



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 12:17 PM UTC

PDB ID : 8BQX / pdb_00008bqx
EMDB ID : EMD-16191
Title : Yeast 80S ribosome in complex with Map1 (conformation 2)
Authors : Knorr, A.G.; Mackens-Kiani, T.; Musial, J.; Berninghausen, O.; Becker, T.;
Beatrix, B.; Beckmann, R.
Deposited on : 2022-11-21
Resolution : 3.80 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

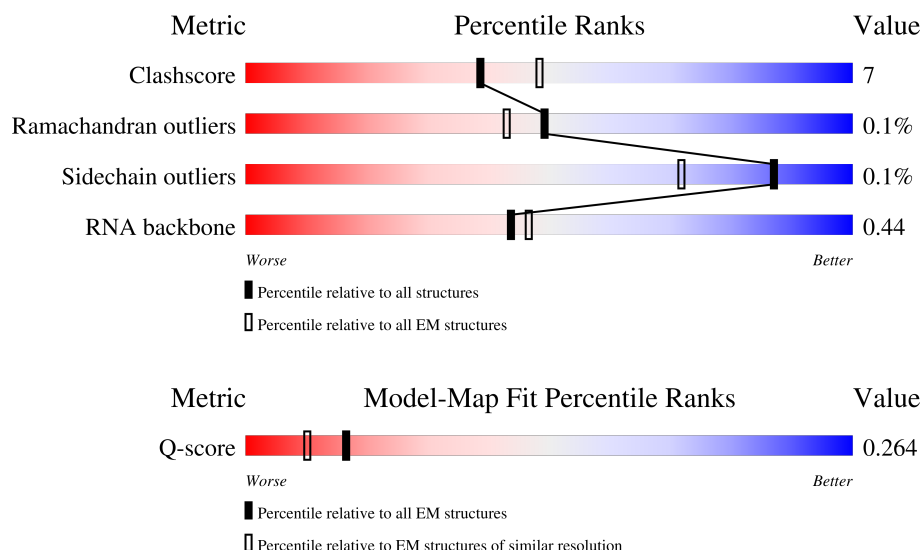
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 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	10198 (3.30 - 4.30)

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	x	387	94% 87% 7% 5%
2	A	222	49% 81% 19%
3	B	206	58% 72% 28%

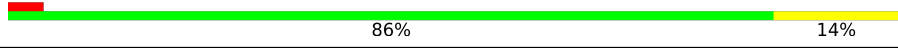
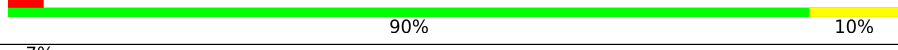
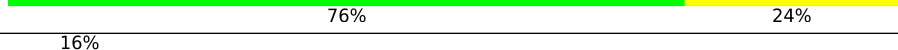
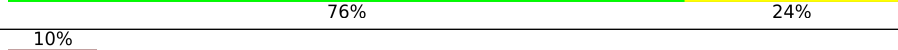
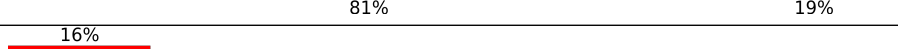
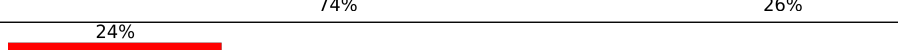
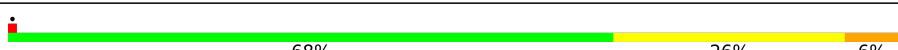
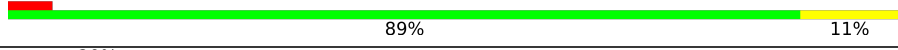
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Mol	Chain	Length	Quality of chain
4	C	92	
5	D	121	
6	E	142	
7	F	141	
8	G	125	
9	H	145	
10	I	143	
11	J	100	
12	K	82	
13	L	63	
14	M	53	
15	N	73	
16	O	312	
17	P	206	
18	Q	232	
19	R	216	
20	S	258	
21	T	228	
22	U	184	
23	V	198	
24	W	184	
25	X	142	
26	Y	150	
27	Z	127	
28	AA	233	

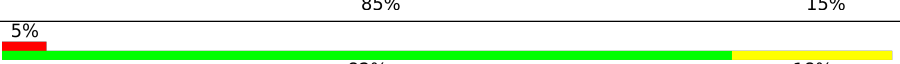
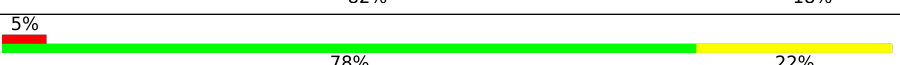
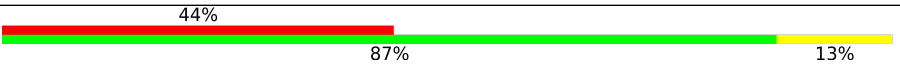
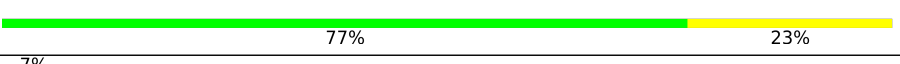
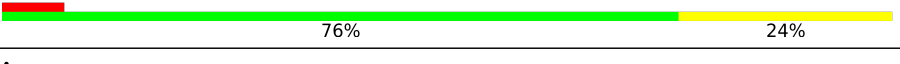
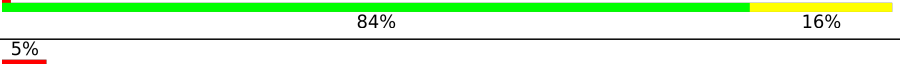
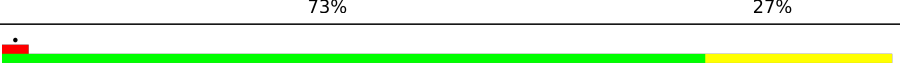
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Mol	Chain	Length	Quality of chain
29	BA	386	
30	AB	136	
31	BB	185	
32	AC	99	
33	BC	109	
34	2	1798	
35	a	87	
36	b	129	
37	c	144	
38	d	134	
39	e	97	
40	f	81	
41	g	60	
42	BQ	3301	
43	BR	121	
44	BS	158	
45	AW	251	
46	BE	361	
47	BI	294	
48	BM	175	
49	BO	222	
50	AD	191	
51	BD	218	
52	AG	169	
53	AJ	193	

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Mol	Chain	Length	Quality of chain
54	AM	136	
55	AQ	203	
56	AU	197	
57	AX	183	
58	BF	188	
59	BH	171	
60	BJ	159	
61	BL	100	
62	AE	126	
63	AH	121	
64	AK	125	
65	AN	135	
66	AR	148	
67	AV	58	
68	AY	96	
69	BG	127	
70	BK	106	
71	BN	112	
72	BP	119	
73	AF	81	
74	AI	77	
75	AL	50	
76	AO	52	
77	AS	25	
78	AP	103	

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Mol	Chain	Length	Quality of chain
79	AT	91	82%18%
80	BT	217	92%86%8%

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 205808 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 protein called Methionine aminopeptidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	x	367	Total	C	N	O	S	0	0
			2899	1825	504	549	21		

- Molecule 2 is a protein called 40S ribosomal protein S3.

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

- Molecule 3 is a protein called 40S ribosomal protein S5.

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

- Molecule 4 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 5 is a protein called 40S ribosomal protein S12.

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

- Molecule 6 is a protein called 40S ribosomal protein S15.

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

- Molecule 7 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S17-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 10 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S20.

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

- Molecule 12 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 14 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S31.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	97	ALA	LYS	conflict	UNP P05759

- Molecule 16 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 17 is a protein called 40S ribosomal protein S0-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 19 is a protein called 40S ribosomal protein S2.

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

- Molecule 20 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 22 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S8-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S13.

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

- Molecule 27 is a protein called 40S ribosomal protein S14-B.

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

- Molecule 28 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 29 is a protein called 60S ribosomal protein L3.

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

- Molecule 30 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 31 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 32 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 33 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 34 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	2	1771	Total	C	N	O	P	0	0
			37739	16872	6683	12413	1771		

- Molecule 35 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 36 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 37 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 38 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
38	d	134	Total	C	N	O	0	0
			1032	651	195	186		

- Molecule 39 is a protein called 40S ribosomal protein S26-B.

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

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

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

- Molecule 41 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 42 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BQ	3301	Total	C	N	O	P	0	0
			70586	31525	12690	23070	3301		

- Molecule 43 is a RNA chain called 5S rRNA.

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

- Molecule 44 is a RNA chain called 5.8S rRNA.

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

- Molecule 45 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L5.

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

- Molecule 48 is a protein called 60S ribosomal protein L6-B.

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

- Molecule 49 is a protein called 60S ribosomal protein L7-A.

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

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

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

- Molecule 51 is a protein called RPL10 isoform 1.

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

- Molecule 52 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	AG	169	Total	C	N	O	S		
			1346	843	252	247	4	0	0

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

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

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

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

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

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

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

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

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

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

- Molecule 58 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L20-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 62 is a protein called 60S ribosomal protein L24-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L25.

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

- Molecule 64 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 65 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 66 is a protein called 60S ribosomal protein L28.

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

- Molecule 67 is a protein called 60S ribosomal protein L29.

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

- Molecule 68 is a protein called 60S ribosomal protein L30.

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

- Molecule 69 is a protein called RPL32 isoform 1.

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

- Molecule 70 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L35-A.

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

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

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

- Molecule 74 is a protein called RPL38 isoform 1.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
75	AL	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	AO	52	Total	C	N	O	S	0	0
			410	254	86	65	5		

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	AS	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	AP	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	AT	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 80 is a protein called 60S ribosomal protein L1-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
80	BT	210	Total	C	N	O	0	0
			1041	621	210	210		

- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	M	1	Total	Zn	0
			1	1	
81	N	1	Total	Zn	0
			1	1	
81	BN	1	Total	Zn	0
			1	1	
81	AF	1	Total	Zn	0
			1	1	
81	AO	1	Total	Zn	0
			1	1	
81	AP	1	Total	Zn	0
			1	1	

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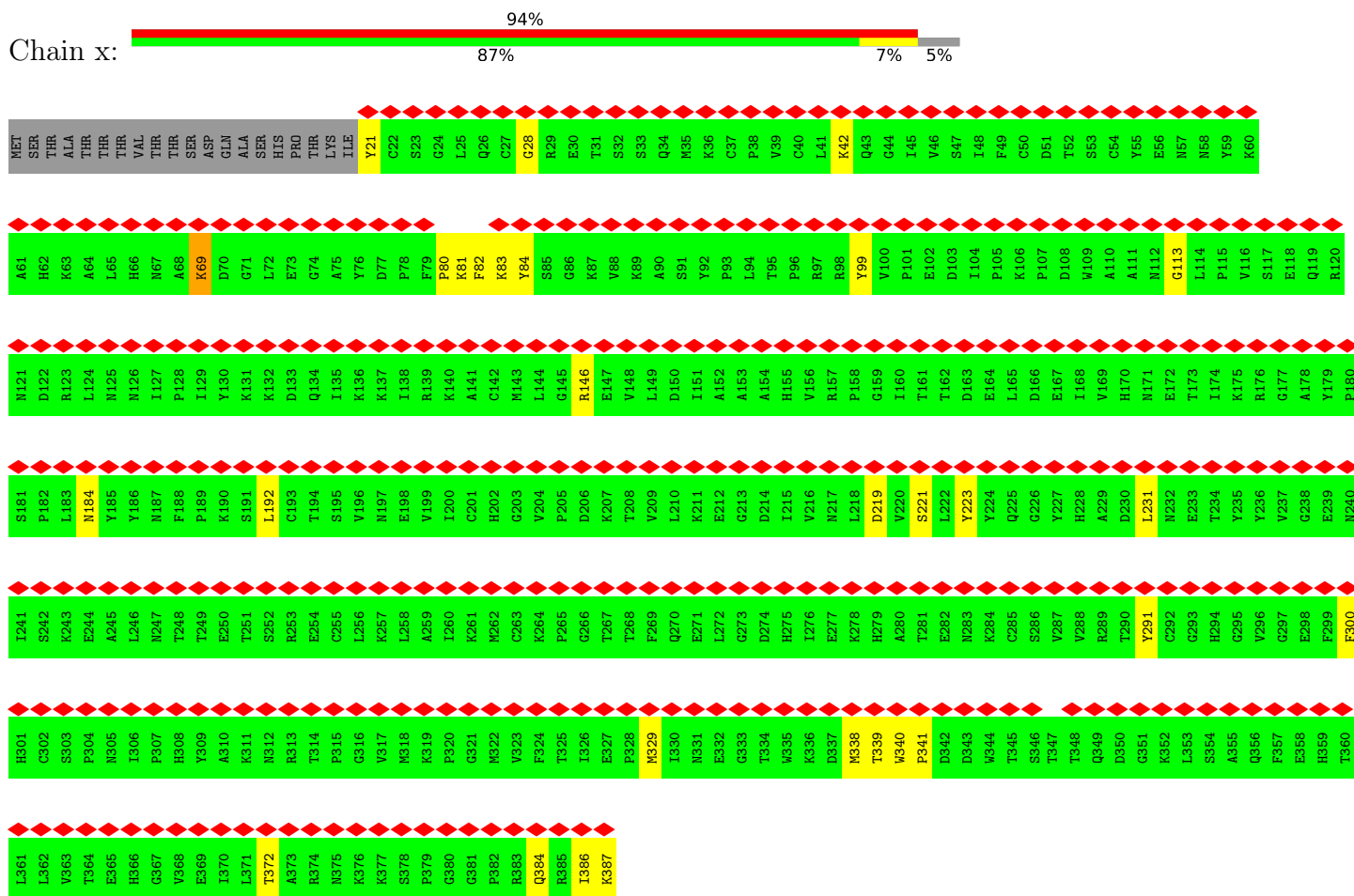
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
81	AT	1	1	1	0

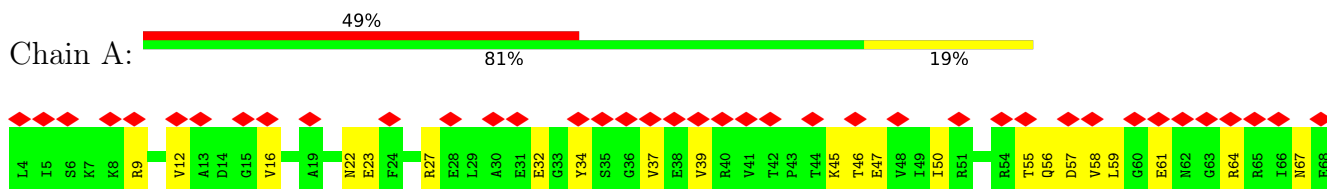
3 Residue-property plots

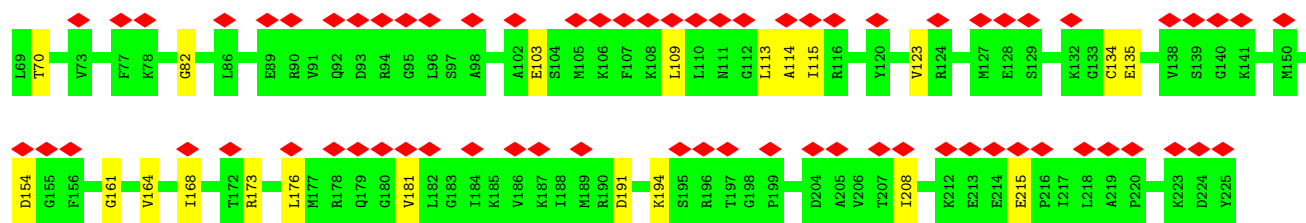
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Methionine aminopeptidase 1

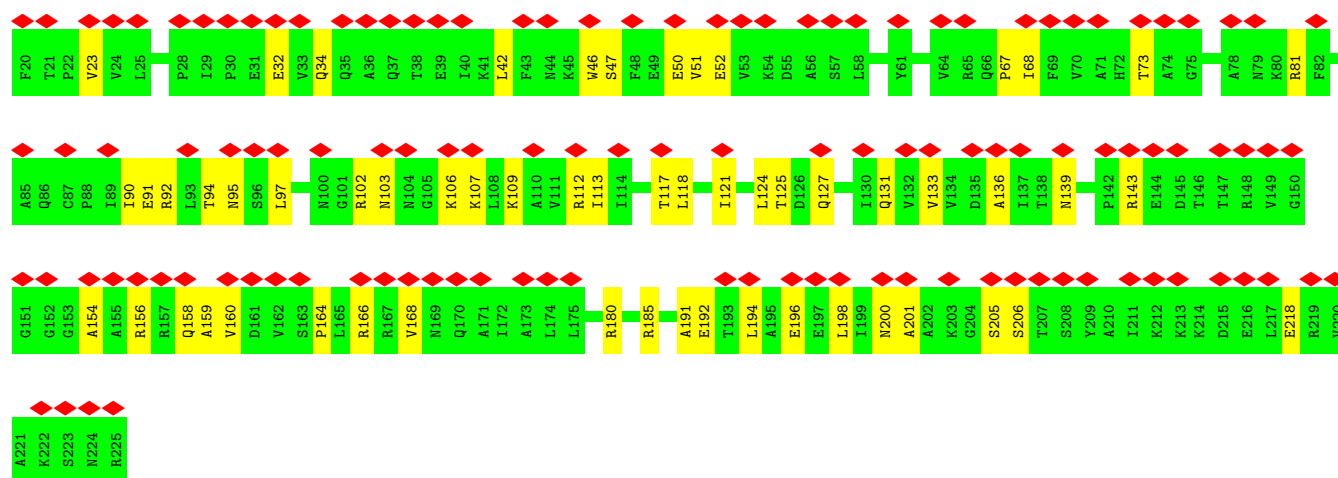
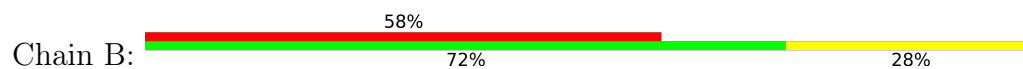


• Molecule 2: 40S ribosomal protein S3

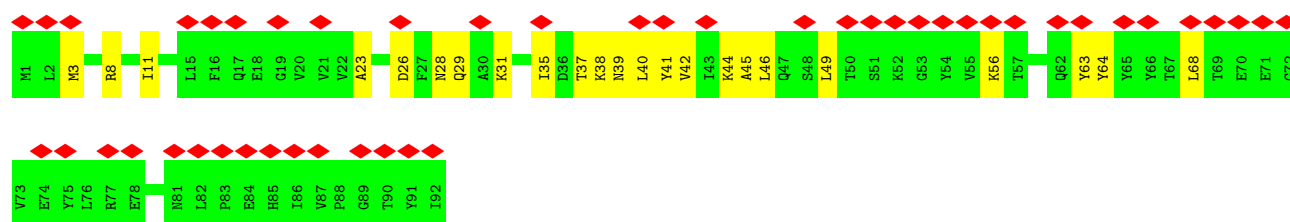




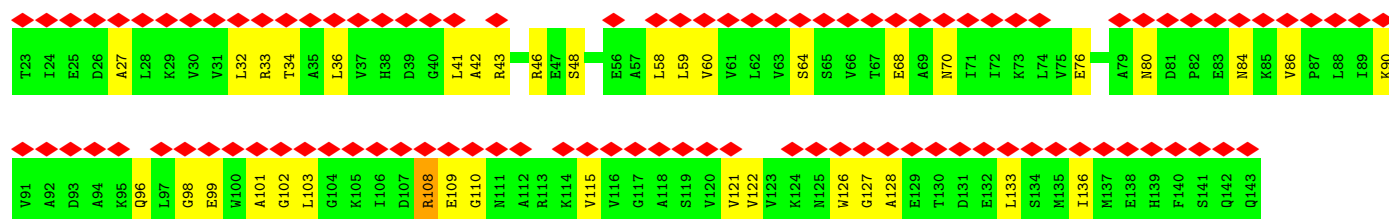
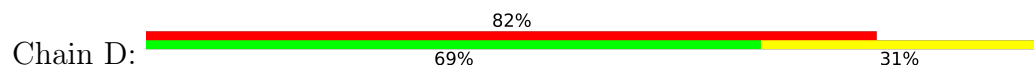
• Molecule 3: 40S ribosomal protein S5



