



wwPDB EM Validation Summary Report ⓘ

Mar 23, 2026 – 11:17 PM UTC

PDB ID : 8EVP / pdb_00008evp
EMDB ID : EMD-28632
Title : Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES), Structure I
Authors : Zhao, Y.; Rai, J.; Li, H.
Deposited on : 2022-10-20
Resolution : 2.38 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:

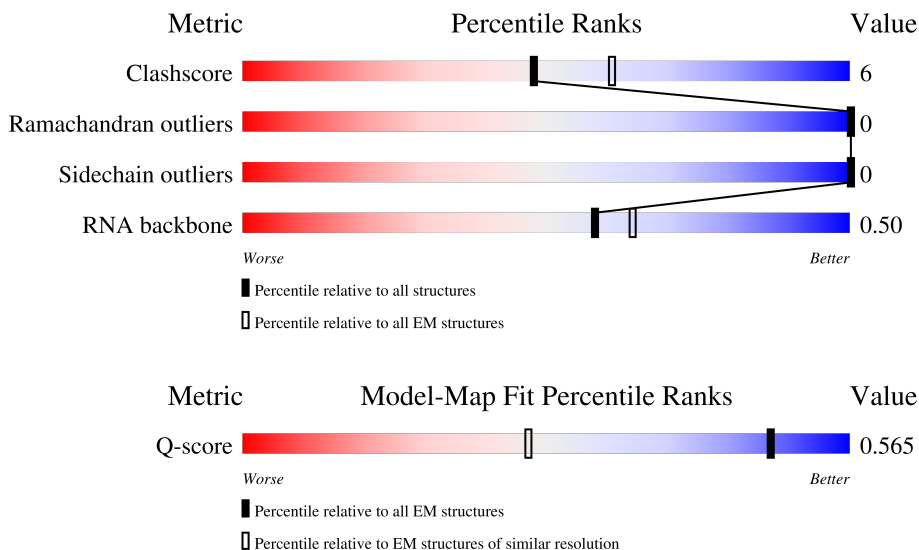
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 2.38 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.















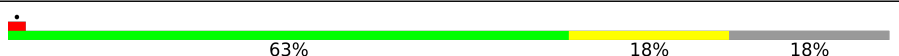
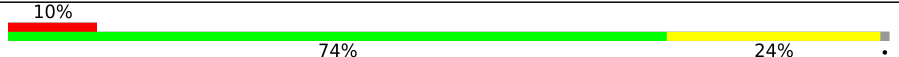
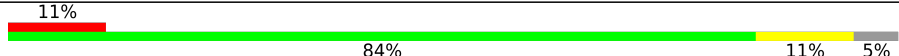

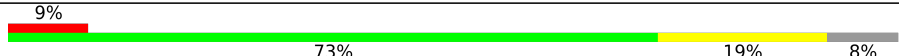
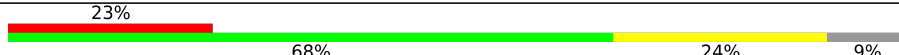
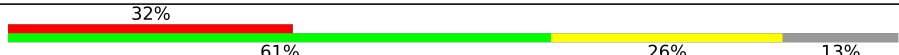
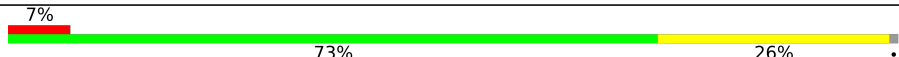
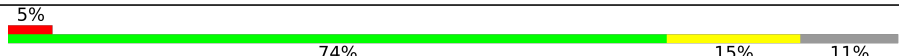



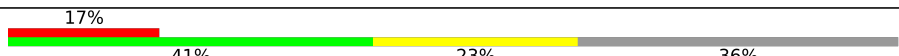
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4811 (1.88 - 2.88)

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	BA	252	70% 12% 18%
2	BB	255	63% 21% 16%
3	BC	254	72% 13% 15%

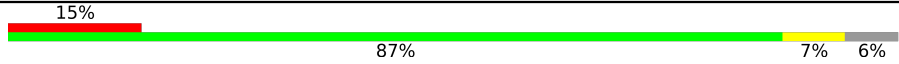







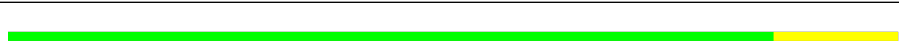

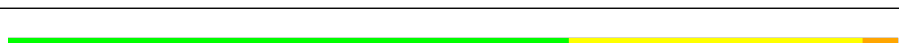


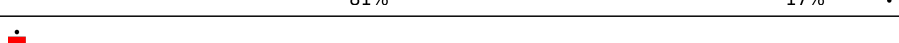
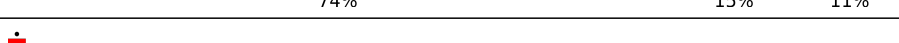
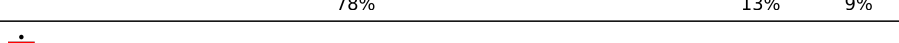
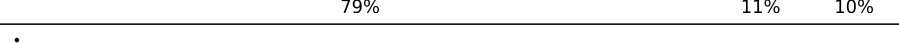
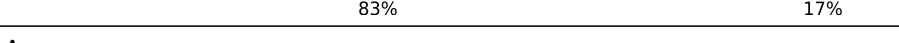
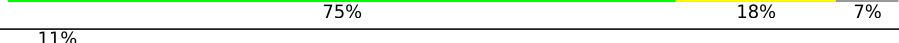






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Mol	Chain	Length	Quality of chain
4	BE	261	
5	BG	236	
6	BH	190	
7	BI	200	
8	BJ	197	
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	

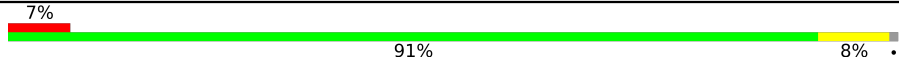







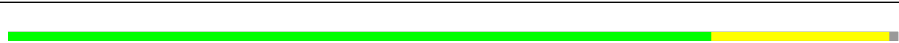

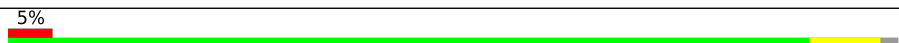


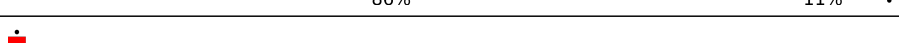
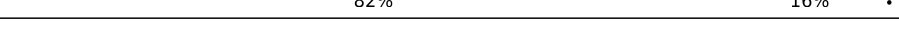
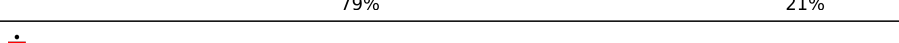
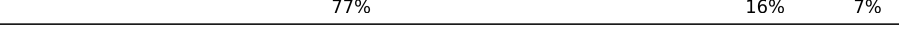
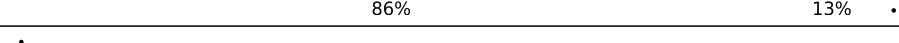
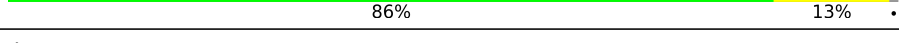






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Mol	Chain	Length	Quality of chain
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	
34	B5	1799	
35	AA	254	
36	AB	387	
37	AC	362	
38	A1	3360	
39	A3	121	
40	A4	158	
41	AD	297	
42	AE	176	
43	AF	244	
44	AG	256	
45	AH	191	
46	AI	221	
47	AJ	174	
48	AL	199	
49	AM	138	
50	AN	204	
51	AO	199	
52	AP	184	
53	AQ	186	

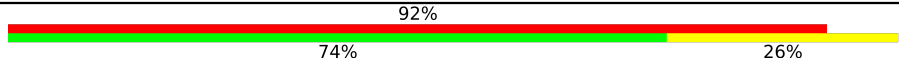

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Mol	Chain	Length	Quality of chain
54	AR	189	
55	AS	178	
56	AT	160	
57	AU	121	
58	AV	137	
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	

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Mol	Chain	Length	Quality of chain
79	E	217	
80	EC	202	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 205919 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 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	BA	206	1612	1034	285	291	2	0	0

- Molecule 2 is a protein called RPS1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	BB	214	1709	1084	310	311	4	0	0

- Molecule 3 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	BC	217	1635	1047	289	297	2	0	0

- Molecule 4 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	BE	260	2068	1316	389	360	3	0	0

- Molecule 5 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	BG	226	1820	1142	350	325	3	0	0

- Molecule 6 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	BH	184	1481	951	265	265	0	0

- Molecule 7 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 8 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 9 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 10 is a protein called 40S ribosomal protein S13.

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

- Molecule 11 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 12 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 13 is a protein called RPS22A isoform 1.

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

- Molecule 14 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 15 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	BY	134	1073	676	208	189		0	0

- Molecule 16 is a protein called RPS26B isoform 1.

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

- Molecule 17 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	Be	60	475	299	98	77	1	0	0

- Molecule 19 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	BD	223	1734	1101	313	314	6	0	0

- Molecule 20 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	BF	206	1609	1007	300	299	3	0	0

- Molecule 21 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 22 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 23 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	BR	121	Total	C	N	O	S	0	0
			975	611	183	179	2		

- Molecule 25 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 27 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BU	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 28 is a protein called RPS25A isoform 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	BZ	69	Total	C	N	O	0	0
			558	357	103	98		

- Molecule 29 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 30 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Bd	53	Total	C	N	O	S	0	0
			443	275	92	72	4		

- Molecule 31 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

- Molecule 32 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Bf	57	Total	C	N	O	S	0	0
			454	288	86	77	3		

- Molecule 33 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BM	121	Total	C	N	O	S	0	0
			913	574	162	175	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B5	1782	Total	C	N	O	P	1	0
			38004	17005	6718	12499	1782		

- Molecule 35 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 36 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	AB	386	Total	C	N	O	S	0	0
			3080	1955	584	533	8		

- Molecule 37 is a protein called RPL4A isoform 1.

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

- Molecule 38 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	A1	3198	Total	C	N	O	P	0	0
			68445	30596	12331	22320	3198		

- Molecule 39 is a RNA chain called 5s rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 40 is a RNA chain called 5.8 S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 41 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 42 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	AE	156	1239	800	222	216	1	0	0

- Molecule 43 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 44 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	AG	230	1798	1149	323	323	3	0	0

- Molecule 45 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	AH	190	1510	957	273	276	4	0	0

- Molecule 46 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	AI	205	1672	1063	316	288	5	0	0

- Molecule 47 is a protein called RPL11A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	AJ	169	1353	847	253	249	4	0	0

- Molecule 48 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	AP	175	1388	862	277	249		0	0

- Molecule 53 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 54 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	AR	188	1521	935	326	260		0	0

- Molecule 55 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	AS	172	1445	930	267	244	4	0	0

- Molecule 56 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 59 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	AW	63	521	336	102	82	1	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	AX	121	968	623	170	173	2	0	0

- Molecule 61 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	AY	126	993	625	192	176		0	0

- Molecule 62 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	AZ	135	1092	710	202	180		0	0

- Molecule 63 is a protein called 60S ribosomal protein L28.

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

- Molecule 64 is a protein called RPL29 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Ab	58	462	289	100	73		0	0

- Molecule 65 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Ac	97	743	479	124	139	1	0	0

- Molecule 66 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Ad	109	890	565	168	156	1	0	0

- Molecule 67 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Ae	127	1020	647	205	167	1	0	0

- Molecule 68 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 69 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ai	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 72 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Aj	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 73 is a protein called RPL38 isoform 1.

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

- Molecule 74 is a protein called 60S ribosomal protein L39.

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

- Molecule 75 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 76 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	An	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 77 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Ao	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 78 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 79 is a protein called RPL1A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	E	217	Total	C	N	O	S	0	0
			1718	1097	299	312	10		

- Molecule 80 is a RNA chain called Internal ribosome entry site.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	EC	192	Total	C	N	O	P	0	0
			4090	1828	729	1341	192		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	BE	1	Total	Mg	0
			1	1	
81	BN	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	B5	60	Total	Mg	0
			60	60	
81	AC	1	Total	Mg	0
			1	1	
81	A1	182	Total	Mg	0
			182	182	
81	A3	2	Total	Mg	0
			2	2	
81	A4	5	Total	Mg	0
			5	5	
81	AD	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
81	AL	1	Total 1	Mg 1	0
81	AP	1	Total 1	Mg 1	0

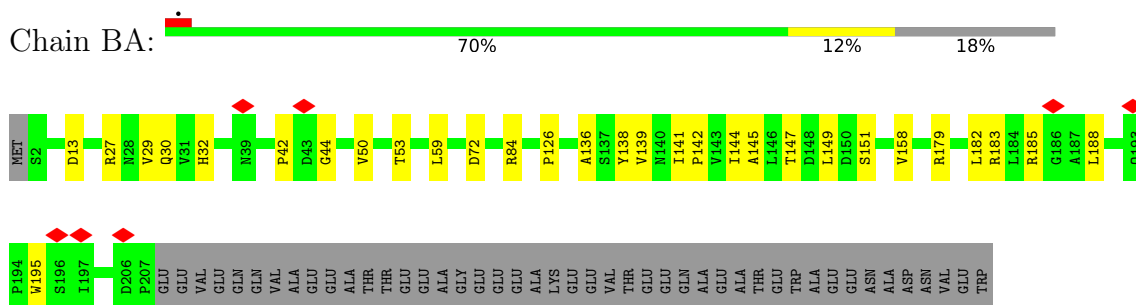
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	Ao	1	Total 1	Zn 1	0

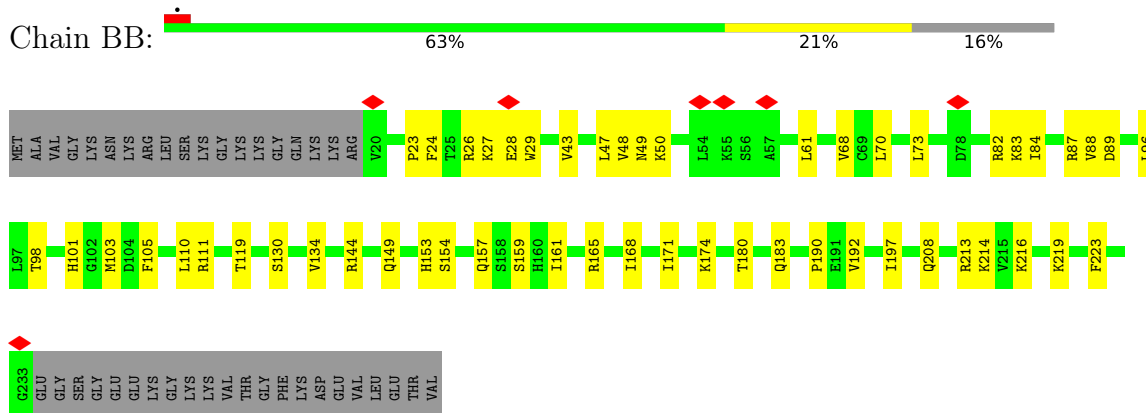
3 Residue-property plots [i](#)

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.

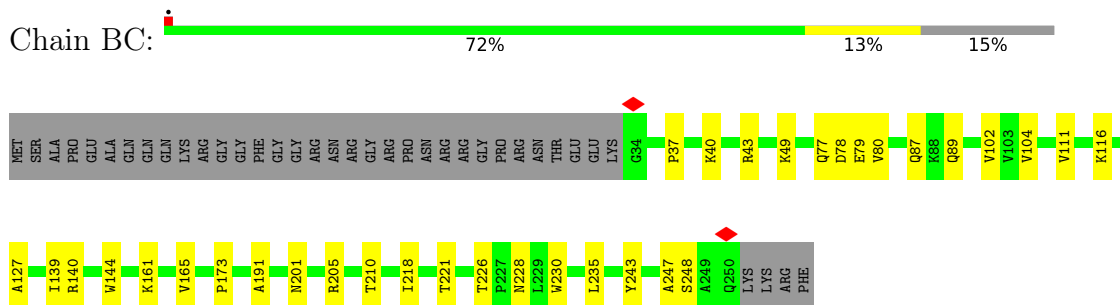
- Molecule 1: 40S ribosomal protein S0-A




- Molecule 2: RPS1A isoform 1

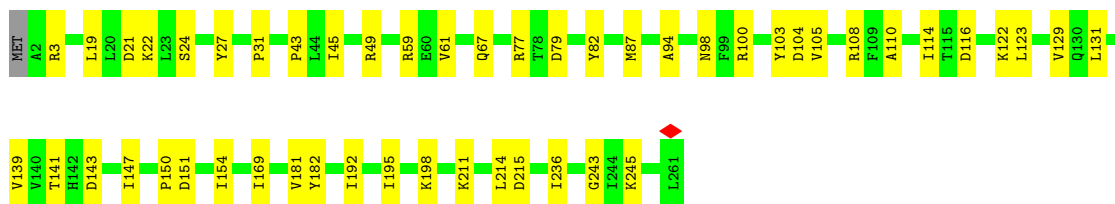


- Molecule 3: RPS2 isoform 1




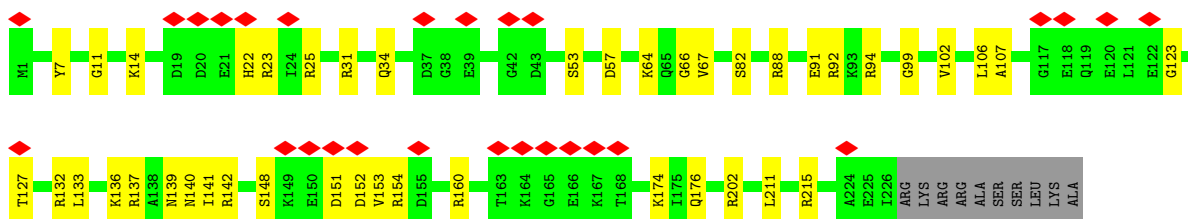
- Molecule 4: 40S ribosomal protein S4-A

Chain BE:  80% 19%




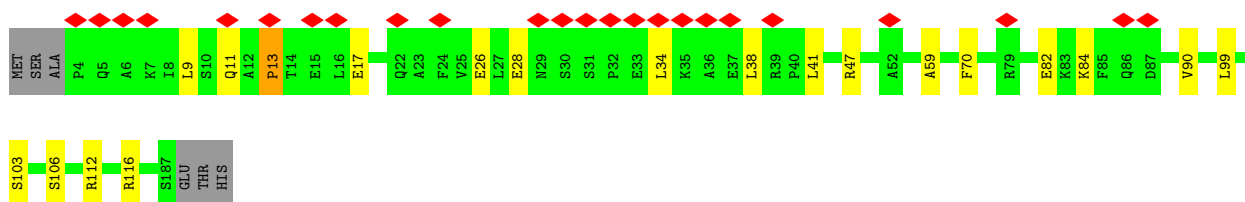
• Molecule 5: 40S ribosomal protein S6-A

