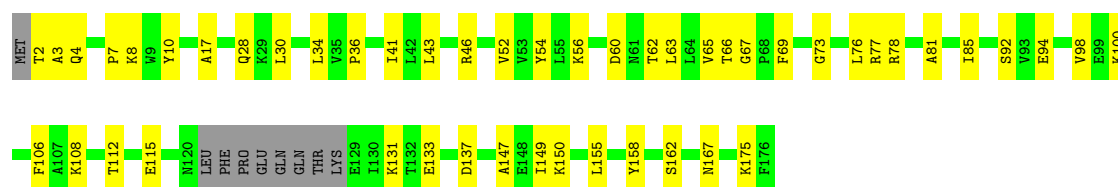
• Molecule 42: RPL5 isoform 1

Chain BD:  65% 35%



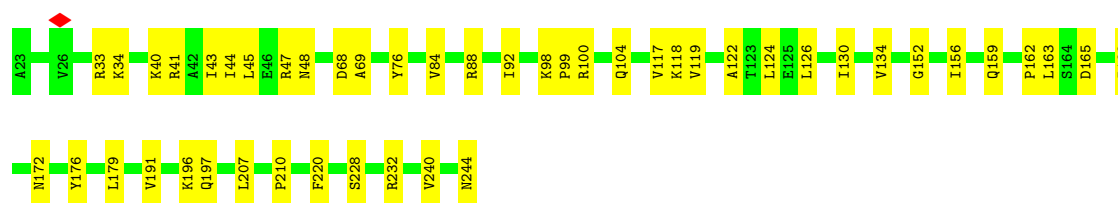
• Molecule 43: 60S ribosomal protein L6-B

Chain BE:  67% 28% 5%



• Molecule 44: 60S ribosomal protein L7-A

Chain BF:  79% 21%

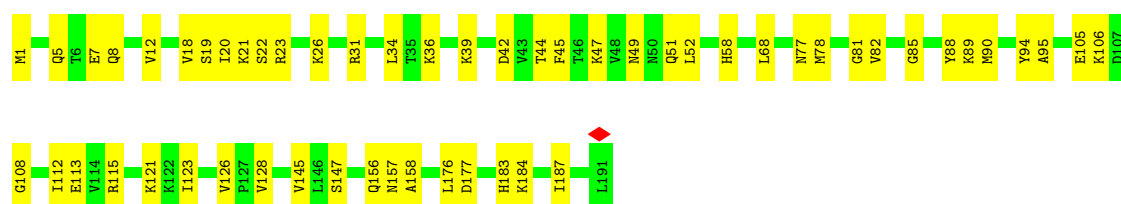


• Molecule 45: 60S ribosomal protein L8

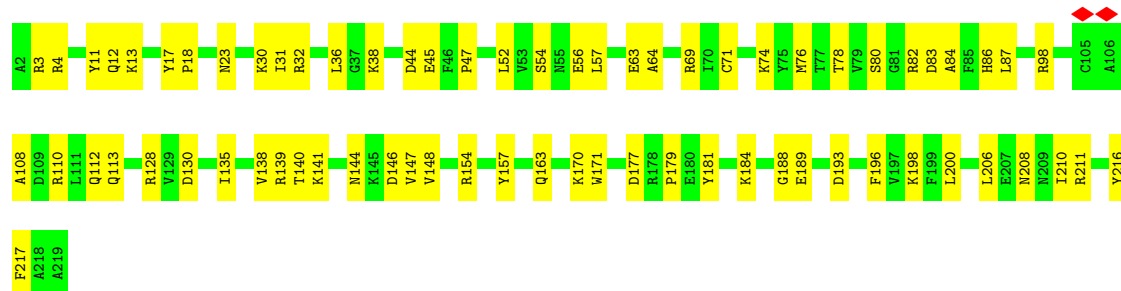
Chain BG:  68% 32%



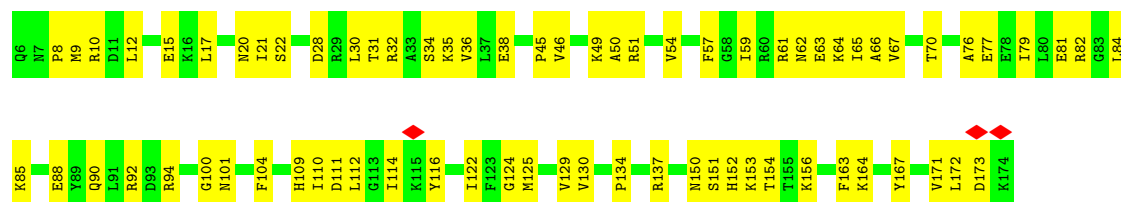
• Molecule 46: RPL9A isoform 1



• Molecule 47: RPL10 isoform 1

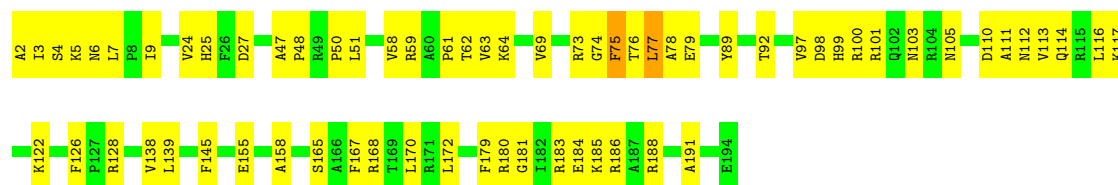


• Molecule 48: RPL11B isoform 1

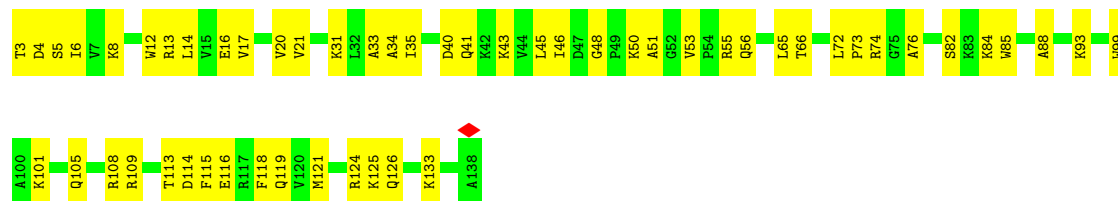


• Molecule 49: 60S ribosomal protein L13-A

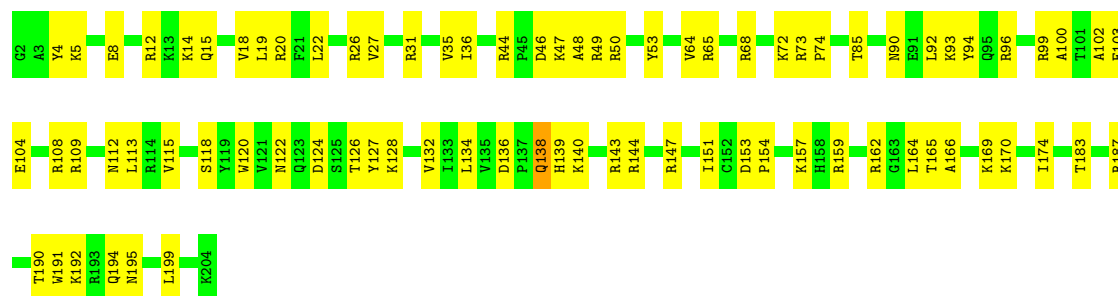




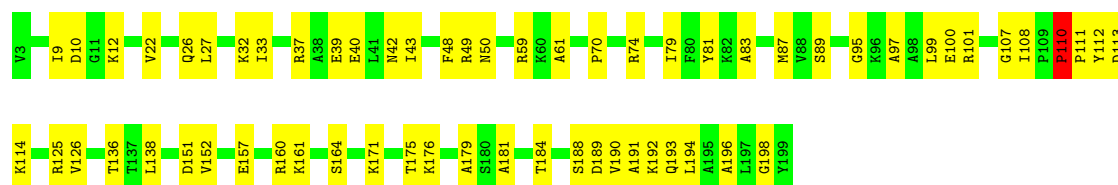
• Molecule 50: 60S ribosomal protein L14-A



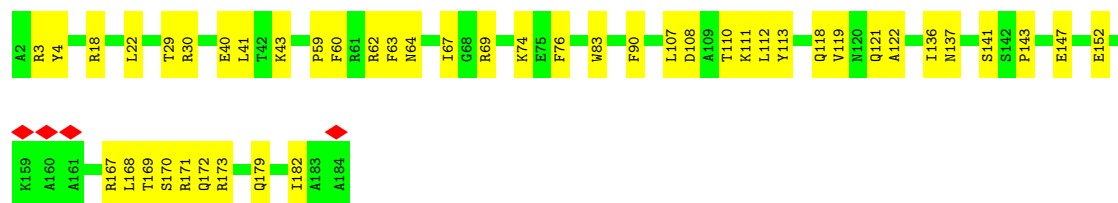
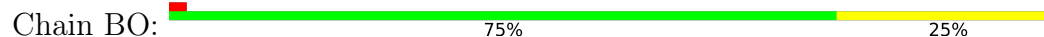
• Molecule 51: Ribosomal protein L15



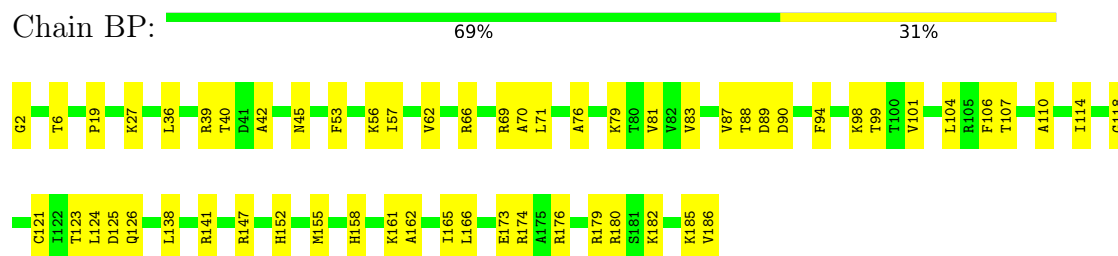
• Molecule 52: 60S ribosomal protein L16-A



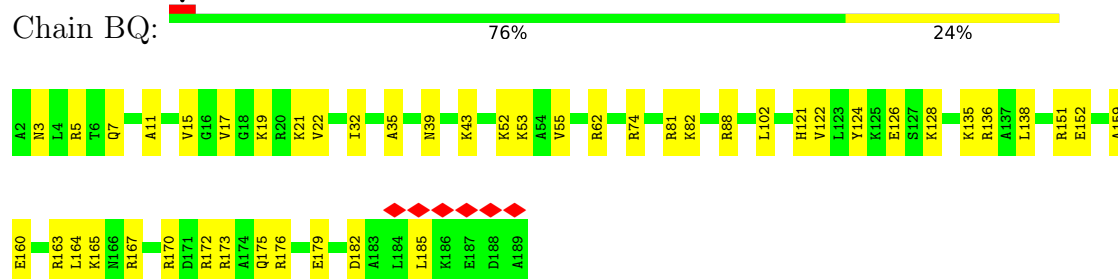
• Molecule 53: 60S ribosomal protein L17-A



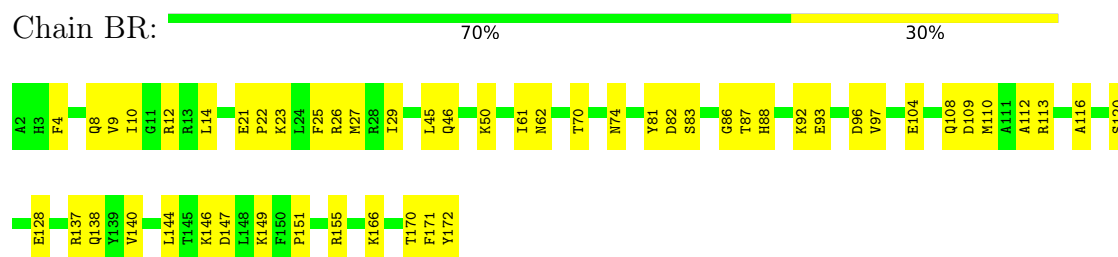
- Molecule 54: 60S ribosomal protein L18-A