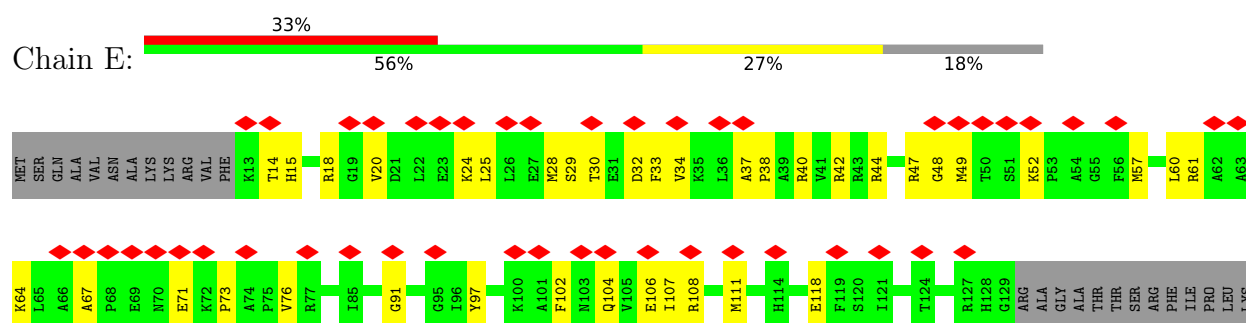
• Molecule 4: 40S ribosomal protein S10-A



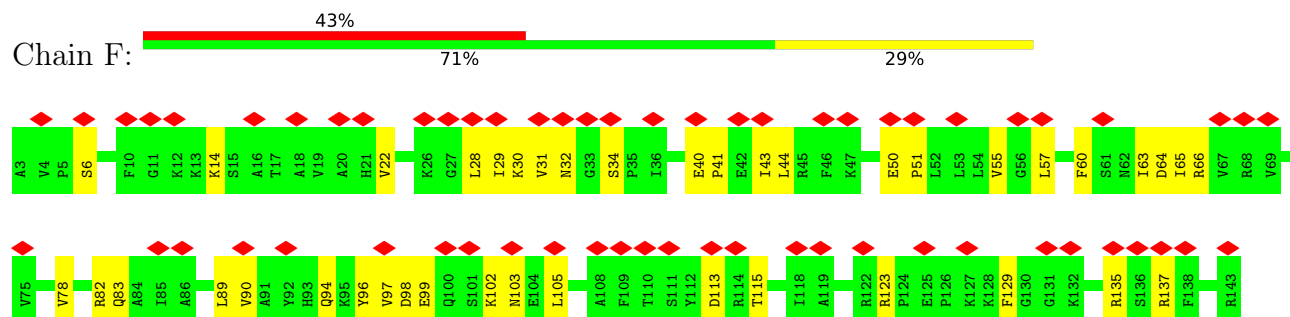
• Molecule 5: 40S ribosomal protein S12



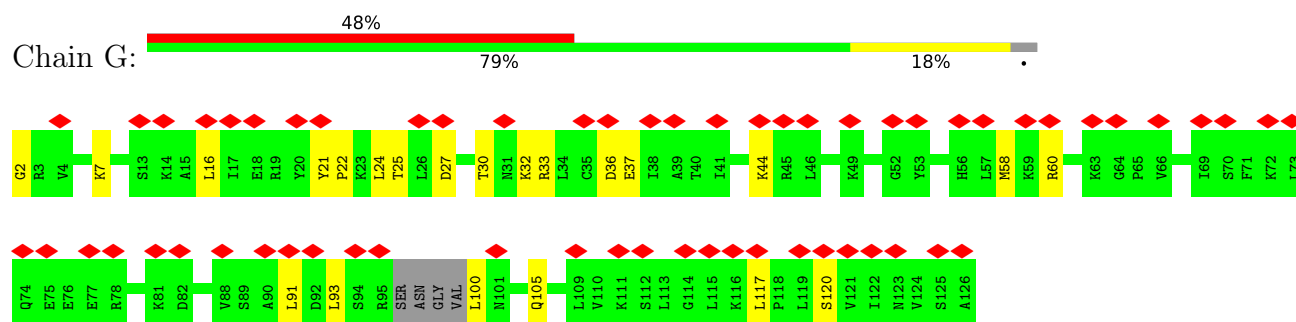
• Molecule 6: 40S ribosomal protein S15



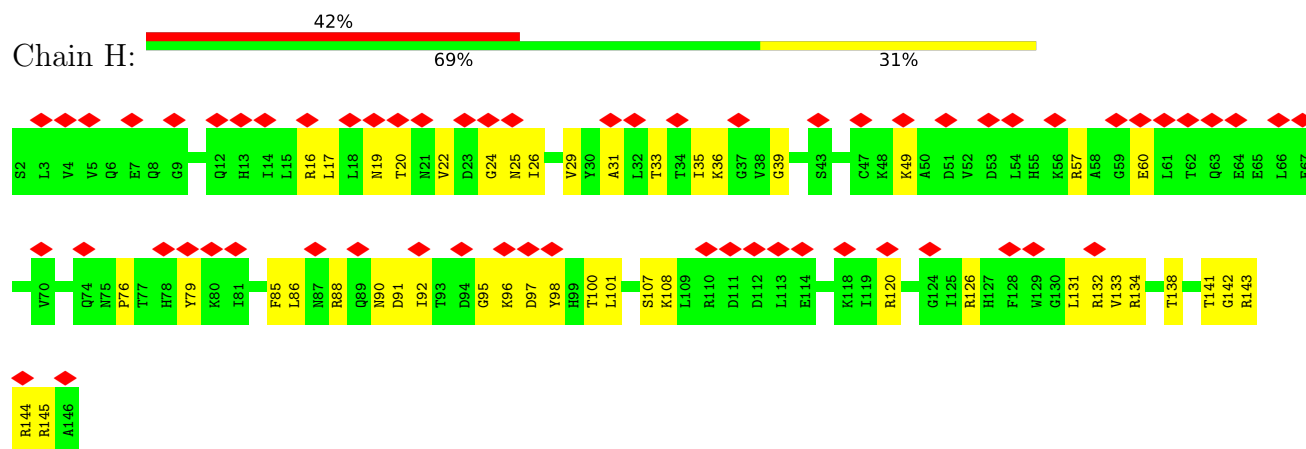
• Molecule 7: 40S ribosomal protein S16-A



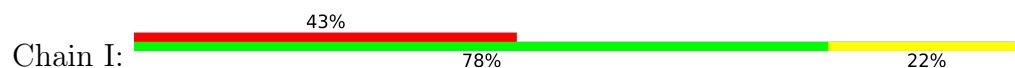
• Molecule 8: 40S ribosomal protein S17-A

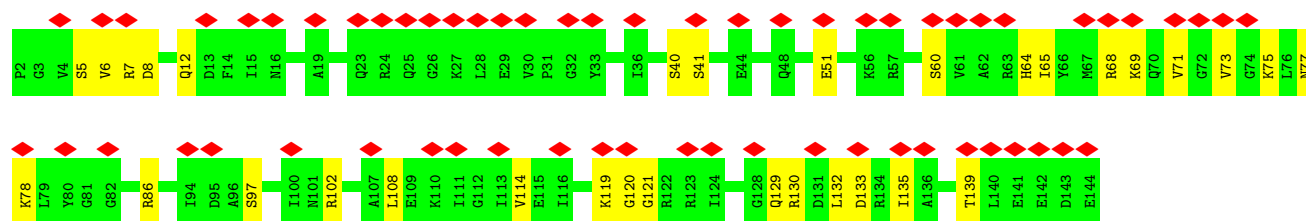


• Molecule 9: 40S ribosomal protein S18-A

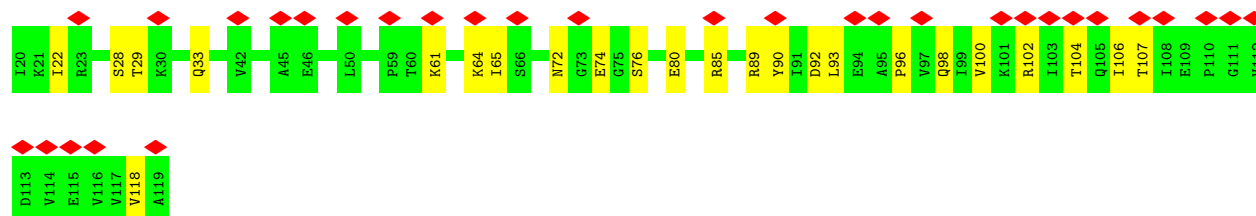
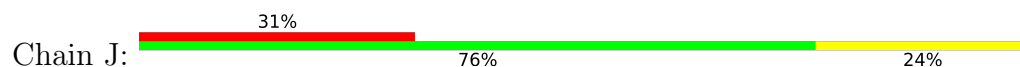


• Molecule 10: 40S ribosomal protein S19-A

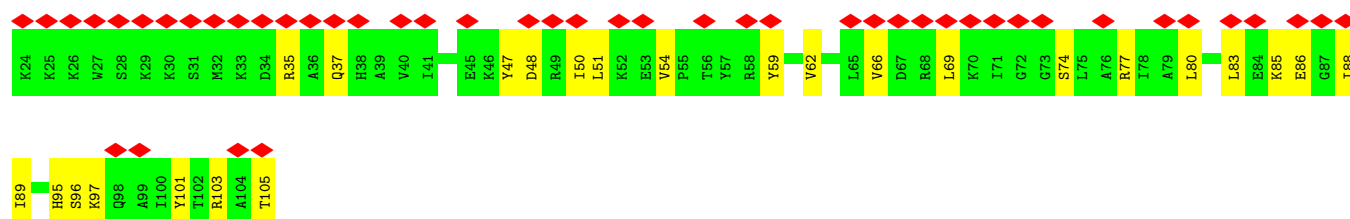




- Molecule 11: 40S ribosomal protein S20



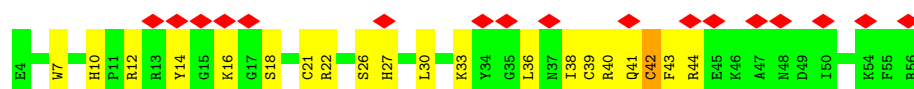
- Molecule 12: 40S ribosomal protein S25-A



- Molecule 13: 40S ribosomal protein S28-A

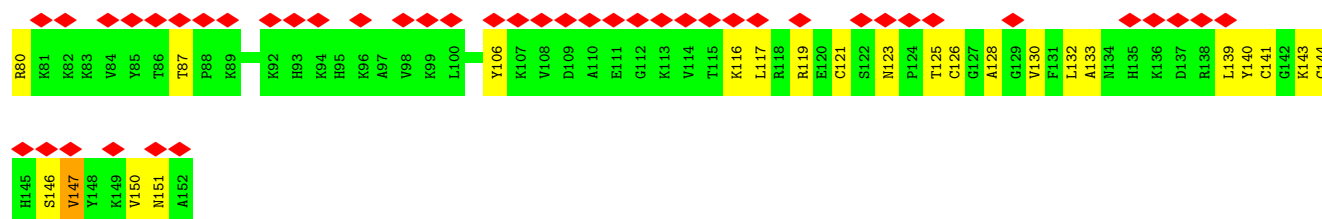


- Molecule 14: 40S ribosomal protein S29-A

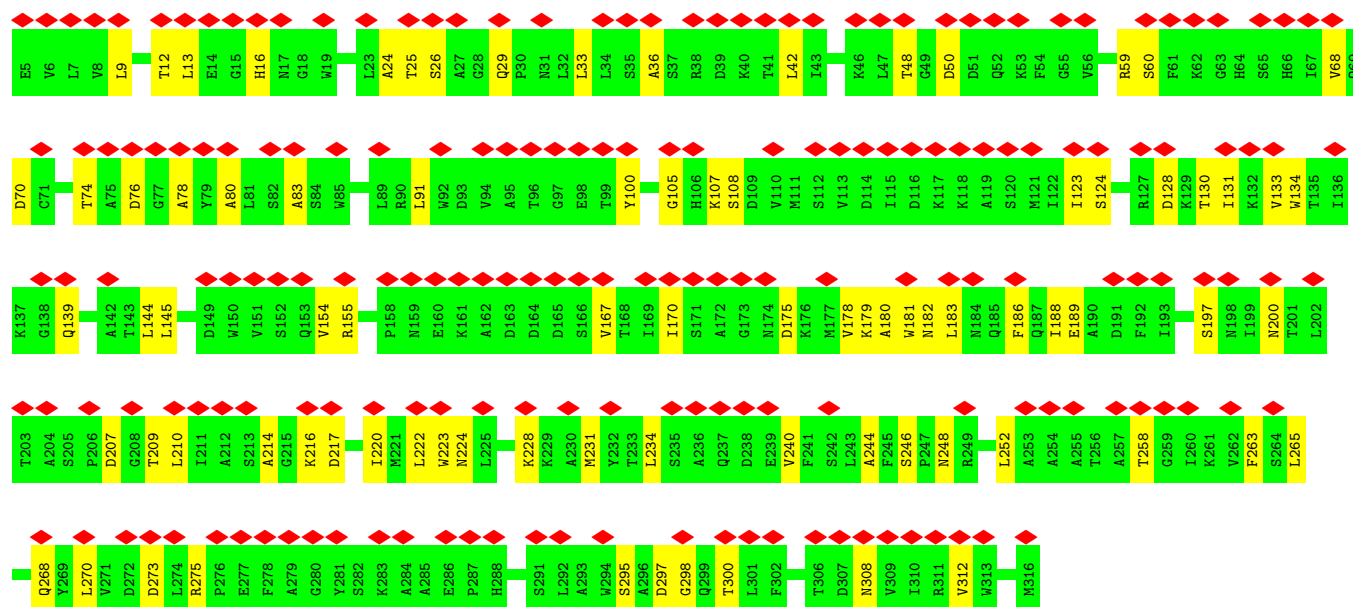
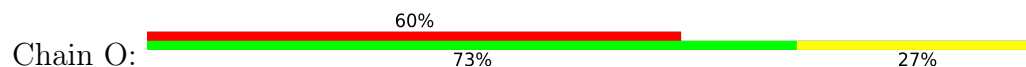


- Molecule 15: 40S ribosomal protein S31

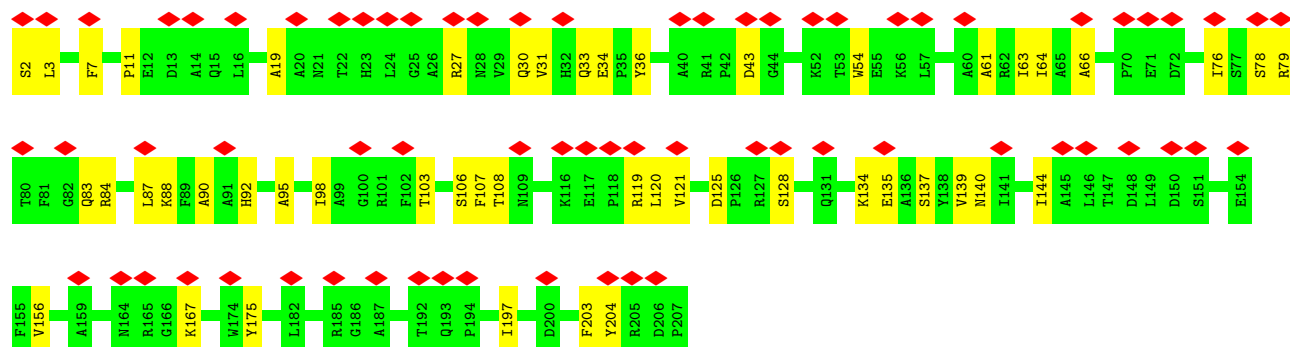
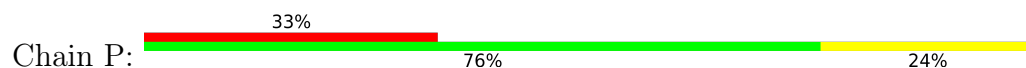




• Molecule 16: Guanine nucleotide-binding protein subunit beta-like protein

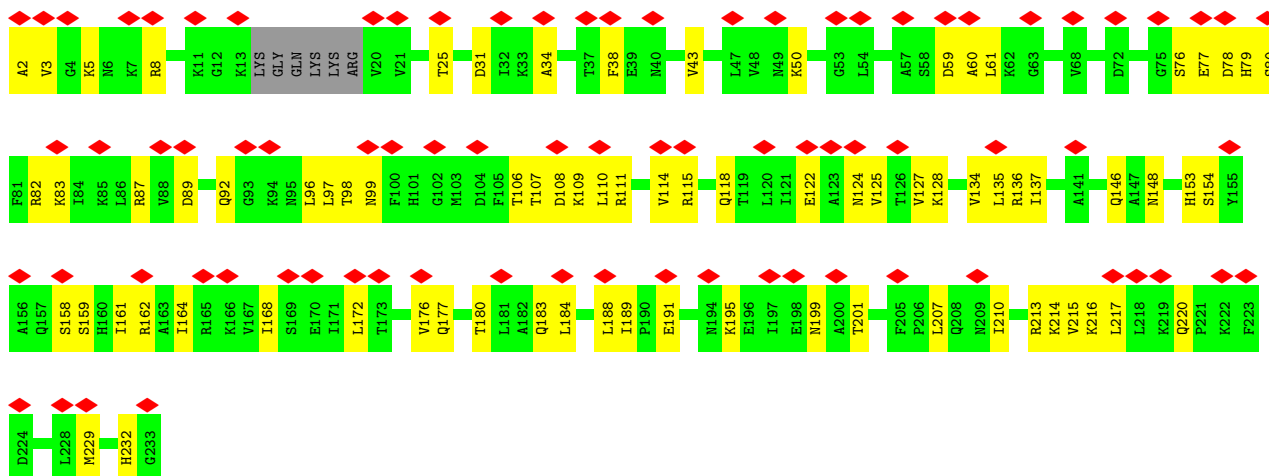


• Molecule 17: 40S ribosomal protein S0-A

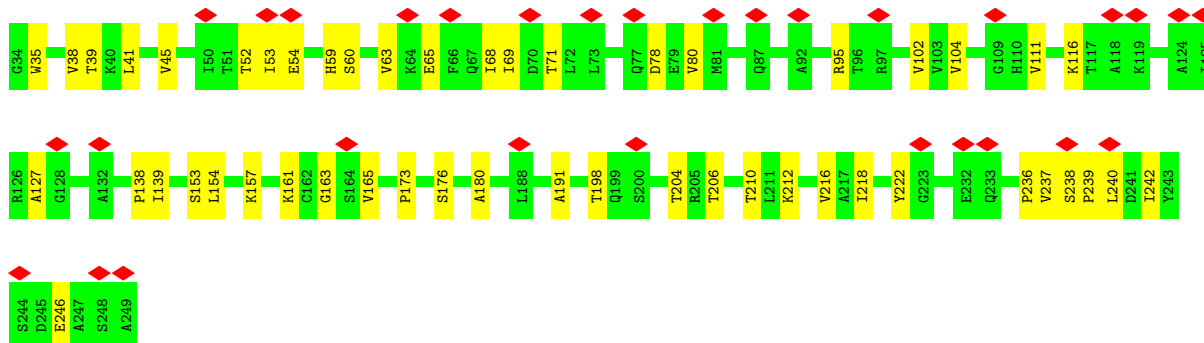
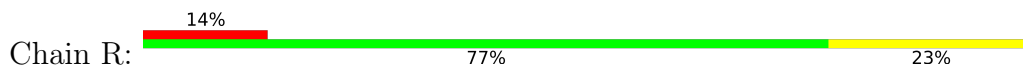