Chain BG:  11% 78% 18%




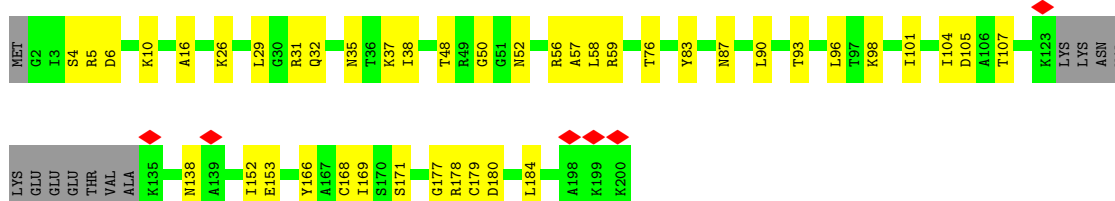
• Molecule 6: 40S ribosomal protein S7-A

Chain BH:  13% 86% 10%




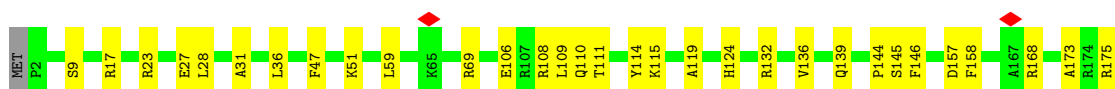
• Molecule 7: 40S ribosomal protein S8-A

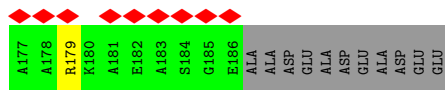
Chain BI:  73% 21% 6%



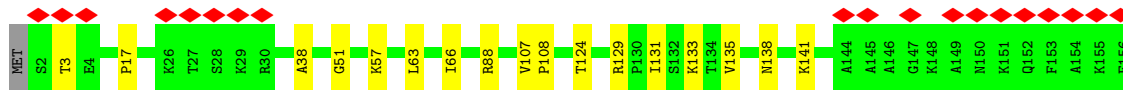
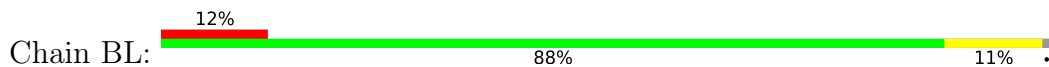
• Molecule 8: 40S ribosomal protein S9-A

Chain BJ:  6% 77% 17% 6%

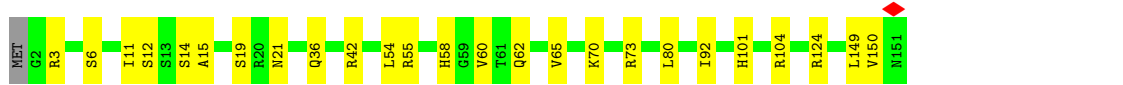
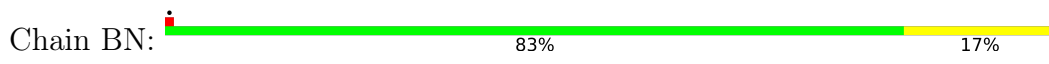




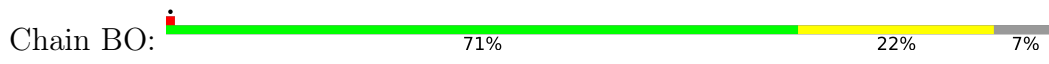
• Molecule 9: 40S ribosomal protein S11-A



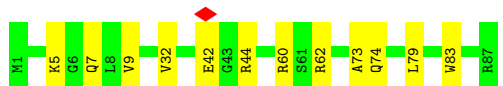
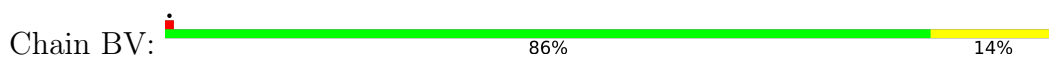
• Molecule 10: 40S ribosomal protein S13



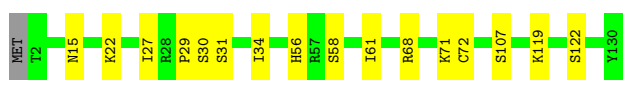
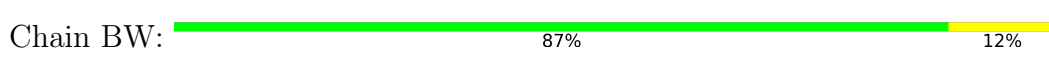
• Molecule 11: 40S ribosomal protein S14-A



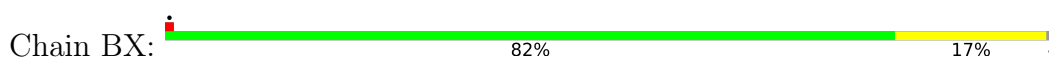
• Molecule 12: 40S ribosomal protein S21-A

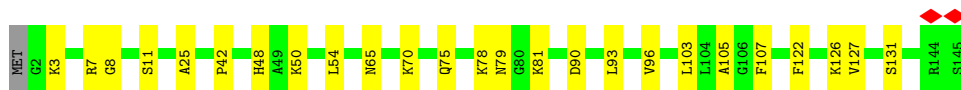


• Molecule 13: RPS22A isoform 1

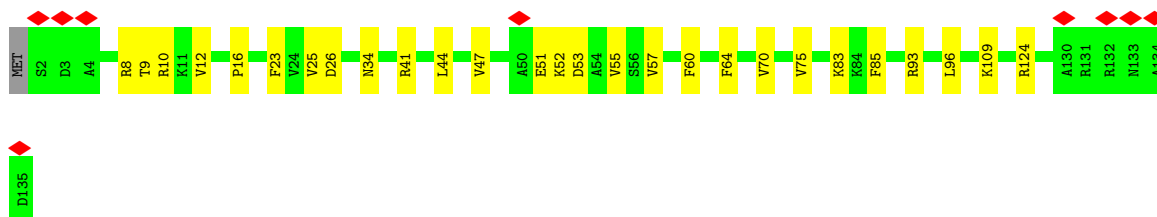
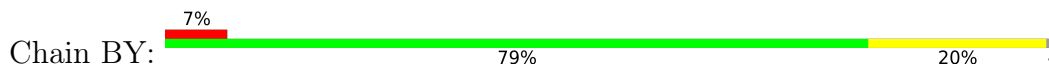


• Molecule 14: 40S ribosomal protein S23-A

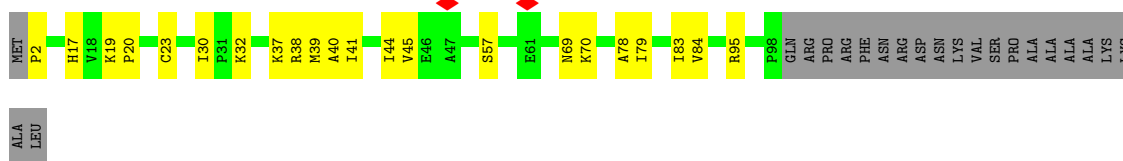




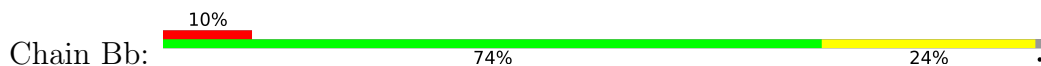
• Molecule 15: 40S ribosomal protein S24-A



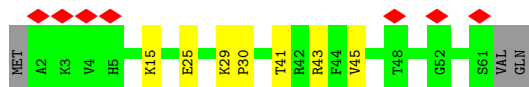
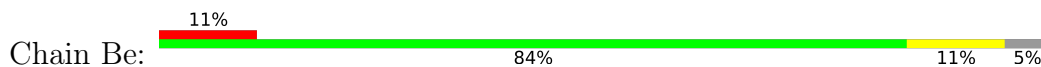
• Molecule 16: RPS26B isoform 1



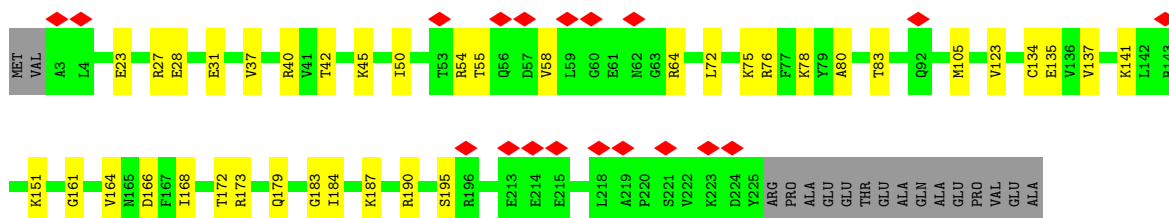
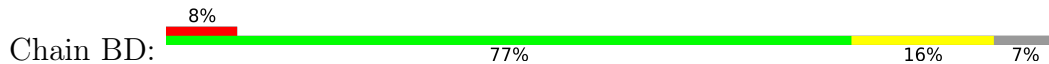
• Molecule 17: 40S ribosomal protein S27-A



• Molecule 18: 40S ribosomal protein S30-A

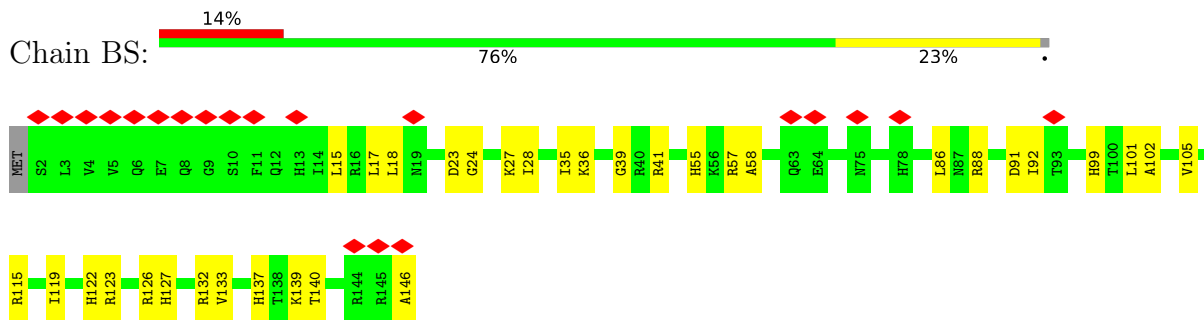


• Molecule 19: RPS3 isoform 1

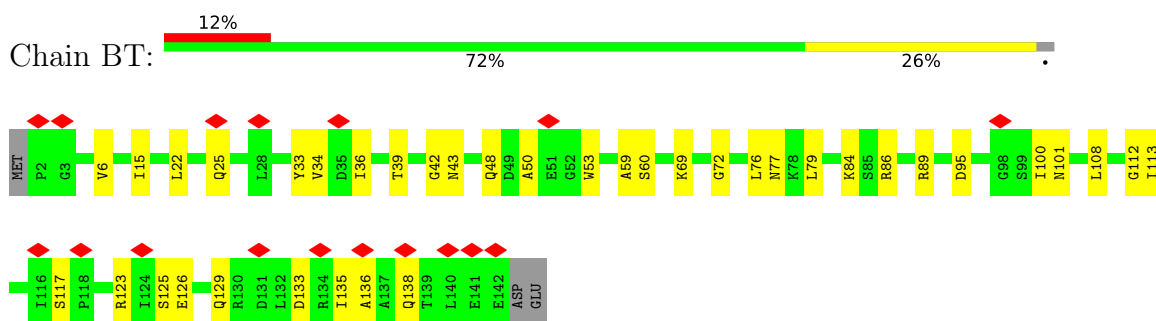


TYR
ARG
LYS
ARG
VAL

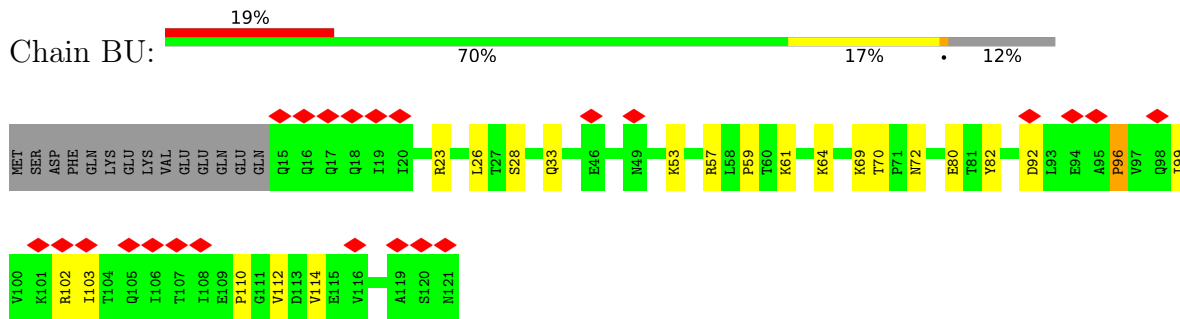
• Molecule 25: 40S ribosomal protein S18-A



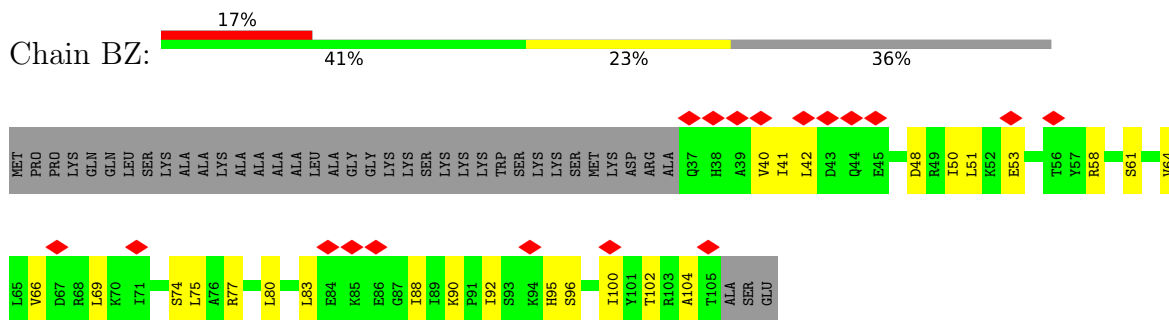
• Molecule 26: 40S ribosomal protein S19-A



• Molecule 27: RPS20 isoform 1

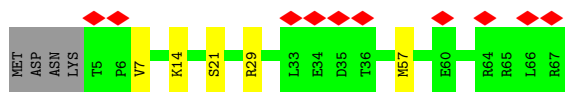


• Molecule 28: RPS25A isoform 1



• Molecule 29: RPS28A isoform 1

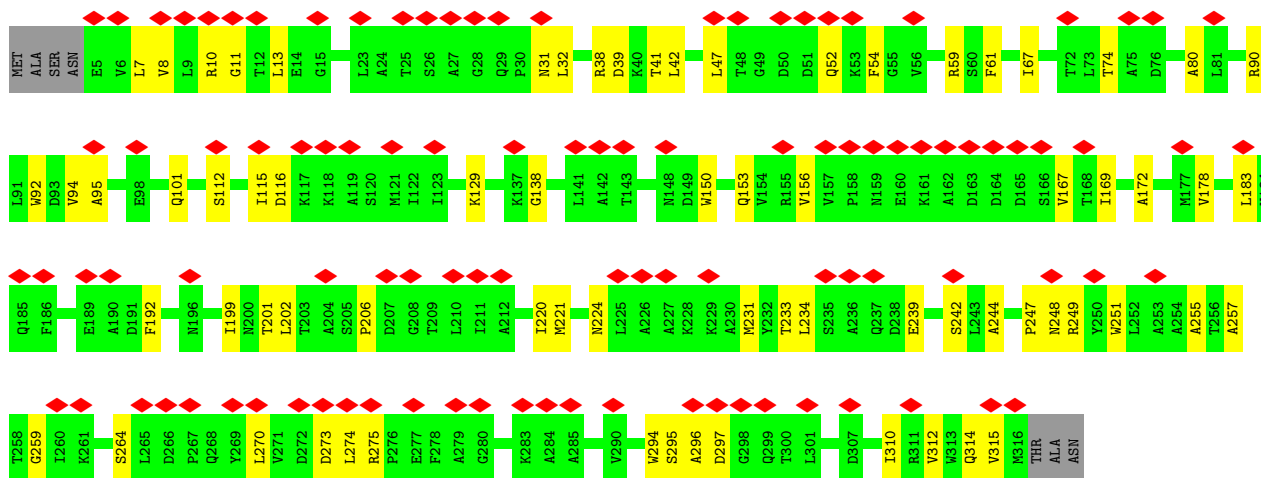
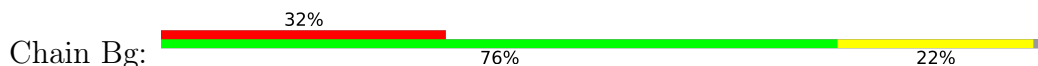




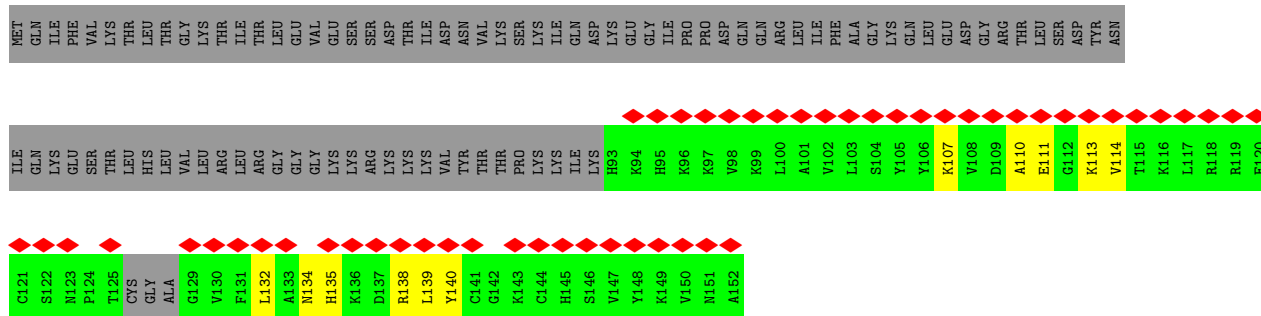
• Molecule 30: RPS29A isoform 1



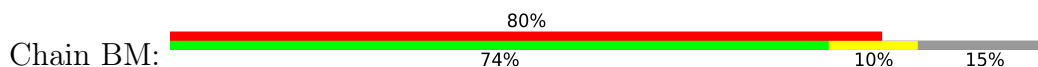
• Molecule 31: Guanine nucleotide-binding protein subunit beta-like protein

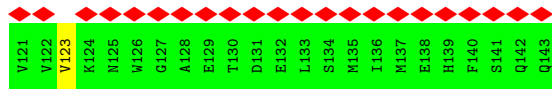
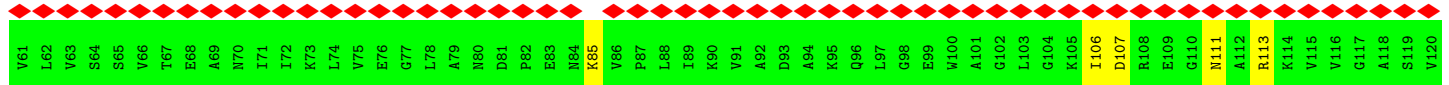


