wwPDB EM Validation Summary Report ⓘ

Oct 22, 2023 – 02:18 PM EDT

PDB ID	:	8EVT
EMDB ID	:	EMD-28636
Title	:	Hypopseudouridylated yeast 80S bound with Taura syndrome virus (TSV) internal ribosome entry site (IRES) refined against a composite map
Authors	:	Zhao, Y.; Rai, J.; Li, H.
Deposited on	:	2022-10-20
Resolution	:	2.20 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:

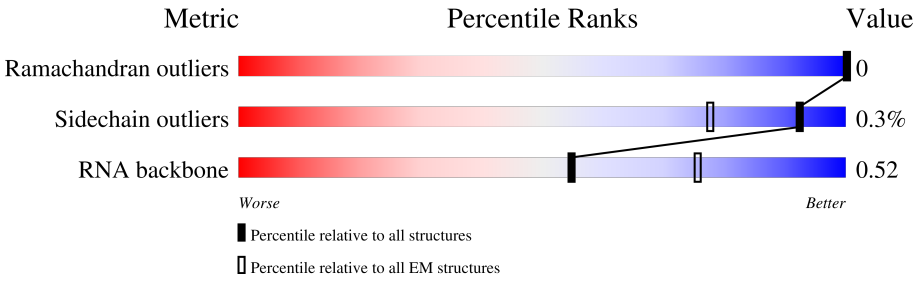
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.20 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	5% 81% 18%
2	BB	255	10% 84% 16%
3	BC	254	85% 15%
4	BE	261	100%
5	BG	236	23% 96%
6	BH	190	31% 96%
7	BI	200	8% 94% 6%
8	BJ	197	6% 93% 6%