• Molecule 18: 40S ribosomal protein S1-A

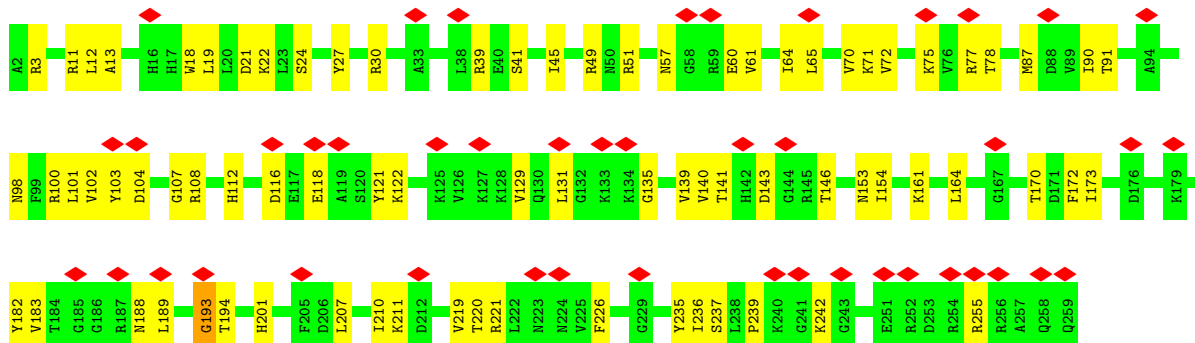




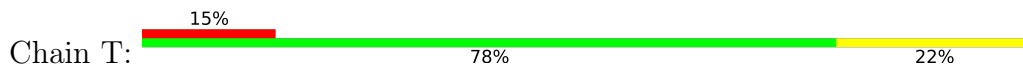
- Molecule 19: 40S ribosomal protein S2

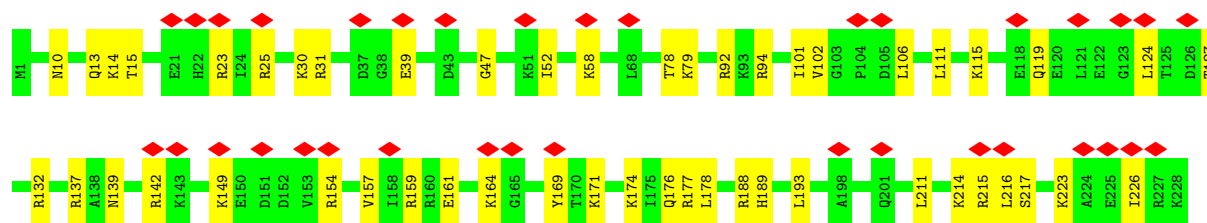


- Molecule 20: 40S ribosomal protein S4-A

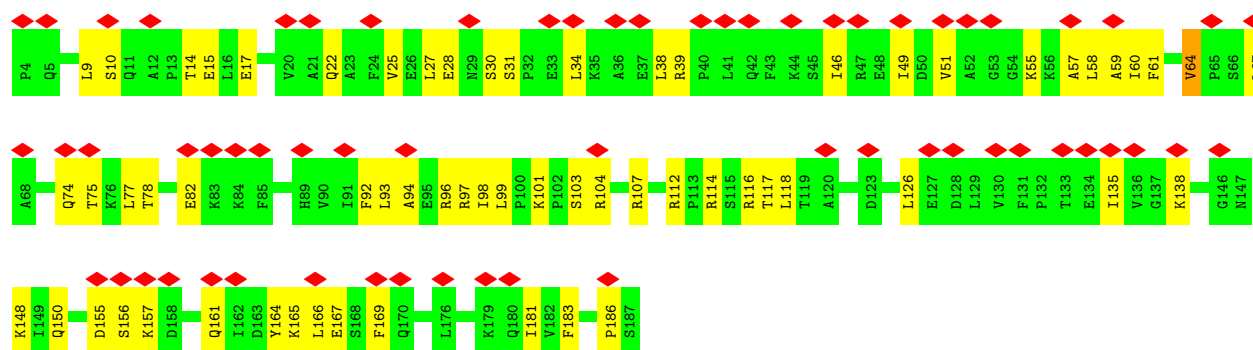


- Molecule 21: 40S ribosomal protein S6-A

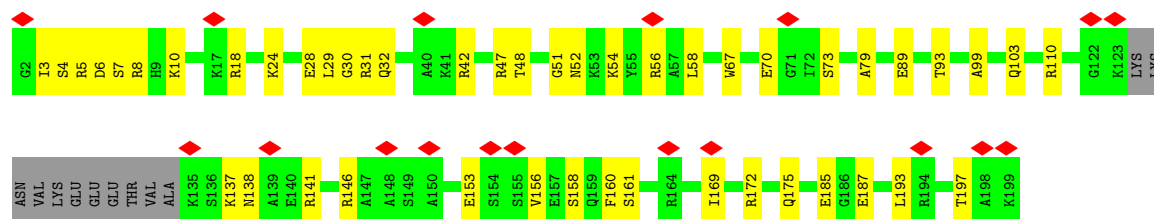




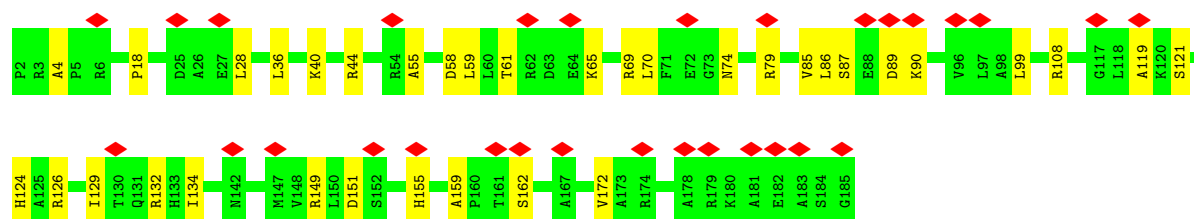
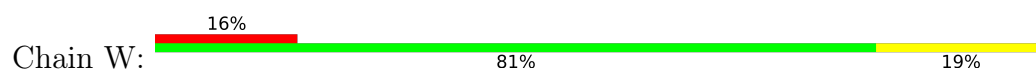
• Molecule 22: 40S ribosomal protein S7-A



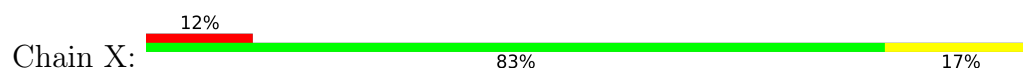
• Molecule 23: 40S ribosomal protein S8-A

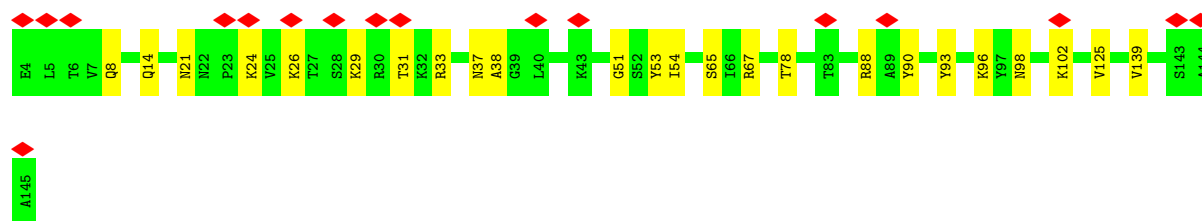


• Molecule 24: 40S ribosomal protein S9-A

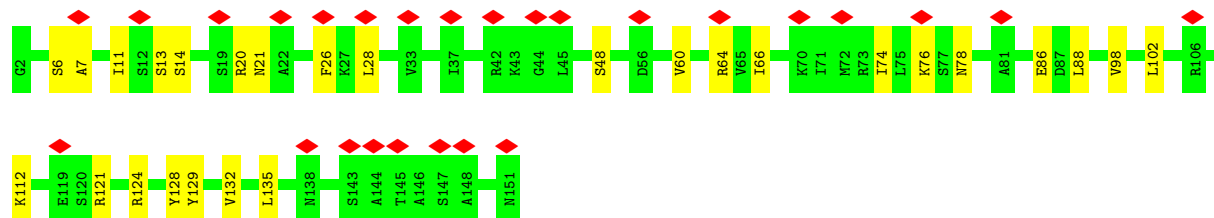
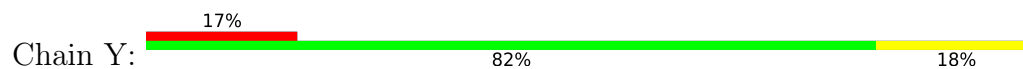


• Molecule 25: 40S ribosomal protein S11-A

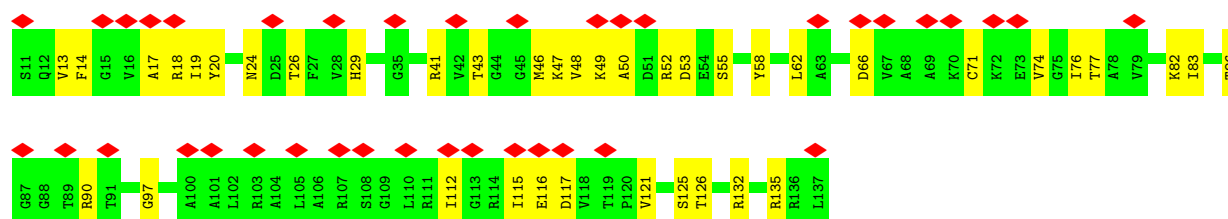




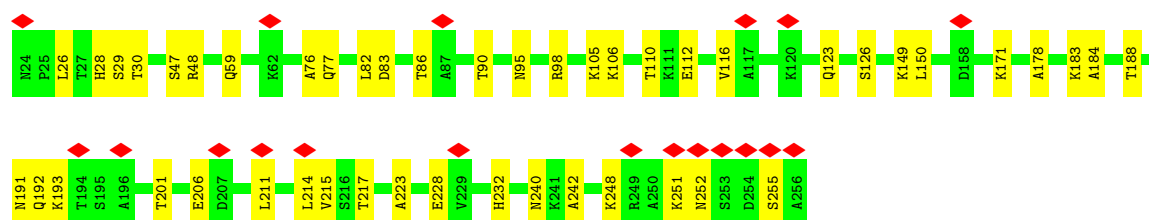
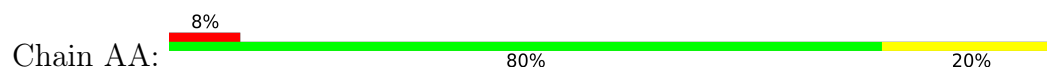
- Molecule 26: 40S ribosomal protein S13



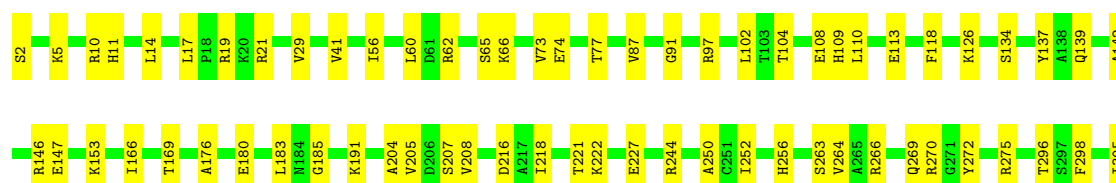
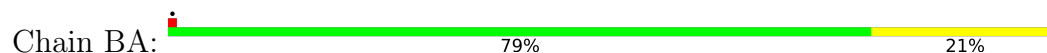
- Molecule 27: 40S ribosomal protein S14-B

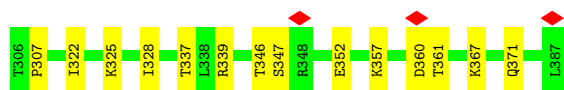


- Molecule 28: 60S ribosomal protein L8-A

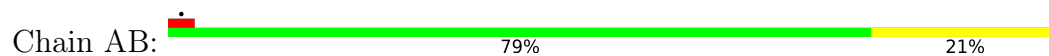


- Molecule 29: 60S ribosomal protein L3

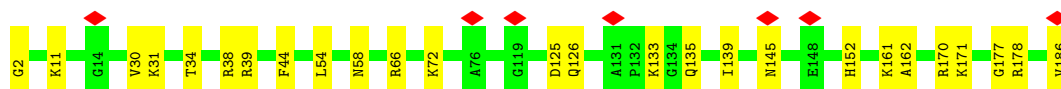




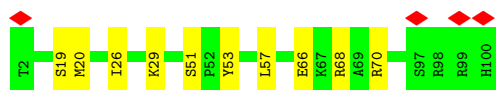
- Molecule 30: 60S ribosomal protein L23-A



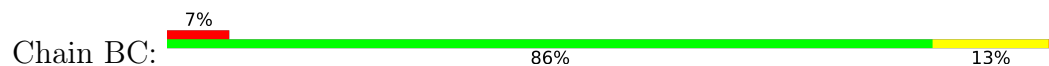
- Molecule 31: 60S ribosomal protein L18-A



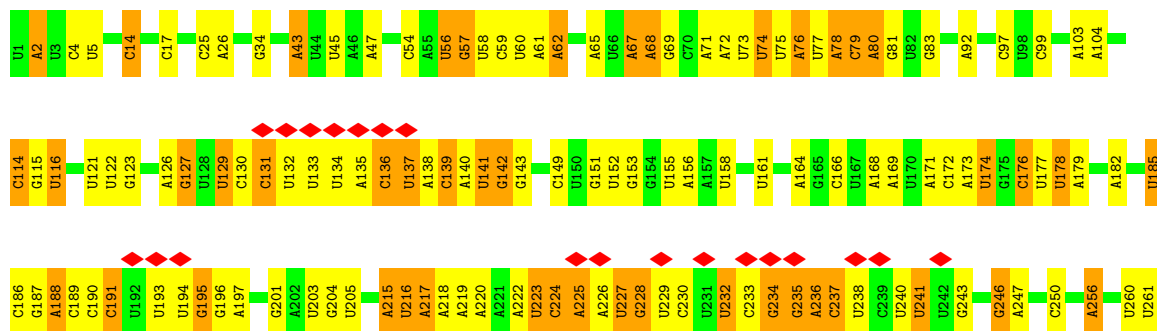
- Molecule 32: 60S ribosomal protein L36-A

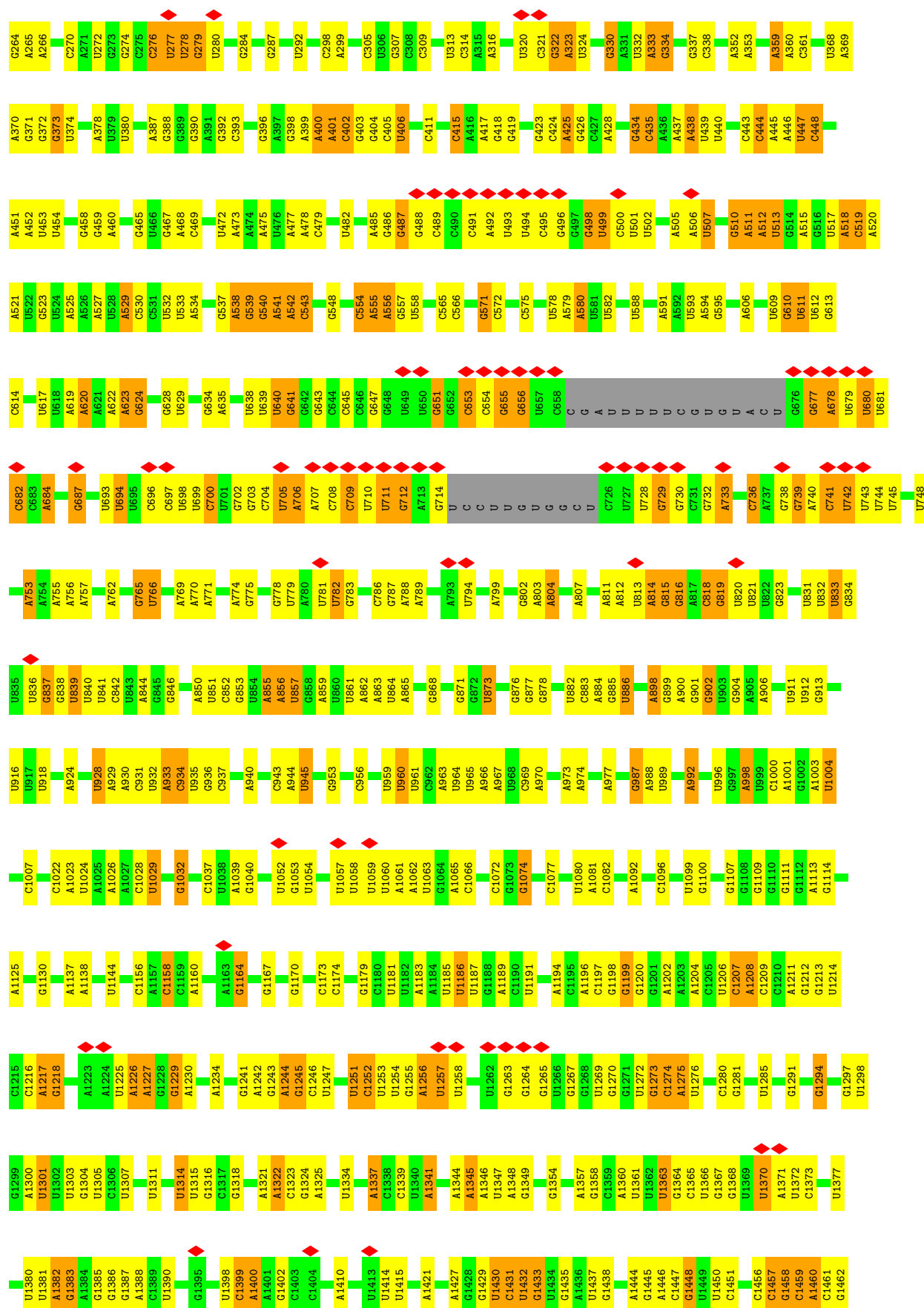


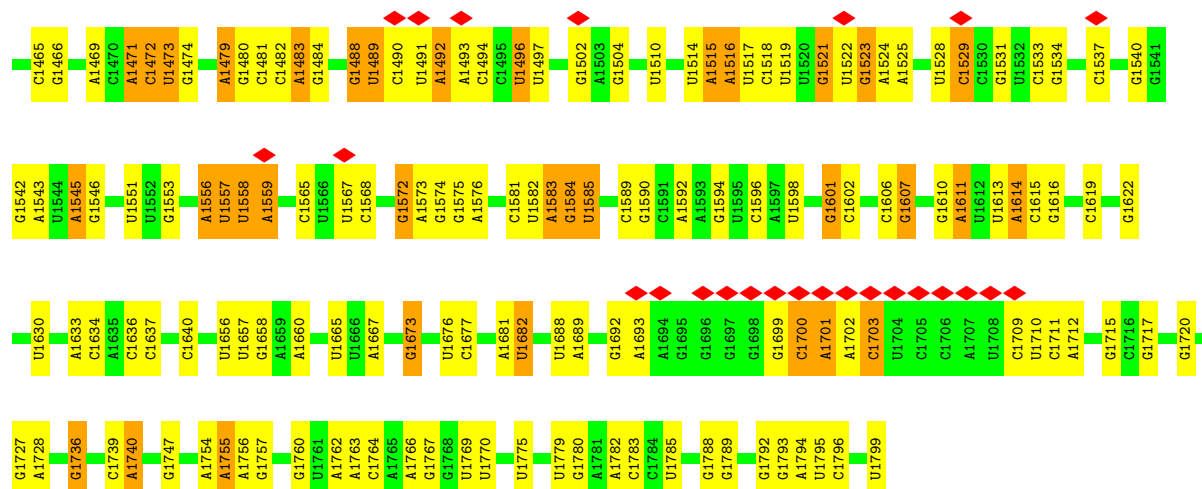
- Molecule 33: 60S ribosomal protein L31-A



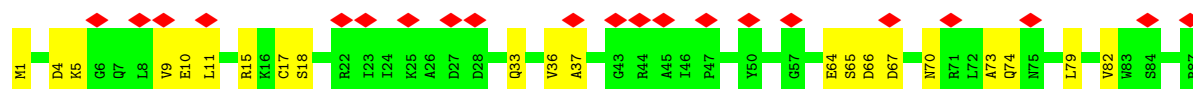
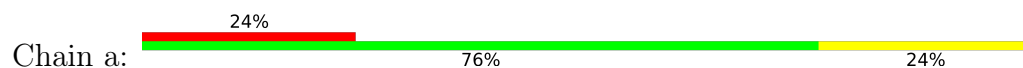
- Molecule 34: 18S rRNA