• Molecule 32: Ubiquitin-40S ribosomal protein S31

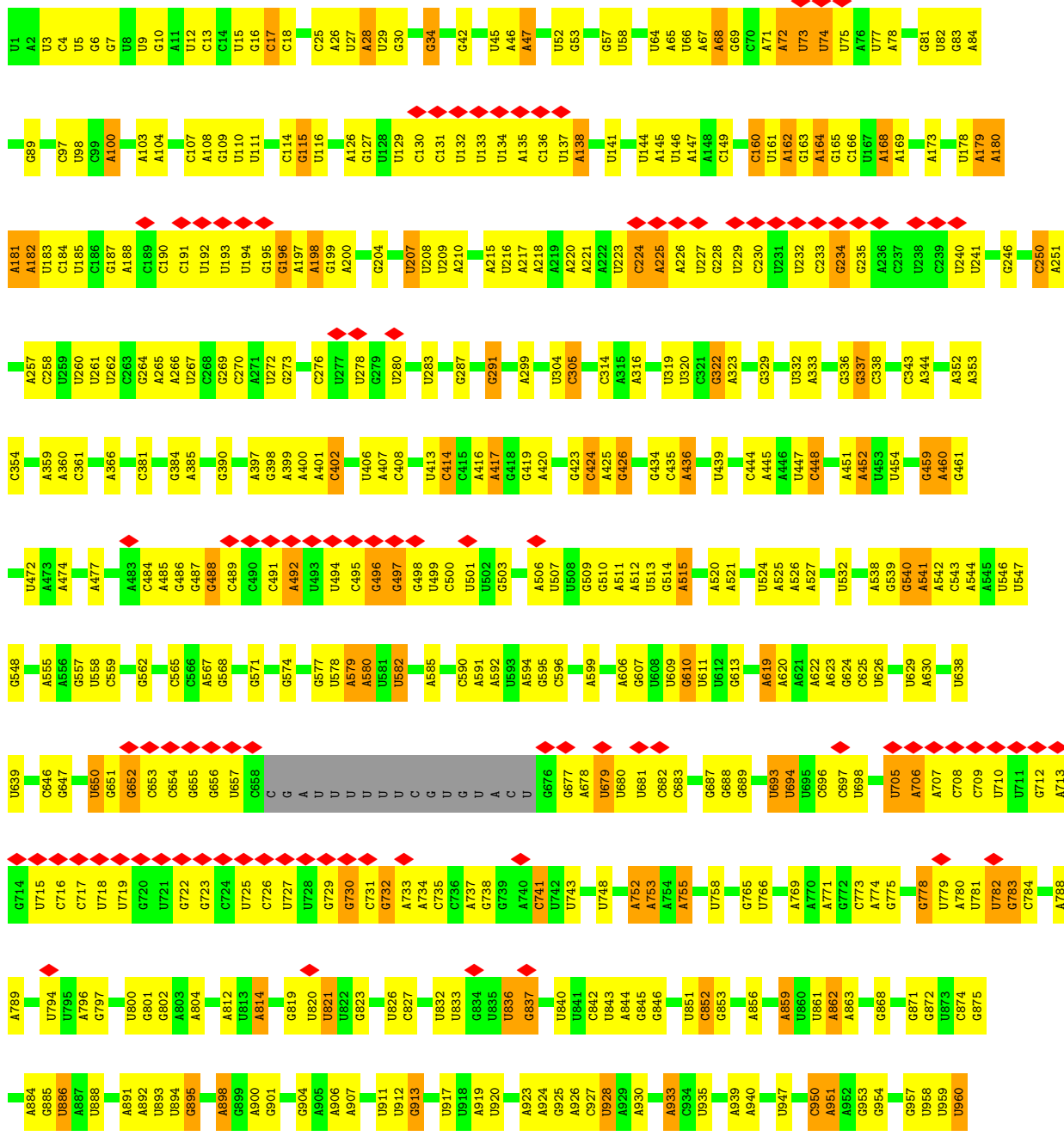


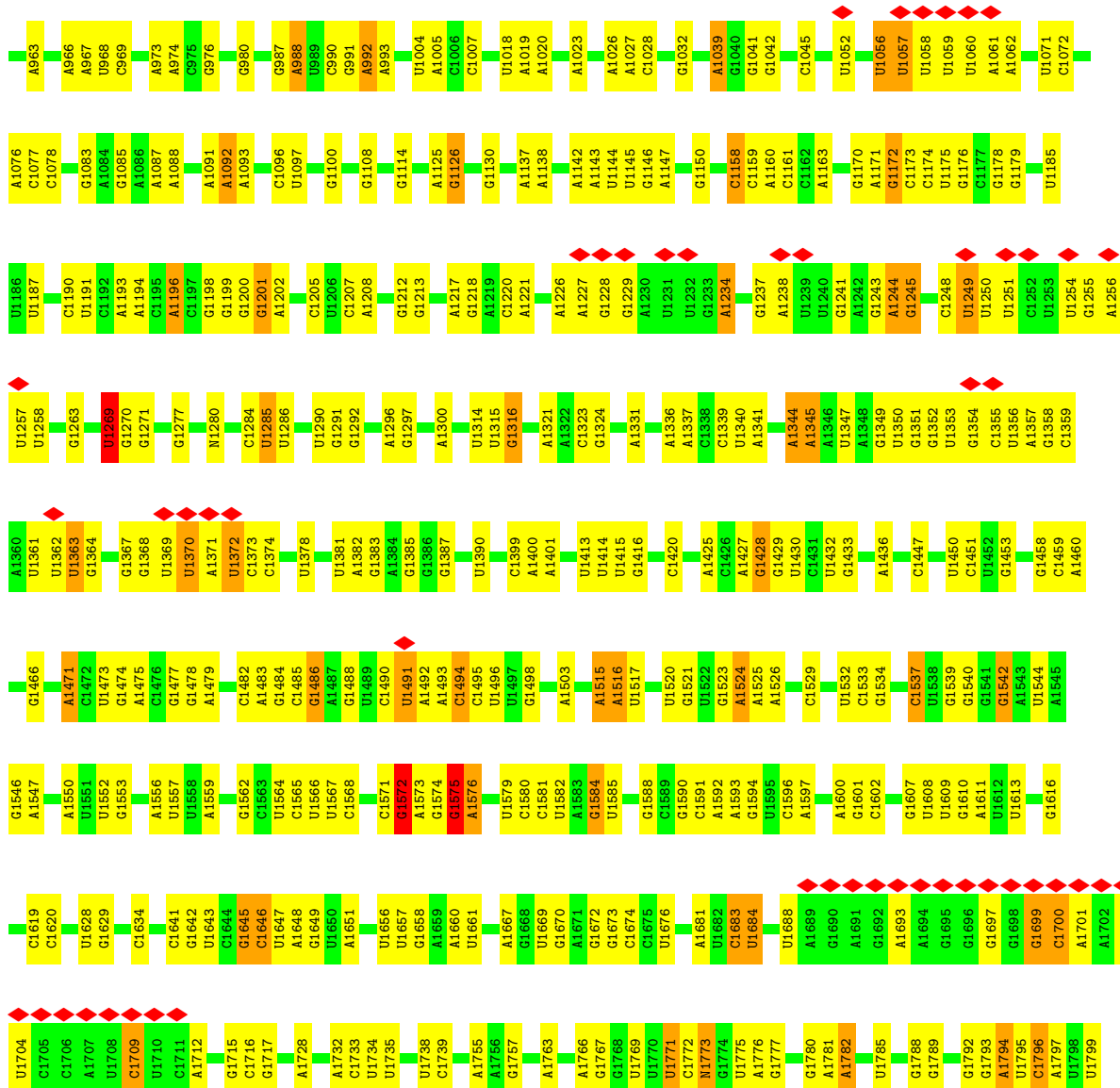
• Molecule 33: 40S ribosomal protein S12



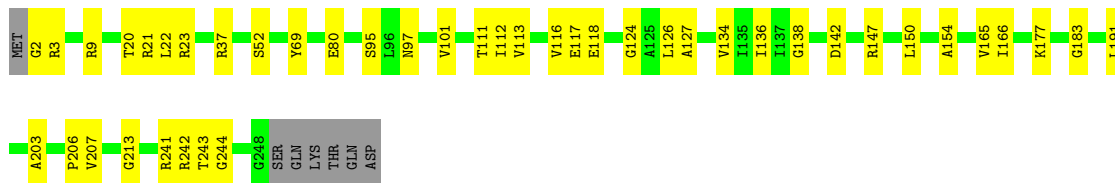
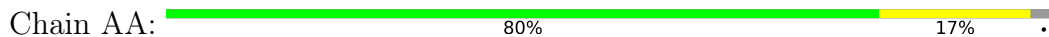


• Molecule 34: 18S rRNA

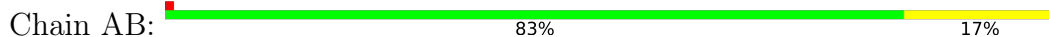


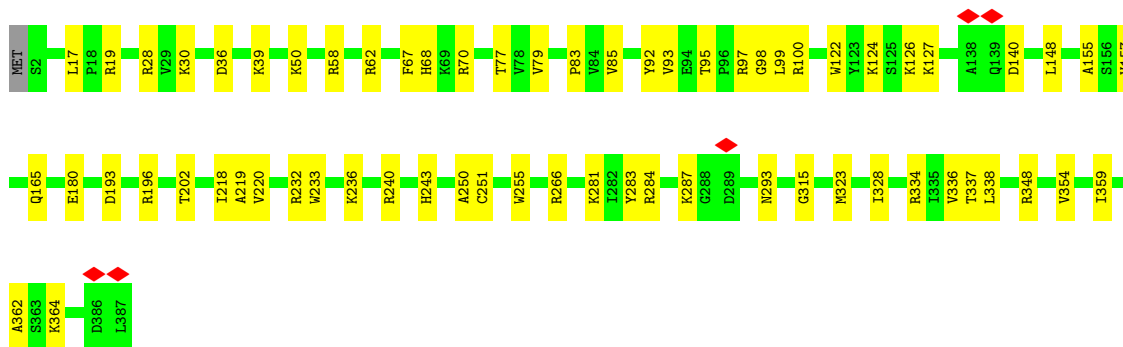


• Molecule 35: 60S ribosomal protein L2-A

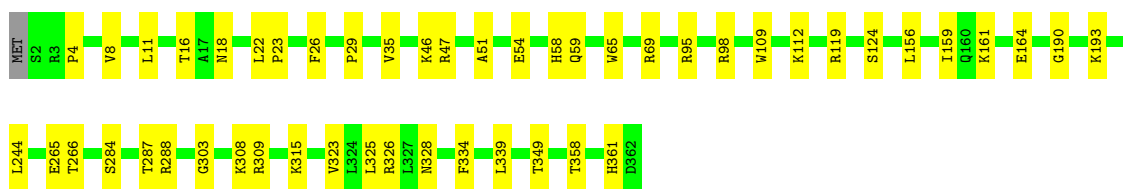
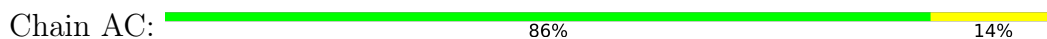


• Molecule 36: 60S ribosomal protein L3

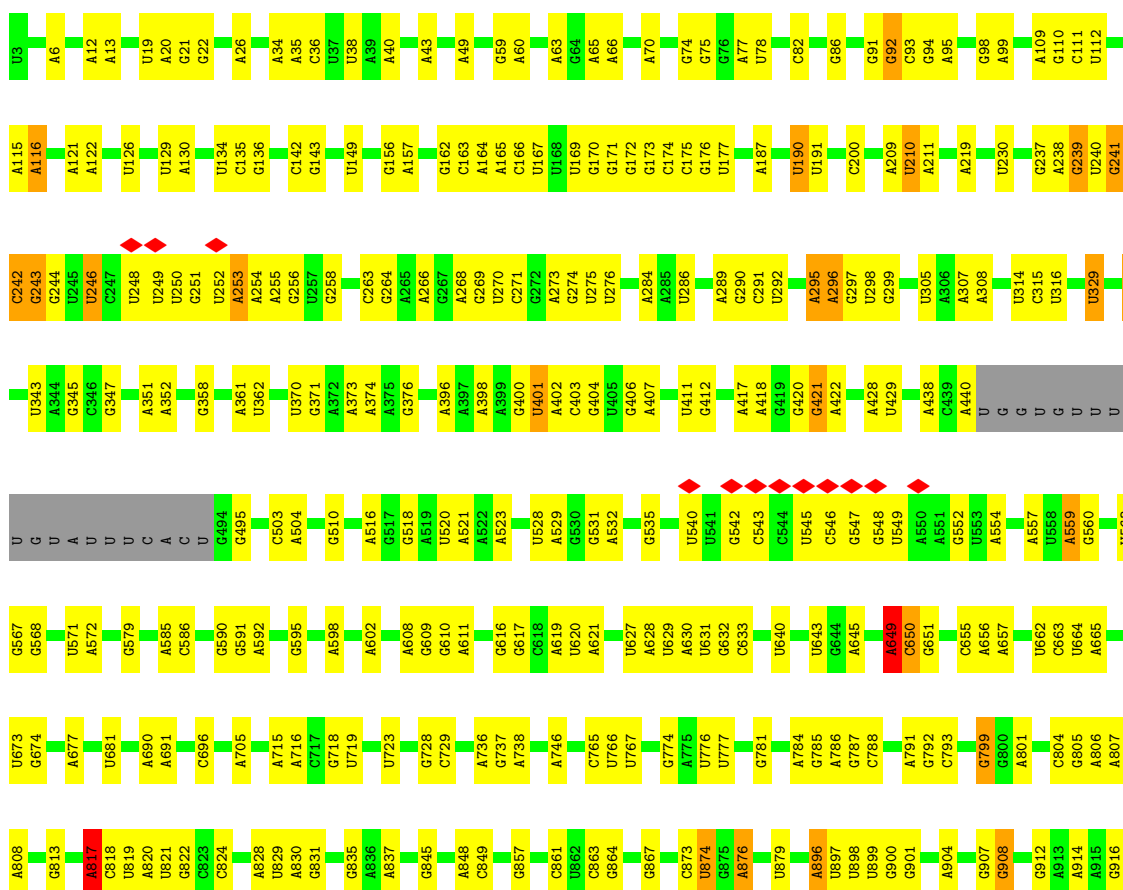




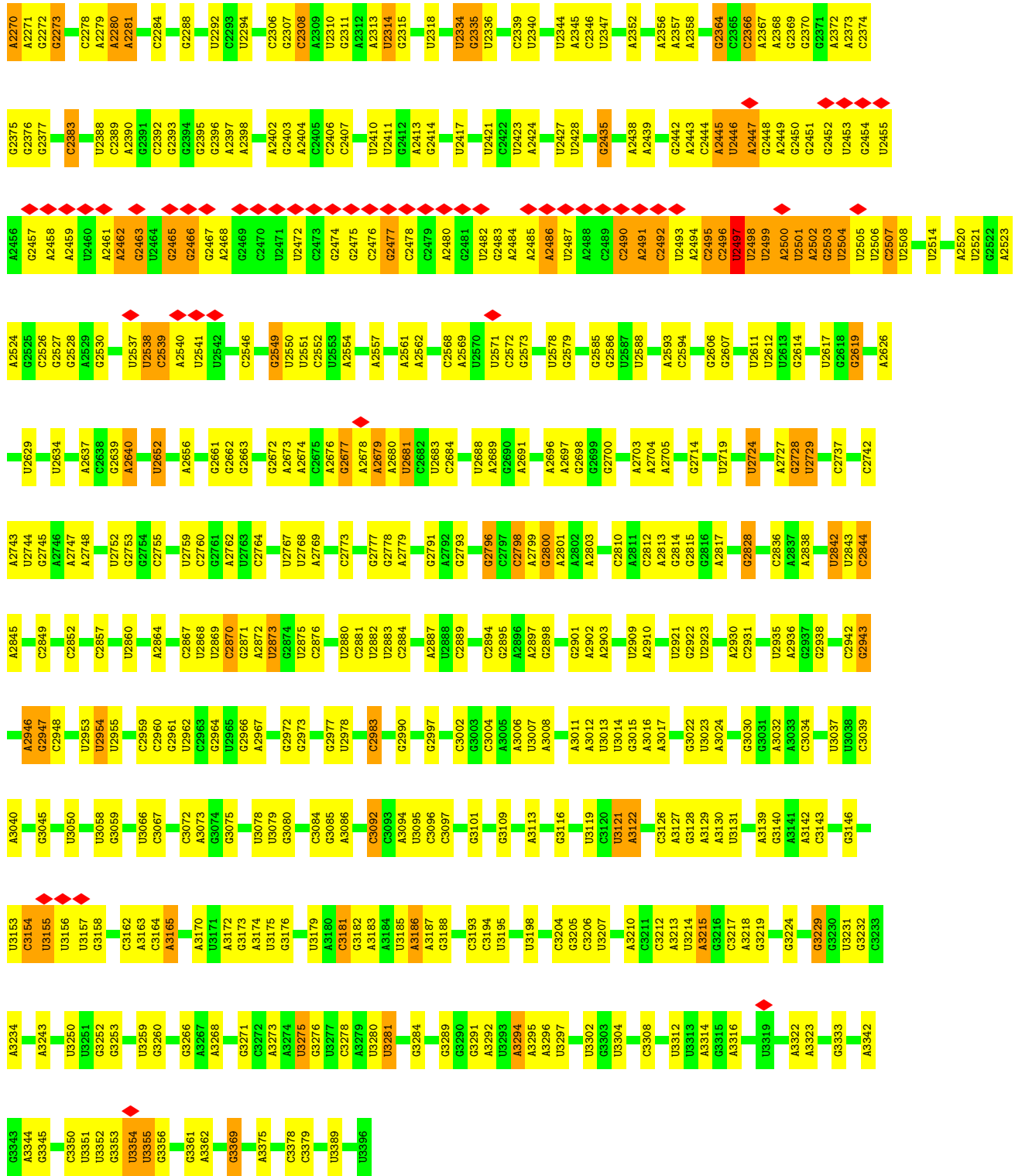
• Molecule 37: RPL4A isoform 1



• Molecule 38: 25S rRNA

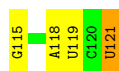


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C	A	C	A1842	G1736	U1618	U1526	G1392	G1282	A1221	C1118	A	C923
C	A	C	C1846	U1737	A1619	A1534	A1393	C1283	G1222	C1119	A	G924
C	A	C	U1738	U1737	U1620	A1535	C1397	G1284	A1223	A1120	G	A925
C	A	C	U1739	U1739	A1621	U1536	U1398	A1286	G1226	U1121	A1030	A933
C	A	C	U1740	U1740	U1622	G1542	A1399	A1287	C1227	C1131	C1032	G934
C	A	C	A1741	G1741	G1623	G1543	A1399	A1287	G1228	C1132	C1032	G937
C	A	C	G1747	G1747	G1624	U1551	G1400	A1290	G1229	U1033	U1034	C938
C	A	C	G1748	G1748	U1627	G1552	G1412	A1291	C1227	A1133	G1035	U943
C	A	C	A1855	U1748	C1628	G1553	A1418	A1292	C1228	C1141	U1039	C944
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C	A	C	G1899	C1763	C1639	U1564	A1446	A1317	A1240	A1159	A1055	C968
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C												