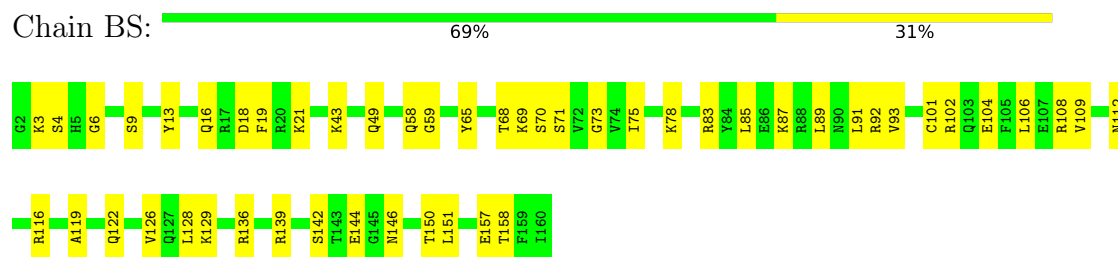
- Molecule 55: 60S ribosomal protein L19-A



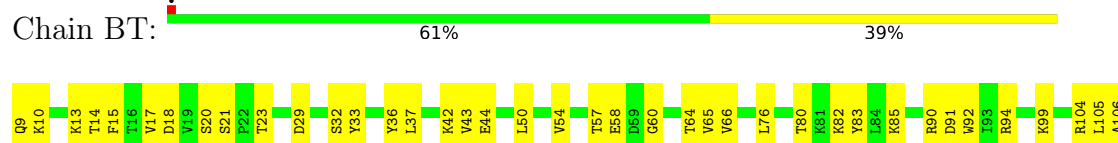
- Molecule 56: 60S ribosomal protein L20-A



- Molecule 57: 60S ribosomal protein L21-A

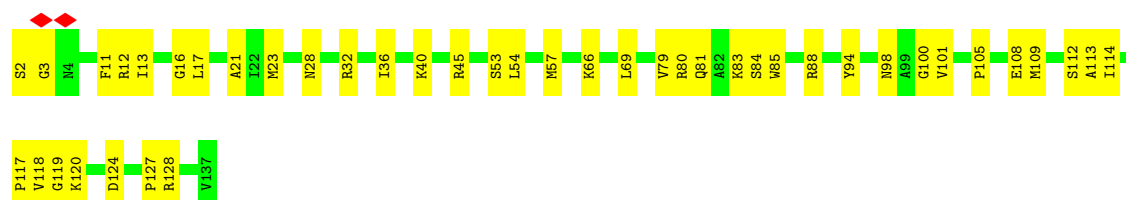


- Molecule 58: 60S ribosomal protein L22-A

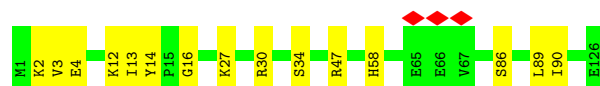




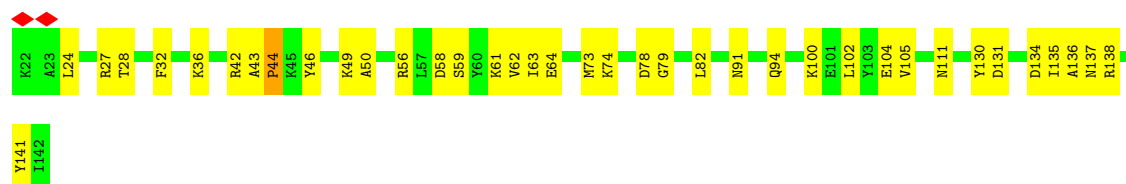
- Molecule 59: 60S ribosomal protein L23-A



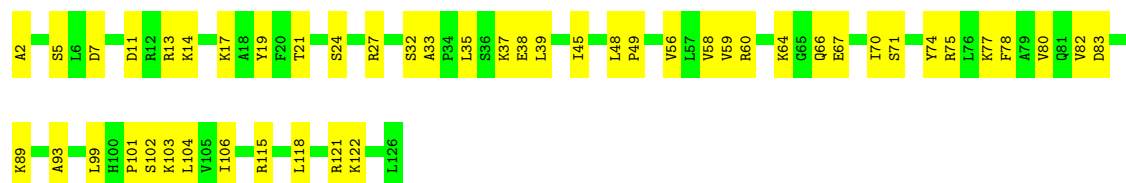
- Molecule 60: RPL24A isoform 1



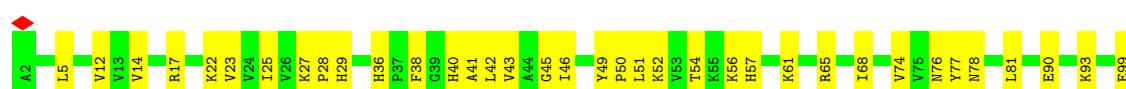
- Molecule 61: 60S ribosomal protein L25



- Molecule 62: 60S ribosomal protein L26-A



- Molecule 63: 60S ribosomal protein L27-A





- Molecule 64: 60S ribosomal protein L28

Chain BZ: 61% 37%



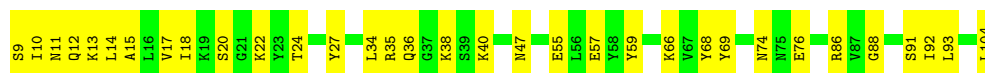
- Molecule 65: 60S ribosomal protein L29

Chain Ba: 86% 14%



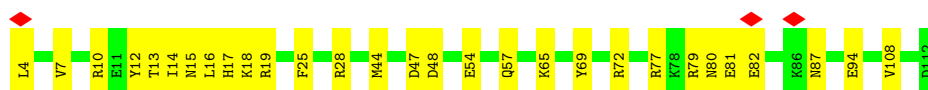
- Molecule 66: 60S ribosomal protein L30

Chain Bb: 66% 34%



- Molecule 67: 60S ribosomal protein L31-A

Chain Bc: 73% 27%



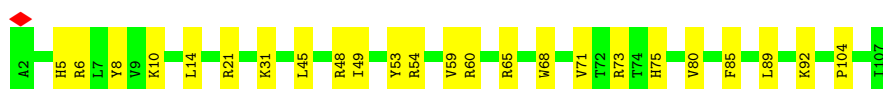
- Molecule 68: RPL32 isoform 1

Chain Bd: 77% 23%

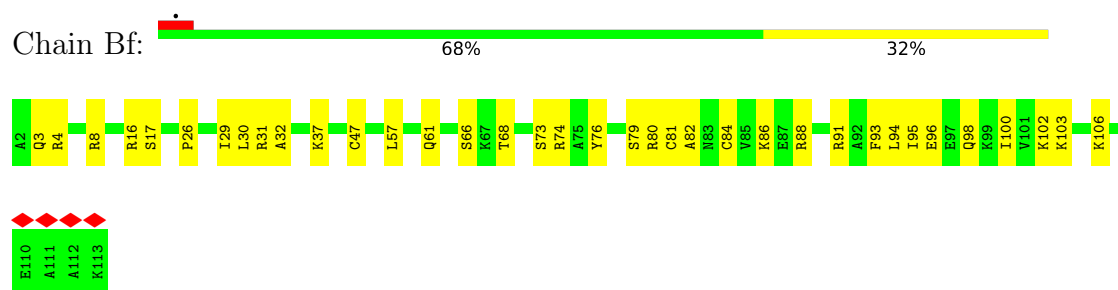


- Molecule 69: 60S ribosomal protein L33-A

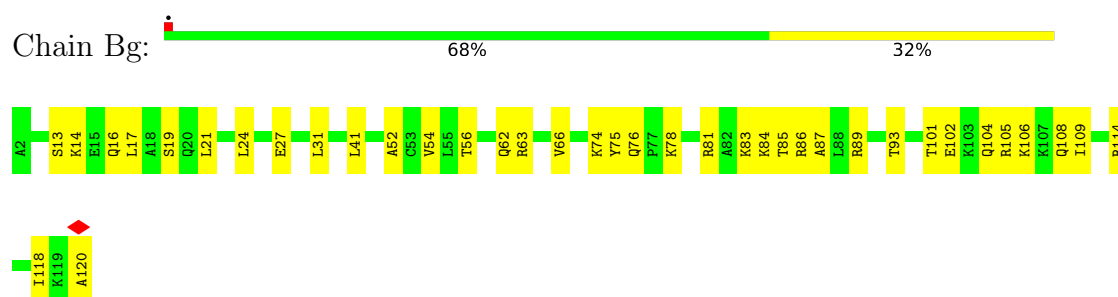
Chain Be: 77% 23%



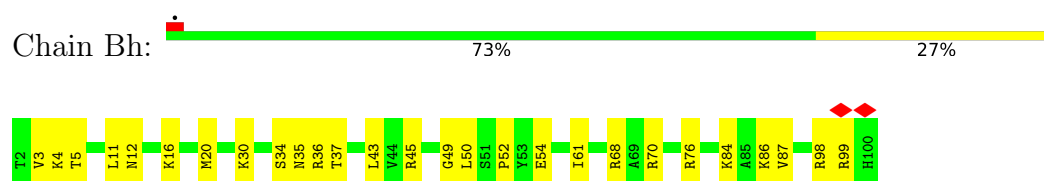
- Molecule 70: 60S ribosomal protein L34-A



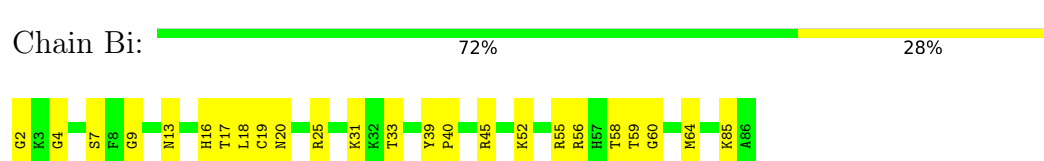
- Molecule 71: 60S ribosomal protein L35-A



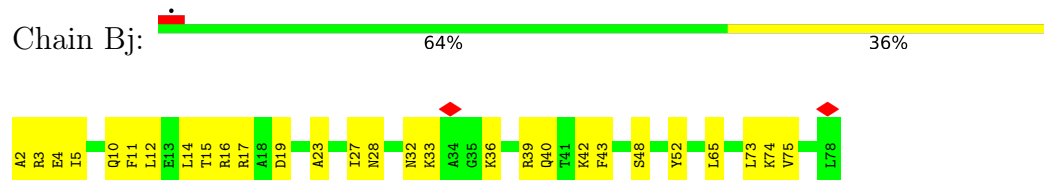
- Molecule 72: 60S ribosomal protein L36-A



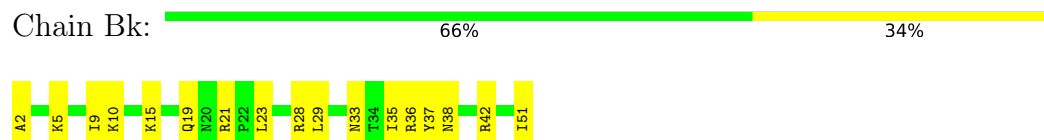
- Molecule 73: 60S ribosomal protein L37-A



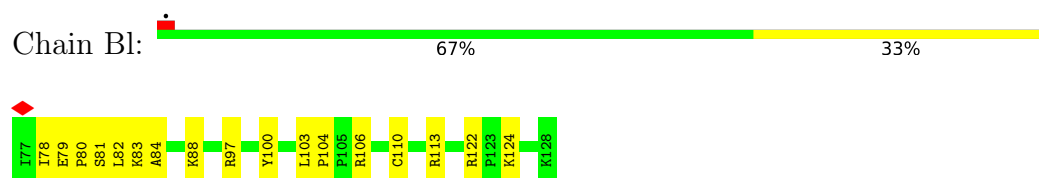
- Molecule 74: RPL38 isoform 1



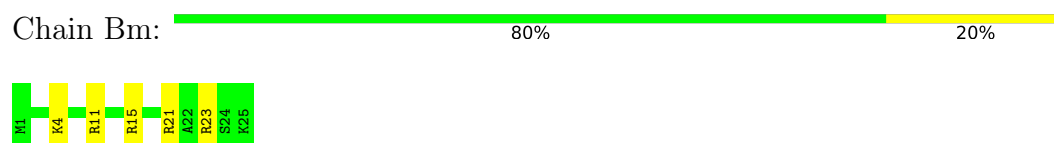
- Molecule 75: 60S ribosomal protein L39