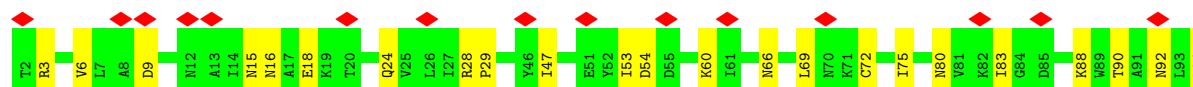
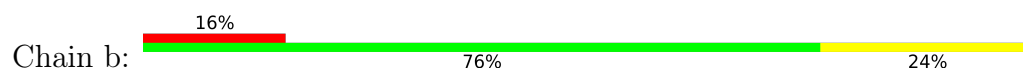




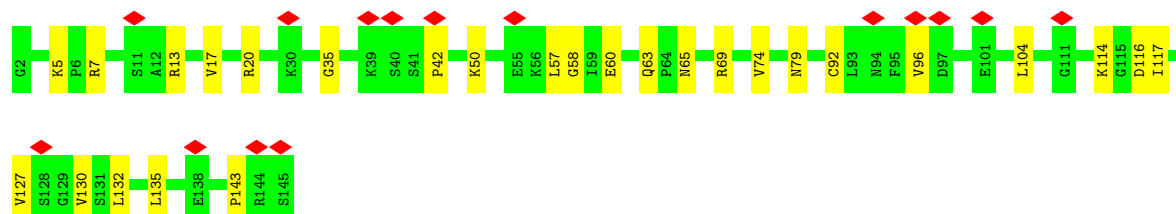
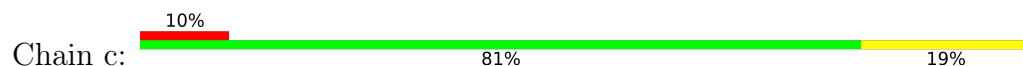
• Molecule 35: 40S ribosomal protein S21-A



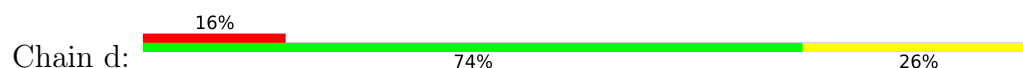
• Molecule 36: 40S ribosomal protein S22-A

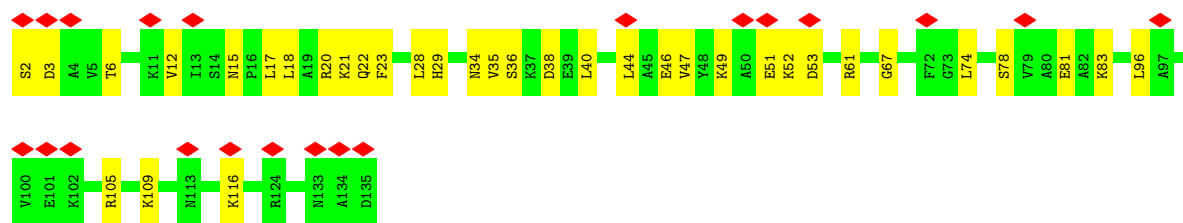


• Molecule 37: 40S ribosomal protein S23-A

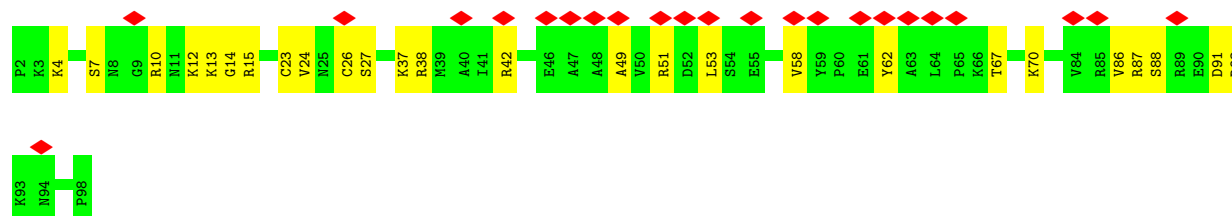
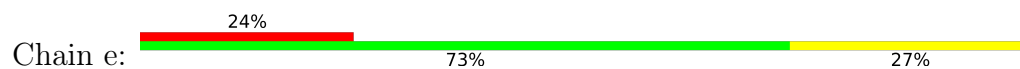


• Molecule 38: 40S ribosomal protein S24-A

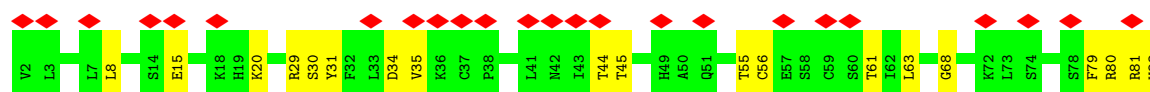
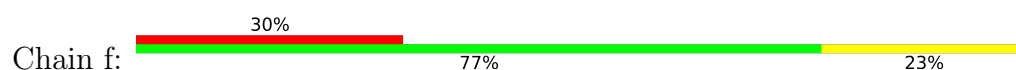




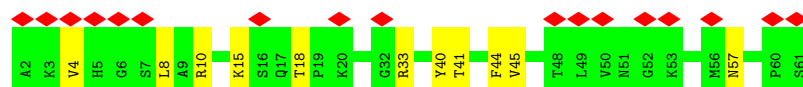
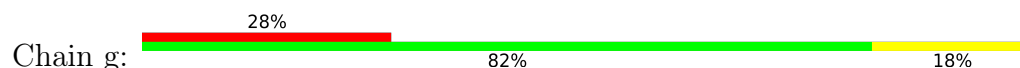
• Molecule 39: 40S ribosomal protein S26-B



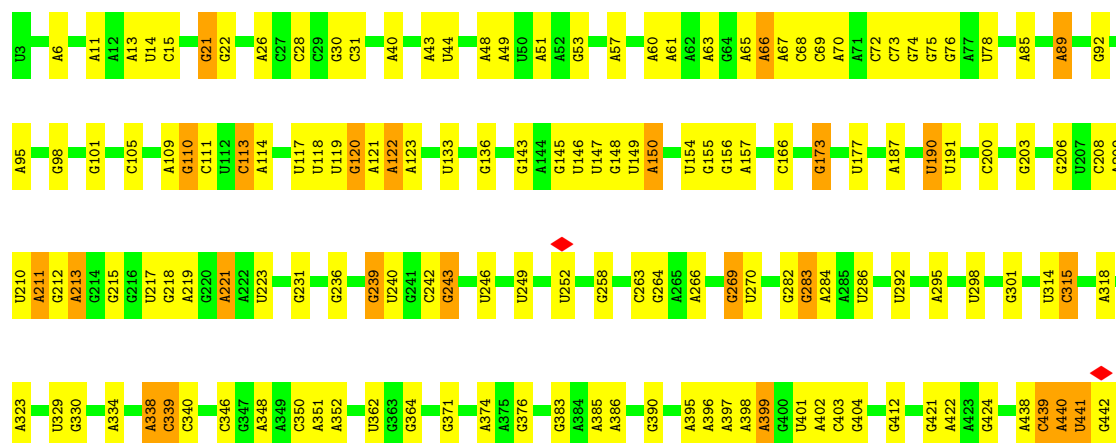
• Molecule 40: 40S ribosomal protein S27-A

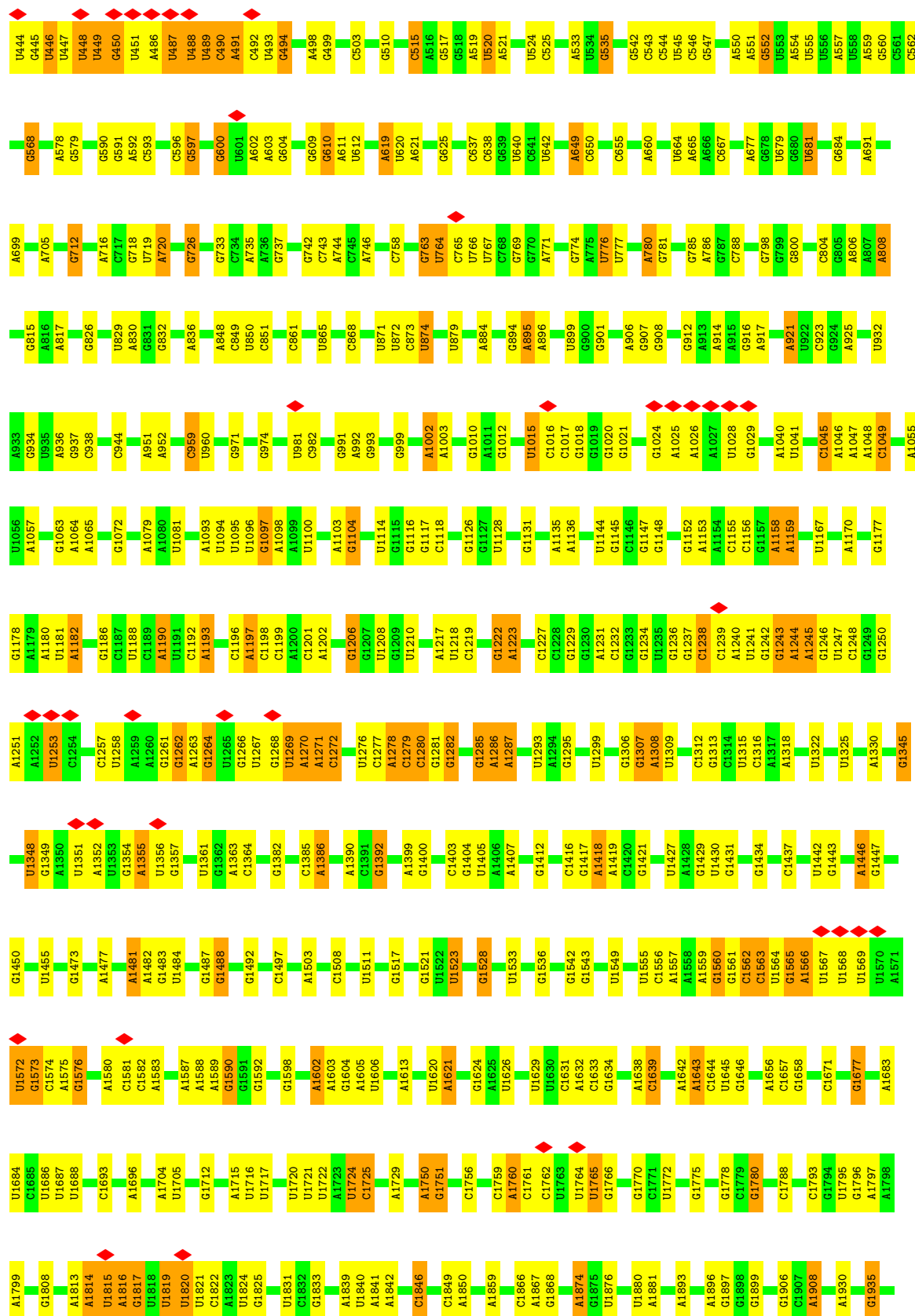


• Molecule 41: 40S ribosomal protein S30-A

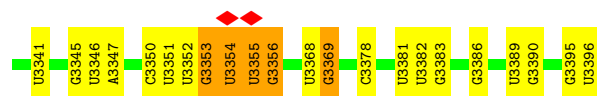


• Molecule 42: 25S rRNA



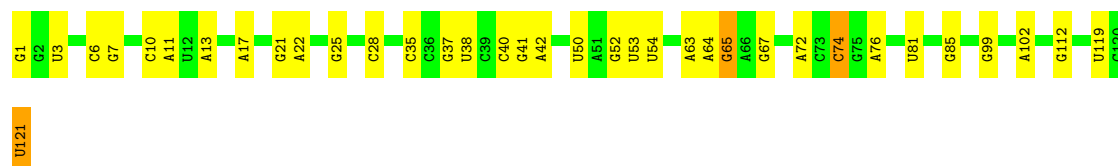






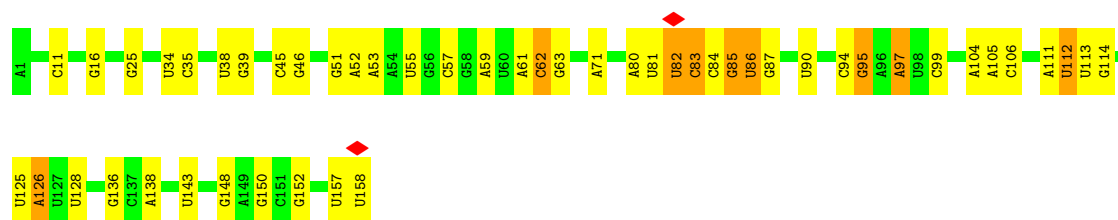
• Molecule 43: 5S rRNA

Chain BR: 70% 27%



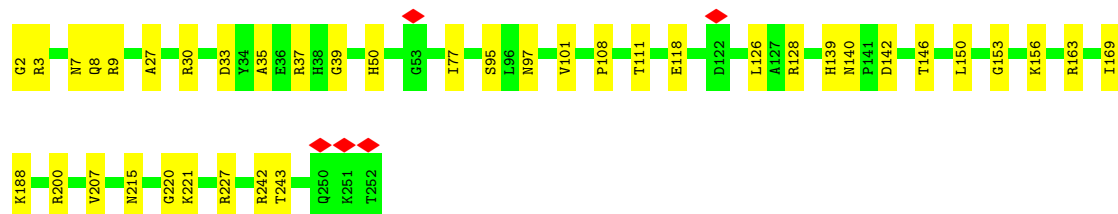
• Molecule 44: 5.8S rRNA

Chain BS: 68% 26% 6%



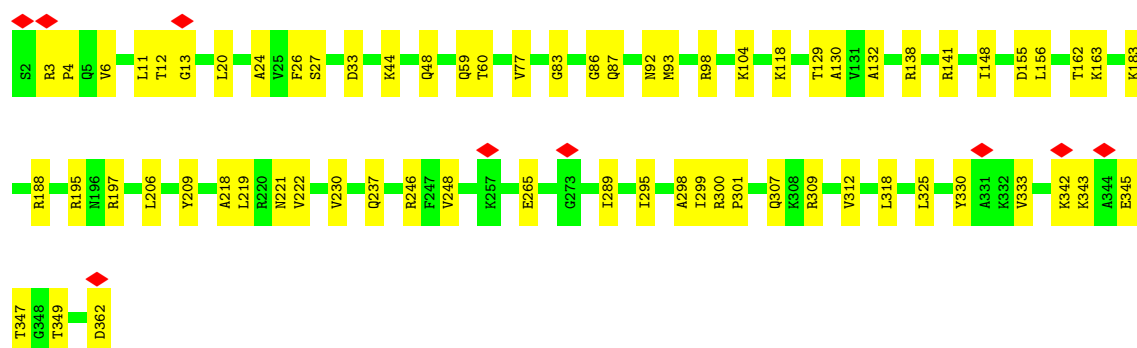
• Molecule 45: 60S ribosomal protein L2-A

Chain AW: 84% 16%



• Molecule 46: 60S ribosomal protein L4-A

Chain BE: 81% 19%



Chain BI: 9% 80% 20%

Q4 K5 D6 Y12 S13 Q17 R22 R23 T28 R33 V37 T38 Q39 R40 K41 R50 V53 R54 P55 D59 I60 I69 D72 S80 R85 Y86 R90 G91 L92 T93 N94 N95 A98 G102 A106 R107 L115 T118 Y119 K120 G121

Y122 E123 E124 G127 E128 D137 R140 L146 D147 V159 L163 K164 E177 F185 E186 T187 E188 E189 L194 S197 Y198 I199 G202 D213 D214 D215 E216 K224 D229 D230 T231 D232 A233 D234 S235 R246 K258 K259 K262 S269 K270

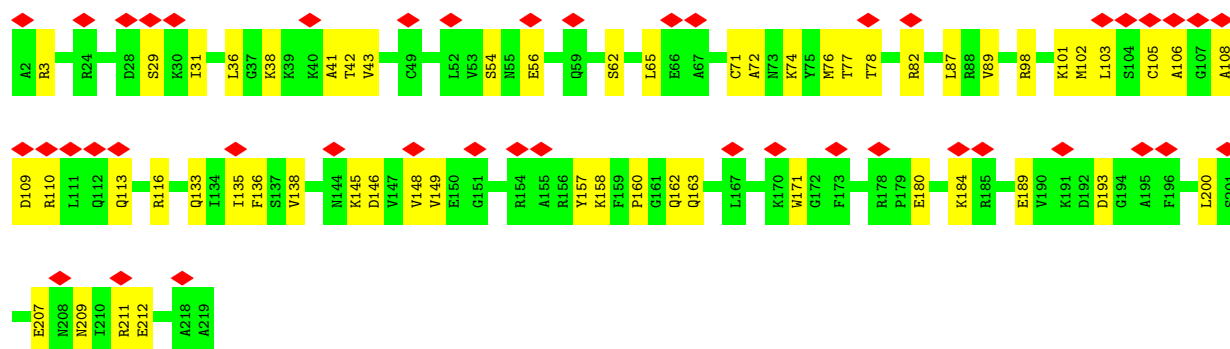
Y272 L277 R282 K289 L290 L293 A294 G295 Q296 Q297

Chain BM:

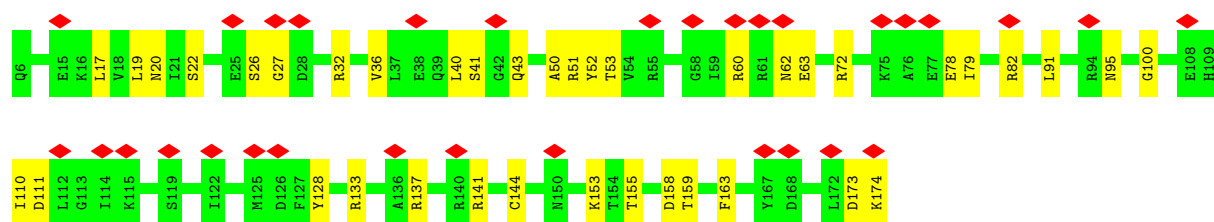
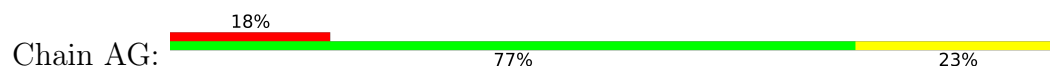
Chain BO: 5% 83% 16%

Chain AD:

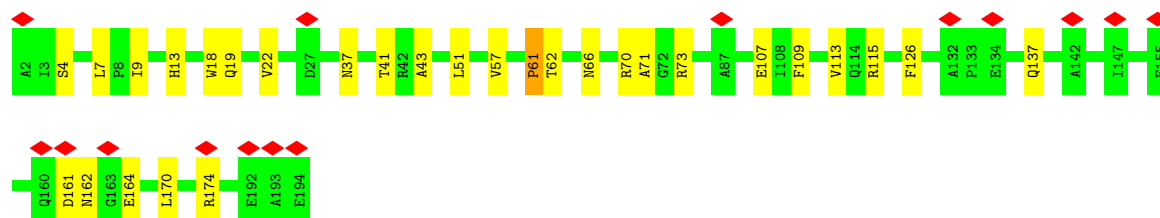
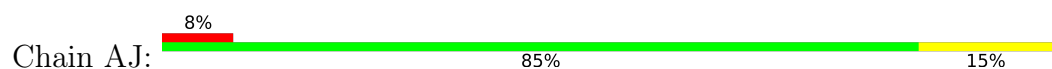
Chain BD:



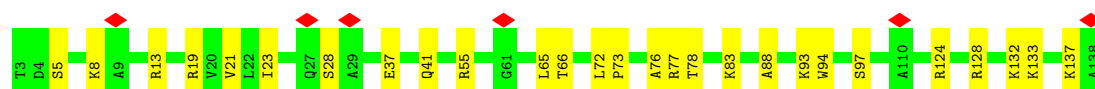
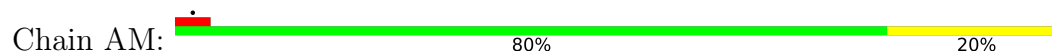
• Molecule 52: RPL11B isoform 1



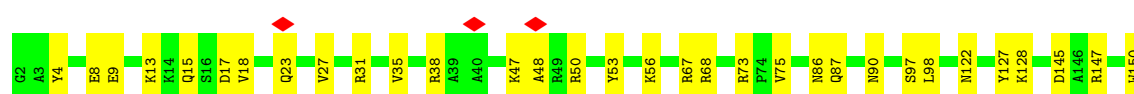
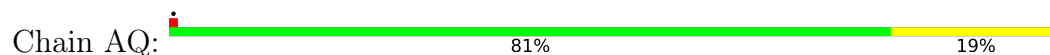
• Molecule 53: 60S ribosomal protein L13-A



• Molecule 54: 60S ribosomal protein L14-A

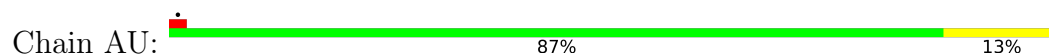


• Molecule 55: 60S ribosomal protein L15-A

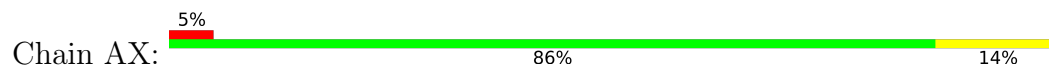




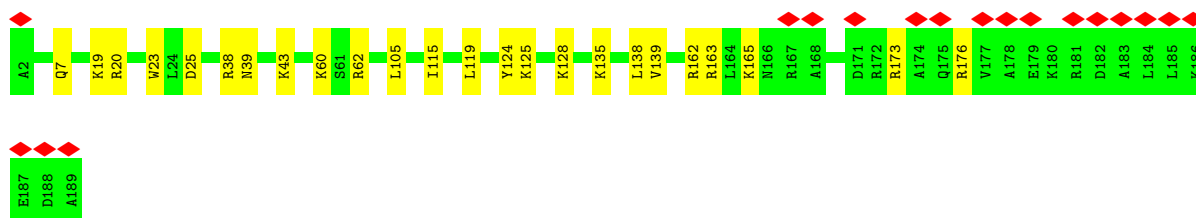
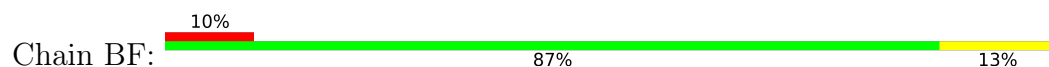
- Molecule 56: 60S ribosomal protein L16-A



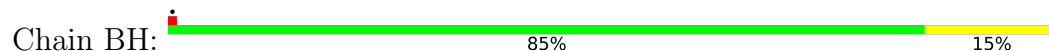
- Molecule 57: 60S ribosomal protein L17-A



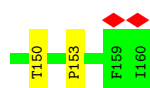
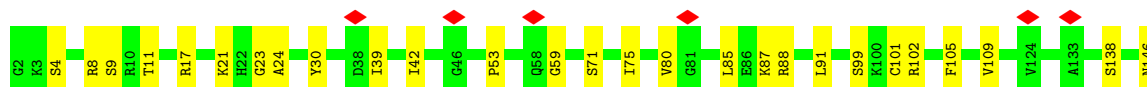
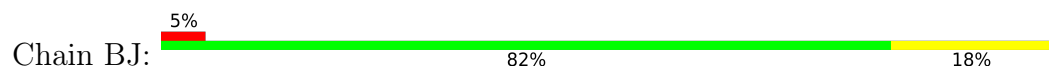
- Molecule 58: 60S ribosomal protein L19-A



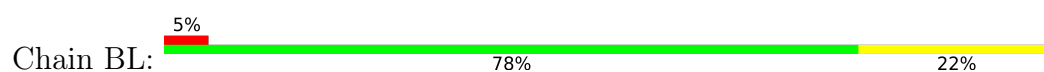
- Molecule 59: 60S ribosomal protein L20-A



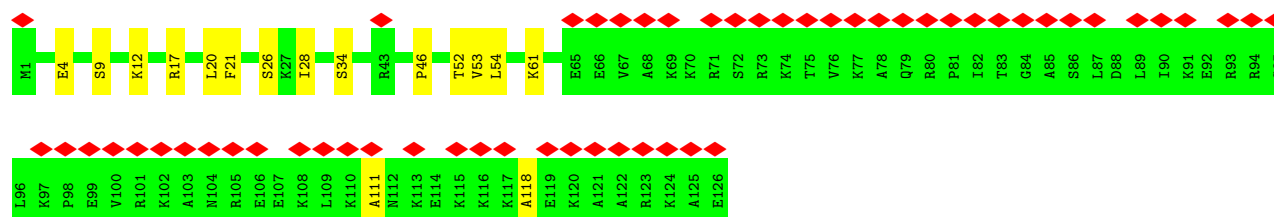
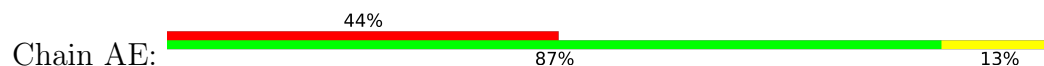
- Molecule 60: 60S ribosomal protein L21-A



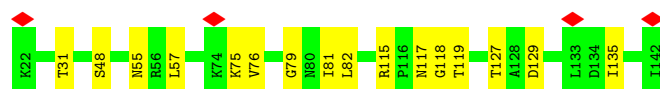
- Molecule 61: 60S ribosomal protein L22-A



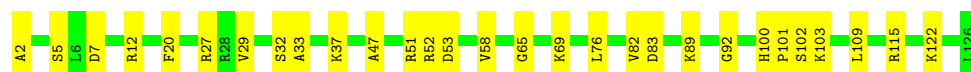
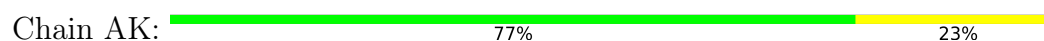
- Molecule 62: 60S ribosomal protein L24-A



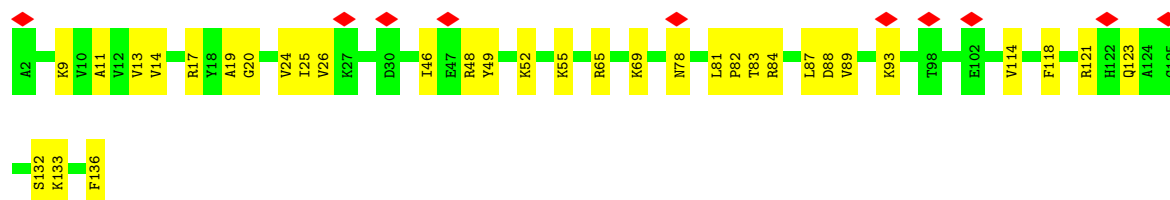
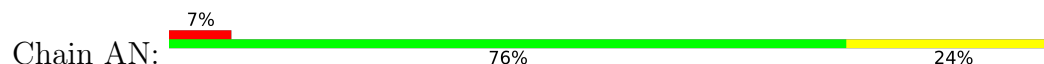
- Molecule 63: 60S ribosomal protein L25



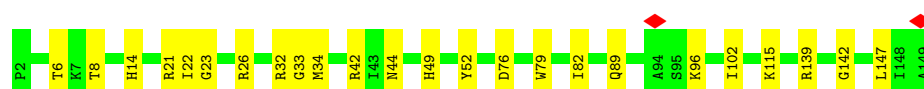
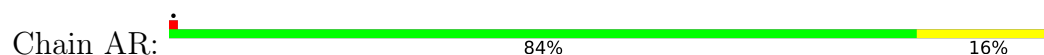
- Molecule 64: 60S ribosomal protein L26-A



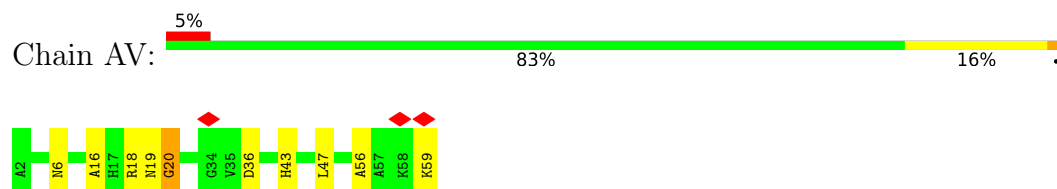
- Molecule 65: 60S ribosomal protein L27-A



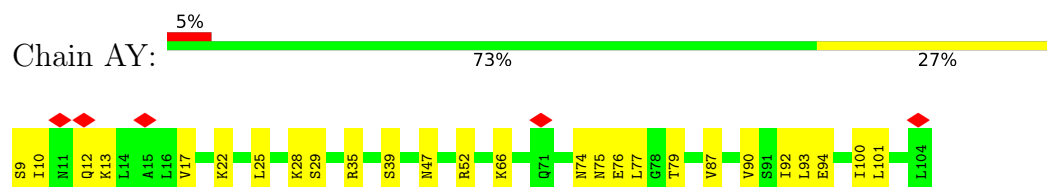
- Molecule 66: 60S ribosomal protein L28



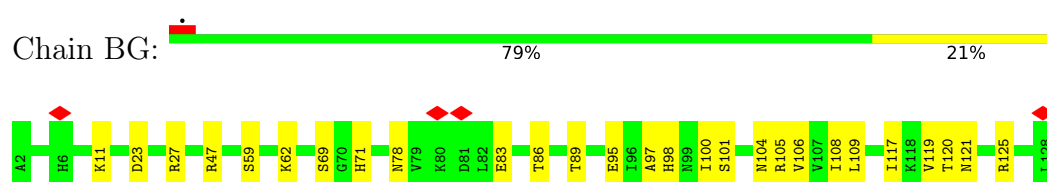
- Molecule 67: 60S ribosomal protein L29



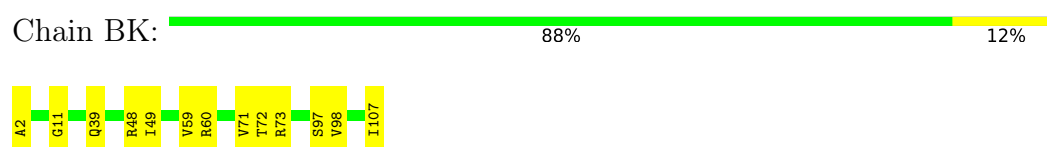
- Molecule 68: 60S ribosomal protein L30



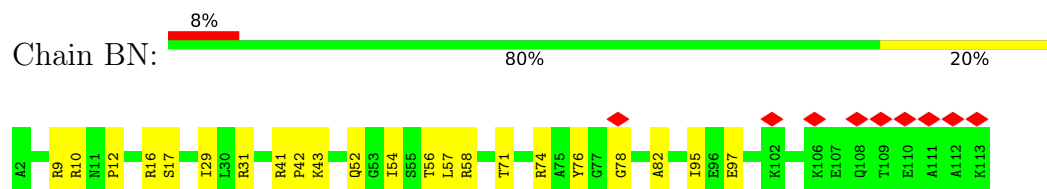
- Molecule 69: RPL32 isoform 1



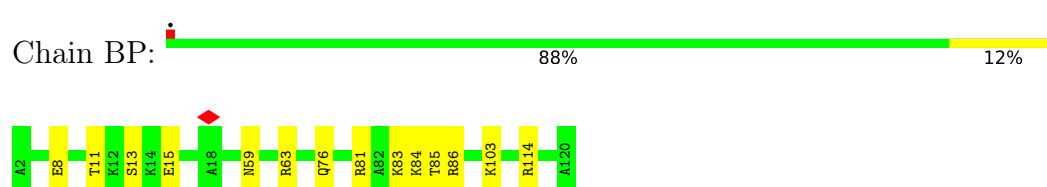
- Molecule 70: 60S ribosomal protein L33-A



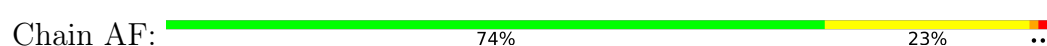
- Molecule 71: 60S ribosomal protein L34-A



- Molecule 72: 60S ribosomal protein L35-A

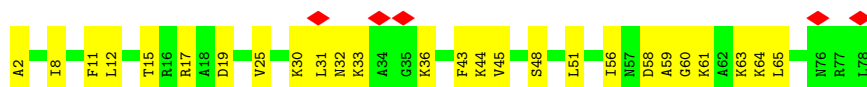


- Molecule 73: 60S ribosomal protein L37-A

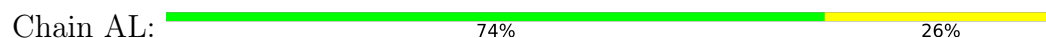




- Molecule 74: RPL38 isoform 1



- Molecule 75: 60S ribosomal protein L39



- Molecule 76: 60S ribosomal protein L40-A



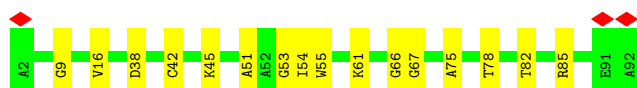
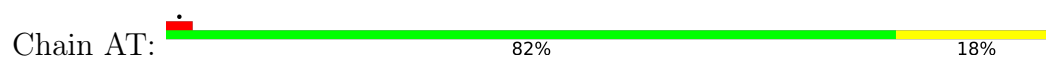
- Molecule 77: 60S ribosomal protein L41-A



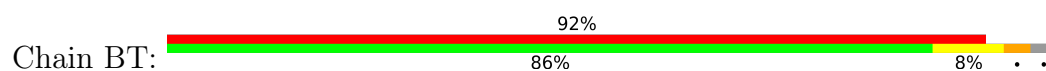
- Molecule 78: 60S ribosomal protein L42-A



- Molecule 79: 60S ribosomal protein L43-A



- Molecule 80: 60S ribosomal protein L1-A



[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	13307	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 ($e^-/\text{\AA}^2$)	56.16	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.096	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	455.28, 455.28, 455.28	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
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	x	0.74	0/2970	1.21	2/4023 (0.0%)
2	A	0.33	0/1754	0.53	0/2361
3	B	0.29	0/1625	0.55	0/2197
4	C	0.26	0/769	0.50	0/1039
5	D	0.24	0/883	0.62	0/1199
6	E	0.28	0/936	0.57	0/1259
7	F	0.33	0/1125	0.54	0/1510
8	G	0.29	0/957	0.47	0/1283
9	H	0.27	0/1207	0.49	0/1623
10	I	0.31	0/1130	0.54	1/1517 (0.1%)
11	J	0.33	0/807	0.52	0/1091
12	K	0.25	0/661	0.52	0/888
13	L	0.29	0/493	0.60	0/663
14	M	0.40	0/452	0.65	0/600
15	N	0.25	0/567	0.59	0/764
16	O	0.25	0/2436	0.51	0/3318
17	P	0.30	0/1644	0.51	0/2249
18	Q	0.29	0/1823	0.60	2/2447 (0.1%)
19	R	0.38	0/1656	0.55	0/2251
20	S	0.32	0/2097	0.56	0/2823
21	T	0.29	0/1839	0.55	0/2460
22	U	0.27	0/1498	0.56	0/2019
23	V	0.36	0/1501	0.53	0/2006
24	W	0.30	0/1504	0.57	0/2016
25	X	0.37	0/1168	0.48	0/1575
26	Y	0.36	0/1215	0.58	0/1638
27	Z	0.32	0/934	0.58	0/1257
28	AA	0.42	0/1836	0.56	0/2481
29	BA	0.56	0/3146	0.57	0/4228
30	AB	0.56	0/1018	0.52	0/1369
31	BB	0.54	0/1465	0.57	0/1965
32	AC	0.41	0/772	0.54	0/1026

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BC	0.55	0/890	0.54	0/1196
34	2	0.33	0/42211	0.44	2/65773 (0.0%)
35	a	0.29	0/682	0.51	0/921
36	b	0.39	0/1038	0.56	1/1395 (0.1%)
37	c	0.42	0/1139	0.59	0/1518
38	d	0.26	0/1046	0.46	0/1401
39	e	0.39	0/778	0.59	0/1042
40	f	0.26	0/620	0.50	0/838
41	g	0.30	0/480	0.53	0/639
42	BQ	0.48	0/78999	0.46	0/123162
43	BR	0.38	0/2883	0.39	0/4491
44	BS	0.50	0/3746	0.46	0/5832
45	AW	0.64	0/1933	0.61	0/2598
46	BE	0.55	0/2800	0.61	0/3790
47	BI	0.39	0/2400	0.51	0/3239
48	BM	0.44	0/1329	0.57	0/1794
49	BO	0.56	0/1821	0.59	0/2451
50	AD	0.39	0/1529	0.50	0/2060
51	BD	0.44	0/1801	0.56	0/2416
52	AG	0.33	0/1367	0.51	0/1834
53	AJ	0.52	0/1568	0.56	0/2106
54	AM	0.43	0/1068	0.55	0/1438
55	AQ	0.66	0/1757	0.63	0/2354
56	AU	0.58	0/1585	0.53	0/2128
57	AX	0.61	0/1439	0.57	0/1938
58	BF	0.50	0/1532	0.53	0/2043
59	BH	0.50	0/1473	0.56	0/1980
60	BJ	0.51	0/1296	0.53	0/1739
61	BL	0.36	0/812	0.48	0/1099
62	AE	0.42	0/850	0.48	0/1152
63	AH	0.51	0/979	0.54	0/1321
64	AK	0.48	0/995	0.53	0/1329
65	AN	0.42	0/1106	0.53	0/1485
66	AR	0.60	0/1200	0.60	0/1607
67	AV	0.48	0/473	0.58	0/629
68	AY	0.44	0/745	0.47	0/1001
69	BG	0.60	0/1038	0.56	0/1390
70	BK	0.63	0/868	0.65	0/1168
71	BN	0.57	0/890	0.63	0/1189
72	BP	0.48	0/978	0.53	0/1301
73	AF	0.76	1/660 (0.2%)	0.88	2/875 (0.2%)
74	AI	0.37	0/618	0.50	0/826
75	AL	0.64	0/443	0.58	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	AO	0.72	1/416 (0.2%)	0.95	2/553 (0.4%)
77	AS	0.49	0/230	0.78	0/296
78	AP	0.74	2/836 (0.2%)	0.75	3/1104 (0.3%)
79	AT	0.72	1/701 (0.1%)	0.80	1/934 (0.1%)
80	BT	0.33	0/1040	0.88	10/1449 (0.7%)
All	All	0.45	5/220976 (0.0%)	0.51	26/324557 (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
1	x	0	1
3	B	0	1
5	D	0	1
7	F	0	1
10	I	0	1
13	L	0	1
15	N	0	1
20	S	0	1
22	U	0	1
27	Z	0	1
28	AA	0	3
31	BB	0	1
33	BC	0	1
36	b	0	1
46	BE	0	3
49	BO	0	1
66	AR	0	2
67	AV	0	2
68	AY	0	1
72	BP	0	1
80	BT	0	4
All	All	0	30

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
78	AP	14	GLY	C-N	7.21	1.43	1.33
79	AT	42	CYS	CA-C	-6.70	1.43	1.52
76	AO	103	LEU	C-N	6.38	1.41	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
73	AF	39	TYR	C-N	6.04	1.45	1.34
78	AP	79	THR	N-CA	-6.03	1.39	1.46

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
78	AP	79	THR	N-CA-C	-7.90	96.43	108.67
80	BT	126	PRO	N-CA-CB	7.77	111.41	103.25
80	BT	135	PRO	N-CA-CB	7.33	110.94	103.25
80	BT	61	PRO	N-CA-CB	7.29	110.91	103.25
76	AO	96	CYS	CA-C-N	6.92	129.44	120.44

There are no chirality outliers.