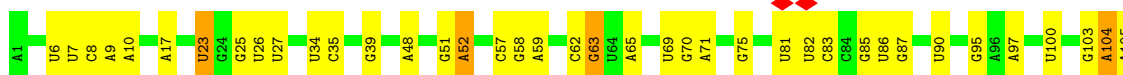


● Molecule 39: 5s rRNA

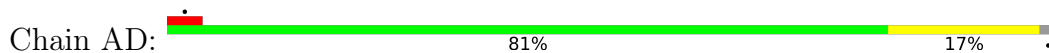




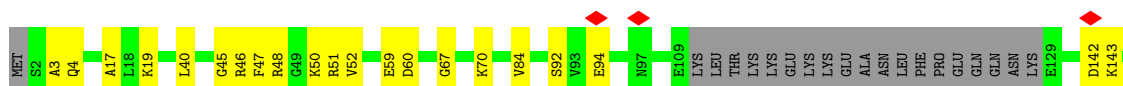
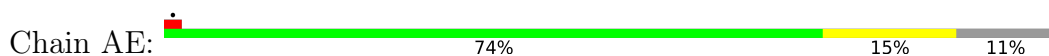
- Molecule 40: 5.8 S rRNA



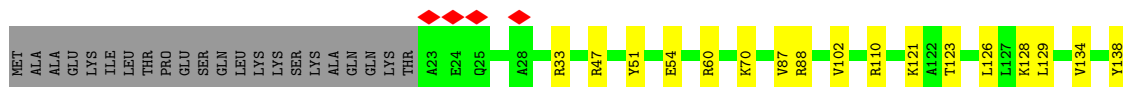
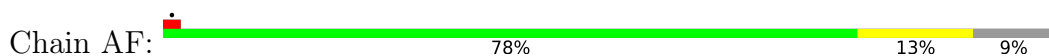
- Molecule 41: RPL5 isoform 1



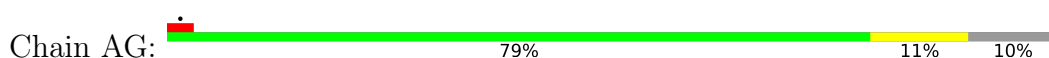
- Molecule 42: 60S ribosomal protein L6-A

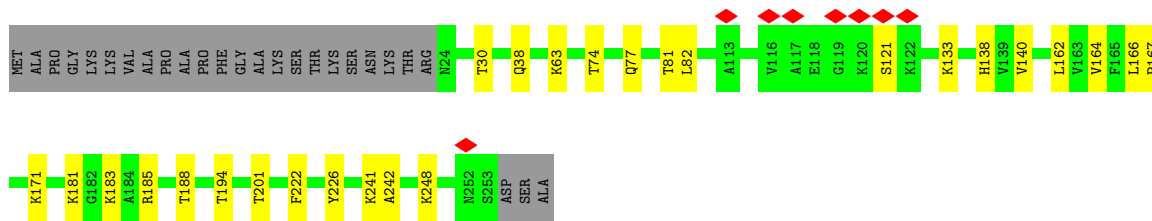


- Molecule 43: 60S ribosomal protein L7-A

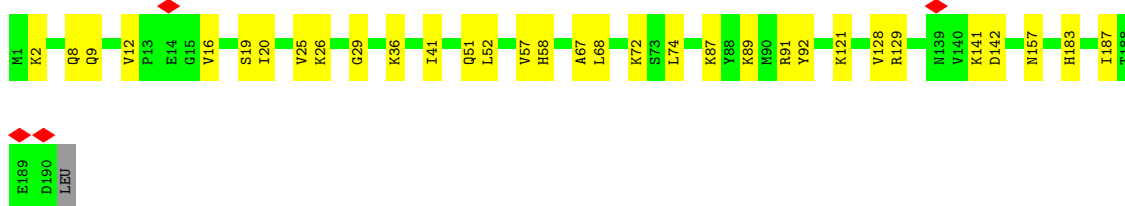
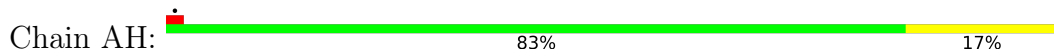


- Molecule 44: 60S ribosomal protein L8-A

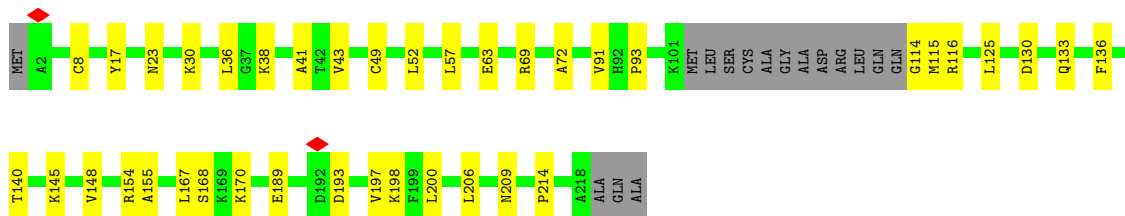
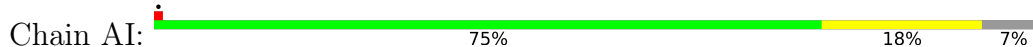




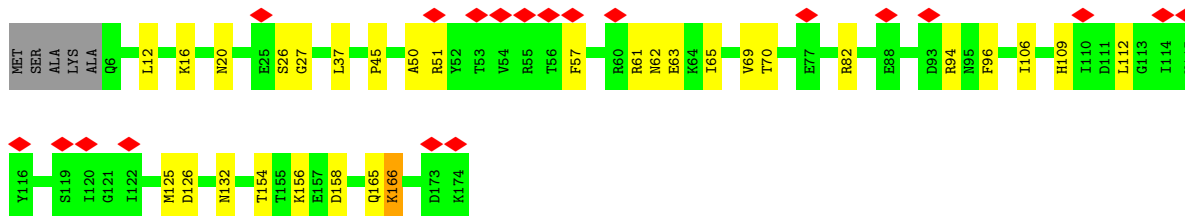
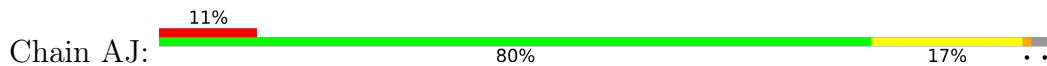
• Molecule 45: 60S ribosomal protein L9-A



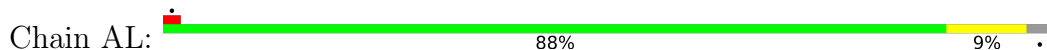
• Molecule 46: RPL10 isoform 1




• Molecule 47: RPL11A isoform 1



• Molecule 48: 60S ribosomal protein L13-A



• Molecule 49: 60S ribosomal protein L14-A

Chain AM:  80% 18%




- Molecule 50: 60S ribosomal protein L15-A

Chain AN:  88% 11%




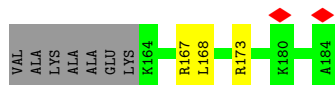
- Molecule 51: 60S ribosomal protein L16-A

Chain AO:  85% 14%




- Molecule 52: 60S ribosomal protein L17-A

Chain AP:  78% 17% 5%



- Molecule 53: 60S ribosomal protein L18-A

Chain AQ:  87% 12%




- Molecule 54: 60S ribosomal protein L19-A


Chain AR:  7% 91% 8%

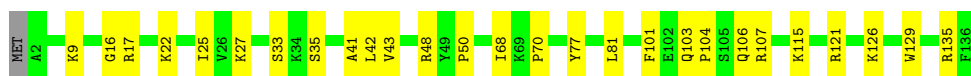


- Molecule 55: 60S ribosomal protein L20


Chain AS:  82% 15%

- Molecule 62: 60S ribosomal protein L27-A

Chain AZ:  79% 20%

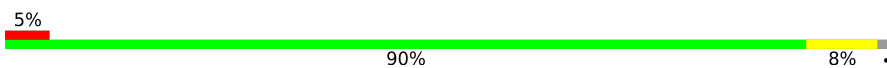


- Molecule 63: 60S ribosomal protein L28

Chain Aa:  80% 19%



- Molecule 64: RPL29 isoform 1

Chain Ab:  5% 90% 8%




- Molecule 65: 60S ribosomal protein L30

Chain Ac:  87% 6% 8%




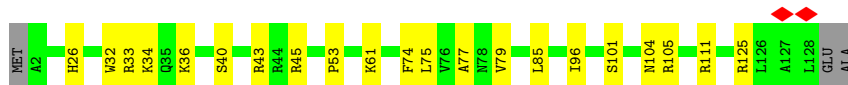
- Molecule 66: 60S ribosomal protein L31-A

Chain Ad:  6% 86% 11%




- Molecule 67: RPL32 isoform 1

Chain Ae:  82% 16%

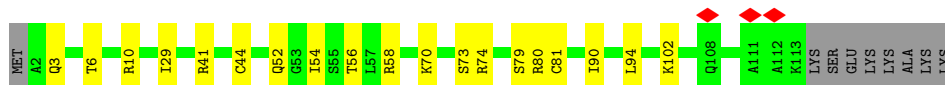
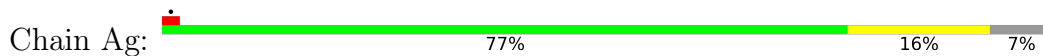


- Molecule 68: 60S ribosomal protein L33-A

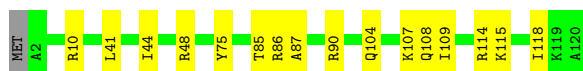
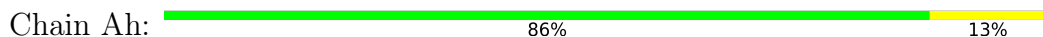
Chain Af:  79% 21%



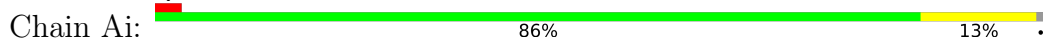
- Molecule 69: 60S ribosomal protein L34-A



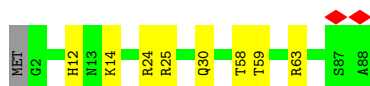
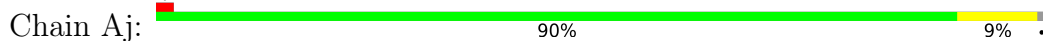
- Molecule 70: 60S ribosomal protein L35-A



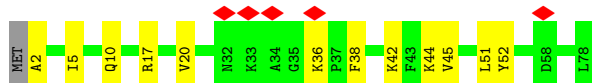
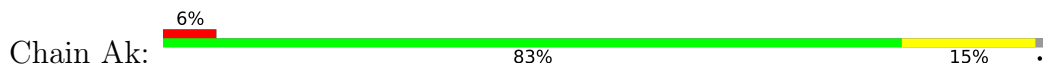
- Molecule 71: 60S ribosomal protein L36-A



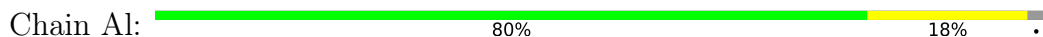
- Molecule 72: 60S ribosomal protein L37-A



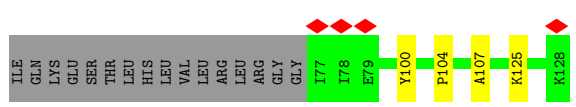
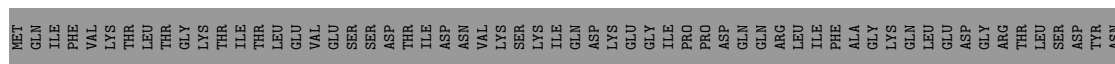
- Molecule 73: RPL38 isoform 1



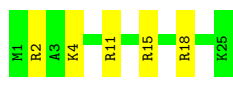
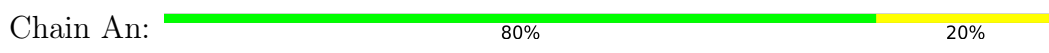
- Molecule 74: 60S ribosomal protein L39



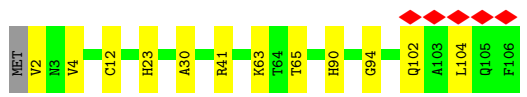
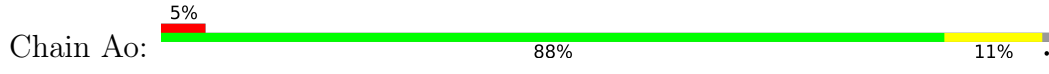
- Molecule 75: Ubiquitin-60S ribosomal protein L40



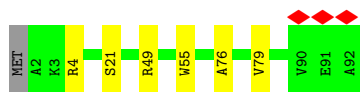
- Molecule 76: 60S ribosomal protein L41-A



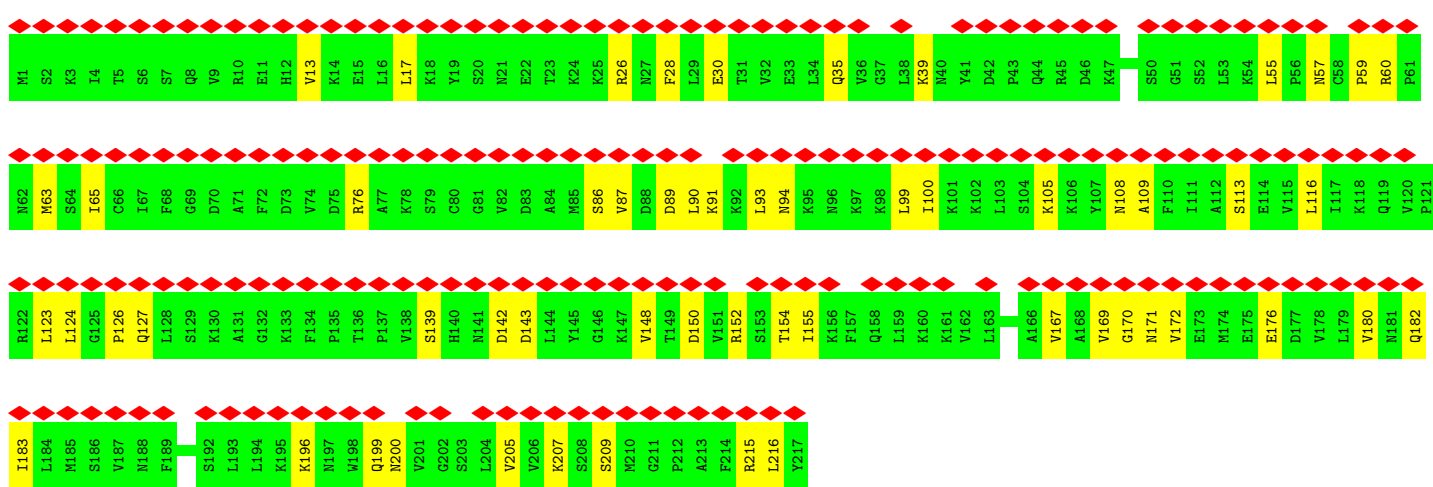
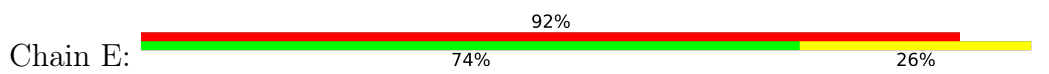
- Molecule 77: 60S ribosomal protein L42-A



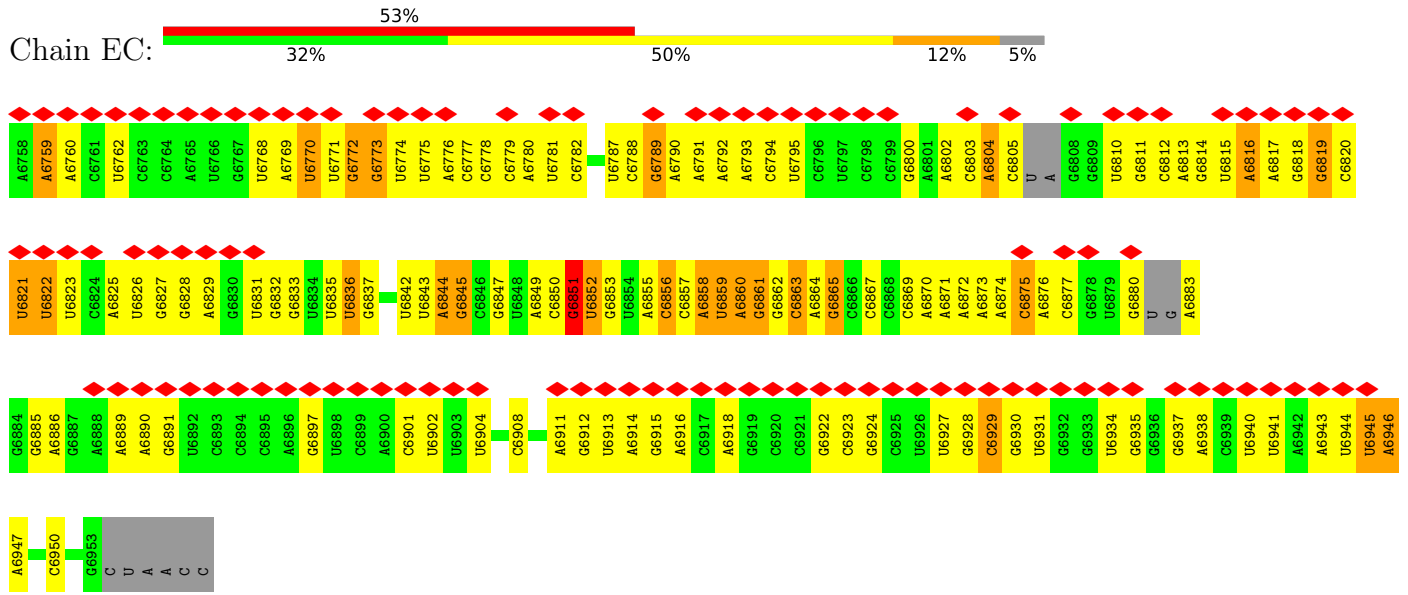
- Molecule 78: 60S ribosomal protein L43-A



- Molecule 79: RPL1A isoform 1



- Molecule 80: Internal ribosome entry site



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112542	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	7.298	Depositor
Minimum map value	-3.391	Depositor
Average map value	0.017	Depositor
Map value standard deviation	0.255	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	423.99997, 423.99997, 423.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: OMG, UR3, MA6, OMC, MG, ZN, 1MA, A2M, 5MC, XSX, HIC, 4AC, G7M, OMU