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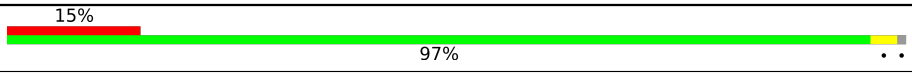
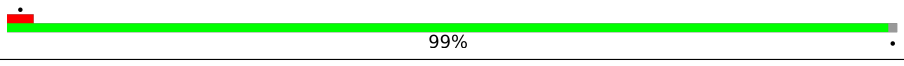
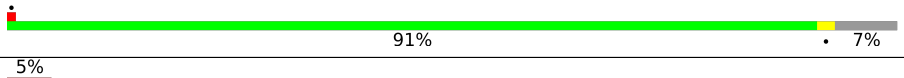
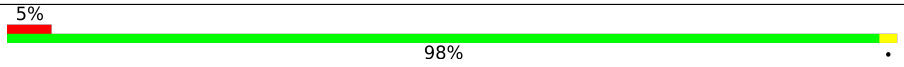
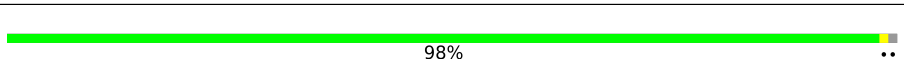
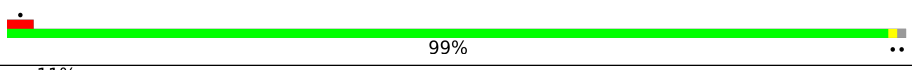
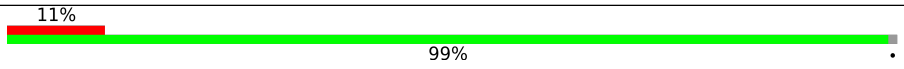
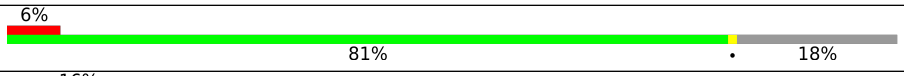
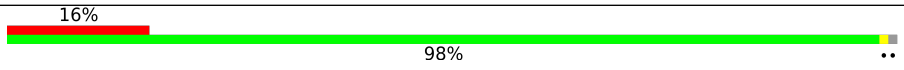
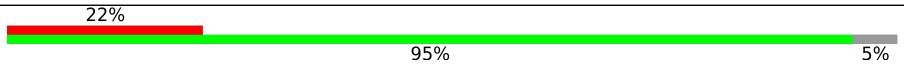
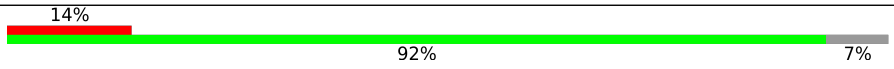
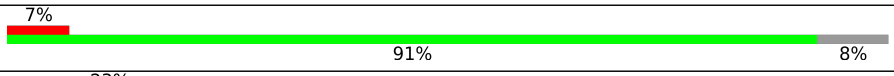
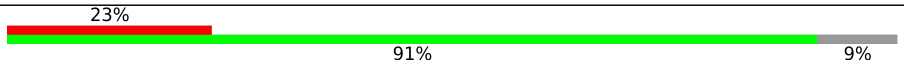
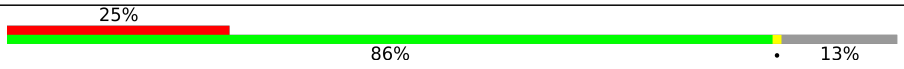
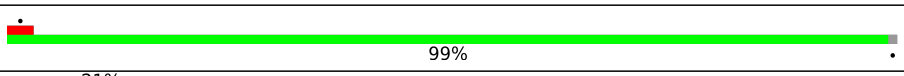
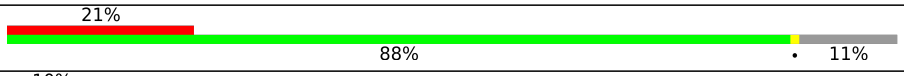
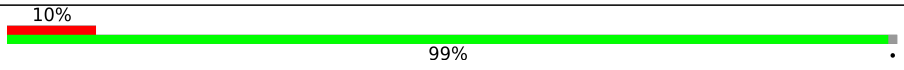
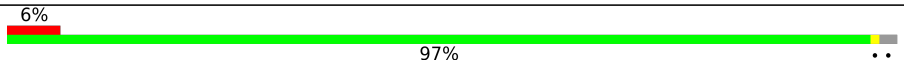
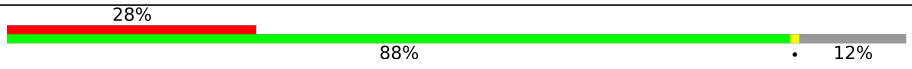
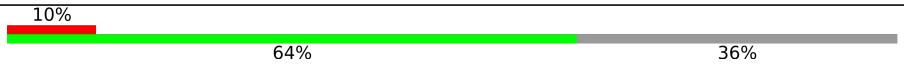
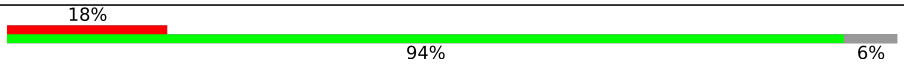
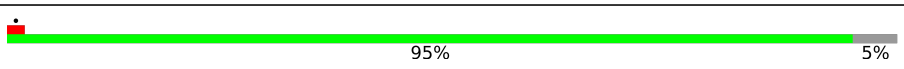
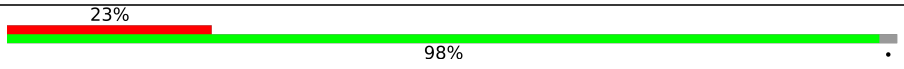
Mol	Chain	Length	Quality of chain
9	BL	156	
10	BN	151	
11	BO	137	
12	BV	87	
13	BW	130	
14	BX	145	
15	BY	135	
16	Ba	119	
17	Bb	82	
18	Be	63	
19	BD	240	
20	BF	225	
21	BK	105	
22	BP	142	
23	BQ	143	
24	BR	136	
25	BS	146	
26	BT	144	
27	BU	121	
28	BZ	108	
29	Bc	67	
30	Bd	56	
31	Bg	319	
32	Bf	152	
33	BM	143	