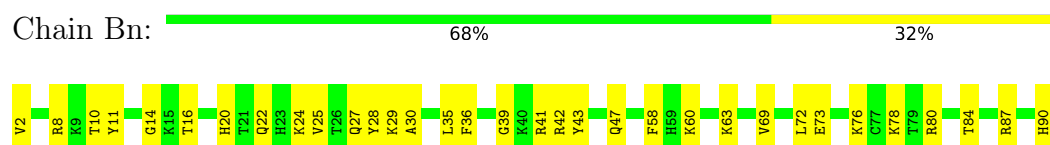
- Molecule 76: 60S ribosomal protein L40-A



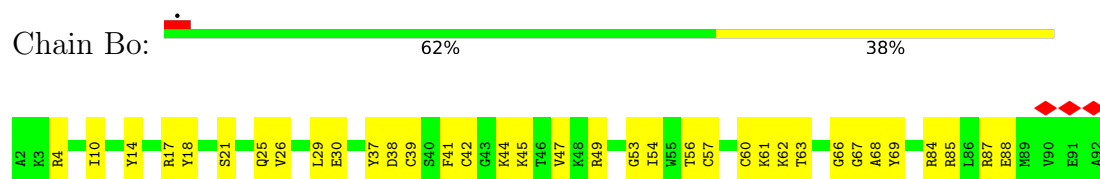
- Molecule 77: 60S ribosomal protein L41



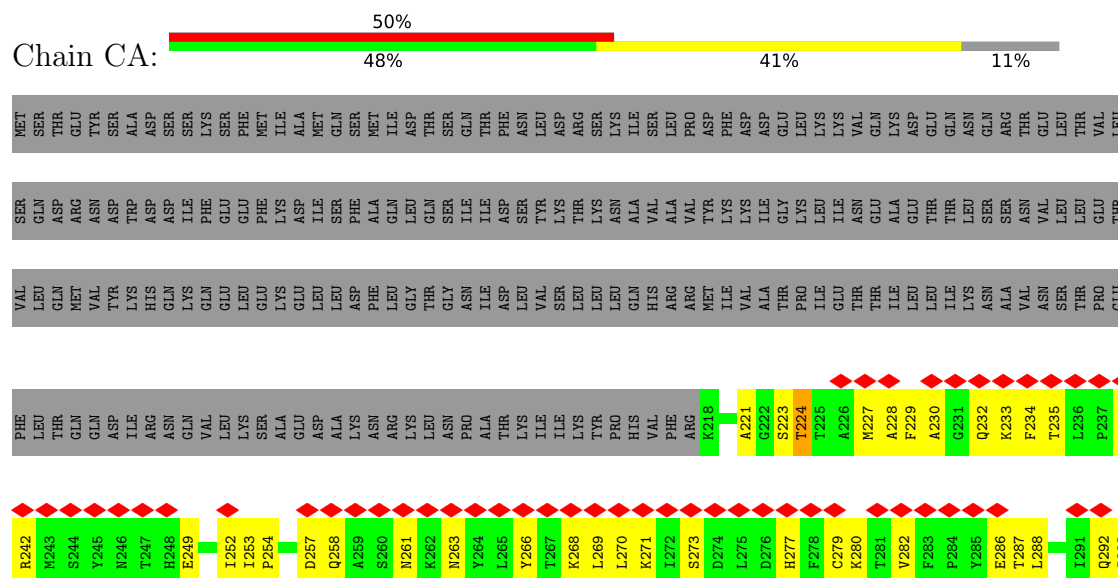
- Molecule 78: 60S ribosomal protein L42-A



- Molecule 79: 60S ribosomal protein L43-A



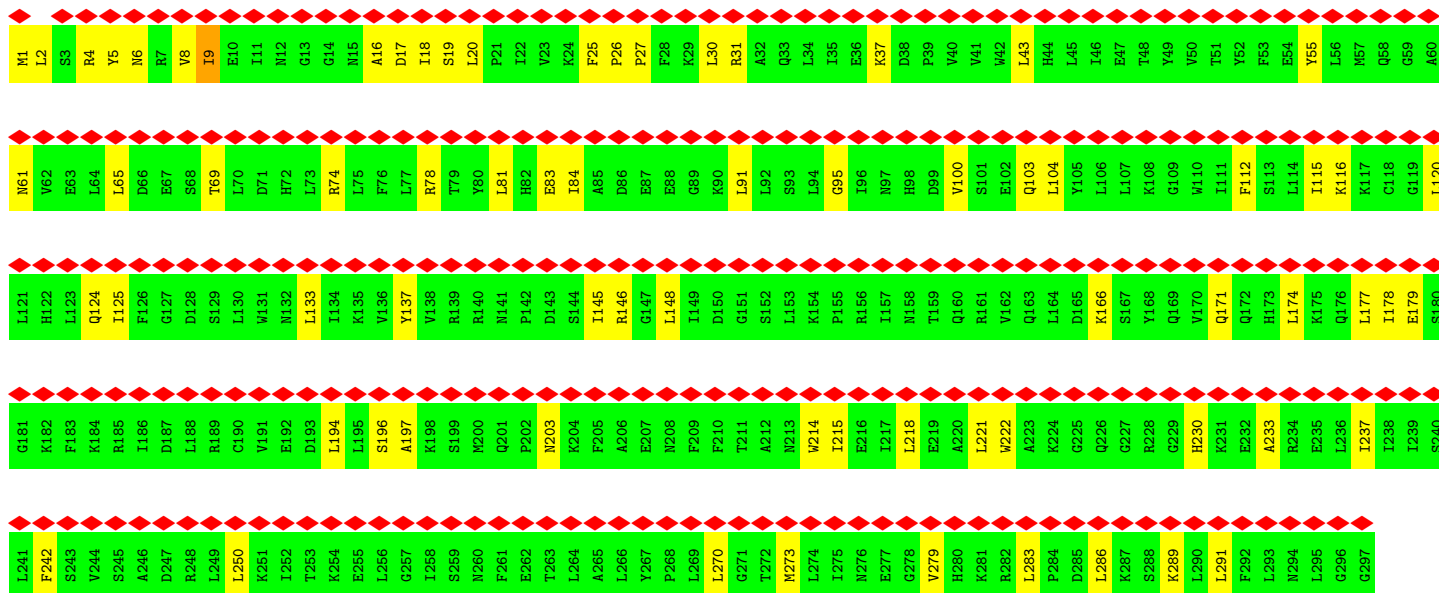
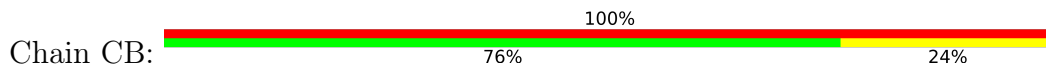
- Molecule 80: RQC trigger complex helicase SLH1