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	BA	0.19	0/1653	0.53	0/2261
2	BB	0.20	0/1735	0.55	0/2335
3	BC	0.16	0/1665	0.39	0/2263
4	BE	0.16	0/2109	0.45	0/2839
5	BG	0.13	0/1844	0.40	0/2464
6	BH	0.20	0/1506	0.53	2/2028 (0.1%)
7	BI	0.18	0/1514	0.53	0/2021
8	BJ	0.15	0/1519	0.43	0/2035
9	BL	0.16	0/1272	0.37	0/1712
10	BN	0.16	0/1215	0.46	0/1638
11	BO	0.21	0/952	0.56	0/1279
12	BV	0.17	0/693	0.44	0/935
13	BW	0.16	0/1038	0.39	0/1395
14	BX	0.18	0/1139	0.49	0/1518
15	BY	0.16	0/1087	0.46	0/1449
16	Ba	0.20	0/782	0.57	0/1047
17	Bb	0.15	0/620	0.46	0/838
18	Be	0.12	0/483	0.43	0/643
19	BD	0.16	0/1759	0.43	0/2368
20	BF	0.17	0/1629	0.47	0/2202
21	BK	0.19	0/837	0.56	0/1131
22	BP	0.16	0/1012	0.45	0/1356
23	BQ	0.17	0/1125	0.46	0/1510
24	BR	0.18	0/984	0.46	0/1318
25	BS	0.16	0/1211	0.47	0/1628
26	BT	0.18	0/1113	0.59	2/1494 (0.1%)
27	BU	0.19	0/865	0.52	1/1169 (0.1%)
28	BZ	0.18	0/566	0.49	0/761
29	Bc	0.15	0/499	0.45	0/670
30	Bd	0.17	0/453	0.43	0/602
31	Bg	0.16	0/2454	0.47	0/3340
32	Bf	0.17	0/462	0.62	2/617 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	BM	0.17	0/921	0.51	0/1245
34	B5	0.18	1/41880 (0.0%)	0.34	4/65248 (0.0%)
35	AA	0.18	0/1912	0.41	0/2569
36	AB	0.18	0/3138	0.41	0/4217
37	AC	0.19	0/2800	0.46	0/3790
38	A1	0.21	2/75561 (0.0%)	0.36	3/117806 (0.0%)
39	A3	0.16	0/2883	0.31	0/4491
40	A4	0.19	0/3746	0.33	0/5832
41	AD	0.15	0/2390	0.42	0/3225
42	AE	0.16	0/1260	0.40	0/1694
43	AF	0.18	0/1821	0.44	0/2451
44	AG	0.18	0/1830	0.47	0/2469
45	AH	0.17	0/1531	0.44	0/2062
46	AI	0.16	0/1708	0.38	1/2290 (0.0%)
47	AJ	0.22	0/1374	0.61	0/1842
48	AL	0.18	0/1568	0.45	0/2106
49	AM	0.16	0/1068	0.38	0/1438
50	AN	0.19	0/1757	0.40	0/2354
51	AO	0.17	0/1585	0.39	0/2128
52	AP	0.17	0/1410	0.41	0/1893
53	AQ	0.16	0/1465	0.38	0/1965
54	AR	0.15	0/1538	0.37	0/2050
55	AS	0.19	0/1481	0.43	0/1990
56	AT	0.20	0/1300	0.45	0/1743
57	AU	0.16	0/812	0.44	0/1099
58	AV	0.18	0/1018	0.43	0/1369
59	AW	0.16	0/533	0.38	0/707
60	AX	0.19	0/983	0.43	0/1325
61	AY	0.17	0/1004	0.40	0/1341
62	AZ	0.16	0/1118	0.37	0/1497
63	Aa	0.19	0/1204	0.48	0/1612
64	Ab	0.17	0/473	0.43	0/629
65	Ac	0.16	0/751	0.40	0/1008
66	Ad	0.16	0/904	0.35	0/1213
67	Ae	0.17	0/1041	0.38	0/1394
68	Af	0.20	0/868	0.42	0/1168
69	Ag	0.23	0/890	0.50	0/1189
70	Ah	0.15	0/978	0.35	0/1301
71	Ai	0.22	0/778	0.47	0/1034
72	Aj	0.21	0/696	0.48	0/923
73	Ak	0.15	0/618	0.39	0/826
74	Al	0.18	0/443	0.42	0/588
75	Am	0.16	0/423	0.37	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	An	0.21	0/234	0.66	0/300
77	Ao	0.17	0/860	0.51	0/1136
78	Ap	0.18	0/701	0.43	0/934
79	E	0.17	0/1745	0.44	0/2342
80	EC	0.16	0/4571	0.40	1/7114 (0.0%)
All	All	0.19	3/219368 (0.0%)	0.39	16/322375 (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
20	BF	0	1
43	AF	0	1
44	AG	0	2
47	AJ	0	1
All	All	0	5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	O3'-P	7.19	1.63	1.56
38	A1	2256	A2M	O3'-P	5.81	1.62	1.56
38	A1	2946	A2M	O3'-P	5.11	1.61	1.56

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BT	34	VAL	CA-C-N	7.62	139.57	126.32
26	BT	34	VAL	C-N-CA	7.62	139.57	126.32
6	BH	13	PRO	CA-C-N	6.92	134.16	121.70
6	BH	13	PRO	C-N-CA	6.92	134.16	121.70
34	B5	1057	U	C2'-C3'-O3'	6.57	119.35	109.50

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
43	AF	232	ARG	Peptide
44	AG	121	SER	Peptide

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Mol	Chain	Res	Type	Group
44	AG	30	THR	Peptide
47	AJ	166	LYS	Peptide
20	BF	124	LEU	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	BA	1612	0	1623	20	0
2	BB	1709	0	1784	38	0
3	BC	1635	0	1723	22	0
4	BE	2068	0	2154	38	0
5	BG	1820	0	1918	32	0
6	BH	1481	0	1572	12	0
7	BI	1489	0	1525	30	0
8	BJ	1494	0	1573	25	0
9	BL	1244	0	1314	10	0
10	BN	1192	0	1255	20	0
11	BO	941	0	979	19	0
12	BV	684	0	672	9	0
13	BW	1021	0	1060	13	0
14	BX	1121	0	1196	20	0
15	BY	1073	0	1132	22	0
16	Ba	769	0	818	15	0
17	Bb	610	0	633	16	0
18	Be	475	0	525	5	0
19	BD	1734	0	1817	30	0
20	BF	1609	0	1675	33	0
21	BK	817	0	804	21	0
22	BP	991	0	1035	32	0
23	BQ	1105	0	1166	29	0
24	BR	975	0	1039	13	0
25	BS	1192	0	1222	26	0
26	BT	1095	0	1114	24	0
27	BU	855	0	917	16	0
28	BZ	558	0	598	17	0
29	Bc	497	0	535	4	0
30	Bd	443	0	436	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	Bg	2401	0	2356	41	0
32	Bf	454	0	465	8	0
33	BM	913	0	955	9	0
34	B5	38004	0	19142	437	0
35	AA	1878	0	1946	30	0
36	AB	3080	0	3158	49	0
37	AC	2748	0	2859	36	0
38	A1	68445	0	34455	602	0
39	A3	2579	0	1304	27	0
40	A4	3353	0	1695	32	0
41	AD	2341	0	2290	34	0
42	AE	1239	0	1326	19	0
43	AF	1784	0	1862	20	0
44	AG	1798	0	1894	16	0
45	AH	1510	0	1576	18	0
46	AI	1672	0	1711	23	0
47	AJ	1353	0	1383	20	0
48	AL	1543	0	1608	16	0
49	AM	1053	0	1149	17	0
50	AN	1720	0	1779	19	0
51	AO	1555	0	1659	21	0
52	AP	1388	0	1423	20	0
53	AQ	1441	0	1543	16	0
54	AR	1521	0	1617	17	0
55	AS	1445	0	1487	24	0
56	AT	1276	0	1323	19	0
57	AU	796	0	812	9	0
58	AV	1003	0	1048	21	0
59	AW	521	0	551	2	0
60	AX	968	0	1036	11	0
61	AY	993	0	1081	12	0
62	AZ	1092	0	1155	19	0
63	Aa	1173	0	1215	27	0
64	Ab	462	0	491	6	0
65	Ac	743	0	797	4	0
66	Ad	890	0	938	7	0
67	Ae	1020	0	1090	17	0
68	Af	850	0	880	17	0
69	Ag	880	0	945	17	0
70	Ah	969	0	1078	12	0
71	Ai	771	0	849	10	0
72	Aj	681	0	687	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	Ak	612	0	682	10	0
74	Al	436	0	475	9	0
75	Am	417	0	459	4	0
76	An	233	0	281	5	0
77	Ao	847	0	914	9	0
78	Ap	694	0	738	6	0
79	E	1718	0	1811	40	0
80	EC	4090	0	2068	41	0
81	A1	182	0	0	0	0
81	A3	2	0	0	0	0
81	A4	5	0	0	0	0
81	AC	1	0	0	0	0
81	AD	1	0	0	0	0
81	AL	1	0	0	0	0
81	AP	1	0	0	0	0
81	B5	60	0	0	0	0
81	BE	1	0	0	0	0
81	BN	1	0	0	0	0
81	Ba	1	0	0	0	0
82	Ao	1	0	0	0	0
All	All	205919	0	151860	2063	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 6.

The worst 5 of 2063 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)
38:A1:2457:G:N2	38:A1:2486:A:C2	1.94	1.35
34:B5:1588:G:H1	34:B5:1608:U:H3	0.99	0.93
34:B5:1697:G:H1	34:B5:1704:U:H3	0.96	0.90
38:A1:2457:G:N2	38:A1:2486:A:H2	1.62	0.87
38:A1:2457:G:C2	38:A1:2486:A:C2	2.73	0.77

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	186 (91%)	18 (9%)	0	100	100
2	BB	212/255 (83%)	185 (87%)	27 (13%)	0	100	100
3	BC	215/254 (85%)	206 (96%)	9 (4%)	0	100	100
4	BE	258/261 (99%)	244 (95%)	14 (5%)	0	100	100
5	BG	224/236 (95%)	215 (96%)	9 (4%)	0	100	100
6	BH	182/190 (96%)	170 (93%)	12 (7%)	0	100	100
7	BI	184/200 (92%)	168 (91%)	16 (9%)	0	100	100
8	BJ	183/197 (93%)	168 (92%)	15 (8%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
10	BN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
11	BO	125/137 (91%)	112 (90%)	13 (10%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
14	BX	142/145 (98%)	131 (92%)	11 (8%)	0	100	100
15	BY	132/135 (98%)	124 (94%)	8 (6%)	0	100	100
16	Ba	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
17	Bb	79/82 (96%)	67 (85%)	12 (15%)	0	100	100
18	Be	58/63 (92%)	53 (91%)	5 (9%)	0	100	100
19	BD	221/240 (92%)	209 (95%)	12 (5%)	0	100	100
20	BF	204/225 (91%)	191 (94%)	13 (6%)	0	100	100
21	BK	94/105 (90%)	83 (88%)	11 (12%)	0	100	100
22	BP	122/142 (86%)	111 (91%)	11 (9%)	0	100	100
23	BQ	139/143 (97%)	133 (96%)	6 (4%)	0	100	100
24	BR	117/136 (86%)	110 (94%)	7 (6%)	0	100	100
25	BS	143/146 (98%)	129 (90%)	14 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BT	139/144 (96%)	127 (91%)	12 (9%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	67/108 (62%)	62 (92%)	5 (8%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
31	Bg	310/319 (97%)	275 (89%)	35 (11%)	0	100	100
32	Bf	53/152 (35%)	39 (74%)	14 (26%)	0	100	100
33	BM	119/143 (83%)	95 (80%)	24 (20%)	0	100	100
35	AA	245/254 (96%)	232 (95%)	13 (5%)	0	100	100
36	AB	383/387 (99%)	367 (96%)	16 (4%)	0	100	100
37	AC	359/362 (99%)	335 (93%)	24 (7%)	0	100	100
41	AD	290/297 (98%)	276 (95%)	14 (5%)	0	100	100
42	AE	152/176 (86%)	141 (93%)	11 (7%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	212 (93%)	16 (7%)	0	100	100
45	AH	188/191 (98%)	172 (92%)	16 (8%)	0	100	100
46	AI	201/221 (91%)	191 (95%)	10 (5%)	0	100	100
47	AJ	167/174 (96%)	142 (85%)	25 (15%)	0	100	100
48	AL	191/199 (96%)	179 (94%)	12 (6%)	0	100	100
49	AM	134/138 (97%)	130 (97%)	4 (3%)	0	100	100
50	AN	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
51	AO	195/199 (98%)	193 (99%)	2 (1%)	0	100	100
52	AP	171/184 (93%)	167 (98%)	4 (2%)	0	100	100
53	AQ	183/186 (98%)	178 (97%)	5 (3%)	0	100	100
54	AR	186/189 (98%)	177 (95%)	9 (5%)	0	100	100
55	AS	170/178 (96%)	160 (94%)	10 (6%)	0	100	100
56	AT	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
57	AU	98/121 (81%)	94 (96%)	4 (4%)	0	100	100
58	AV	134/137 (98%)	132 (98%)	2 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	115 (97%)	4 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AY	124/127 (98%)	121 (98%)	3 (2%)	0	100	100
62	AZ	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
63	Aa	146/149 (98%)	130 (89%)	16 (11%)	0	100	100
64	Ab	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
65	Ac	95/105 (90%)	94 (99%)	1 (1%)	0	100	100
66	Ad	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
67	Ae	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
68	Af	104/107 (97%)	101 (97%)	3 (3%)	0	100	100
69	Ag	110/121 (91%)	106 (96%)	4 (4%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	90 (93%)	7 (7%)	0	100	100
72	Aj	85/88 (97%)	82 (96%)	3 (4%)	0	100	100
73	Ak	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
74	Al	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
75	Am	50/128 (39%)	47 (94%)	3 (6%)	0	100	100
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
78	Ap	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
79	E	215/217 (99%)	205 (95%)	10 (5%)	0	100	100
All	All	11086/12103 (92%)	10364 (94%)	722 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	BA	173/210 (82%)	173 (100%)	0	100	100
2	BB	191/224 (85%)	191 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	BC	176/205 (86%)	176 (100%)	0	100	100
4	BE	221/222 (100%)	221 (100%)	0	100	100
5	BG	193/201 (96%)	193 (100%)	0	100	100
6	BH	165/170 (97%)	165 (100%)	0	100	100
7	BI	150/161 (93%)	150 (100%)	0	100	100
8	BJ	158/166 (95%)	158 (100%)	0	100	100
9	BL	136/137 (99%)	136 (100%)	0	100	100
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	96 (100%)	0	100	100
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	110 (100%)	0	100	100
14	BX	119/120 (99%)	119 (100%)	0	100	100
15	BY	112/113 (99%)	112 (100%)	0	100	100
16	Ba	83/100 (83%)	83 (100%)	0	100	100
17	Bb	70/71 (99%)	70 (100%)	0	100	100
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	182 (100%)	0	100	100
20	BF	173/191 (91%)	173 (100%)	0	100	100
21	BK	89/98 (91%)	89 (100%)	0	100	100
22	BP	104/118 (88%)	104 (100%)	0	100	100
23	BQ	117/119 (98%)	117 (100%)	0	100	100
24	BR	110/124 (89%)	110 (100%)	0	100	100
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	113 (100%)	0	100	100
27	BU	100/114 (88%)	100 (100%)	0	100	100
28	BZ	61/89 (68%)	61 (100%)	0	100	100
29	Bc	56/60 (93%)	56 (100%)	0	100	100
30	Bd	47/49 (96%)	47 (100%)	0	100	100
31	Bg	256/262 (98%)	256 (100%)	0	100	100
32	Bf	49/135 (36%)	49 (100%)	0	100	100
33	BM	98/119 (82%)	98 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	321 (100%)	0	100	100
37	AC	288/289 (100%)	288 (100%)	0	100	100
41	AD	241/245 (98%)	241 (100%)	0	100	100
42	AE	134/153 (88%)	134 (100%)	0	100	100
43	AF	186/205 (91%)	186 (100%)	0	100	100
44	AG	189/208 (91%)	189 (100%)	0	100	100
45	AH	170/171 (99%)	170 (100%)	0	100	100
46	AI	176/187 (94%)	176 (100%)	0	100	100
47	AJ	147/150 (98%)	147 (100%)	0	100	100
48	AL	154/159 (97%)	154 (100%)	0	100	100
49	AM	107/109 (98%)	107 (100%)	0	100	100
50	AN	175/176 (99%)	175 (100%)	0	100	100
51	AO	160/162 (99%)	160 (100%)	0	100	100
52	AP	141/146 (97%)	141 (100%)	0	100	100
53	AQ	150/151 (99%)	150 (100%)	0	100	100
54	AR	153/154 (99%)	153 (100%)	0	100	100
55	AS	156/162 (96%)	156 (100%)	0	100	100
56	AT	136/137 (99%)	136 (100%)	0	100	100
57	AU	87/107 (81%)	87 (100%)	0	100	100
58	AV	104/105 (99%)	104 (100%)	0	100	100
59	AW	55/129 (43%)	55 (100%)	0	100	100
60	AX	105/118 (89%)	105 (100%)	0	100	100
61	AY	109/110 (99%)	109 (100%)	0	100	100
62	AZ	115/116 (99%)	115 (100%)	0	100	100
63	Aa	118/119 (99%)	118 (100%)	0	100	100
64	Ab	46/47 (98%)	46 (100%)	0	100	100
65	Ac	81/88 (92%)	81 (100%)	0	100	100
66	Ad	96/97 (99%)	96 (100%)	0	100	100
67	Ae	109/111 (98%)	109 (100%)	0	100	100
68	Af	90/91 (99%)	90 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	Ag	95/103 (92%)	95 (100%)	0	100	100
70	Ah	104/105 (99%)	104 (100%)	0	100	100
71	Ai	81/82 (99%)	81 (100%)	0	100	100
72	Aj	70/71 (99%)	70 (100%)	0	100	100
73	Ak	68/69 (99%)	68 (100%)	0	100	100
74	Al	45/46 (98%)	45 (100%)	0	100	100
75	Am	47/116 (40%)	47 (100%)	0	100	100
76	An	23/23 (100%)	23 (100%)	0	100	100
77	Ao	90/91 (99%)	90 (100%)	0	100	100
78	Ap	71/72 (99%)	71 (100%)	0	100	100
79	E	198/198 (100%)	198 (100%)	0	100	100
All	All	9468/10186 (93%)	9468 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 178 such sidechains are listed below:

Mol	Chain	Res	Type
46	AI	23	ASN
60	AX	65	GLN
46	AI	92	HIS
51	AO	31[A]	GLN
62	AZ	123	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1780/1799 (98%)	403 (22%)	12 (0%)
38	A1	3194/3360 (95%)	606 (18%)	27 (0%)
39	A3	120/121 (99%)	12 (10%)	1 (0%)
40	A4	157/158 (99%)	26 (16%)	0
80	EC	189/202 (93%)	87 (46%)	11 (5%)
All	All	5440/5640 (96%)	1134 (20%)	51 (0%)

5 of 1134 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	17	C
34	B5	25	C
34	B5	26	A
34	B5	34	G
34	B5	42	G

5 of 51 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	2496	C
38	A1	2506	U
80	EC	6911	A
38	A1	2497	U
38	A1	2501	U