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Mol	Chain	Length	Quality of chain
34	B5	1798	13% 74% 24%
35	AA	254	97%
36	AB	387	99%
37	AC	362	99%
38	A1	3360	8% 75% 19% 5%
39	A3	121	88% 12%
40	A4	158	82% 18%
41	AD	297	14% 98%
42	AE	176	9% 88% 11%
43	AF	244	91% 9%
44	AG	256	8% 89% 10%
45	AH	191	5% 99%
46	AI	221	5% 92% 7%
47	AJ	174	41% 97%
48	AL	199	8% 97%
49	AM	138	99%
50	AN	204	100%
51	AO	199	99%
52	AP	184	95% 5%
53	AQ	186	99%
54	AR	189	18% 98%
55	AS	178	97%
56	AT	160	6% 99%
57	AU	121	15% 82% 17%
58	AV	137	99%

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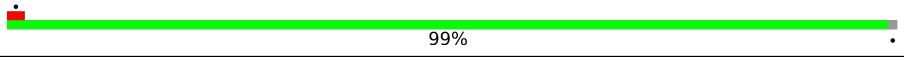
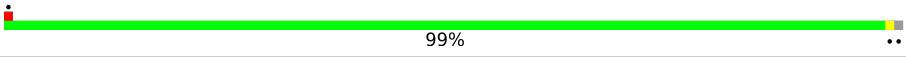
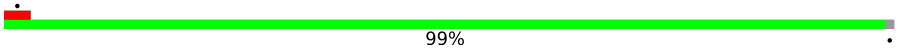
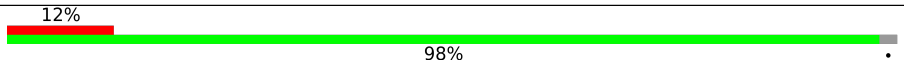
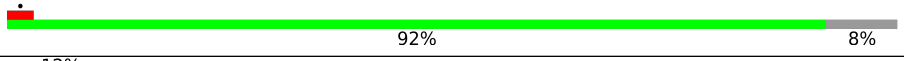
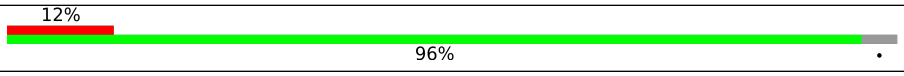
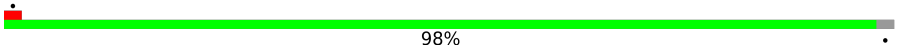
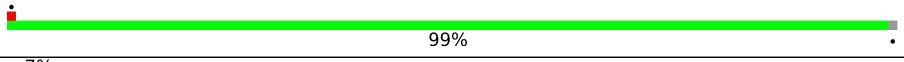
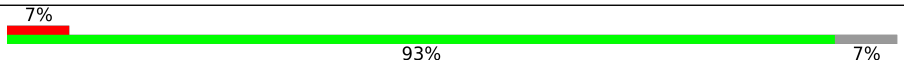
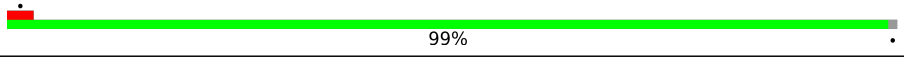
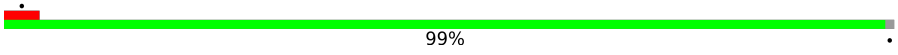
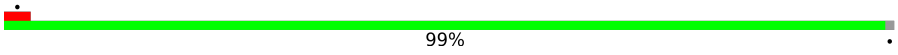
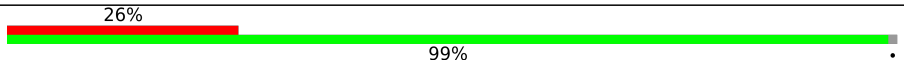
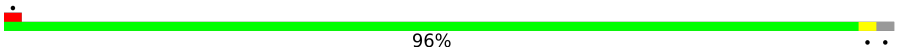
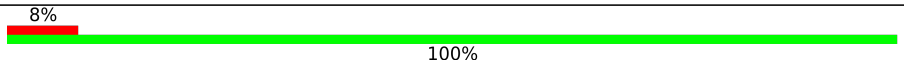
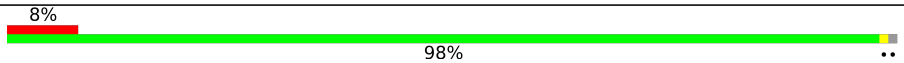
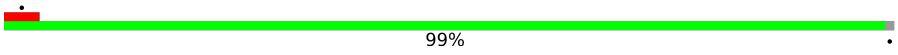
Mol	Chain	Length	Quality of chain
59	AW	155	
60	AX	142	
61	AY	127	
62	AZ	136	
63	Aa	149	
64	Ab	59	
65	Ac	105	
66	Ad	113	
67	Ae	130	
68	Af	107	
69	Ag	121	
70	Ah	120	
71	Ai	100	
72	Aj	88	
73	Ak	78	
74	Al	51	
75	Am	128	
76	An	25	
77	Ao	106	
78	Ap	92	
79	E	217	
80	EC	202	