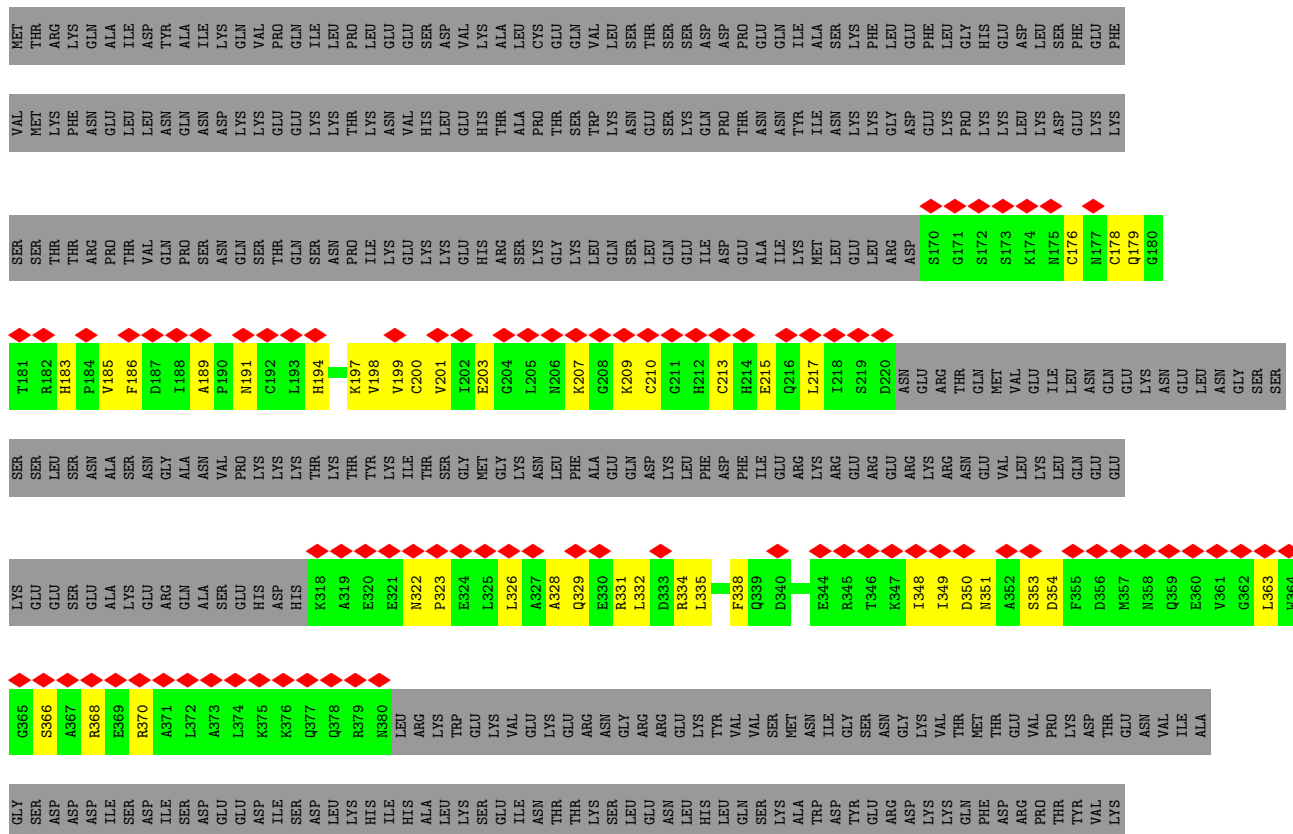




- Molecule 81: CUE3 isoform 1



- Molecule 82: RQC trigger complex subunit RQT4



LYS
ASN
SER
ASP
THR
ALA
GLN
GLN
ASN
ARG
LYS
THR
GLU
GLU
LYS
ALA
HIS
ASP
MET
GLN
ALA
TYR
ASP
LEU
LYS
SER
ARG
VAL
GLN
VAL
VAL
ASP
GLN
ASN
ALA
ASP
ALA
SER
VAL
GLU
GLN
ASN
ILE
LEU
ALA
VAL
LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17885	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 ($e^-/\text{\AA}^2$)	44	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	4.383	Depositor
Minimum map value	-1.015	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.109	Depositor
Recommended contour level	0.3	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	0.44	0/42211	0.40	1/65773 (0.0%)
2	3	0.51	0/3746	0.42	0/5832
3	4	0.43	0/2883	0.37	0/4491
4	5	0.55	0/75723	0.42	0/118057
5	6	0.31	0/1808	0.30	0/2816
6	AA	0.32	0/1644	0.44	0/2249
7	AB	0.34	0/1823	0.53	2/2447 (0.1%)
8	AC	0.43	0/1656	0.47	0/2251
9	AD	0.33	0/1754	0.47	0/2361
10	AE	0.39	0/2097	0.53	1/2823 (0.0%)
11	AF	0.32	0/1625	0.50	0/2197
12	AG	0.30	0/1839	0.47	0/2460
13	AH	0.28	0/1498	0.49	0/2019
14	AI	0.44	0/1501	0.58	0/2006
15	AJ	0.38	0/1504	0.51	0/2016
16	AK	0.31	0/769	0.62	0/1039
17	AL	0.44	0/1185	0.45	0/1598
18	AM	0.20	0/883	0.60	0/1199
19	AN	0.40	0/1215	0.48	0/1638
20	AO	0.38	0/937	0.60	0/1261
21	AP	0.27	0/936	0.50	0/1259
22	AQ	0.31	0/1125	0.58	0/1510
23	AR	0.30	0/957	0.52	0/1283
24	AS	0.30	0/1211	0.53	0/1628
25	AT	0.28	0/1130	0.54	0/1517
26	AU	0.32	0/807	0.50	0/1091
27	AV	0.37	0/682	0.54	0/921
28	AW	0.44	0/1038	0.55	0/1395
29	AX	0.49	0/1139	0.58	0/1518
30	AY	0.34	0/1087	0.46	0/1449
31	AZ	0.24	0/661	0.52	0/888
32	Aa	0.42	0/782	0.63	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ab	0.35	0/620	0.52	0/838
34	Ac	0.34	0/493	0.60	0/663
35	Ad	0.39	0/452	0.54	0/600
36	Ae	0.32	0/480	0.50	0/639
37	Af	0.21	0/567	0.51	0/764
38	Ag	0.19	0/2436	0.43	0/3318
39	BA	0.52	0/1933	0.54	0/2598
40	BB	0.47	0/3146	0.50	0/4228
41	BC	0.48	0/2800	0.52	0/3790
42	BD	0.34	0/2400	0.48	0/3239
43	BE	0.32	0/1327	0.42	0/1790
44	BF	0.47	0/1821	0.46	0/2451
45	BG	0.33	0/1836	0.47	0/2481
46	BH	0.38	0/1529	0.48	0/2060
47	BI	0.45	0/1801	0.49	0/2416
48	BJ	0.34	0/1371	0.53	0/1838
49	BK	0.42	0/1568	0.52	0/2106
50	BL	0.35	0/1068	0.47	0/1438
51	BM	0.48	0/1757	0.51	0/2354
52	BN	0.49	0/1585	0.49	0/2128
53	BO	0.51	0/1439	0.51	0/1938
54	BP	0.47	0/1465	0.48	0/1965
55	BQ	0.44	0/1532	0.45	0/2043
56	BR	0.46	0/1473	0.49	0/1980
57	BS	0.45	0/1300	0.51	0/1743
58	BT	0.35	0/812	0.50	0/1099
59	BU	0.53	0/1018	0.46	0/1369
60	BV	0.39	0/850	0.43	0/1152
61	BW	0.40	0/979	0.47	0/1321
62	BX	0.42	0/995	0.49	0/1329
63	BY	0.33	0/1118	0.43	0/1497
64	BZ	0.52	0/1204	0.59	1/1612 (0.1%)
65	Ba	0.42	0/473	0.52	0/629
66	Bb	0.38	0/745	0.42	0/1001
67	Bc	0.44	0/890	0.50	1/1196 (0.1%)
68	Bd	0.50	0/1038	0.50	0/1390
69	Be	0.51	0/868	0.52	0/1168
70	Bf	0.45	0/890	0.46	0/1189
71	Bg	0.37	0/978	0.49	0/1301
72	Bh	0.31	0/772	0.41	0/1026
73	Bi	0.54	0/685	0.51	0/908
74	Bj	0.30	0/618	0.44	0/826
75	Bk	0.51	0/443	0.45	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bl	0.41	0/423	0.52	0/562
77	Bm	0.52	0/230	0.42	0/296
78	Bn	0.43	0/836	0.52	0/1104
79	Bo	0.50	0/701	0.51	0/934
80	CA	0.15	0/14309	0.37	1/19348 (0.0%)
81	CB	0.09	0/2463	0.25	0/3324
82	CC	0.12	0/897	0.36	0/1203
All	All	0.45	0/233290	0.44	7/340819 (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	1
10	AE	0	1
12	AG	0	1
14	AI	0	1
18	AM	0	3
22	AQ	0	1
29	AX	0	1
32	Aa	0	2
37	Af	0	1
38	Ag	0	1
40	BB	0	1
41	BC	0	1
45	BG	0	2
49	BK	0	1
52	BN	0	1
61	BW	0	1
64	BZ	0	1
65	Ba	0	1
All	All	0	22

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
64	BZ	116	GLY	N-CA-C	6.46	118.08	111.95
10	AE	193	GLY	N-CA-C	5.34	125.83	113.18
80	CA	1633	SER	N-CA-C	-5.33	107.79	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
67	Bc	7	VAL	N-CA-C	-5.14	107.34	111.91
1	2	322	G	C2'-C3'-O3'	5.10	117.15	109.50

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	AB	81	PHE	Peptide
10	AE	42	LEU	Peptide
12	AG	68	LEU	Peptide
14	AI	9	HIS	Peptide
18	AM	83	GLU	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	18987	1041	0
2	3	3353	0	1695	76	0
3	4	2579	0	1304	62	0
4	5	67650	0	33997	1298	0
5	6	1619	0	821	53	0
6	AA	1603	0	1610	74	0
7	AB	1798	0	1890	86	0
8	AC	1626	0	1715	82	0
9	AD	1729	0	1812	67	0
10	AE	2056	0	2140	75	0
11	AF	1605	0	1669	88	0
12	AG	1815	0	1894	84	0
13	AH	1473	0	1555	62	0
14	AI	1476	0	1501	57	0
15	AJ	1479	0	1556	68	0
16	AK	752	0	719	49	0
17	AL	1159	0	1225	31	0
18	AM	875	0	878	54	0
19	AN	1192	0	1255	40	0
20	AO	926	0	950	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	AP	916	0	941	66	0
22	AQ	1105	0	1166	63	0
23	AR	948	0	990	62	0
24	AS	1192	0	1222	77	0
25	AT	1112	0	1124	68	0
26	AU	797	0	863	49	0
27	AV	673	0	662	36	0
28	AW	1021	0	1060	30	0
29	AX	1121	0	1196	42	0
30	AY	1073	0	1132	48	0
31	AZ	651	0	682	37	0
32	Aa	769	0	818	42	0
33	Ab	610	0	633	34	0
34	Ac	491	0	524	23	0
35	Ad	442	0	428	33	0
36	Ae	472	0	521	27	0
37	Af	556	0	546	48	0
38	Ag	2383	0	2332	112	0
39	BA	1899	0	1957	67	0
40	BB	3075	0	3142	75	0
41	BC	2748	0	2859	77	0
42	BD	2351	0	2294	81	0
43	BE	1305	0	1370	45	0
44	BF	1784	0	1862	38	0
45	BG	1804	0	1877	54	0
46	BH	1508	0	1572	51	0
47	BI	1764	0	1804	48	0
48	BJ	1350	0	1381	71	0
49	BK	1543	0	1608	61	0
50	BL	1053	0	1149	46	0
51	BM	1720	0	1779	73	0
52	BN	1555	0	1659	47	0
53	BO	1416	0	1433	40	0
54	BP	1441	0	1543	46	0
55	BQ	1515	0	1606	47	0
56	BR	1437	0	1475	54	0
57	BS	1276	0	1323	44	0
58	BT	796	0	812	32	0
59	BU	1003	0	1048	30	0
60	BV	836	0	709	13	0
61	BW	964	0	1025	35	0
62	BX	984	0	1075	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
63	BY	1092	0	1155	37	0
64	BZ	1173	0	1215	58	0
65	Ba	462	0	491	6	0
66	Bb	737	0	792	24	0
67	Bc	876	0	912	22	0
68	Bd	1017	0	1081	25	0
69	Be	850	0	880	19	0
70	Bf	880	0	941	29	0
71	Bg	969	0	1078	39	0
72	Bh	766	0	844	25	0
73	Bi	670	0	673	23	0
74	Bj	612	0	682	26	0
75	Bk	436	0	475	14	0
76	Bl	417	0	455	25	0
77	Bm	229	0	273	9	0
78	Bn	824	0	888	29	0
79	Bo	694	0	735	29	0
80	CA	14008	0	14058	612	0
81	CB	2415	0	2508	52	0
82	CC	886	0	857	39	0
83	2	84	0	0	0	0
83	AC	1	0	0	0	0
83	AQ	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	218071	0	165368	5820	0

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

The worst 5 of 5820 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)
1:2:69:G:H1	1:2:82:U:H3	1.09	0.99
1:2:521:A:N3	30:AY:34:ASN:ND2	2.12	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:AO:29:HIS:HB3	20:AO:41:ARG:HA	1.47	0.97
4:5:2139:A:HO2'	73:Bi:2:GLY:N	1.62	0.95
1:2:992:A:H2	1:2:1012:U:H3	1.12	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	AA	204/206 (99%)	186 (91%)	18 (9%)	0	100	100
7	AB	222/255 (87%)	207 (93%)	13 (6%)	2 (1%)	14	49
8	AC	214/216 (99%)	204 (95%)	10 (5%)	0	100	100
9	AD	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
10	AE	256/258 (99%)	237 (93%)	18 (7%)	1 (0%)	30	66
11	AF	204/206 (99%)	197 (97%)	7 (3%)	0	100	100
12	AG	226/228 (99%)	212 (94%)	13 (6%)	1 (0%)	30	66
13	AH	182/184 (99%)	171 (94%)	11 (6%)	0	100	100
14	AI	183/200 (92%)	167 (91%)	14 (8%)	2 (1%)	11	45
15	AJ	182/184 (99%)	171 (94%)	10 (6%)	1 (0%)	24	62
16	AK	90/92 (98%)	86 (96%)	4 (4%)	0	100	100
17	AL	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
18	AM	119/121 (98%)	95 (80%)	23 (19%)	1 (1%)	16	52
19	AN	148/150 (99%)	141 (95%)	7 (5%)	0	100	100
20	AO	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
21	AP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
22	AQ	139/141 (99%)	127 (91%)	12 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	AR	117/136 (86%)	113 (97%)	4 (3%)	0	100	100
24	AS	143/145 (99%)	130 (91%)	13 (9%)	0	100	100
25	AT	141/143 (99%)	130 (92%)	11 (8%)	0	100	100
26	AU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
27	AV	85/87 (98%)	72 (85%)	13 (15%)	0	100	100
28	AW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
29	AX	142/144 (99%)	129 (91%)	12 (8%)	1 (1%)	18	55
30	AY	132/134 (98%)	124 (94%)	7 (5%)	1 (1%)	16	52
31	AZ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
32	Aa	95/97 (98%)	77 (81%)	16 (17%)	2 (2%)	5	30
33	Ab	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
34	Ac	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
35	Ad	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
36	Ae	58/60 (97%)	54 (93%)	4 (7%)	0	100	100
37	Af	71/73 (97%)	62 (87%)	9 (13%)	0	100	100
38	Ag	310/312 (99%)	300 (97%)	10 (3%)	0	100	100
39	BA	249/251 (99%)	236 (95%)	12 (5%)	1 (0%)	30	66
40	BB	384/386 (100%)	361 (94%)	22 (6%)	1 (0%)	36	71
41	BC	359/361 (99%)	338 (94%)	19 (5%)	2 (1%)	21	58
42	BD	292/294 (99%)	280 (96%)	11 (4%)	1 (0%)	36	71
43	BE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
44	BF	220/222 (99%)	209 (95%)	11 (5%)	0	100	100
45	BG	231/233 (99%)	217 (94%)	14 (6%)	0	100	100
46	BH	189/191 (99%)	183 (97%)	6 (3%)	0	100	100
47	BI	216/218 (99%)	210 (97%)	6 (3%)	0	100	100
48	BJ	167/169 (99%)	154 (92%)	13 (8%)	0	100	100
49	BK	191/193 (99%)	176 (92%)	13 (7%)	2 (1%)	12	47
50	BL	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
51	BM	201/203 (99%)	189 (94%)	12 (6%)	0	100	100
52	BN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	12	47
53	BO	181/183 (99%)	172 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
54	BP	183/185 (99%)	174 (95%)	9 (5%)	0	100	100
55	BQ	186/188 (99%)	177 (95%)	9 (5%)	0	100	100
56	BR	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
57	BS	157/159 (99%)	147 (94%)	10 (6%)	0	100	100
58	BT	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	BU	134/136 (98%)	130 (97%)	4 (3%)	0	100	100
60	BV	124/126 (98%)	122 (98%)	2 (2%)	0	100	100
61	BW	119/121 (98%)	114 (96%)	4 (3%)	1 (1%)	16	52
62	BX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
63	BY	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
64	BZ	146/148 (99%)	135 (92%)	10 (7%)	1 (1%)	18	55
65	Ba	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Bb	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
67	Bc	107/109 (98%)	99 (92%)	8 (8%)	0	100	100
68	Bd	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
69	Be	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
70	Bf	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
71	Bg	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
72	Bh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
73	Bi	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
74	Bj	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
75	Bk	48/50 (96%)	47 (98%)	1 (2%)	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%)	97 (96%)	4 (4%)	0	100	100
79	Bo	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
80	CA	1738/1967 (88%)	1664 (96%)	70 (4%)	4 (0%)	43	77
81	CB	295/297 (99%)	291 (99%)	3 (1%)	1 (0%)	36	71
82	CC	110/530 (21%)	107 (97%)	3 (3%)	0	100	100
All	All	13127/14000 (94%)	12439 (95%)	660 (5%)	28 (0%)	44	77