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

67 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
38	OMU	A1	2724	38	19,22,23	1.22	3 (15%)	25,31,34	1.82	5 (20%)
34	OMG	B5	1126	34	23,26,27	1.18	3 (13%)	32,38,41	2.00	6 (18%)
38	OMU	A1	2347	38	19,22,23	1.29	4 (21%)	25,31,34	1.84	5 (20%)
38	A2M	A1	2220	38	22,25,26	1.54	5 (22%)	30,36,39	1.94	8 (26%)
34	OMC	B5	1007	34	19,22,23	0.78	0	25,31,34	0.91	1 (4%)
38	OMC	A1	663	38	19,22,23	0.79	0	25,31,34	0.80	0
38	A2M	A1	1449	81,38	22,25,26	1.48	4 (18%)	30,36,39	2.03	7 (23%)
34	OMC	B5	414	34	19,22,23	0.81	0	25,31,34	0.80	1 (4%)
34	A2M	B5	436	34	22,25,26	1.51	4 (18%)	30,36,39	2.06	7 (23%)
38	5MC	A1	2278	81,38	19,22,23	1.55	3 (15%)	26,32,35	1.22	3 (11%)
38	OMU	A1	2421	38	19,22,23	1.23	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	2793	38	23,26,27	1.18	3 (13%)	32,38,41	2.02	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
38	1MA	A1	645	81,38	21,25,26	1.34	4 (19%)	30,37,40	1.66	6 (20%)
36	HIC	AB	243	36	10,11,12	1.49	1 (10%)	9,14,16	1.48	1 (11%)
38	1MA	A1	2142	81,38	21,25,26	1.33	4 (19%)	30,37,40	1.72	4 (13%)
38	A2M	A1	2640	38	22,25,26	1.48	3 (13%)	30,36,39	2.06	7 (23%)
34	G7M	B5	1575	34	23,26,27	2.59	9 (39%)	34,39,42	2.96	12 (35%)
38	OMG	A1	867	38	23,26,27	1.18	3 (13%)	32,38,41	2.01	6 (18%)
34	4AC	B5	1773	34	21,24,25	0.99	1 (4%)	28,34,37	1.97	7 (25%)
34	OMC	B5	1639	34	19,22,23	0.76	0	25,31,34	0.76	0
38	OMC	A1	650	38	19,22,23	0.77	0	25,31,34	0.83	1 (4%)
38	OMC	A1	1437	81,38	19,22,23	0.83	0	25,31,34	1.32	4 (16%)
34	A2M	B5	796	34	22,25,26	1.49	4 (18%)	30,36,39	2.29	9 (30%)
34	OMG	B5	1428	34	23,26,27	1.19	3 (13%)	32,38,41	1.95	6 (18%)
38	OMG	A1	908	38	23,26,27	1.20	3 (13%)	32,38,41	2.06	6 (18%)
38	OMG	A1	1450	38	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2337	38	19,22,23	0.78	0	25,31,34	0.79	0
34	4AC	B5	1280	34	21,24,25	1.01	1 (4%)	28,34,37	1.09	4 (14%)
38	UR3	A1	2634	38	19,22,23	0.97	0	26,32,35	1.73	2 (7%)
38	OMC	A1	2197	38	19,22,23	0.78	0	25,31,34	0.86	0
34	A2M	B5	28	81,34	22,25,26	1.49	4 (18%)	30,36,39	2.08	9 (30%)
34	A2M	B5	100	81,34	22,25,26	1.50	3 (13%)	30,36,39	2.06	7 (23%)
38	A2M	A1	1133	81,38	22,25,26	1.48	4 (18%)	30,36,39	2.24	10 (33%)
38	OMG	A1	2922	38	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)
38	OMC	A1	2948	38	19,22,23	0.80	0	25,31,34	1.01	1 (4%)
38	OMU	A1	898	38	19,22,23	1.26	3 (15%)	25,31,34	1.82	5 (20%)
34	A2M	B5	541	34	22,25,26	1.50	4 (18%)	30,36,39	2.16	8 (26%)
38	A2M	A1	649	38	22,25,26	1.44	3 (13%)	30,36,39	1.99	7 (23%)
38	OMU	A1	1888	38	19,22,23	1.26	3 (15%)	25,31,34	1.89	5 (20%)
38	OMU	A1	2729	38	19,22,23	1.33	4 (21%)	25,31,34	1.83	7 (28%)
38	A2M	A1	2256	80,38	22,25,26	1.50	5 (22%)	30,36,39	2.15	10 (33%)
38	OMG	A1	2619	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	6 (18%)
38	A2M	A1	817	81,38	22,25,26	1.48	5 (22%)	30,36,39	2.04	9 (30%)
34	A2M	B5	619	81,34	22,25,26	1.48	5 (22%)	30,36,39	2.05	9 (30%)
34	XSX	B5	1191	34	24,28,29	0.98	0	30,40,43	2.48	4 (13%)
38	A2M	A1	2281	38	22,25,26	1.37	4 (18%)	30,36,39	2.42	12 (40%)
34	OMG	B5	562	34	23,26,27	1.19	3 (13%)	32,38,41	1.94	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
34	OMG	B5	1271	34	23,26,27	1.18	3 (13%)	32,38,41	1.94	6 (18%)
34	MA6	B5	1782	34	23,26,27	1.51	5 (21%)	33,38,41	2.08	10 (30%)
38	OMG	A1	2815	38	23,26,27	1.20	3 (13%)	32,38,41	1.98	6 (18%)
34	A2M	B5	420	34	22,25,26	1.50	4 (18%)	30,36,39	2.07	10 (33%)
34	OMU	B5	1269	34	19,22,23	1.27	4 (21%)	25,31,34	1.87	5 (20%)
38	A2M	A1	876	38	22,25,26	1.47	3 (13%)	30,36,39	2.00	7 (23%)
34	A2M	B5	974	34	22,25,26	1.47	5 (22%)	30,36,39	2.01	11 (36%)
34	MA6	B5	1781	34	23,26,27	1.53	5 (21%)	33,38,41	2.12	10 (30%)
38	OMG	A1	2288	38	23,26,27	1.19	3 (13%)	32,38,41	1.97	6 (18%)
38	OMU	A1	2417	38	19,22,23	1.22	3 (15%)	25,31,34	1.79	5 (20%)
38	A2M	A1	2946	81,38	22,25,26	1.49	5 (22%)	30,36,39	2.14	11 (36%)
38	5MC	A1	2870	38	19,22,23	1.58	3 (15%)	26,32,35	1.30	3 (11%)
34	OMG	B5	1572	34	23,26,27	1.19	3 (13%)	32,38,41	1.96	6 (18%)
38	OMC	A1	2959	38	19,22,23	0.81	0	25,31,34	0.83	1 (4%)
38	A2M	A1	807	38	22,25,26	1.48	4 (18%)	30,36,39	2.10	8 (26%)
38	OMU	A1	2921	81,38	19,22,23	1.24	3 (15%)	25,31,34	1.85	5 (20%)
38	OMG	A1	805	38	23,26,27	1.19	3 (13%)	32,38,41	2.03	7 (21%)
38	A2M	A1	2280	38	22,25,26	1.48	4 (18%)	30,36,39	2.10	9 (30%)
34	OMU	B5	578	34	19,22,23	1.21	3 (15%)	25,31,34	1.82	5 (20%)
38	OMG	A1	2791	38	23,26,27	1.18	3 (13%)	32,38,41	1.98	6 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	2724	38	-	1/9/27/28	0/2/2/2
34	OMG	B5	1126	34	-	1/9/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
38	A2M	A1	2220	38	-	1/9/27/28	0/3/3/3
34	OMC	B5	1007	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	663	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	1449	81,38	-	0/9/27/28	0/3/3/3
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
34	A2M	B5	436	34	-	0/9/27/28	0/3/3/3
38	5MC	A1	2278	81,38	-	0/7/25/26	0/2/2/2
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMG	A1	2793	38	-	0/9/27/28	0/3/3/3
38	1MA	A1	645	81,38	-	2/7/25/26	0/3/3/3
36	HIC	AB	243	36	-	1/5/6/8	0/1/1/1
38	1MA	A1	2142	81,38	-	0/7/25/26	0/3/3/3
38	A2M	A1	2640	38	-	0/9/27/28	0/3/3/3
34	G7M	B5	1575	34	-	0/7/25/26	0/3/3/3
38	OMG	A1	867	38	-	0/9/27/28	0/3/3/3
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
38	OMC	A1	650	38	-	1/9/27/28	0/2/2/2
38	OMC	A1	1437	81,38	-	3/9/27/28	0/2/2/2
34	A2M	B5	796	34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1428	34	-	3/9/27/28	0/3/3/3
38	OMG	A1	908	38	-	0/9/27/28	0/3/3/3
38	OMG	A1	1450	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2337	38	-	0/9/27/28	0/2/2/2
34	4AC	B5	1280	34	-	2/11/29/30	0/2/2/2
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
34	A2M	B5	28	81,34	-	0/9/27/28	0/3/3/3
34	A2M	B5	100	81,34	-	0/9/27/28	0/3/3/3
38	A2M	A1	1133	81,38	-	0/9/27/28	0/3/3/3
38	OMG	A1	2922	38	-	0/9/27/28	0/3/3/3
38	OMC	A1	2948	38	-	1/9/27/28	0/2/2/2
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
34	A2M	B5	541	34	-	4/9/27/28	0/3/3/3
38	A2M	A1	649	38	-	1/9/27/28	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
38	OMU	A1	2729	38	-	3/9/27/28	0/2/2/2
38	A2M	A1	2256	80,38	-	1/9/27/28	0/3/3/3
38	OMG	A1	2619	38	-	3/9/27/28	0/3/3/3
38	A2M	A1	817	81,38	-	1/9/27/28	0/3/3/3
34	A2M	B5	619	81,34	-	3/9/27/28	0/3/3/3
34	XSX	B5	1191	34	-	3/16/34/35	0/2/2/2
38	A2M	A1	2281	38	-	0/9/27/28	0/3/3/3
34	OMG	B5	562	34	-	0/9/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/9/27/28	0/3/3/3
34	MA6	B5	1782	34	-	3/11/29/30	0/3/3/3
38	OMG	A1	2815	38	-	0/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	A2M	B5	420	34	-	1/9/27/28	0/3/3/3
34	OMU	B5	1269	34	-	5/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	1/9/27/28	0/3/3/3
34	A2M	B5	974	34	-	0/9/27/28	0/3/3/3
34	MA6	B5	1781	34	-	0/11/29/30	0/3/3/3
38	OMG	A1	2288	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2417	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2946	81,38	-	0/9/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMG	B5	1572	34	-	3/9/27/28	0/3/3/3
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	807	38	-	0/9/27/28	0/3/3/3
38	OMU	A1	2921	81,38	-	0/9/27/28	0/2/2/2
38	OMG	A1	805	38	-	1/9/27/28	0/3/3/3
38	A2M	A1	2280	38	-	2/9/27/28	0/3/3/3
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	OMG	A1	2791	38	-	1/9/27/28	0/3/3/3

The worst 5 of 196 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	G7M	C8-N7	7.56	1.45	1.33
38	A1	2870	5MC	C5-C4	5.57	1.48	1.44
38	A1	2278	5MC	C5-C4	5.48	1.48	1.44
34	B5	1575	G7M	C5-N7	-5.02	1.33	1.39
34	B5	541	A2M	C5-C4	4.75	1.47	1.39

The worst 5 of 393 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	B5	1191	XSX	C3-C1-N3	11.43	132.13	112.16
34	B5	1575	G7M	CN7-N7-C8	-7.87	112.87	124.79
34	B5	1773	4AC	N4-C4-N3	7.05	125.31	113.87
38	A1	2634	UR3	C4-N3-C2	-6.90	119.02	124.58
34	B5	1575	G7M	N9-C8-N7	-6.55	96.59	112.48

There are no chirality outliers.

5 of 72 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	414	OMC	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
34	B5	420	A2M	C1'-C2'-O2'-CM'
34	B5	1271	OMG	C1'-C2'-O2'-CM2
34	B5	1280	4AC	N3-C4-N4-C7
34	B5	1280	4AC	C5-C4-N4-C7

There are no ring outliers.

23 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
38	A1	2724	OMU	1	0
34	B5	1126	OMG	3	0
38	A1	2220	A2M	2	0
38	A1	663	OMC	1	0
38	A1	1449	A2M	1	0
34	B5	414	OMC	1	0
34	B5	436	A2M	1	0
38	A1	2640	A2M	1	0
34	B5	1575	G7M	3	0
34	B5	1773	4AC	1	0
38	A1	650	OMC	1	0
38	A1	2197	OMC	2	0
34	B5	28	A2M	1	0
34	B5	100	A2M	1	0
38	A1	1133	A2M	1	0
38	A1	649	A2M	2	0
38	A1	2256	A2M	1	0
38	A1	2619	OMG	1	0
38	A1	817	A2M	1	0
34	B5	1269	OMU	1	0
38	A1	876	A2M	1	0
38	A1	2946	A2M	1	0
34	B5	1572	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 257 ligands modelled in this entry, 257 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.

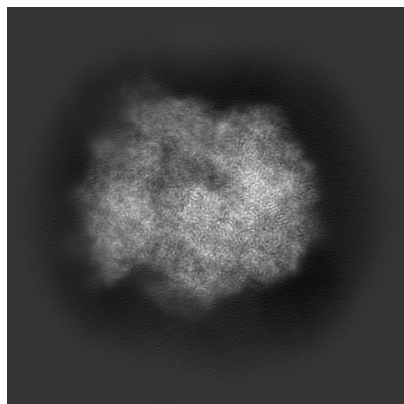
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28632. These allow visual inspection of the internal detail of the map and identification of artifacts.

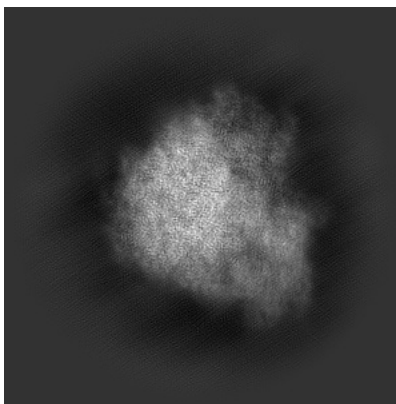
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

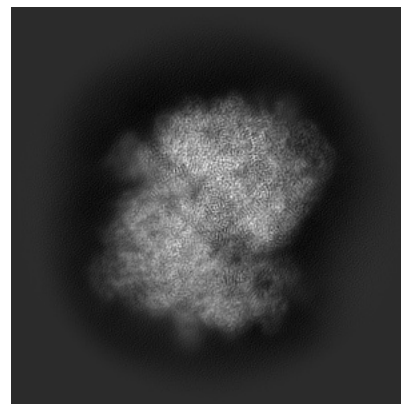
6.1.1 Primary map



X

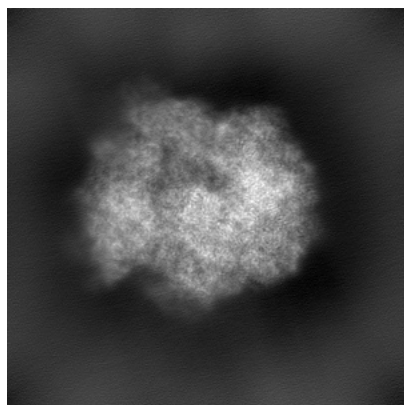


Y

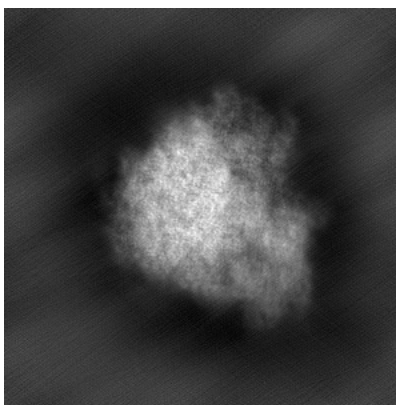


Z

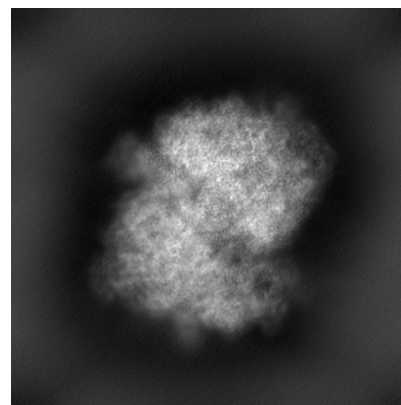
6.1.2 Raw map



X



Y

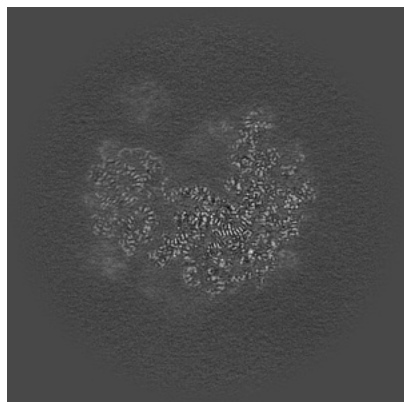


Z

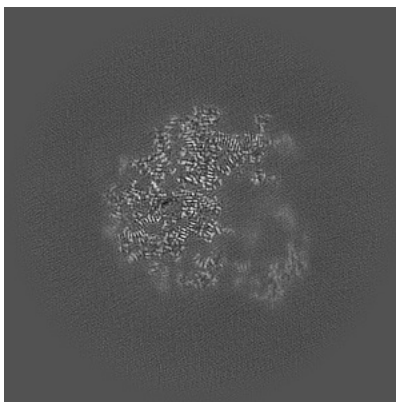
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