5 of 30 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	42	LEU	Peptide
5	D	108	ARG	Peptide
7	F	40	GLU	Peptide
10	I	120	GLY	Peptide
1	x	223	TYR	Sidechain

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	x	2899	0	2843	121	0
2	A	1729	0	1812	27	0
3	B	1605	0	1669	46	0
4	C	752	0	719	17	0
5	D	875	0	878	23	0
6	E	916	0	941	29	0
7	F	1105	0	1166	30	0
8	G	948	0	990	20	0
9	H	1188	0	1218	35	0
10	I	1112	0	1124	25	0
11	J	797	0	863	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	K	651	0	682	18	0
13	L	491	0	524	13	0
14	M	442	0	428	20	0
15	N	556	0	549	25	0
16	O	2383	0	2332	57	0
17	P	1603	0	1610	36	0
18	Q	1798	0	1890	58	0
19	R	1626	0	1715	40	0
20	S	2056	0	2140	68	0
21	T	1815	0	1894	41	0
22	U	1473	0	1555	51	0
23	V	1476	0	1501	35	0
24	W	1479	0	1556	27	0
25	X	1142	0	1209	20	0
26	Y	1192	0	1255	23	0
27	Z	923	0	948	27	0
28	AA	1804	0	1877	32	0
29	BA	3075	0	3142	58	0
30	AB	1003	0	1048	22	0
31	BB	1441	0	1543	20	0
32	AC	766	0	844	7	0
33	BC	876	0	912	9	0
34	2	37739	0	18988	513	0
35	a	673	0	662	17	0
36	b	1021	0	1060	21	0
37	c	1121	0	1196	24	0
38	d	1032	0	1044	32	0
39	e	765	0	814	19	0
40	f	610	0	633	15	0
41	g	472	0	521	12	0
42	BQ	70586	0	35467	705	0
43	BR	2579	0	1304	22	0
44	BS	3353	0	1695	26	0
45	AW	1899	0	1957	30	0
46	BE	2748	0	2859	55	0
47	BI	2351	0	2294	45	0
48	BM	1307	0	1377	22	0
49	BO	1784	0	1862	28	0
50	AD	1508	0	1572	17	0
51	BD	1764	0	1804	37	0
52	AG	1346	0	1370	28	0
53	AJ	1543	0	1608	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	AM	1053	0	1149	23	0
55	AQ	1720	0	1779	27	0
56	AU	1555	0	1659	19	0
57	AX	1416	0	1433	18	0
58	BF	1515	0	1606	22	0
59	BH	1437	0	1475	20	0
60	BJ	1272	0	1312	24	0
61	BL	796	0	812	15	0
62	AE	836	0	706	12	0
63	AH	964	0	1025	13	0
64	AK	984	0	1075	19	0
65	AN	1080	0	1122	23	0
66	AR	1169	0	1211	19	0
67	AV	462	0	491	8	0
68	AY	737	0	792	17	0
69	BG	1017	0	1081	19	0
70	BK	850	0	880	12	0
71	BN	880	0	942	22	0
72	BP	969	0	1078	9	0
73	AF	645	0	645	16	0
74	AI	612	0	675	57	0
75	AL	436	0	475	13	0
76	AO	410	0	442	13	0
77	AS	229	0	273	2	0
78	AP	824	0	890	12	0
79	AT	694	0	734	12	0
80	BT	1041	0	447	4	0
81	AF	1	0	0	0	0
81	AO	1	0	0	0	0
81	AP	1	0	0	0	0
81	AT	1	0	0	0	0
81	BN	1	0	0	0	0
81	M	1	0	0	0	0
81	N	1	0	0	0	0
All	All	205808	0	151673	2493	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 7.

The worst 5 of 2493 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:x:338:MET:HE3	42:BQ:1762:C:C5	1.54	1.40
1:x:386:ILE:CG2	42:BQ:2024:G:C4	2.02	1.40
1:x:339:THR:O	42:BQ:1762:C:C1'	1.69	1.39
1:x:338:MET:HB2	42:BQ:1762:C:C4	1.58	1.39
1:x:386:ILE:HG21	42:BQ:2024:G:C1'	1.53	1.38

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	
1	x	365/387 (94%)	349 (96%)	14 (4%)	2 (0%)	24	57
2	A	220/222 (99%)	208 (94%)	12 (6%)	0	100	100
3	B	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
4	C	90/92 (98%)	77 (86%)	13 (14%)	0	100	100
5	D	119/121 (98%)	89 (75%)	29 (24%)	1 (1%)	16	48
6	E	115/142 (81%)	100 (87%)	15 (13%)	0	100	100
7	F	139/141 (99%)	124 (89%)	15 (11%)	0	100	100
8	G	117/125 (94%)	112 (96%)	5 (4%)	0	100	100
9	H	143/145 (99%)	129 (90%)	14 (10%)	0	100	100
10	I	141/143 (99%)	128 (91%)	13 (9%)	0	100	100
11	J	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
12	K	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
13	L	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
14	M	51/53 (96%)	49 (96%)	2 (4%)	0	100	100
15	N	71/73 (97%)	48 (68%)	23 (32%)	0	100	100
16	O	310/312 (99%)	265 (86%)	45 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	P	204/206 (99%)	181 (89%)	23 (11%)	0	100	100
18	Q	222/232 (96%)	196 (88%)	26 (12%)	0	100	100
19	R	214/216 (99%)	189 (88%)	25 (12%)	0	100	100
20	S	256/258 (99%)	224 (88%)	32 (12%)	0	100	100
21	T	226/228 (99%)	210 (93%)	16 (7%)	0	100	100
22	U	182/184 (99%)	160 (88%)	22 (12%)	0	100	100
23	V	183/198 (92%)	164 (90%)	19 (10%)	0	100	100
24	W	182/184 (99%)	162 (89%)	19 (10%)	1 (0%)	24	57
25	X	140/142 (99%)	125 (89%)	15 (11%)	0	100	100
26	Y	148/150 (99%)	131 (88%)	17 (12%)	0	100	100
27	Z	125/127 (98%)	108 (86%)	17 (14%)	0	100	100
28	AA	231/233 (99%)	209 (90%)	22 (10%)	0	100	100
29	BA	384/386 (100%)	354 (92%)	30 (8%)	0	100	100
30	AB	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
31	BB	183/185 (99%)	170 (93%)	13 (7%)	0	100	100
32	AC	97/99 (98%)	91 (94%)	6 (6%)	0	100	100
33	BC	107/109 (98%)	92 (86%)	15 (14%)	0	100	100
35	a	85/87 (98%)	72 (85%)	13 (15%)	0	100	100
36	b	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
37	c	142/144 (99%)	122 (86%)	20 (14%)	0	100	100
38	d	132/134 (98%)	123 (93%)	9 (7%)	0	100	100
39	e	95/97 (98%)	85 (90%)	10 (10%)	0	100	100
40	f	79/81 (98%)	71 (90%)	8 (10%)	0	100	100
41	g	58/60 (97%)	48 (83%)	10 (17%)	0	100	100
45	AW	249/251 (99%)	220 (88%)	29 (12%)	0	100	100
46	BE	359/361 (99%)	320 (89%)	38 (11%)	1 (0%)	36	67
47	BI	292/294 (99%)	268 (92%)	24 (8%)	0	100	100
48	BM	163/175 (93%)	146 (90%)	17 (10%)	0	100	100
49	BO	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
50	AD	189/191 (99%)	172 (91%)	17 (9%)	0	100	100
51	BD	216/218 (99%)	188 (87%)	28 (13%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
52	AG	167/169 (99%)	155 (93%)	12 (7%)	0	100	100
53	AJ	191/193 (99%)	169 (88%)	21 (11%)	1 (0%)	24	57
54	AM	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
55	AQ	201/203 (99%)	181 (90%)	20 (10%)	0	100	100
56	AU	195/197 (99%)	186 (95%)	9 (5%)	0	100	100
57	AX	181/183 (99%)	165 (91%)	16 (9%)	0	100	100
58	BF	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
59	BH	169/171 (99%)	157 (93%)	12 (7%)	0	100	100
60	BJ	157/159 (99%)	142 (90%)	15 (10%)	0	100	100
61	BL	98/100 (98%)	92 (94%)	6 (6%)	0	100	100
62	AE	124/126 (98%)	106 (86%)	18 (14%)	0	100	100
63	AH	119/121 (98%)	110 (92%)	9 (8%)	0	100	100
64	AK	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
65	AN	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
66	AR	146/148 (99%)	128 (88%)	18 (12%)	0	100	100
67	AV	56/58 (97%)	46 (82%)	10 (18%)	0	100	100
68	AY	94/96 (98%)	91 (97%)	3 (3%)	0	100	100
69	BG	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
70	BK	104/106 (98%)	98 (94%)	6 (6%)	0	100	100
71	BN	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
72	BP	117/119 (98%)	109 (93%)	8 (7%)	0	100	100
73	AF	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
74	AI	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
75	AL	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
76	AO	50/52 (96%)	43 (86%)	7 (14%)	0	100	100
77	AS	23/25 (92%)	23 (100%)	0	0	100	100
78	AP	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
79	AT	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
80	BT	208/217 (96%)	166 (80%)	31 (15%)	11 (5%)	1	16
All	All	11551/11792 (98%)	10413 (90%)	1121 (10%)	17 (0%)	49	79

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
80	BT	56	PRO
80	BT	59	PRO
80	BT	87	VAL
80	BT	121	PRO
80	BT	126	PRO

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	
1	x	322/340 (95%)	321 (100%)	1 (0%)	86	84
2	A	182/182 (100%)	181 (100%)	1 (0%)	81	81
3	B	172/173 (99%)	172 (100%)	0	100	100
4	C	77/85 (91%)	77 (100%)	0	100	100
5	D	88/98 (90%)	88 (100%)	0	100	100
6	E	95/118 (80%)	95 (100%)	0	100	100
7	F	117/117 (100%)	117 (100%)	0	100	100
8	G	101/113 (89%)	101 (100%)	0	100	100
9	H	127/128 (99%)	127 (100%)	0	100	100
10	I	115/115 (100%)	115 (100%)	0	100	100
11	J	93/93 (100%)	93 (100%)	0	100	100
12	K	67/73 (92%)	67 (100%)	0	100	100
13	L	55/56 (98%)	55 (100%)	0	100	100
14	M	47/47 (100%)	46 (98%)	1 (2%)	47	64
15	N	56/63 (89%)	56 (100%)	0	100	100
16	O	250/257 (97%)	250 (100%)	0	100	100
17	P	170/173 (98%)	170 (100%)	0	100	100
18	Q	200/205 (98%)	200 (100%)	0	100	100
19	R	175/175 (100%)	175 (100%)	0	100	100
20	S	220/220 (100%)	220 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	T	189/195 (97%)	189 (100%)	0	100	100
22	U	163/165 (99%)	163 (100%)	0	100	100
23	V	148/159 (93%)	148 (100%)	0	100	100
24	W	156/157 (99%)	156 (100%)	0	100	100
25	X	126/127 (99%)	126 (100%)	0	100	100
26	Y	127/127 (100%)	127 (100%)	0	100	100
27	Z	90/96 (94%)	90 (100%)	0	100	100
28	AA	187/191 (98%)	187 (100%)	0	100	100
29	BA	318/322 (99%)	317 (100%)	1 (0%)	86	84
30	AB	104/104 (100%)	104 (100%)	0	100	100
31	BB	150/150 (100%)	150 (100%)	0	100	100
32	AC	80/81 (99%)	80 (100%)	0	100	100
33	BC	92/96 (96%)	92 (100%)	0	100	100
35	a	71/74 (96%)	71 (100%)	0	100	100
36	b	110/110 (100%)	110 (100%)	0	100	100
37	c	119/119 (100%)	119 (100%)	0	100	100
38	d	102/112 (91%)	102 (100%)	0	100	100
39	e	82/83 (99%)	82 (100%)	0	100	100
40	f	70/70 (100%)	70 (100%)	0	100	100
41	g	50/51 (98%)	50 (100%)	0	100	100
45	AW	190/193 (98%)	190 (100%)	0	100	100
46	BE	288/288 (100%)	287 (100%)	1 (0%)	86	84
47	BI	241/243 (99%)	241 (100%)	0	100	100
48	BM	139/154 (90%)	139 (100%)	0	100	100
49	BO	186/186 (100%)	186 (100%)	0	100	100
50	AD	168/171 (98%)	168 (100%)	0	100	100
51	BD	185/185 (100%)	185 (100%)	0	100	100
52	AG	145/147 (99%)	145 (100%)	0	100	100
53	AJ	154/154 (100%)	154 (100%)	0	100	100
54	AM	107/107 (100%)	107 (100%)	0	100	100
55	AQ	175/175 (100%)	174 (99%)	1 (1%)	78	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
56	AU	160/160 (100%)	160 (100%)	0	100	100
57	AX	138/145 (95%)	138 (100%)	0	100	100
58	BF	152/153 (99%)	152 (100%)	0	100	100
59	BH	155/155 (100%)	155 (100%)	0	100	100
60	BJ	135/136 (99%)	135 (100%)	0	100	100
61	BL	87/87 (100%)	87 (100%)	0	100	100
62	AE	56/108 (52%)	56 (100%)	0	100	100
63	AH	104/105 (99%)	104 (100%)	0	100	100
64	AK	108/108 (100%)	108 (100%)	0	100	100
65	AN	112/115 (97%)	112 (100%)	0	100	100
66	AR	117/118 (99%)	117 (100%)	0	100	100
67	AV	46/46 (100%)	46 (100%)	0	100	100
68	AY	81/81 (100%)	81 (100%)	0	100	100
69	BG	108/109 (99%)	108 (100%)	0	100	100
70	BK	90/90 (100%)	90 (100%)	0	100	100
71	BN	95/95 (100%)	95 (100%)	0	100	100
72	BP	104/104 (100%)	104 (100%)	0	100	100
73	AF	67/67 (100%)	65 (97%)	2 (3%)	36	57
74	AI	68/68 (100%)	68 (100%)	0	100	100
75	AL	45/45 (100%)	45 (100%)	0	100	100
76	AO	45/47 (96%)	43 (96%)	2 (4%)	25	49
77	AS	22/23 (96%)	22 (100%)	0	100	100
78	AP	87/88 (99%)	87 (100%)	0	100	100
79	AT	71/71 (100%)	71 (100%)	0	100	100
All	All	9494/9747 (97%)	9484 (100%)	10 (0%)	87	89

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
73	AF	22	CYS
76	AO	112	LYS
76	AO	115	CYS
29	BA	104	THR
46	BE	12	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
69	BG	35	GLN
70	BK	26	ASN
75	AL	32	ASN
31	BB	126	GLN
31	BB	23	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	2	1768/1798 (98%)	536 (30%)	53 (2%)
42	BQ	3296/3301 (99%)	760 (23%)	44 (1%)
43	BR	120/121 (99%)	15 (12%)	1 (0%)
44	BS	157/158 (99%)	32 (20%)	3 (1%)
All	All	5341/5378 (99%)	1343 (25%)	101 (1%)

5 of 1343 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	2	2	A
34	2	4	C
34	2	14	C
34	2	25	C
34	2	26	A

5 of 101 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
42	BQ	763	G
42	BQ	1716	U
44	BS	85	G
42	BQ	873	C
42	BQ	1271	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
42	BQ	4
68	AY	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BQ	2452:G	O3'	2492:C	P	17.28
1	BQ	2059:U	O3'	2080:C	P	10.98
1	BQ	451:U	O3'	486:A	P	8.84
1	BQ	1984:C	O3'	1985:G	P	6.36
1	AY	47:ASN	C	48:THR	N	1.17

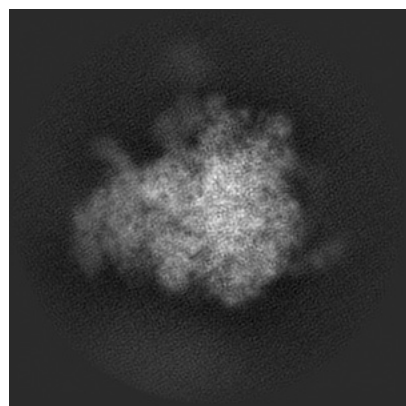
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16191. These allow visual inspection of the internal detail of the map and identification of artifacts.

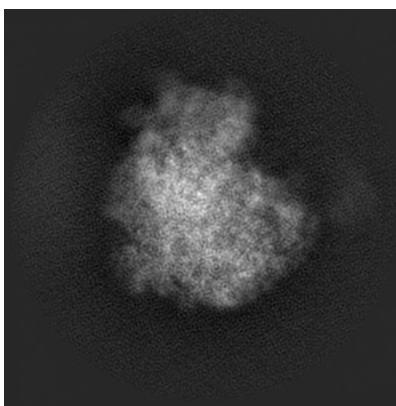
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

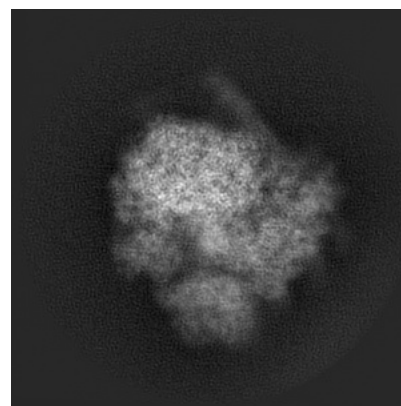
6.1.1 Primary map



X

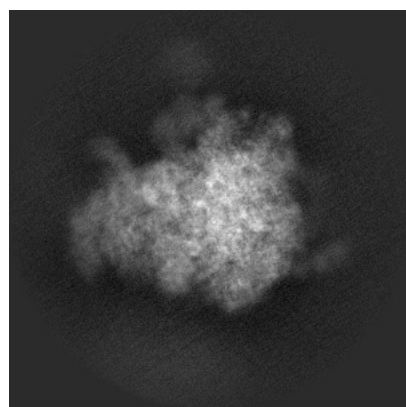


Y

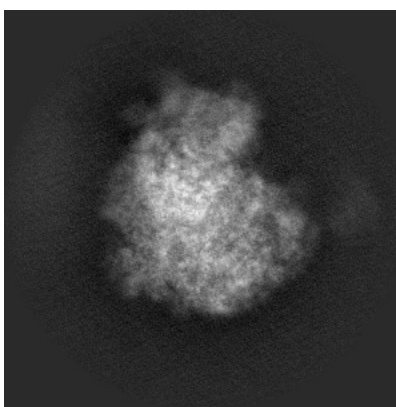


Z

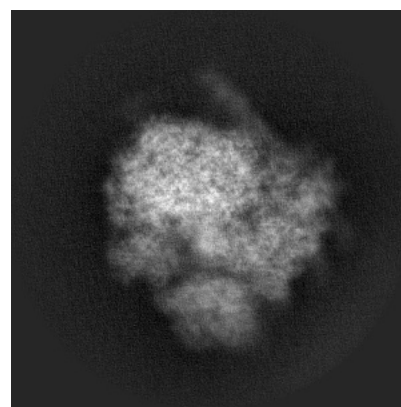
6.1.2 Raw map



X



Y

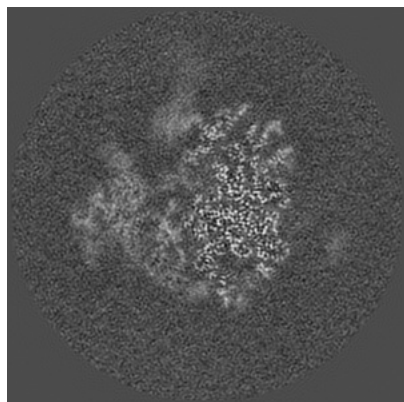


Z

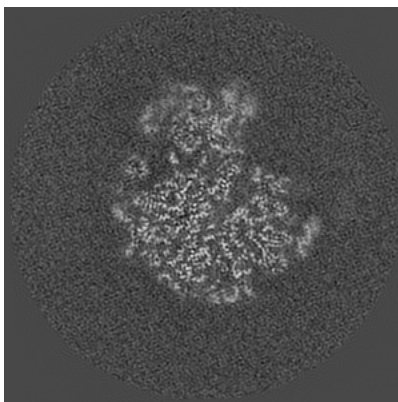
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