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%)	94 (99%)	1 (1%)	65	74
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	320 (100%)	1 (0%)	86	84
41	BC	288/288 (100%)	287 (100%)	1 (0%)	86	84
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%)	185 (100%)	0	100	100
48	BJ	146/147 (99%)	146 (100%)	0	100	100
49	BK	154/154 (100%)	153 (99%)	1 (1%)	78	80
50	BL	107/107 (100%)	107 (100%)	0	100	100
51	BM	175/175 (100%)	174 (99%)	1 (1%)	78	80
52	BN	160/160 (100%)	159 (99%)	1 (1%)	78	80
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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%)	11117 (100%)	6 (0%)	87	88

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
49	BK	6	ASN
51	BM	138	GLN

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Mol	Chain	Res	Type
52	BN	50[A]	ASN
40	BB	90	VAL
21	AP	103	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 108 such sidechains are listed below:

Mol	Chain	Res	Type
53	BO	137	ASN
65	Ba	42	ASN
80	CA	1649	GLN
55	BQ	141	HIS
57	BS	131	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1800 (98%)	434 (24%)	36 (2%)
2	3	157/158 (99%)	31 (19%)	1 (0%)
3	4	120/121 (99%)	14 (11%)	1 (0%)
4	5	3159/3396 (93%)	584 (18%)	32 (1%)
5	6	75/76 (98%)	14 (18%)	0
All	All	5279/5551 (95%)	1077 (20%)	70 (1%)

5 of 1077 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	5	U
1	2	9	U
1	2	17	C

5 of 70 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	2496	C
4	5	2538	U
4	5	3229	C
1	2	1256	A
1	2	1226	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

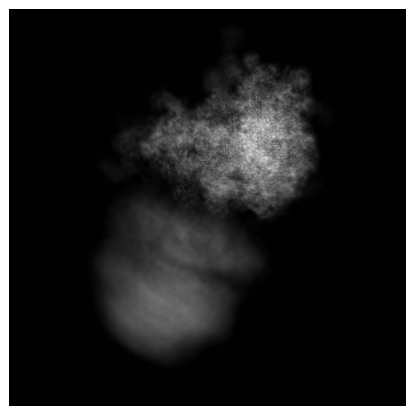
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14978. These allow visual inspection of the internal detail of the map and identification of artifacts.

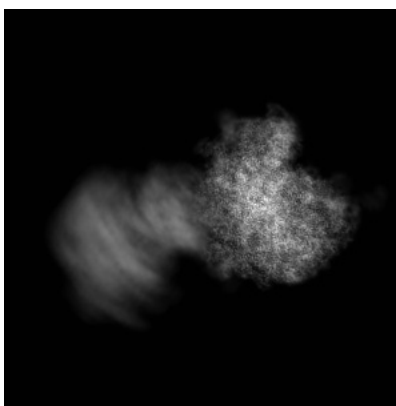
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

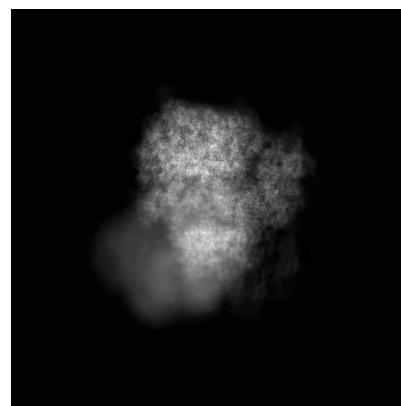
6.1.1 Primary map



X

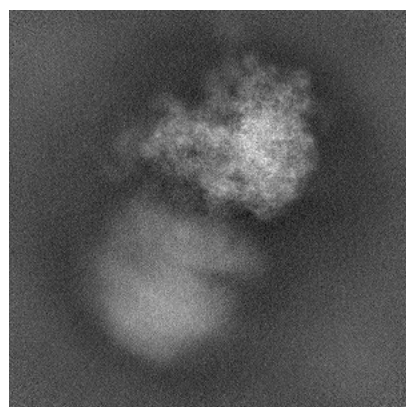


Y

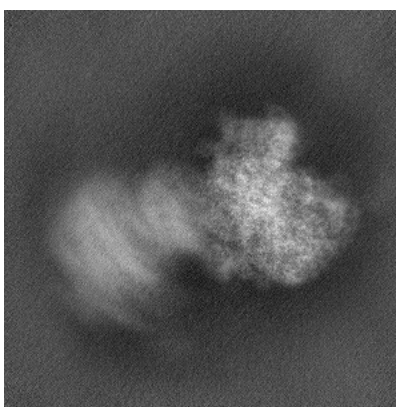


Z

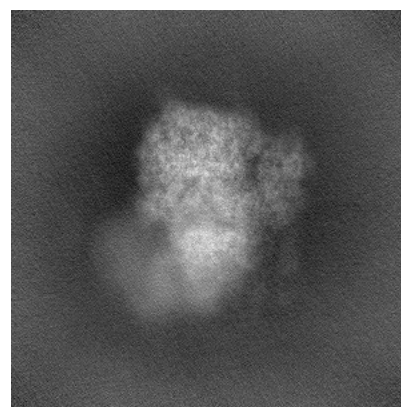
6.1.2 Raw map



X



Y

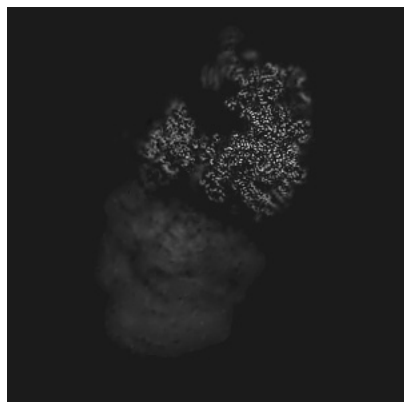


Z

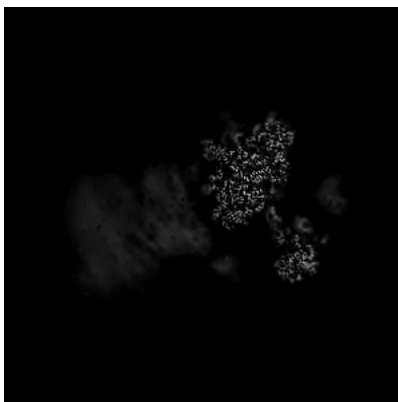
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 280

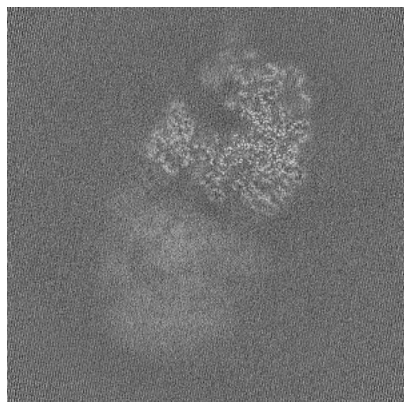


Y Index: 280

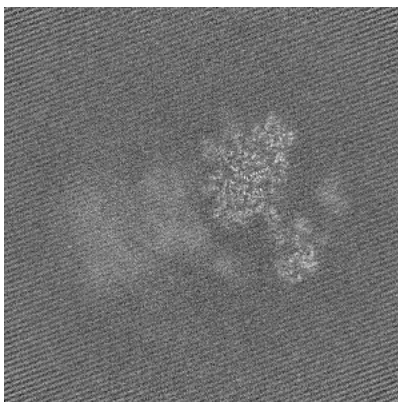


Z Index: 280

6.2.2 Raw map



X Index: 280



Y Index: 280

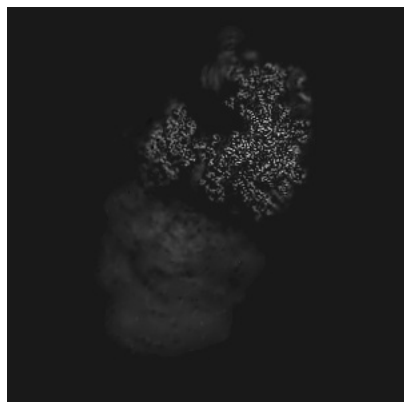


Z Index: 280

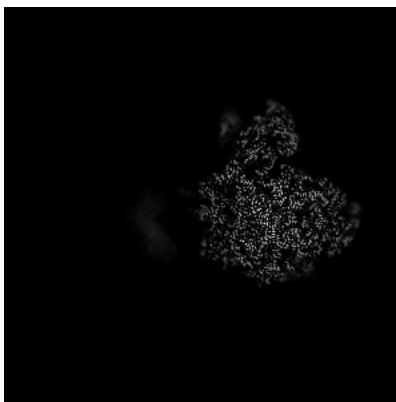
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

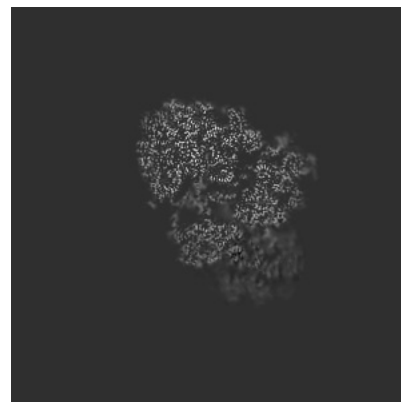
6.3.1 Primary map



X Index: 281

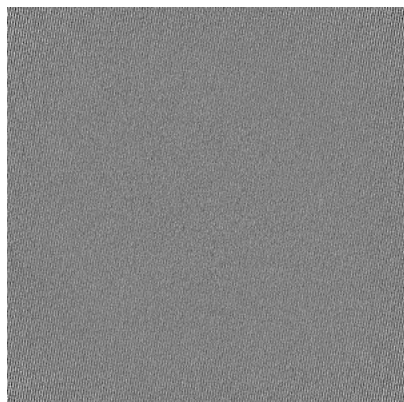


Y Index: 345

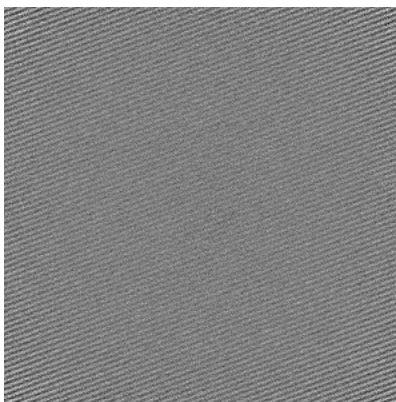


Z Index: 380

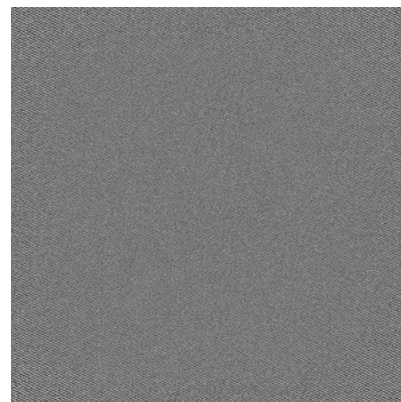
6.3.2 Raw map



X Index: 0



Y Index: 0

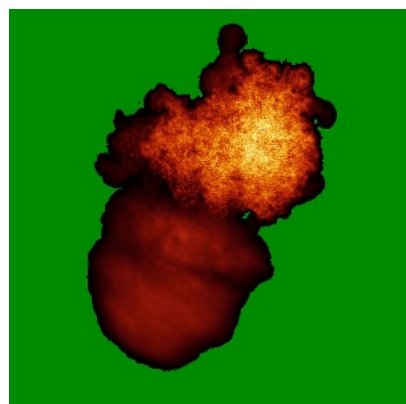


Z Index: 0

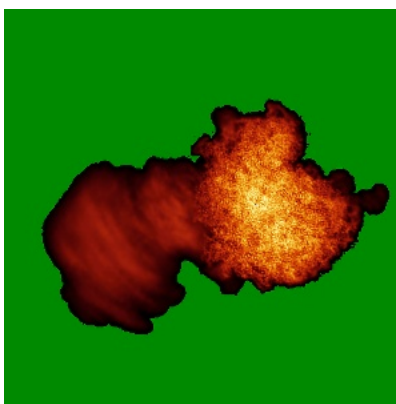
The images above show the largest variance slices of the map in three orthogonal directions.