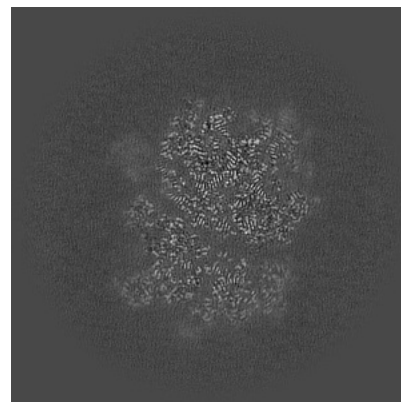
6.2.1 Primary map



X Index: 200

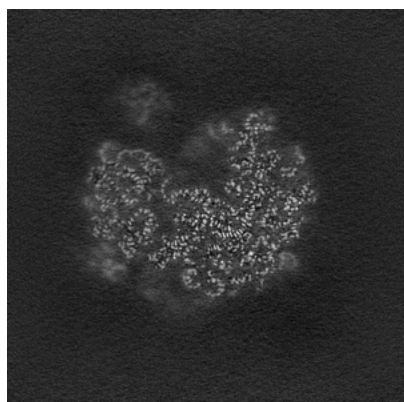


Y Index: 200

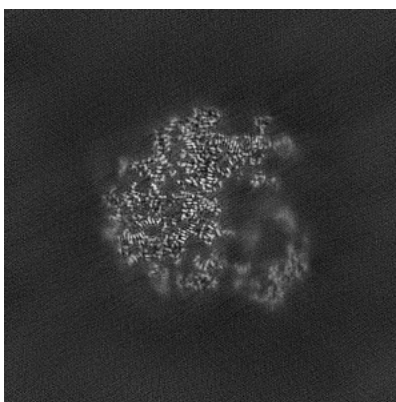


Z Index: 200

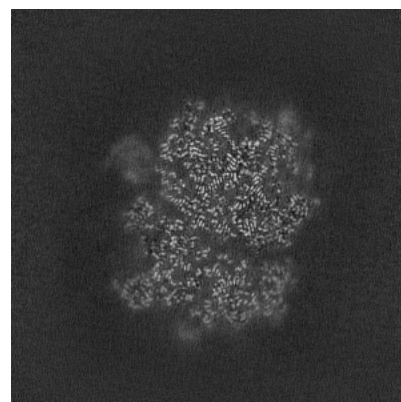
6.2.2 Raw map



X Index: 200



Y Index: 200

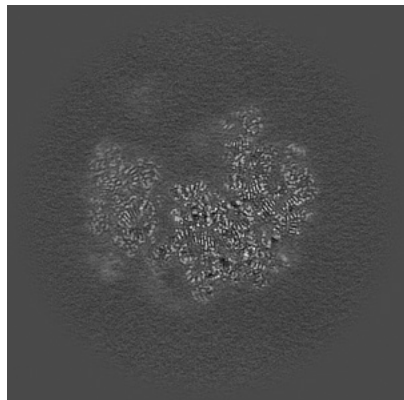


Z Index: 200

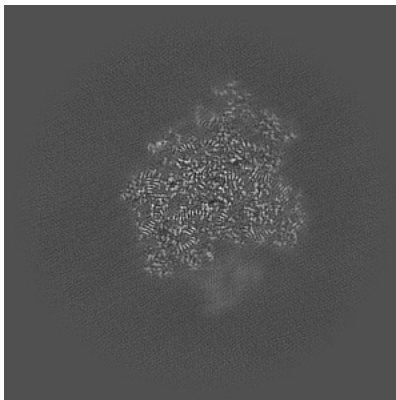
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

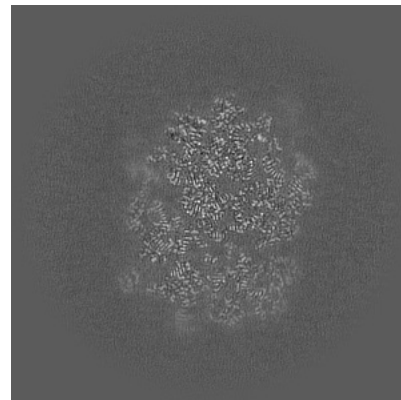
6.3.1 Primary map



X Index: 205

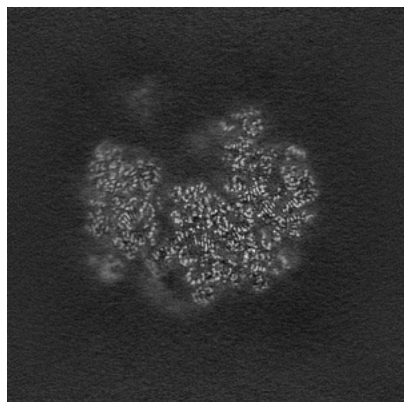


Y Index: 246

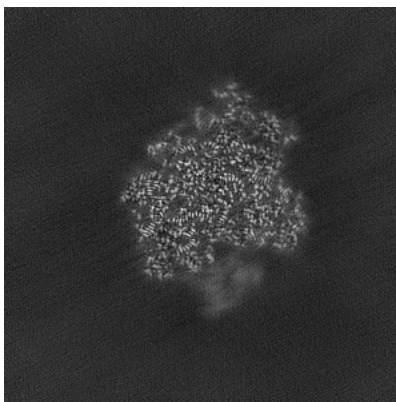


Z Index: 191

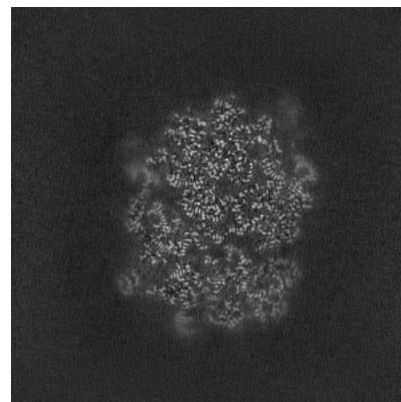
6.3.2 Raw map



X Index: 205



Y Index: 246

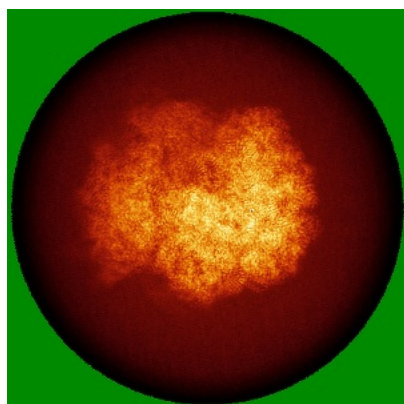


Z Index: 191

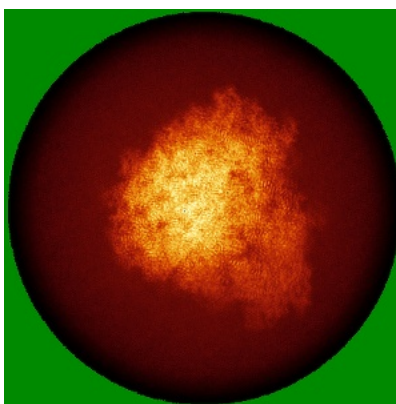
The images above show the largest variance slices of the map in three orthogonal directions.

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

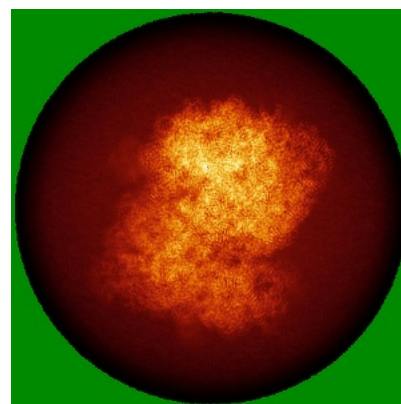
6.4.1 Primary map



X

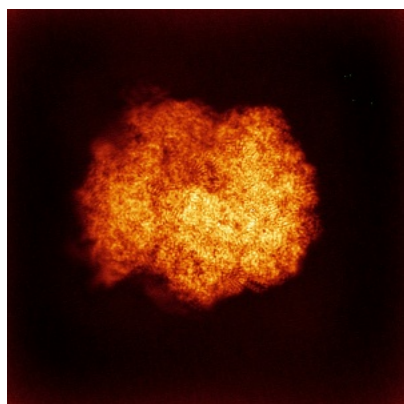


Y

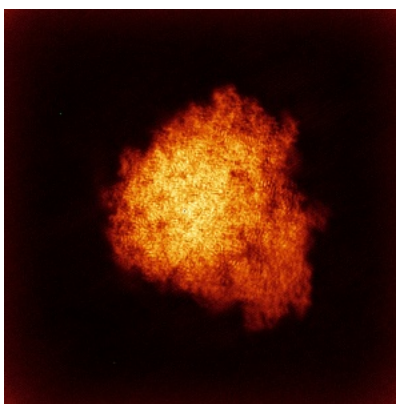


Z

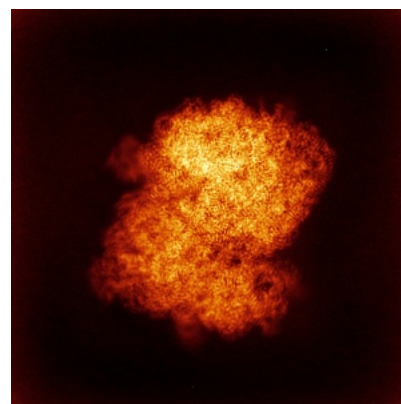
6.4.2 Raw map



X



Y

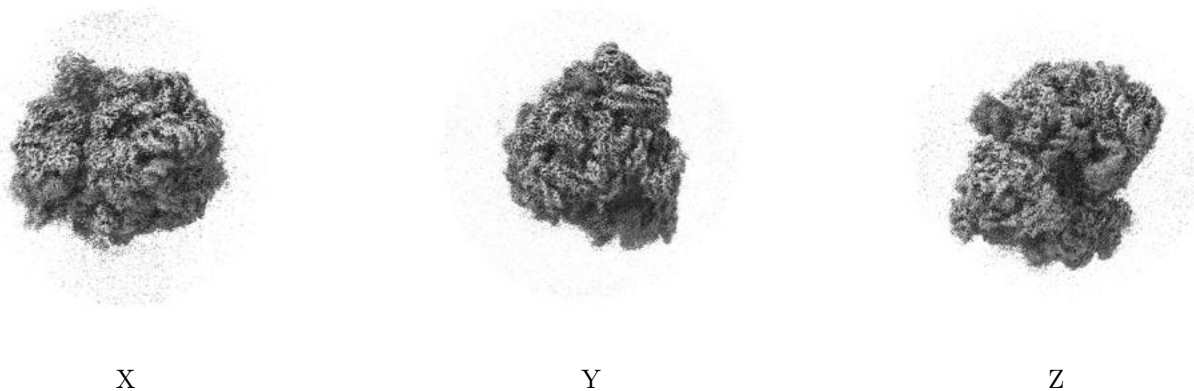


Z

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.

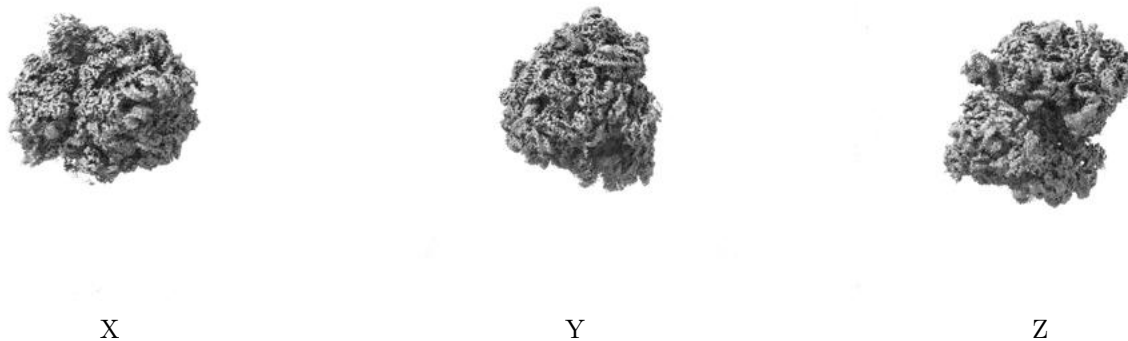
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. 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.

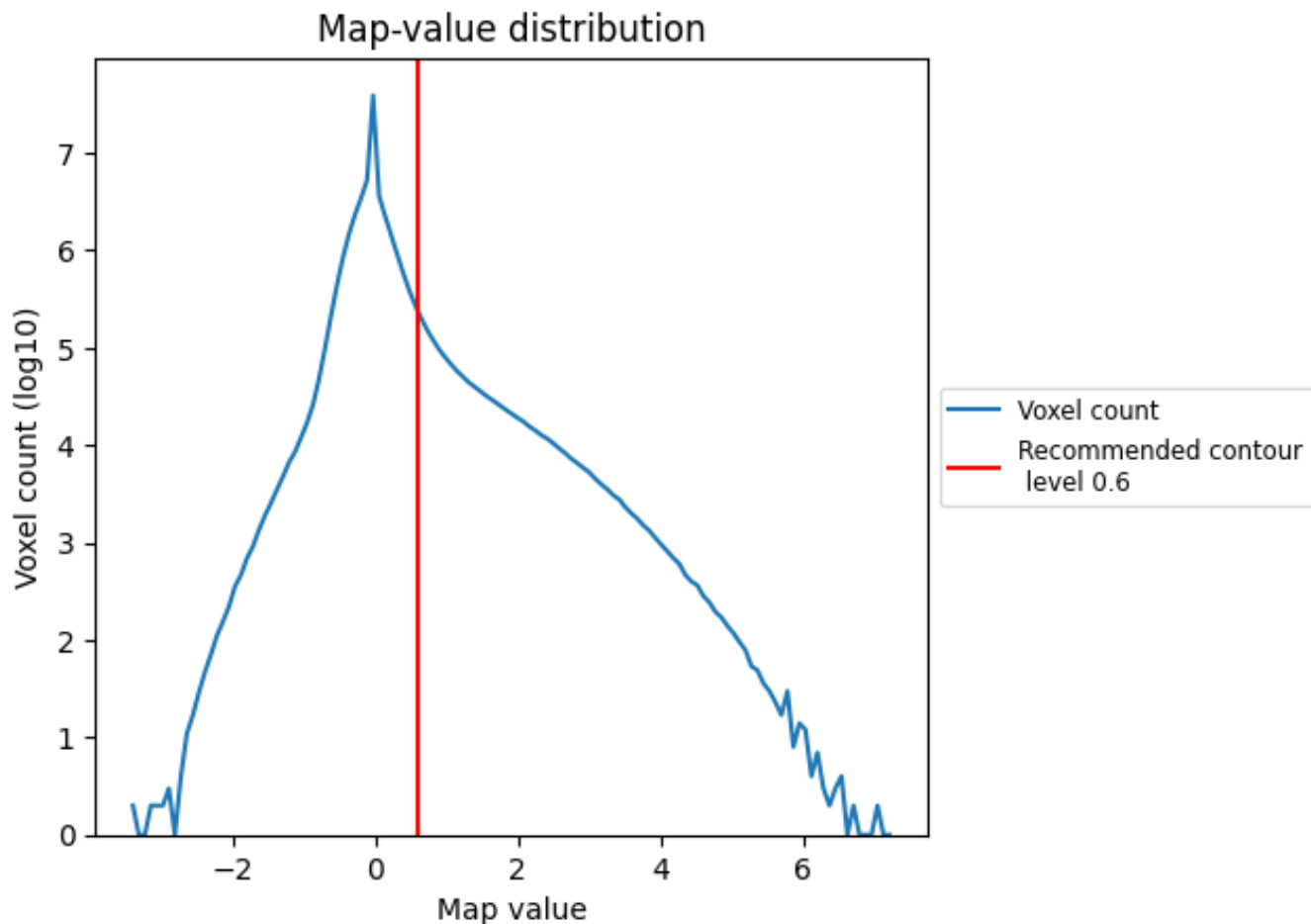
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

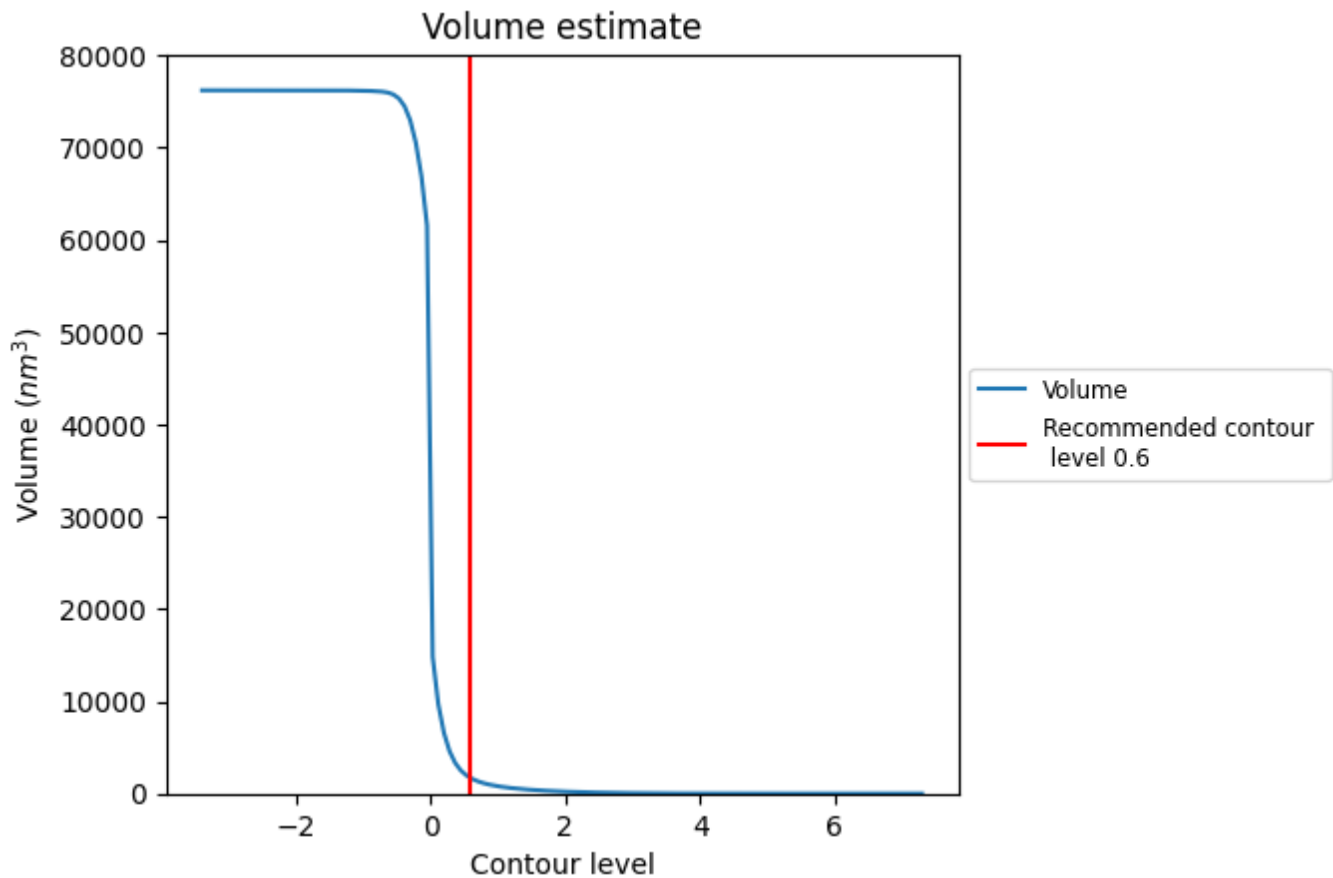
This section contains the results of statistical analysis of the map.

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.