2 Entry composition (i)

There are 82 unique types of molecules in this entry. The entry contains 202928 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
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
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
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
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
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
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
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
14	BX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

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

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

- Molecule 16 is a protein called RPS26B isoform 1.

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

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

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

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

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

- Molecule 19 is a protein called RPS3 isoform 1.

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

- Molecule 20 is a protein called Rps5p.

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

- 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		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B5	1280	4AC	C	conflict	GB 1329886537
B5	1773	4AC	C	conflict	GB 1329886537

- 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	3192	Total	C	N	O	P	0	0
			68319	30539	12310	22278	3192		

- 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
42	AE	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

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

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

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

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

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

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

- Molecule 46 is a protein called RPL10 isoform 1.

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

- Molecule 47 is a protein called RPL11A isoform 1.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 59 is a protein called RPL24A isoform 1.

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

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

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

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

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

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

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

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

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

- Molecule 64 is a protein called RPL29 isoform 1.

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

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

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

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

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

- Molecule 67 is a protein called RPL32 isoform 1.

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

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

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

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

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

- 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 TSV IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	EC	57	Total	C	N	O	P	0	0
			1209	541	213	398	57		

- Molecule 81 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	BN	1	Total	Mg	0
			1	1	
81	Ba	1	Total	Mg	0
			1	1	
81	B5	73	Total	Mg	0
			73	73	
81	AB	1	Total	Mg	0
			1	1	
81	AC	1	Total	Mg	0
			1	1	
81	A1	180	Total	Mg	0
			180	180	

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Mol	Chain	Residues	Atoms	AltConf
81	A3	2	Total Mg 2 2	0
81	A4	4	Total Mg 4 4	0
81	AN	2	Total Mg 2 2	0
81	AO	1	Total Mg 1 1	0
81	AP	1	Total Mg 1 1	0
81	Ae	2	Total Mg 2 2	0
81	Af	1	Total Mg 1 1	0
81	Ah	1	Total Mg 1 1	0
81	Aj	1	Total Mg 1 1	0

- Molecule 82 is ZINC ION (three-letter code: ZN) (formula: Zn).