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

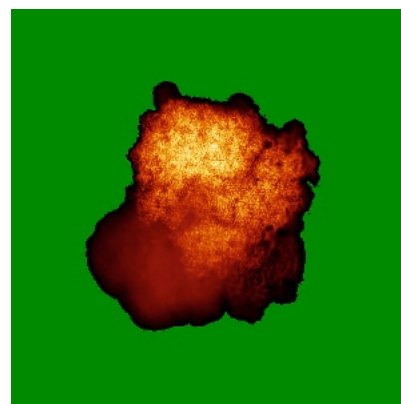
6.4.1 Primary map



X

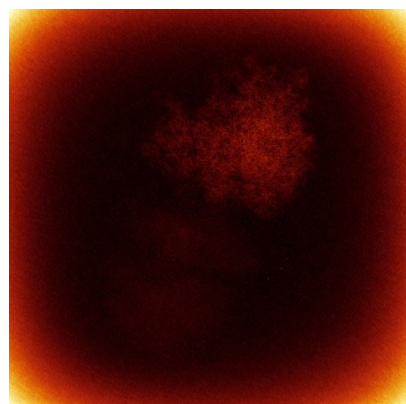


Y

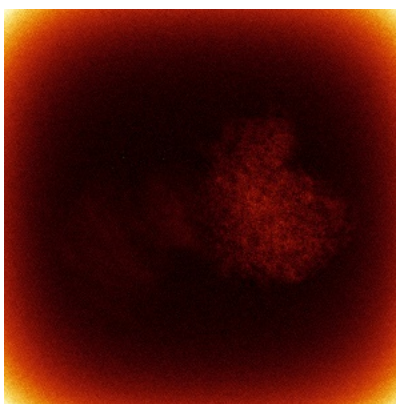


Z

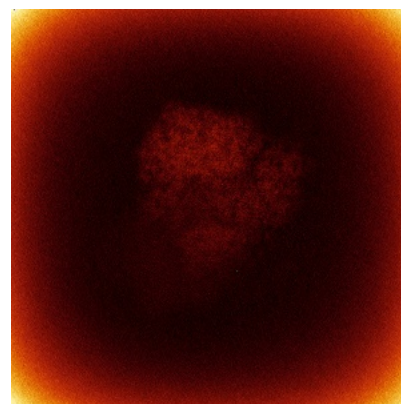
6.4.2 Raw map



X



Y



Z

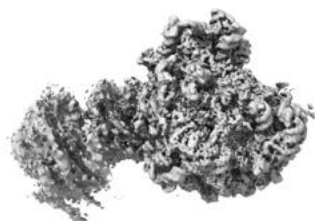
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



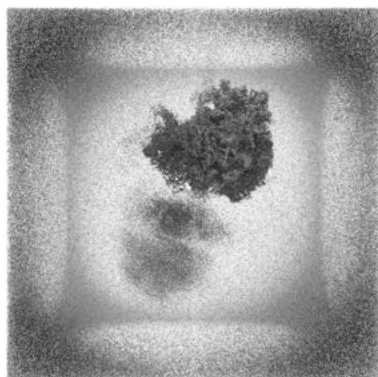
Y



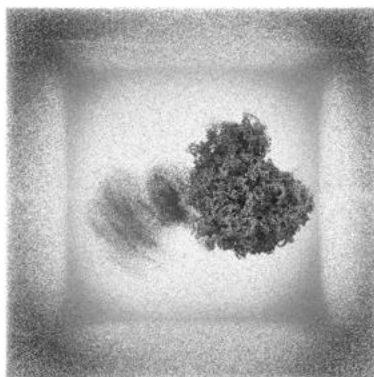
Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

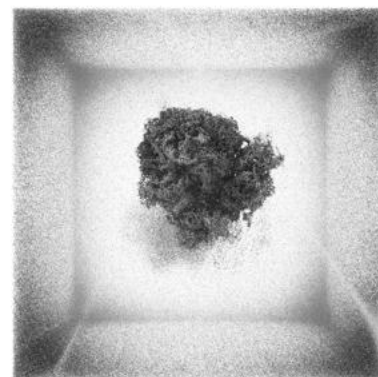
6.5.2 Raw map



X



Y



Z

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.

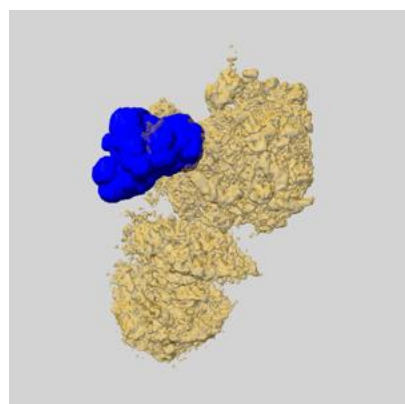
6.6 Mask visualisation [i](#)

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

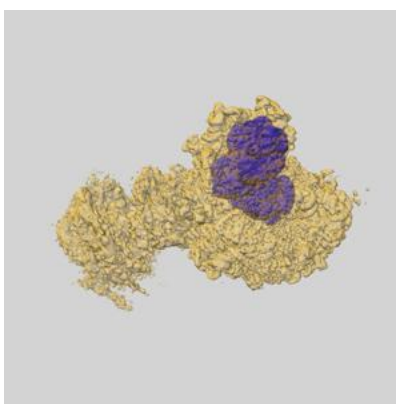
A mask typically either:

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

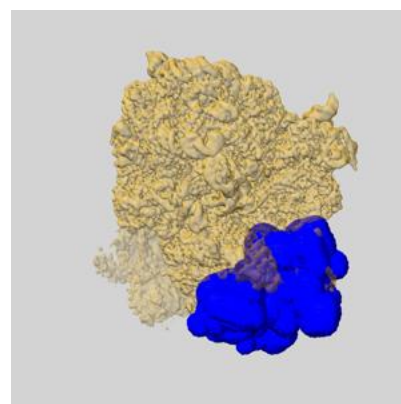
6.6.1 emd_14978_msk_1.map [i](#)



X

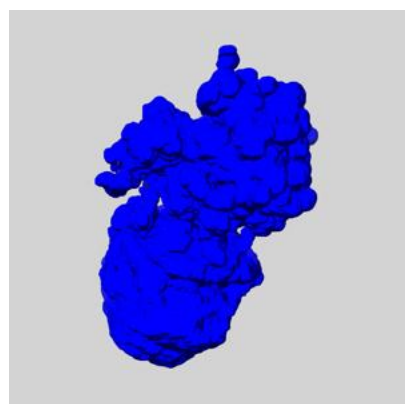


Y

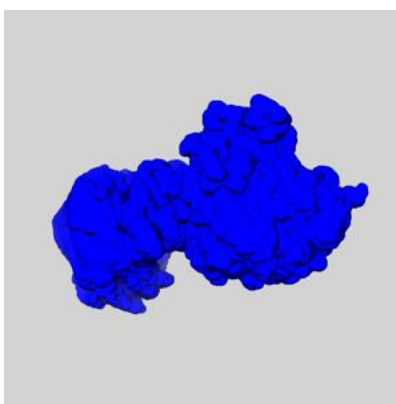


Z

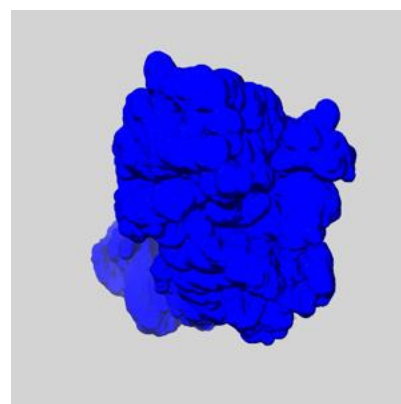
6.6.2 emd_14978_msk_2.map [i](#)