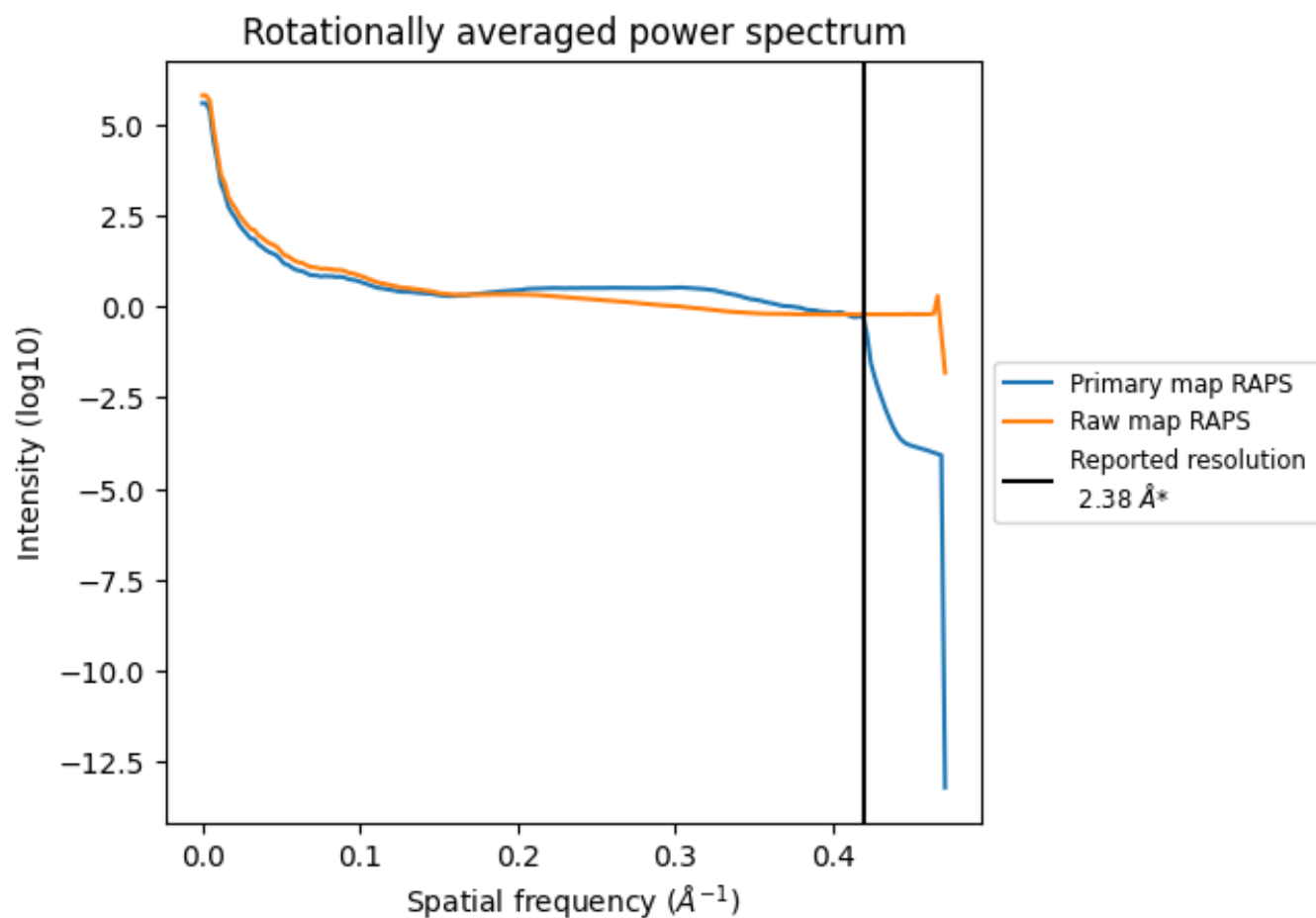
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1679 nm³; this corresponds to an approximate mass of 1517 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 i

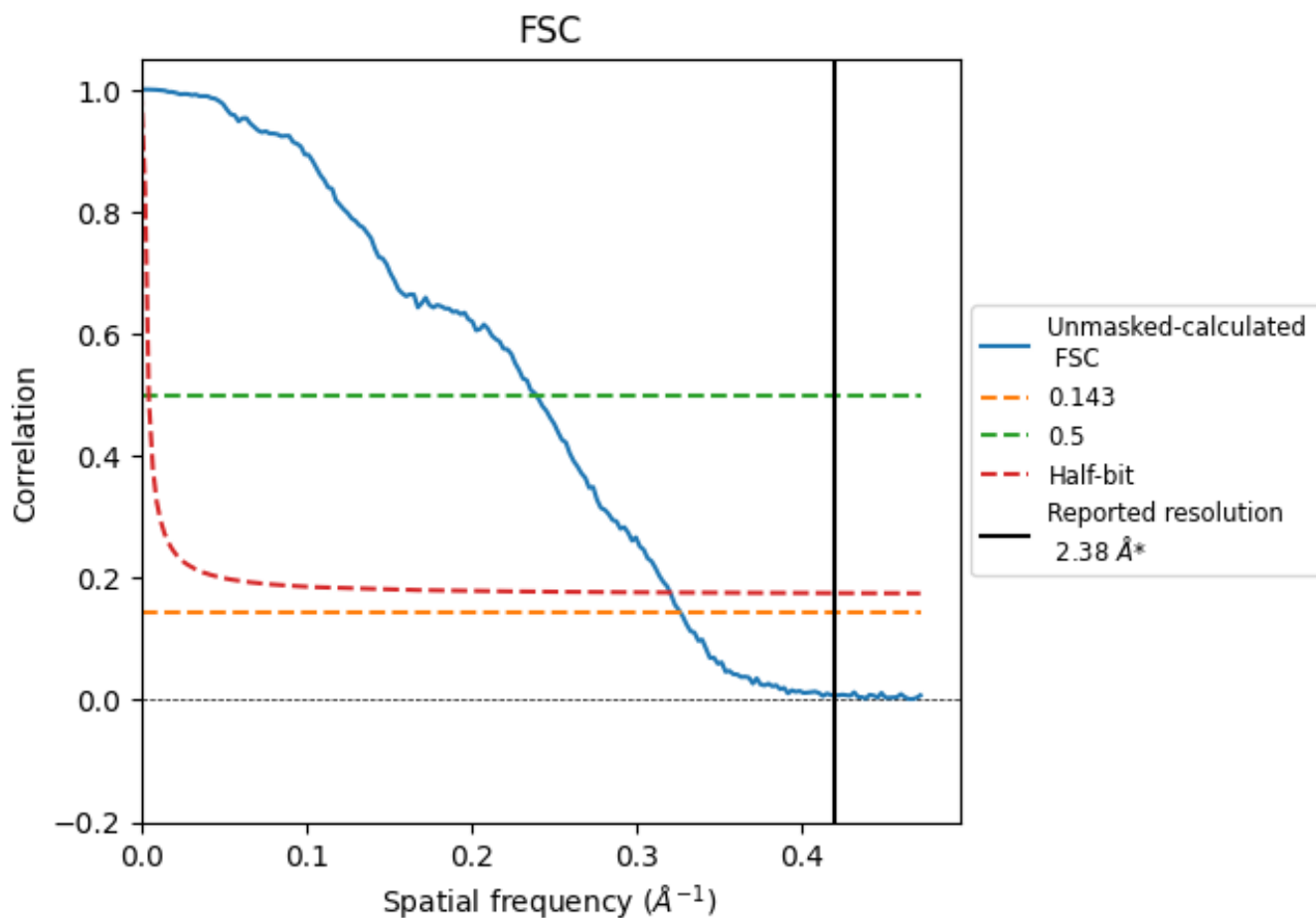


*Reported resolution corresponds to spatial frequency of 0.420 Å⁻¹

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 0.420 Å⁻¹

8.2 Resolution estimates [i](#)

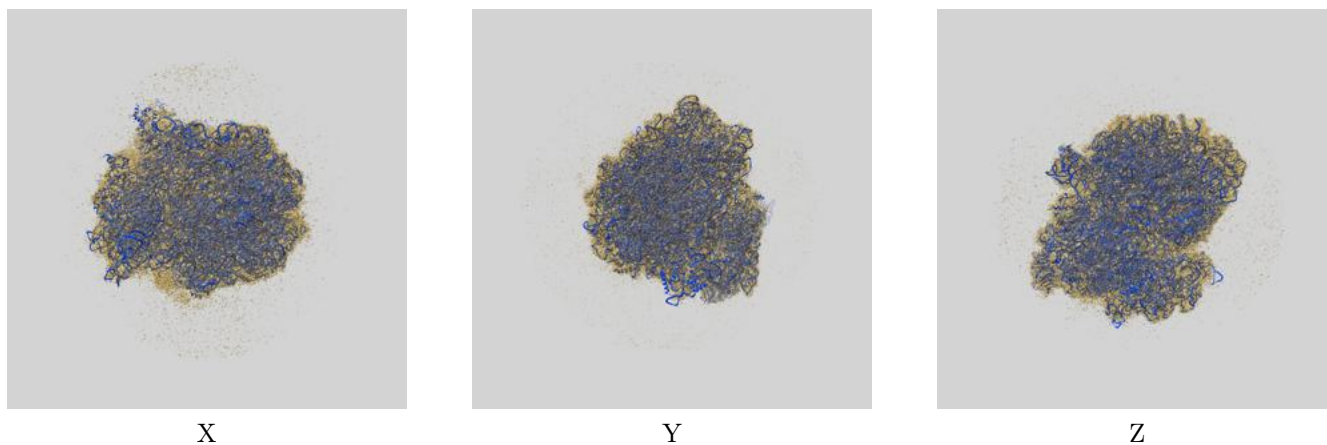
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.38	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.06	4.19	3.12

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.06 differs from the reported value 2.38 by more than 10 %

9 Map-model fit [i](#)

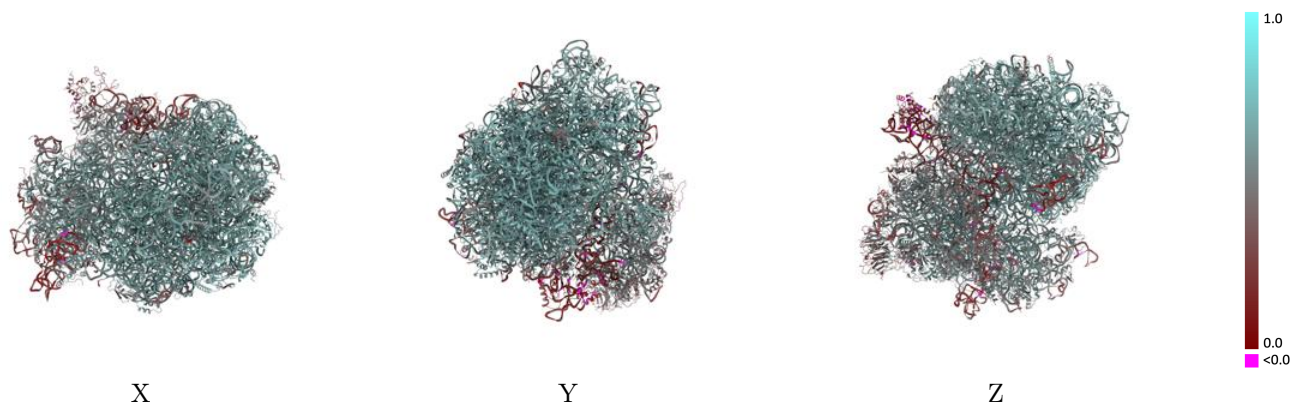
This section contains information regarding the fit between EMDB map EMD-28632 and PDB model 8EVP. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)



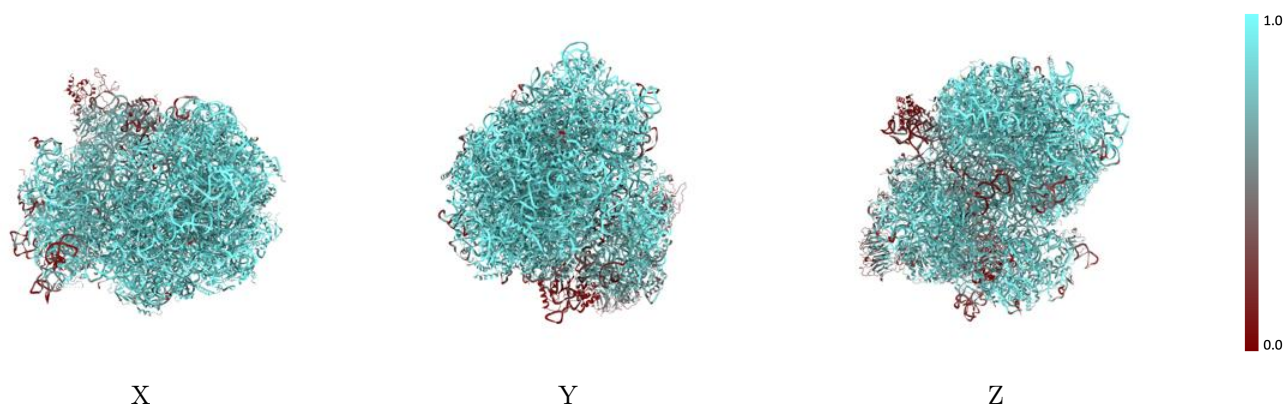
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



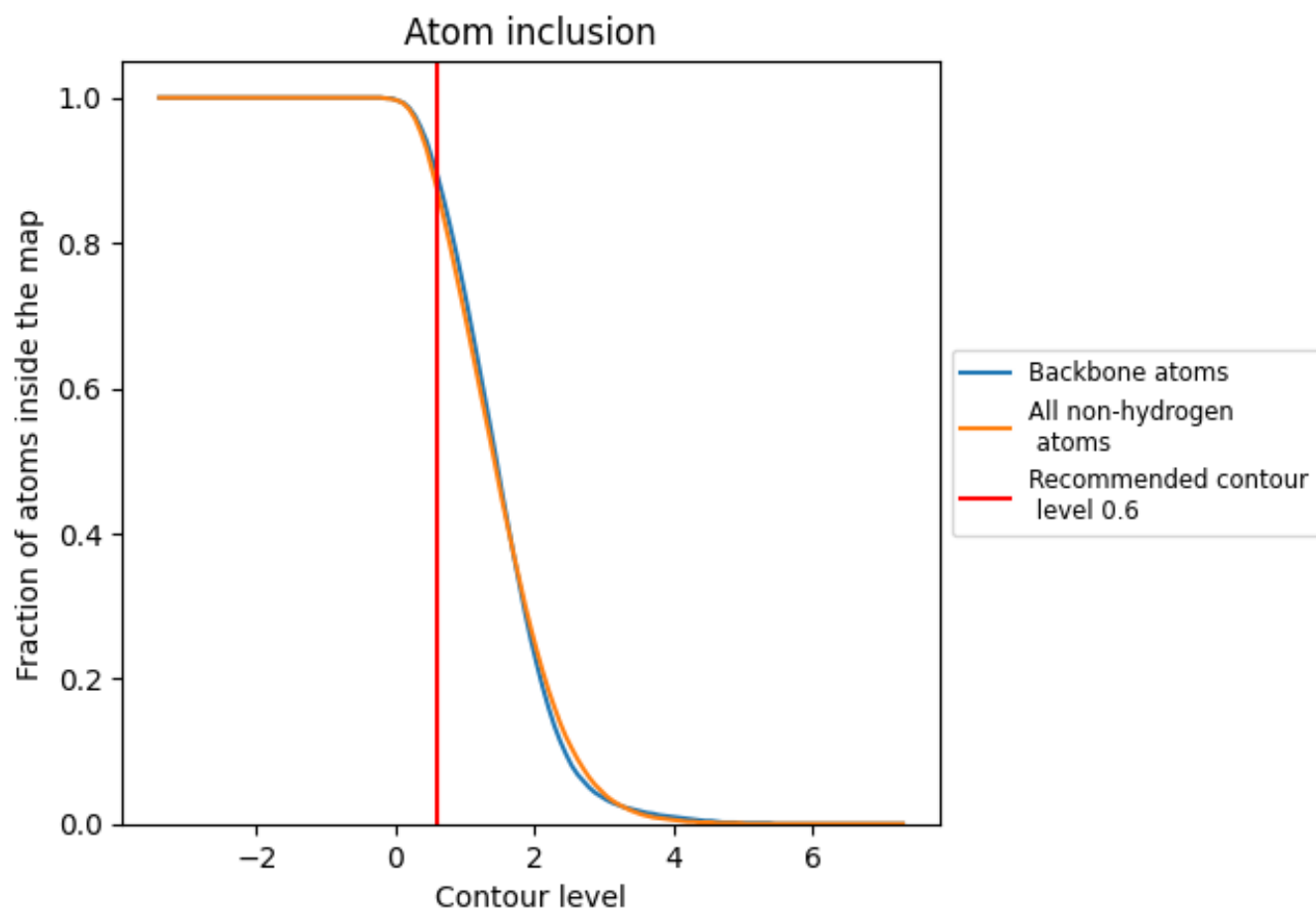
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.6).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.5650
A1	 0.9390	 0.6040
A3	 0.9820	 0.6100
A4	 0.9730	 0.6340
AA	 0.9810	 0.6660
AB	 0.9490	 0.6220
AC	 0.9580	 0.6390
AD	 0.8710	 0.5650
AE	 0.8710	 0.5700
AF	 0.9500	 0.6400
AG	 0.8920	 0.5810
AH	 0.8940	 0.5930
AI	 0.9330	 0.6150
AJ	 0.7510	 0.4710
AL	 0.9310	 0.6260
AM	 0.9200	 0.6030
AN	 0.9870	 0.6620
AO	 0.9600	 0.6330
AP	 0.9500	 0.6330
AQ	 0.9820	 0.6660
AR	 0.8780	 0.5910
AS	 0.9350	 0.6210
AT	 0.9380	 0.6160
AU	 0.8310	 0.5360
AV	 0.9430	 0.6340
AW	 0.9600	 0.6340
AX	 0.9420	 0.6240
AY	 0.9230	 0.6130
AZ	 0.9360	 0.6040
Aa	 0.9560	 0.6450
Ab	 0.9270	 0.6080
Ac	 0.9430	 0.6250
Ad	 0.8840	 0.5900
Ae	 0.9620	 0.6520
Af	 0.9640	 0.6410











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Chain	Atom inclusion	Q-score
Ag	 0.9400	 0.6180
Ah	 0.9420	 0.6230
Ai	 0.9170	 0.5930
Aj	 0.9680	 0.6580
Ak	 0.7810	 0.5550
Al	 0.9780	 0.6530
Am	 0.8930	 0.6150
An	 0.9340	 0.5920
Ao	 0.9020	 0.6070
Ap	 0.9400	 0.6370
B5	 0.8700	 0.5300
BA	 0.8620	 0.5530
BB	 0.8560	 0.5560
BC	 0.9340	 0.6080
BD	 0.7480	 0.4850
BE	 0.9100	 0.5800
BF	 0.7220	 0.4750
BG	 0.7310	 0.4860
BH	 0.7250	 0.4970
BI	 0.8860	 0.5880
BJ	 0.8660	 0.5570
BK	 0.5850	 0.3940
BL	 0.8570	 0.5810
BM	 0.0820	 0.2560
BN	 0.9300	 0.6100
BO	 0.9000	 0.5730
BP	 0.5180	 0.3960
BQ	 0.7750	 0.4850
BR	 0.7780	 0.4970
BS	 0.6730	 0.4460
BT	 0.7490	 0.4730
BU	 0.6440	 0.4400
BV	 0.9080	 0.5810
BW	 0.9630	 0.6390
BX	 0.9150	 0.6060
BY	 0.7900	 0.5040
BZ	 0.6220	 0.4250
Ba	 0.9000	 0.5700
Bb	 0.8450	 0.5610
Bc	 0.6960	 0.4810
Bd	 0.8840	 0.5350
Be	 0.8000	 0.5130

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Chain	Atom inclusion	Q-score
Bf	 0.1190	 0.2320
Bg	 0.5440	 0.4010
E	 0.1450	 0.1950
EC	 0.3860	 0.2180