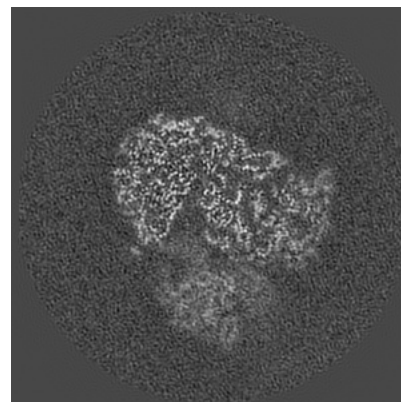
6.2.1 Primary map



X Index: 210

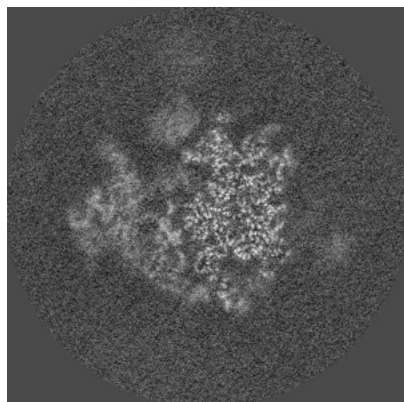


Y Index: 210

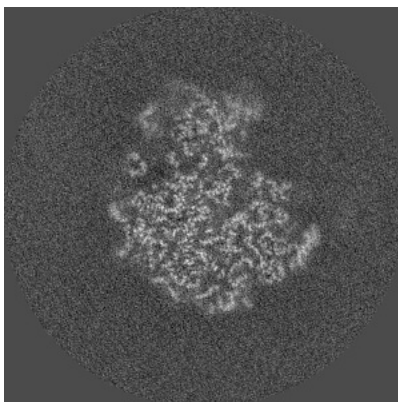


Z Index: 210

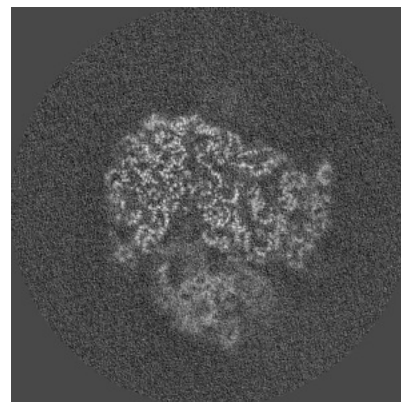
6.2.2 Raw map



X Index: 210



Y Index: 210

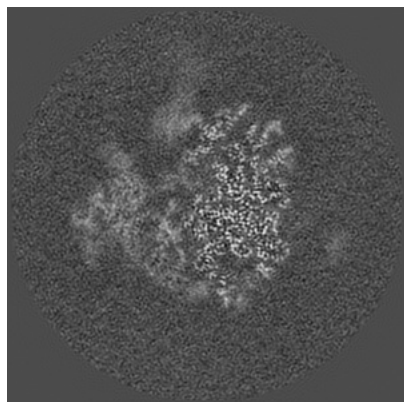


Z Index: 210

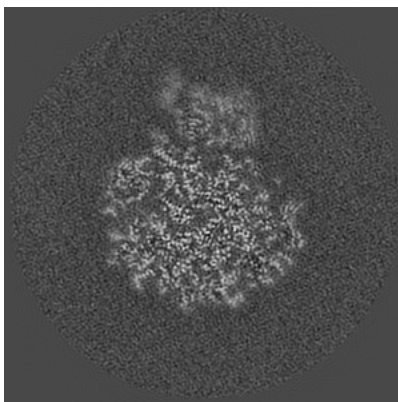
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

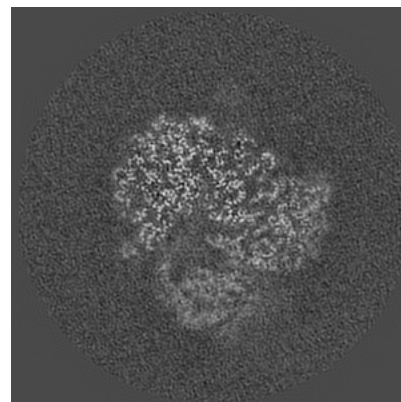
6.3.1 Primary map



X Index: 210

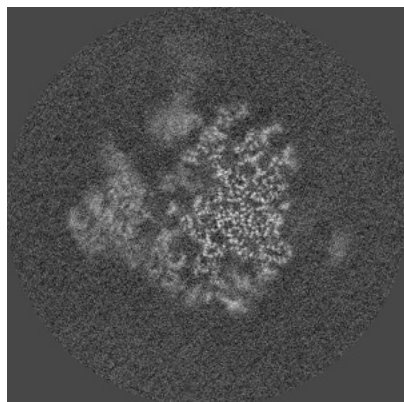


Y Index: 234

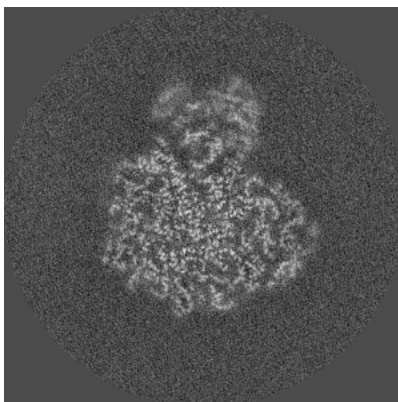


Z Index: 215

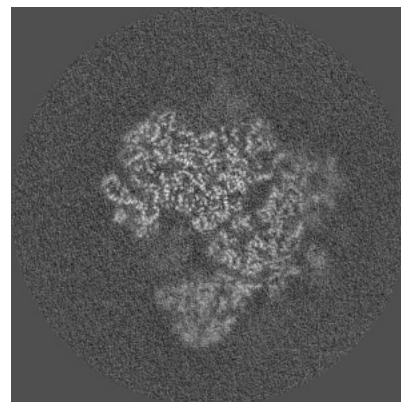
6.3.2 Raw map



X Index: 206



Y Index: 226

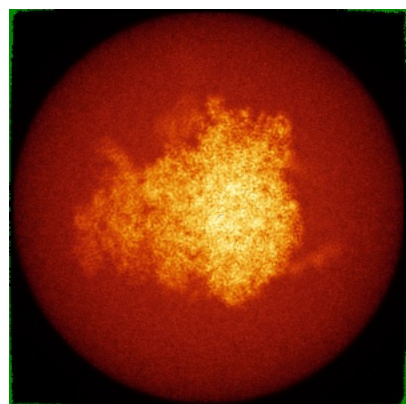


Z Index: 189

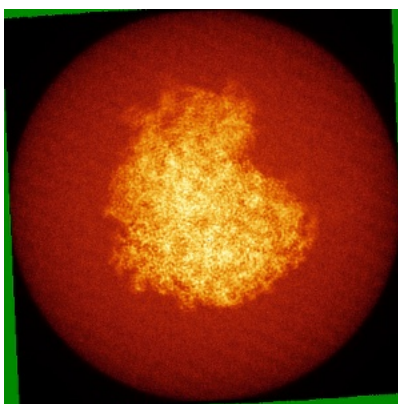
The images above show the largest variance slices of the map in three orthogonal directions.

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

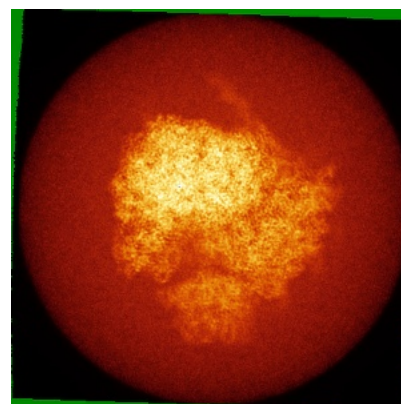
6.4.1 Primary map



X

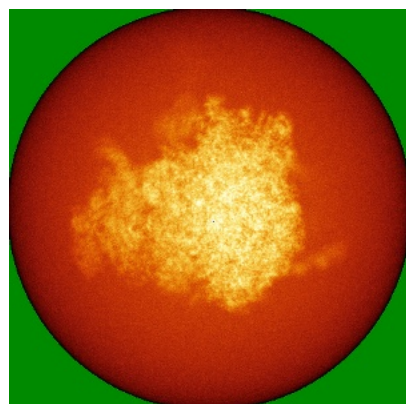


Y

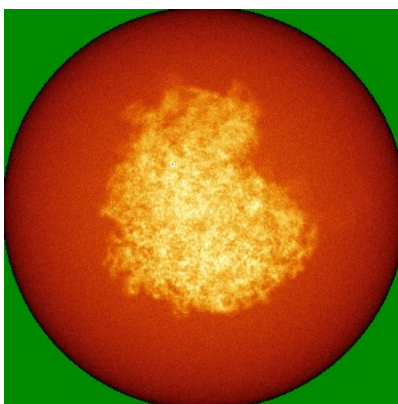


Z

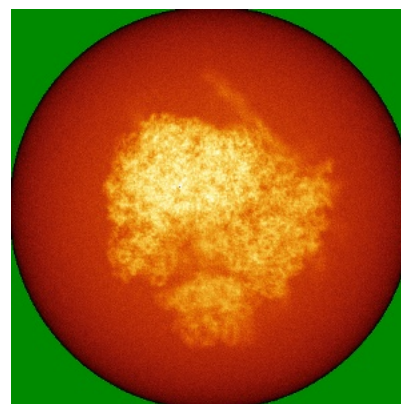
6.4.2 Raw map



X



Y

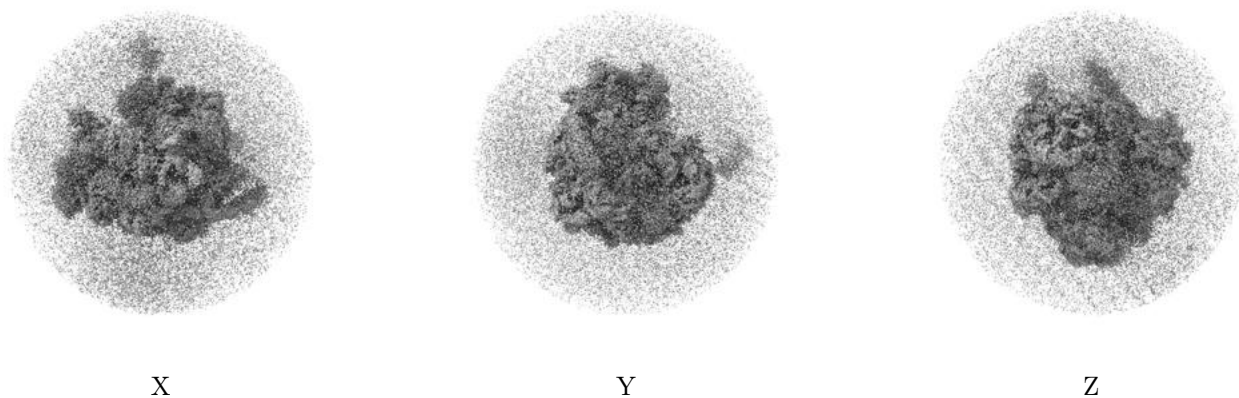


Z

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.

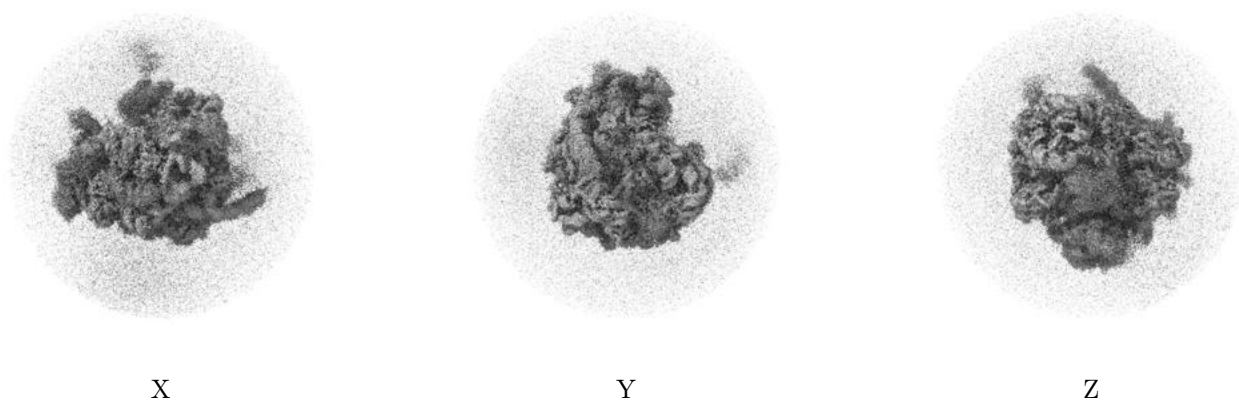
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

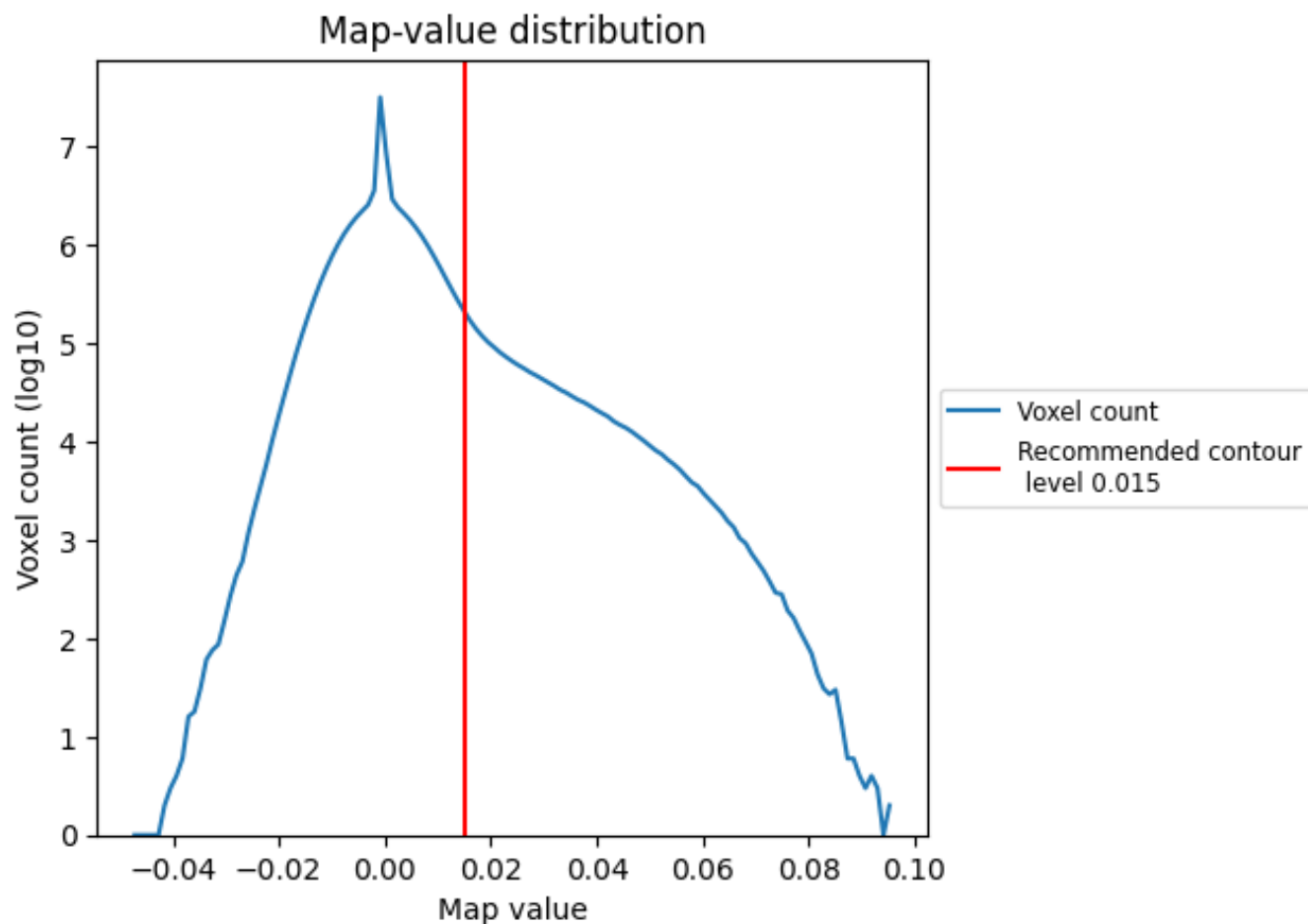
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

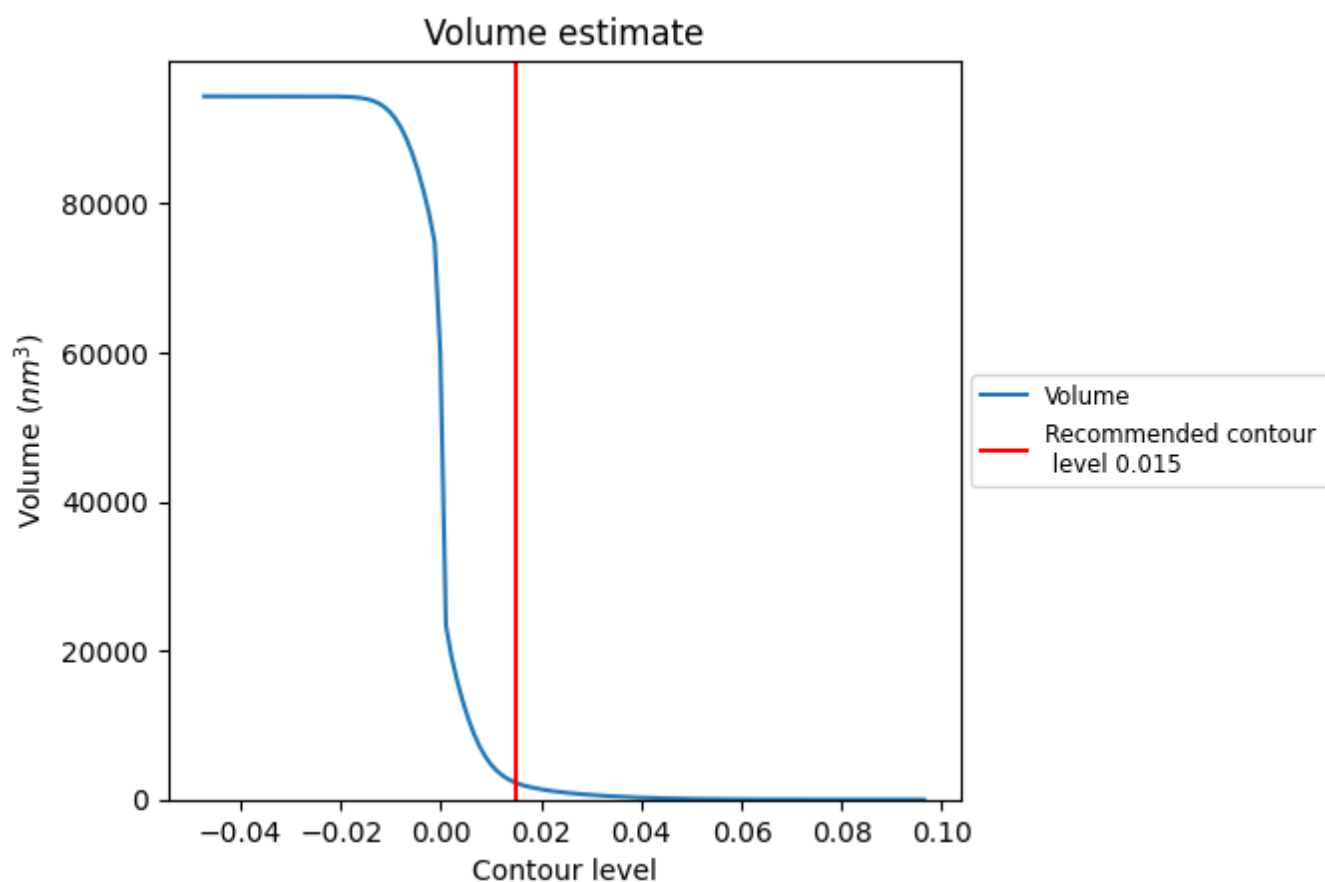
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