X



Y

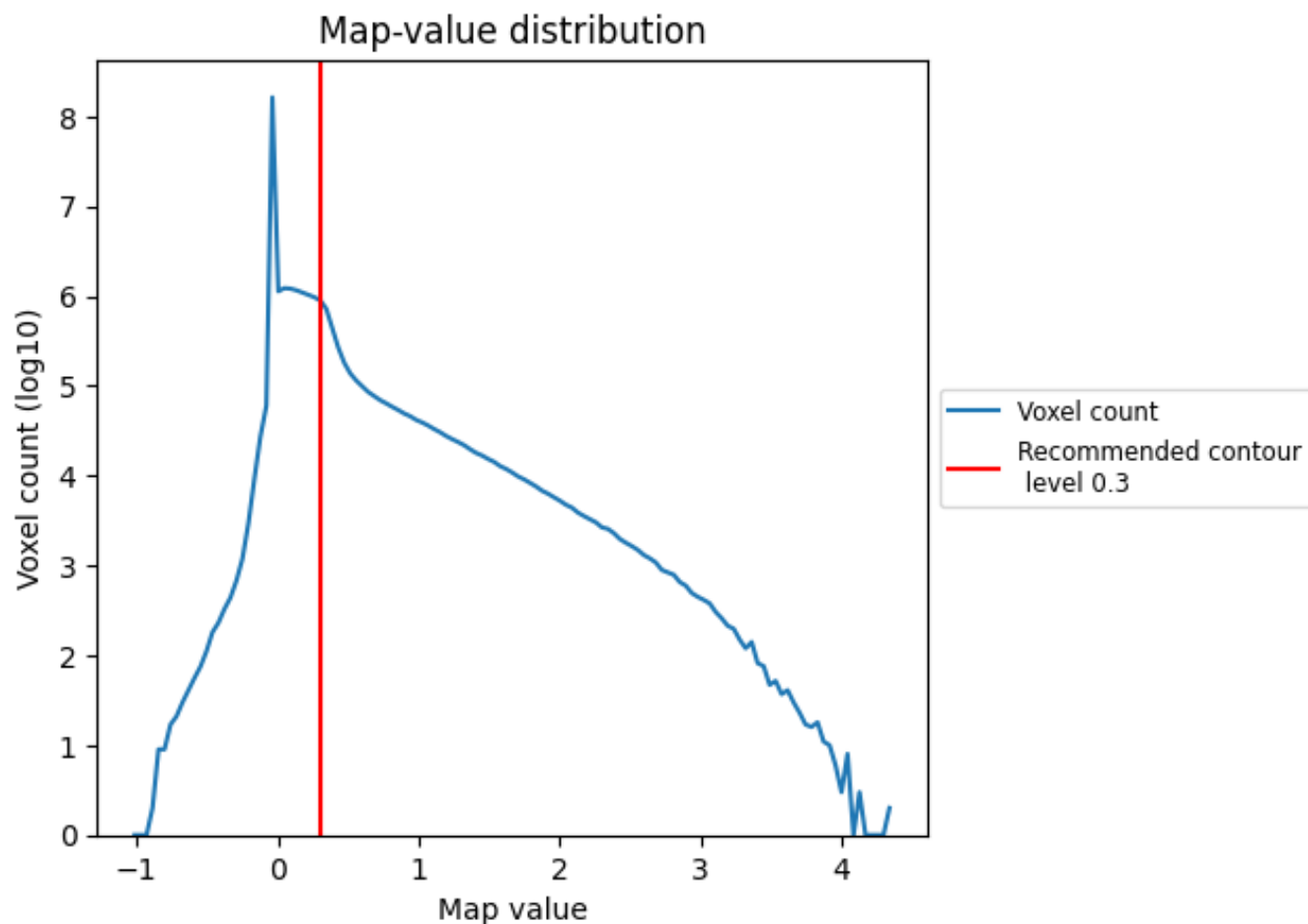


Z

7 Map analysis [i](#)

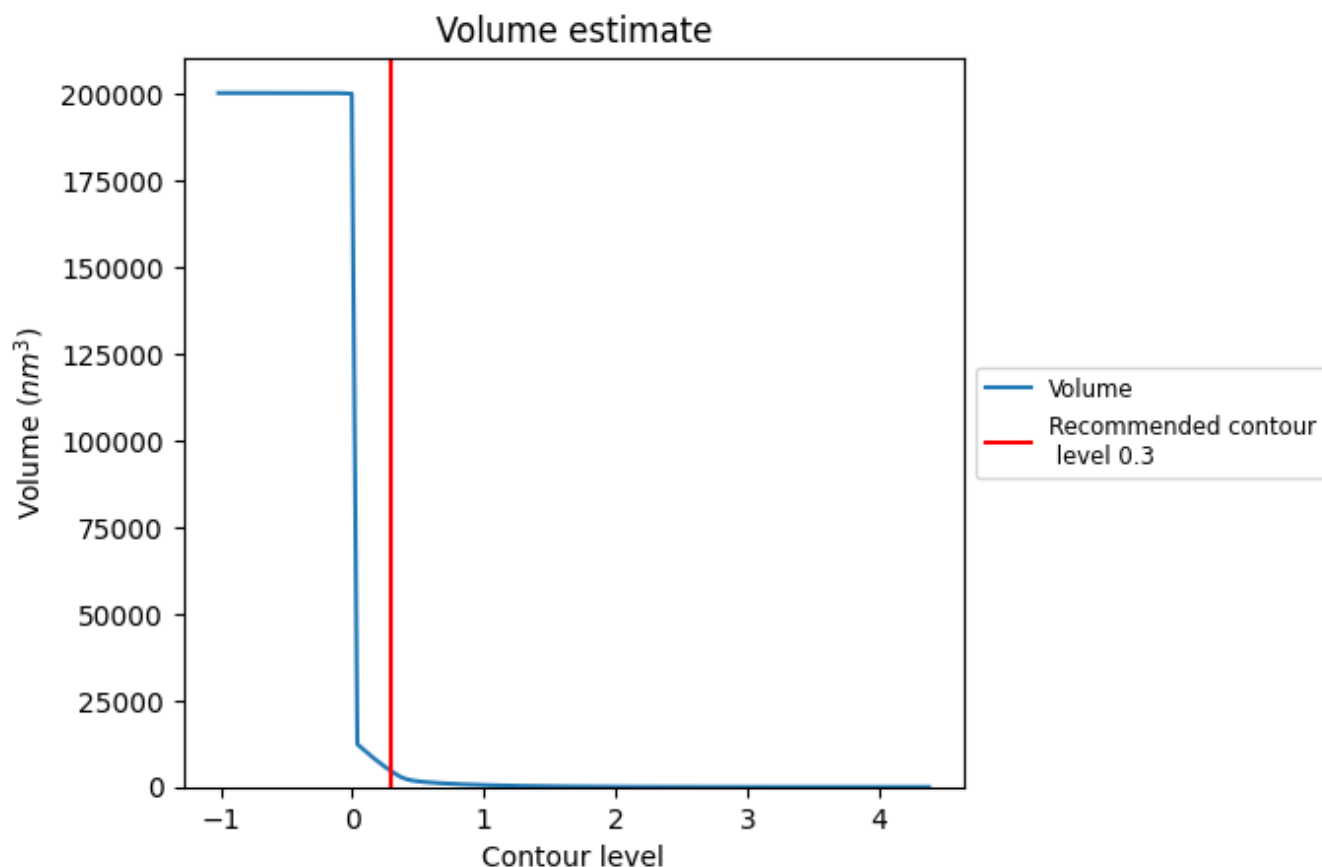
This section contains the results of statistical analysis of the map.

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.

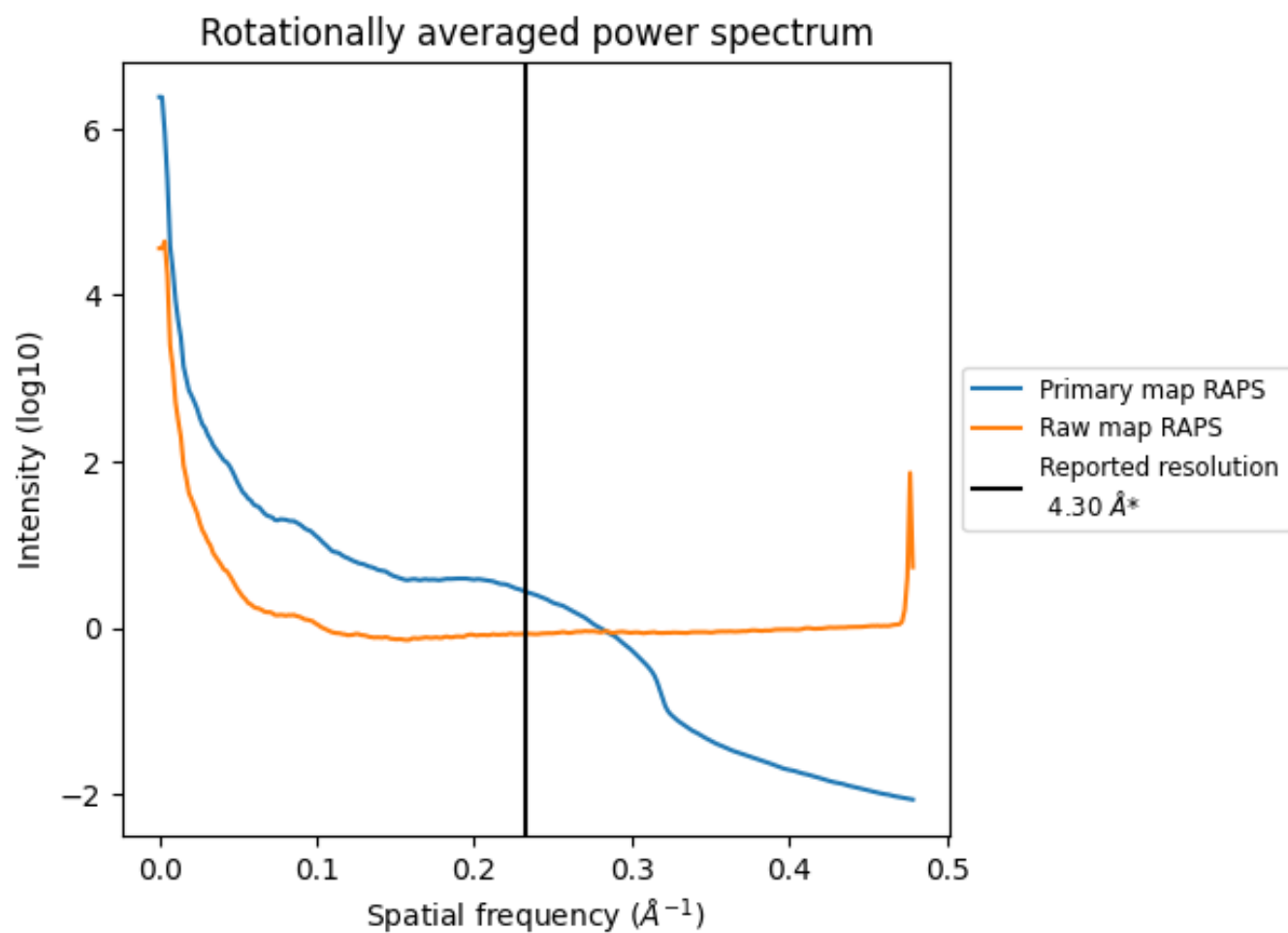
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4493 nm³; this corresponds to an approximate mass of 4059 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 ⓘ

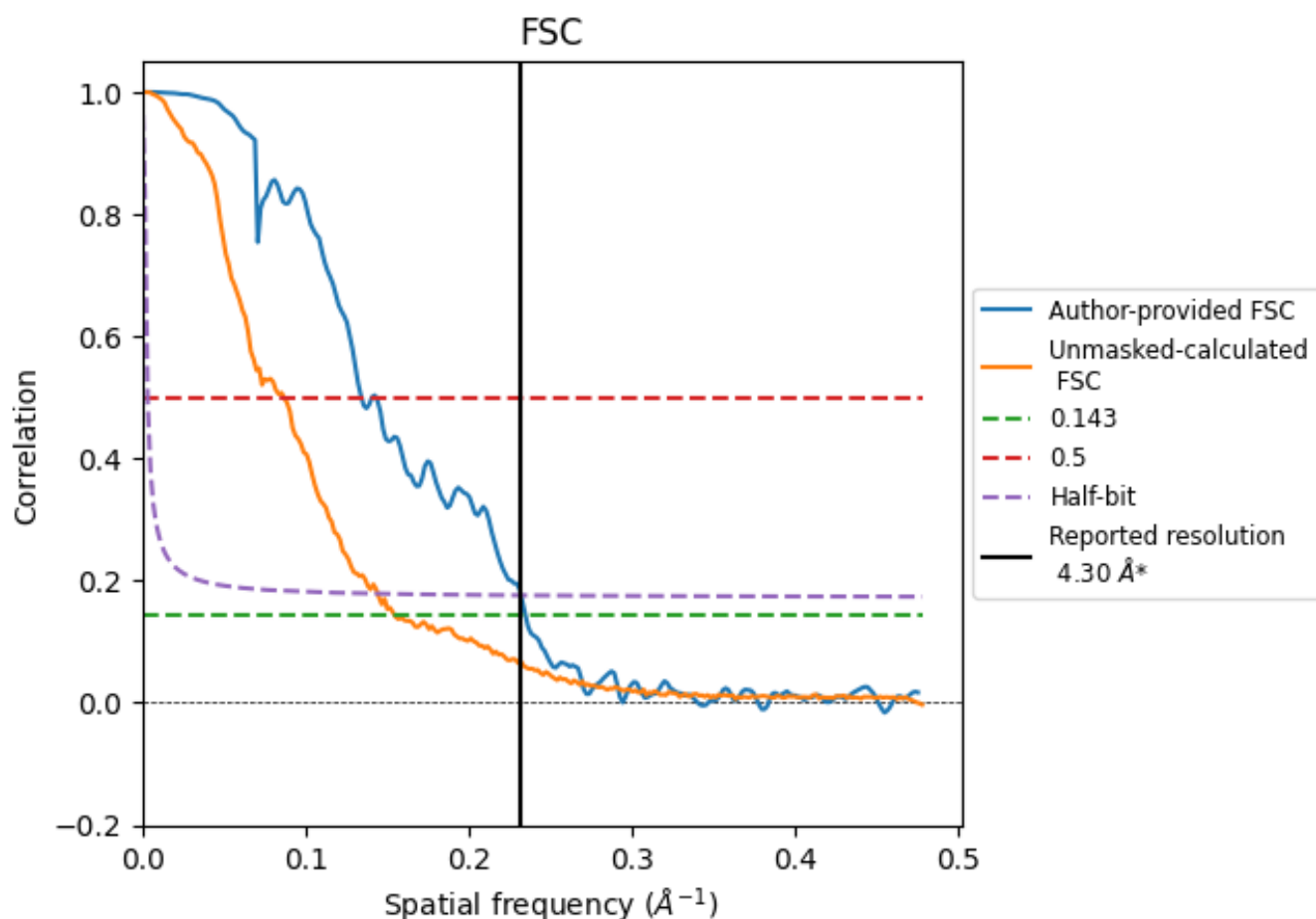


*Reported resolution corresponds to spatial frequency of 0.233 Å⁻¹

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 0.233 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

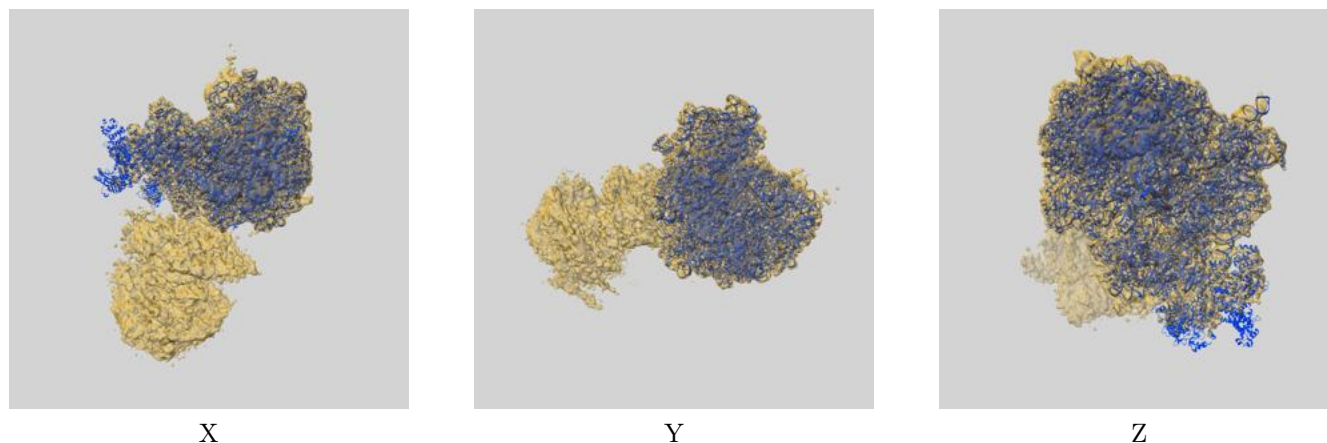
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.30	-	-
Author-provided FSC curve	4.25	7.43	4.30
Unmasked-calculated*	6.46	11.49	6.92

*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 6.46 differs from the reported value 4.3 by more than 10 %

9 Map-model fit [i](#)

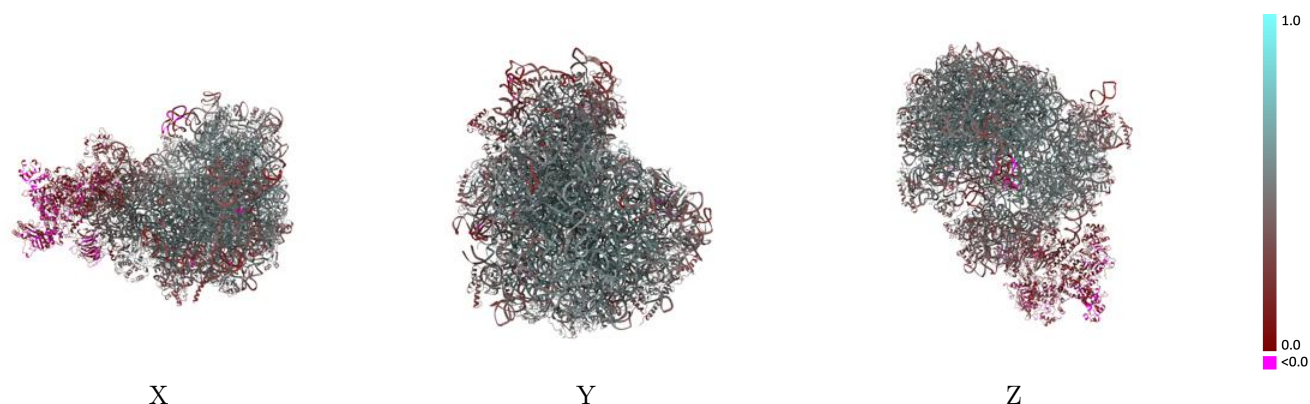
This section contains information regarding the fit between EMDB map EMD-14978 and PDB model 7ZUW. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



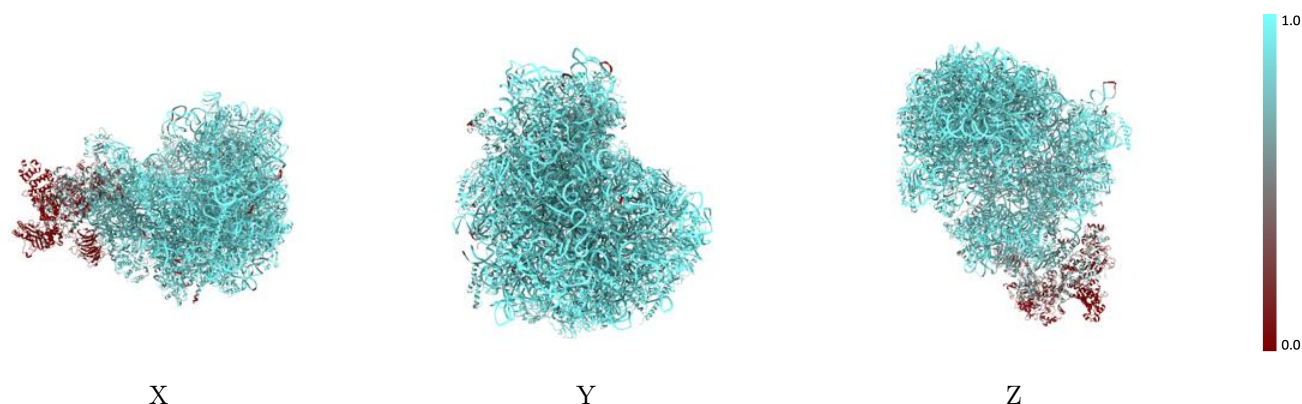
The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



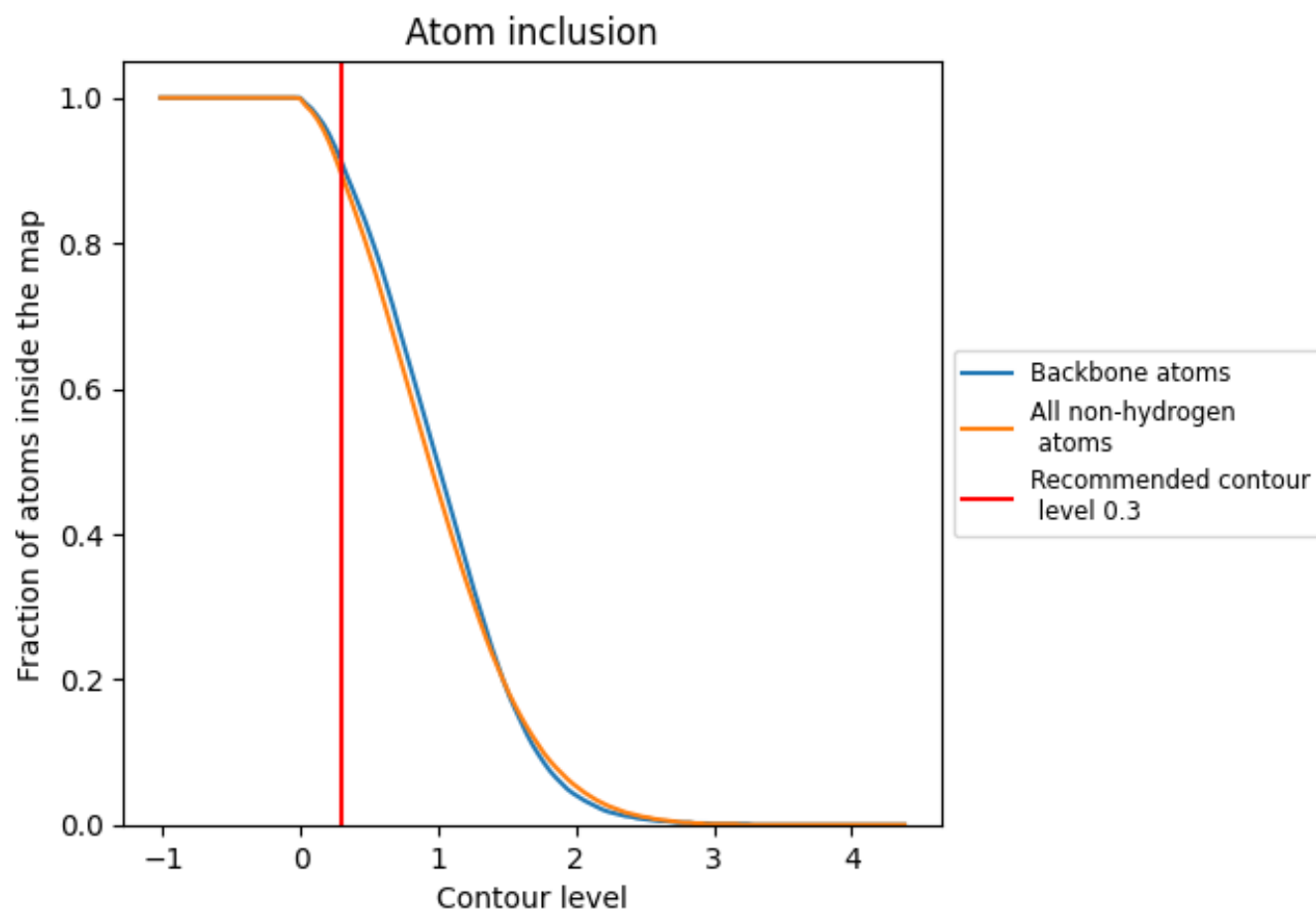
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8940	 0.4470
2	 0.9700	 0.4490
3	 0.9880	 0.5060
4	 0.9930	 0.4820
5	 0.9790	 0.5100
6	 0.9660	 0.3900
AA	 0.8950	 0.4260
AB	 0.8510	 0.4360
AC	 0.9320	 0.4800
AD	 0.8650	 0.3930
AE	 0.9540	 0.4910
AF	 0.8550	 0.3850
AG	 0.9110	 0.3870
AH	 0.8330	 0.3740
AI	 0.9590	 0.4980
AJ	 0.9500	 0.4460
AK	 0.8970	 0.3180
AL	 0.9220	 0.5140
AM	 0.7540	 0.2070
AN	 0.9140	 0.4800
AO	 0.9180	 0.4910
AP	 0.9100	 0.3570
AQ	 0.8830	 0.3830
AR	 0.8230	 0.3630
AS	 0.9050	 0.3610
AT	 0.8810	 0.3400
AU	 0.8860	 0.3600
AV	 0.9080	 0.4500
AW	 0.9560	 0.5190
AX	 0.9700	 0.5350
AY	 0.9440	 0.4420
AZ	 0.7330	 0.3040
Aa	 0.9200	 0.4790
Ab	 0.8600	 0.4290
Ac	 0.8010	 0.4040



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Chain	Atom inclusion	Q-score
Ad	 0.9690	 0.4690
Ae	 0.8840	 0.4330
Af	 0.8220	 0.2180
Ag	 0.0700	 0.1180
BA	 0.9590	 0.5570
BB	 0.9760	 0.5300
BC	 0.9670	 0.5180
BD	 0.9160	 0.4200
BE	 0.9280	 0.4320
BF	 0.9670	 0.5180
BG	 0.8670	 0.4130
BH	 0.9420	 0.4780
BI	 0.9420	 0.4950
BJ	 0.9020	 0.4000
BK	 0.9450	 0.4840
BL	 0.9510	 0.4520
BM	 0.9730	 0.5520
BN	 0.9700	 0.5230
BO	 0.9670	 0.5300
BP	 0.9770	 0.5400
BQ	 0.9200	 0.4810
BR	 0.9530	 0.5150
BS	 0.9650	 0.5140
BT	 0.9360	 0.4360
BU	 0.9560	 0.5600
BV	 0.9420	 0.4570
BW	 0.9500	 0.4830
BX	 0.9720	 0.4800
BY	 0.9170	 0.4450
BZ	 0.9530	 0.5280
Ba	 0.9490	 0.5030
Bb	 0.9350	 0.4890
Bc	 0.9540	 0.5040
Bd	 0.9740	 0.5520
Be	 0.9610	 0.5490
Bf	 0.9170	 0.5050
Bg	 0.9510	 0.4680
Bh	 0.9010	 0.4400
Bi	 0.9950	 0.5690
Bj	 0.9160	 0.4040
Bk	 0.9830	 0.5650
Bl	 0.9510	 0.5160

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Chain	Atom inclusion	Q-score
Bm	 0.9860	 0.5870
Bn	 0.9430	 0.5110
Bo	 0.9390	 0.5410
CA	 0.3620	 0.1550
CB	 0.0060	 0.0480
CC	 0.2120	 0.1450