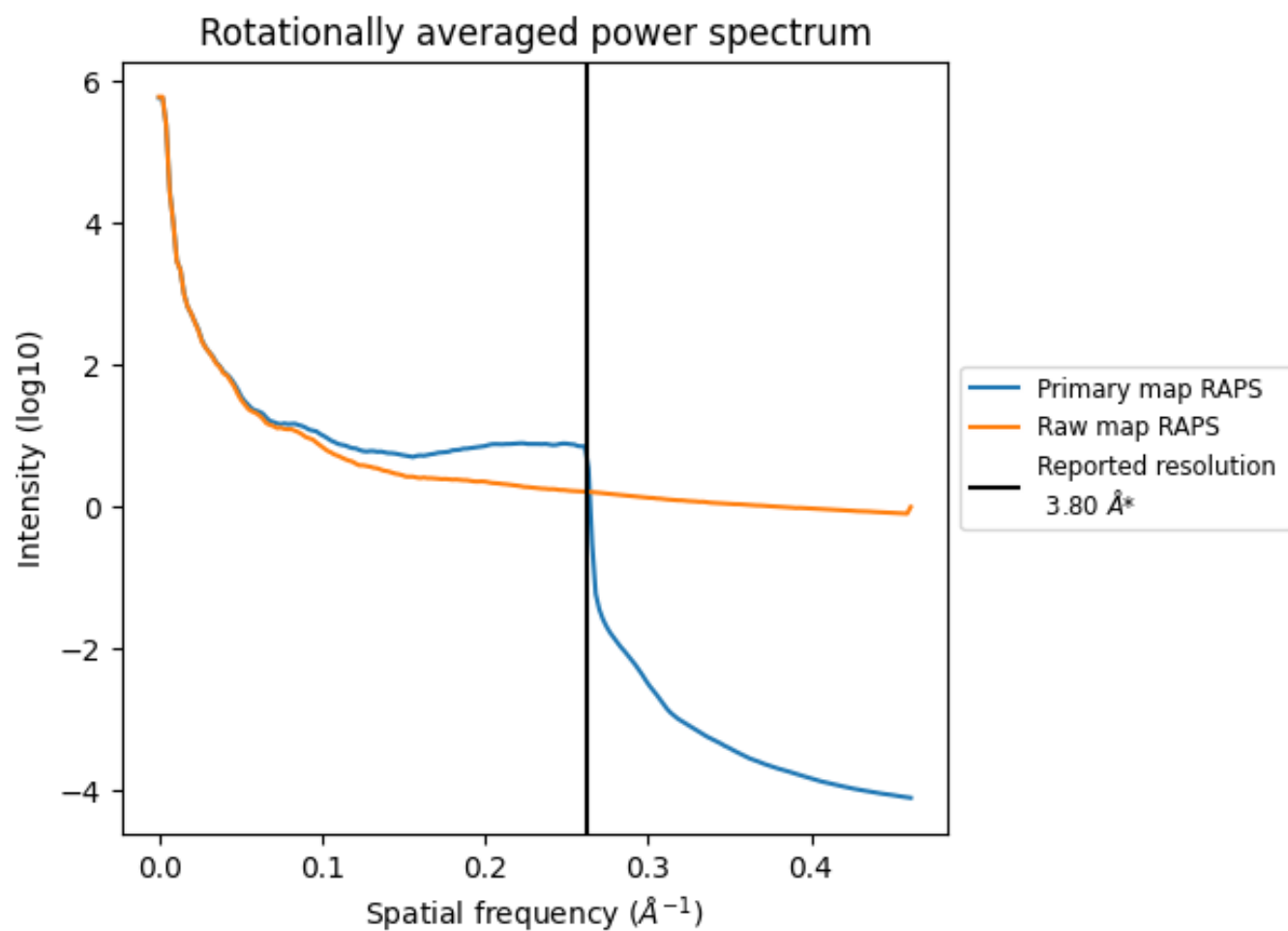
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2255 nm³; this corresponds to an approximate mass of 2037 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 ⓘ

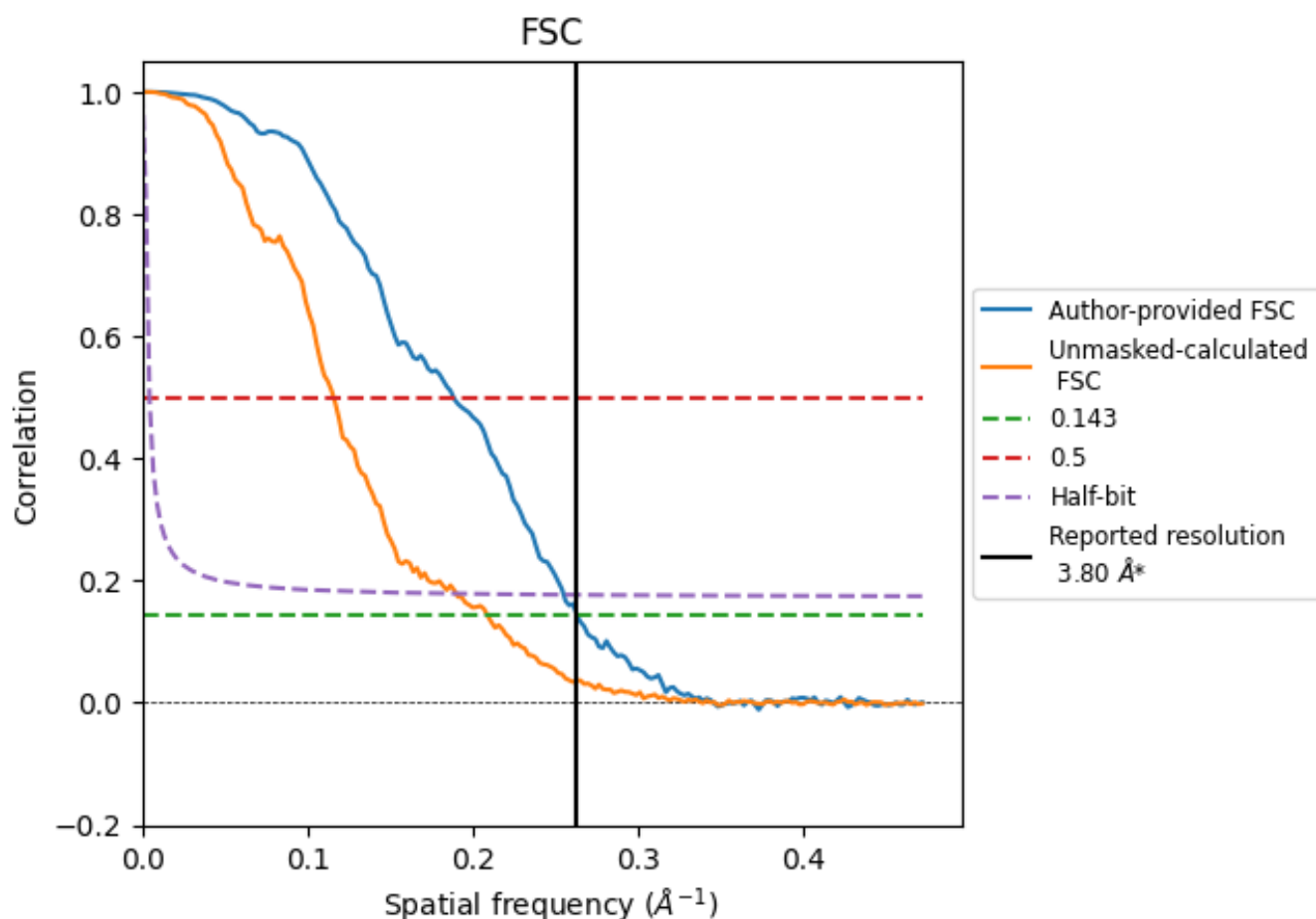


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 0.263 Å⁻¹

8.2 Resolution estimates [i](#)

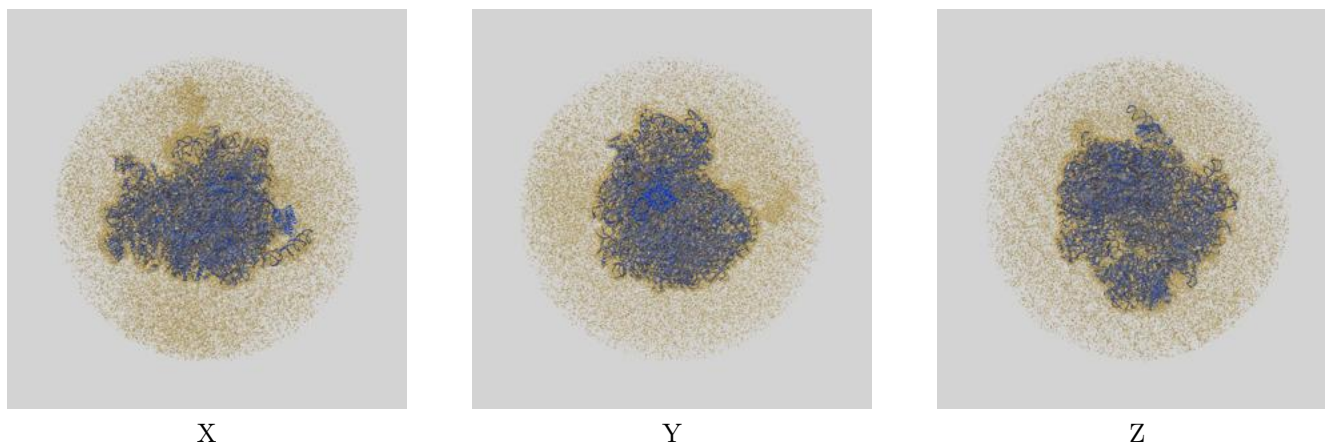
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.80	5.31	3.92
Unmasked-calculated*	4.78	8.64	5.26

*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 4.78 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

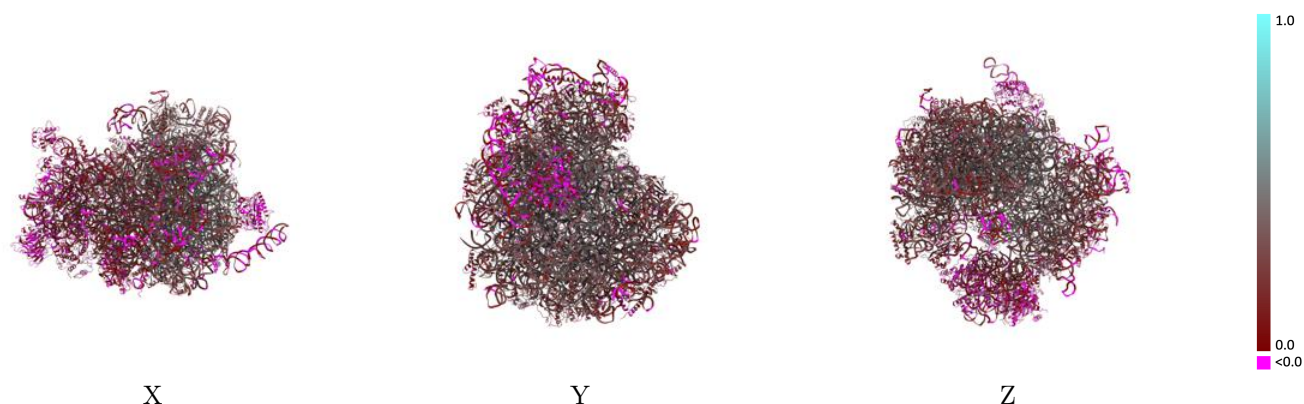
This section contains information regarding the fit between EMDB map EMD-16191 and PDB model 8BQX. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



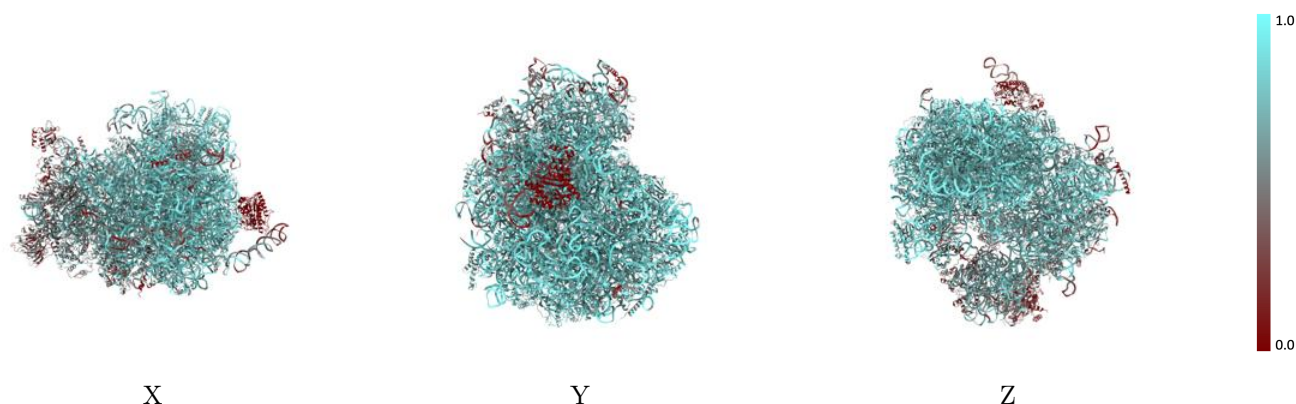
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



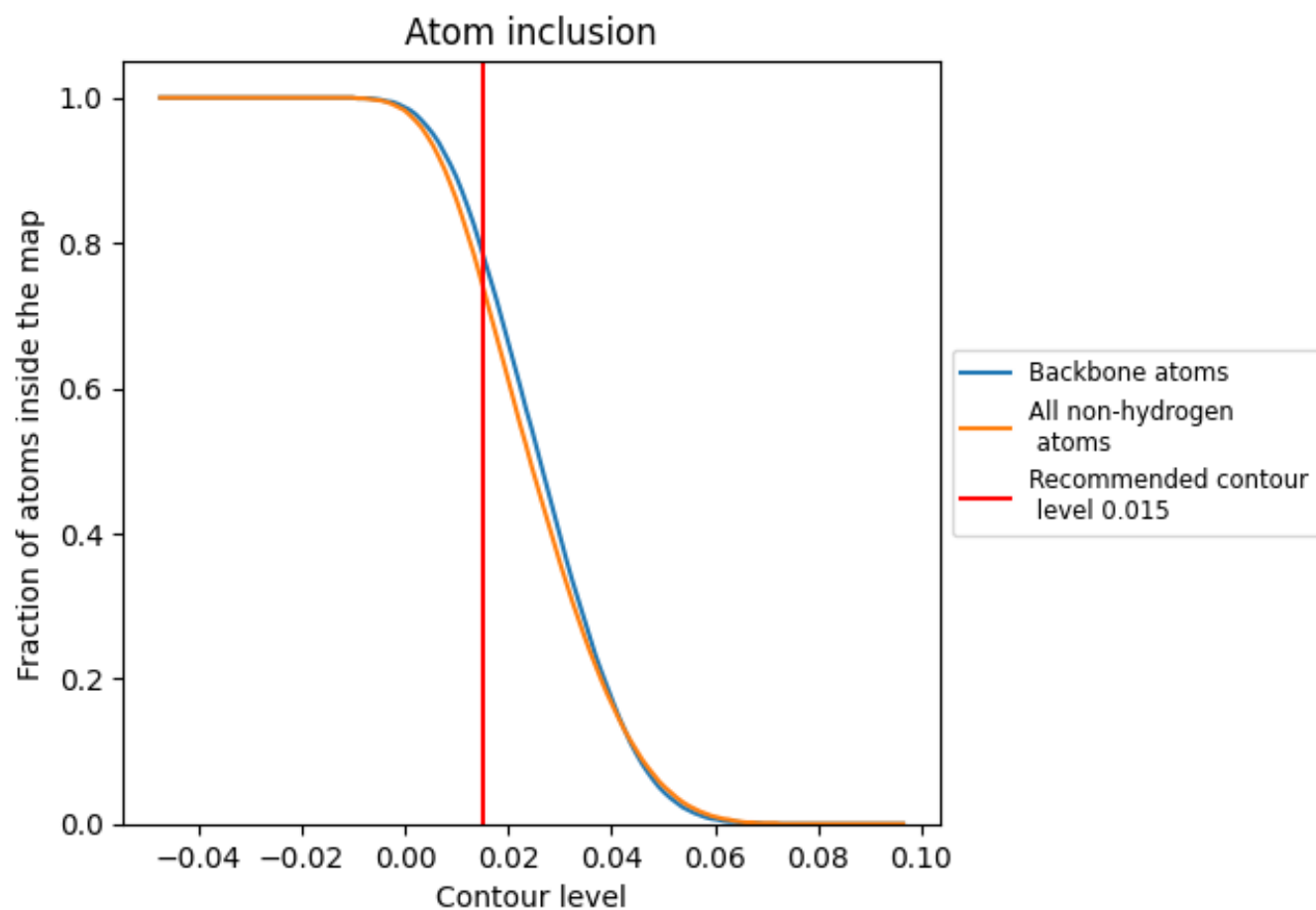
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 74% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7440	 0.2640
2	 0.7690	 0.2120
A	 0.4230	 0.1180
AA	 0.7240	 0.2760
AB	 0.7670	 0.3980
AC	 0.7320	 0.2980
AD	 0.7450	 0.2870
AE	 0.5510	 0.2380
AF	 0.8710	 0.4150
AG	 0.6290	 0.1890
AH	 0.7590	 0.3470
AI	 0.7180	 0.2810
AJ	 0.7580	 0.3050
AK	 0.7980	 0.3400
AL	 0.7780	 0.3790
AM	 0.7320	 0.2440
AN	 0.7020	 0.2560
AO	 0.7810	 0.2960
AP	 0.7650	 0.3530
AQ	 0.7870	 0.3580
AR	 0.7870	 0.3420
AS	 0.6830	 0.2560
AT	 0.7690	 0.3790
AU	 0.7640	 0.3230
AV	 0.7480	 0.3250
AW	 0.7910	 0.4020
AX	 0.7950	 0.3800
AY	 0.7270	 0.3270
B	 0.3570	 0.0370
BA	 0.8010	 0.3730
BB	 0.7570	 0.3120
BC	 0.7730	 0.3630
BD	 0.6230	 0.2070
BE	 0.7650	 0.3060
BF	 0.7410	 0.3280



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Chain	Atom inclusion	Q-score
BG	 0.7800	 0.3580
BH	 0.7600	 0.3120
BI	 0.7210	 0.2340
BJ	 0.7400	 0.2980
BK	 0.7560	 0.3290
BL	 0.7520	 0.3020
BM	 0.6960	 0.2250
BN	 0.7370	 0.3540
BO	 0.7470	 0.2860
BP	 0.7590	 0.3080
BQ	 0.8700	 0.3310
BR	 0.8750	 0.2710
BS	 0.9050	 0.3610
BT	 0.1370	 0.0880
C	 0.4350	 0.0770
D	 0.2120	 0.0460
E	 0.4600	 0.0740
F	 0.4600	 0.0600
G	 0.4240	 0.0860
H	 0.4920	 0.0760
I	 0.4540	 0.0580
J	 0.5140	 0.0990
K	 0.3730	 0.0400
L	 0.3760	 0.0940
M	 0.5450	 0.1100
N	 0.3930	 0.0680
O	 0.3540	 0.0420
P	 0.5380	 0.1250
Q	 0.4960	 0.1520
R	 0.6190	 0.2150
S	 0.6130	 0.2010
T	 0.6330	 0.1920
U	 0.5020	 0.1130
V	 0.7040	 0.2670
W	 0.6460	 0.1990
X	 0.6700	 0.2860
Y	 0.6230	 0.2310
Z	 0.5430	 0.1620
a	 0.5510	 0.1460
b	 0.6160	 0.2190
c	 0.6560	 0.2790
d	 0.6480	 0.1920

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Chain	Atom inclusion	Q-score
e	 0.5850	 0.1910
f	 0.5460	 0.1750
g	 0.5480	 0.1520
x	 0.0330	 0.0050