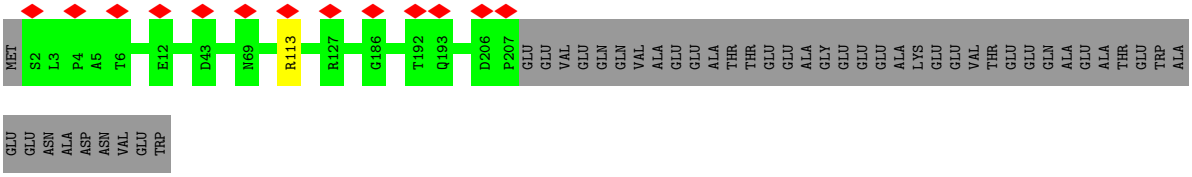
Mol	Chain	Residues	Atoms	AltConf
82	Ao	1	Total Zn 1 1	0

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.

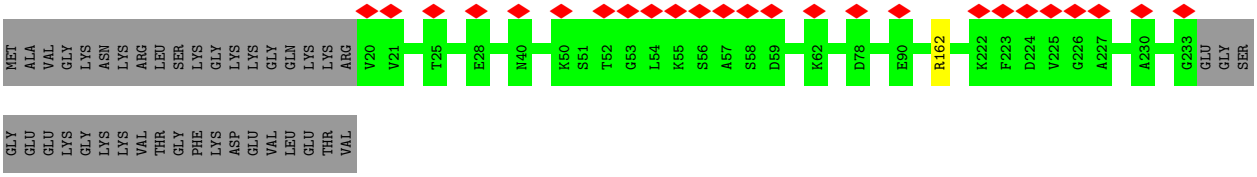
• Molecule 1: 40S ribosomal protein S0-A

Chain BA:



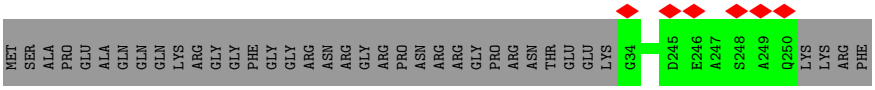
• Molecule 2: RPS1A isoform 1

Chain BB:



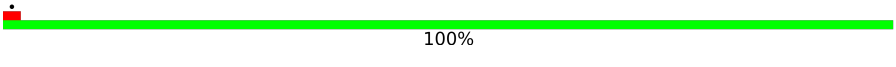
• Molecule 3: RPS2 isoform 1

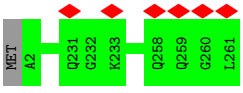
Chain BC:



• Molecule 4: 40S ribosomal protein S4-A

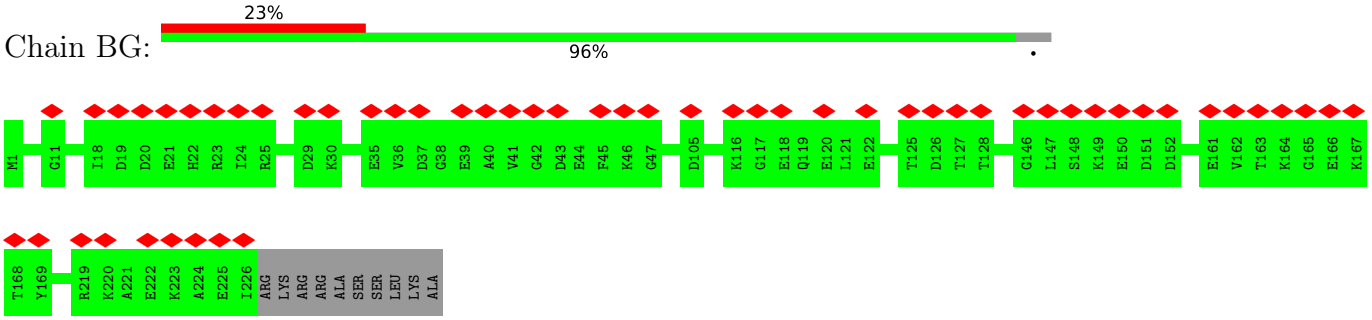
Chain BE:





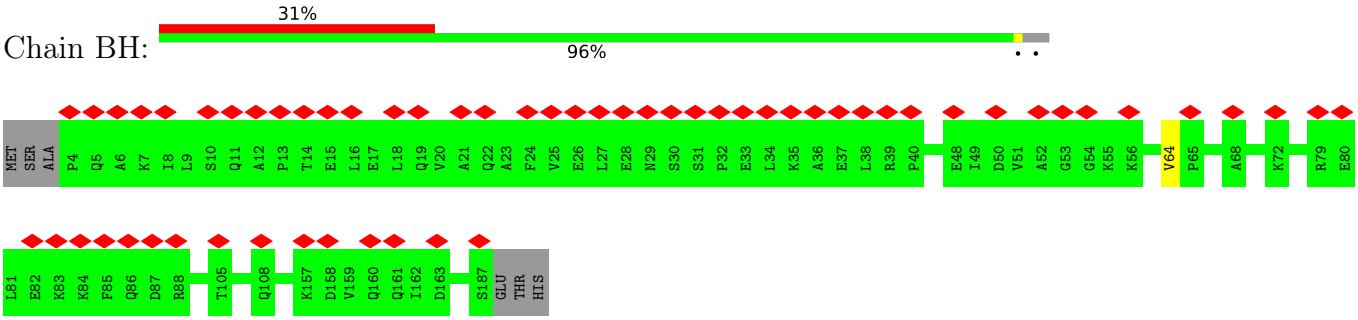
• Molecule 5: 40S ribosomal protein S6-A

Chain BG:



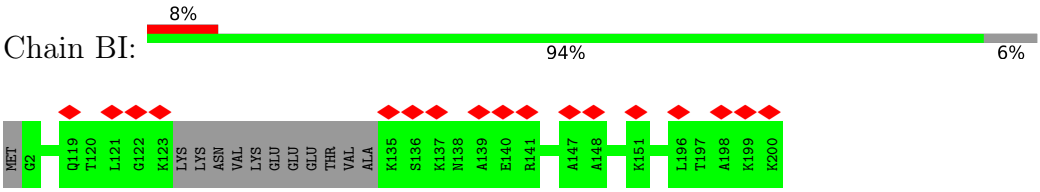
• Molecule 6: 40S ribosomal protein S7-A

Chain BH:



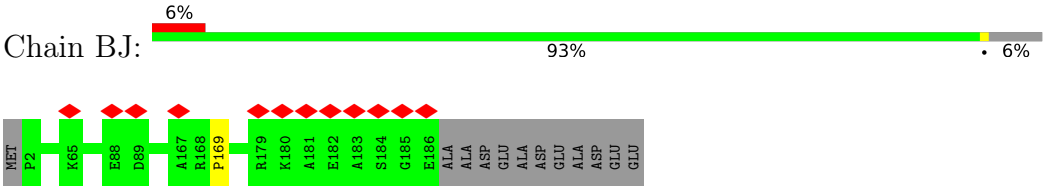
• Molecule 7: 40S ribosomal protein S8-A

Chain BI:



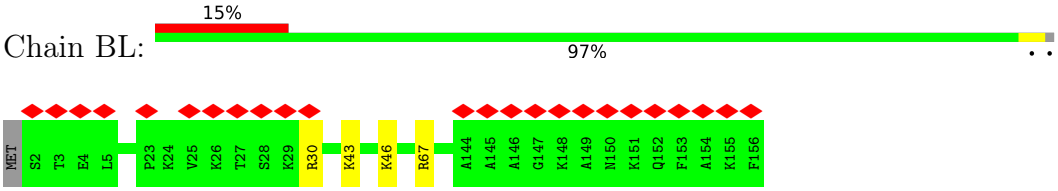
• Molecule 8: 40S ribosomal protein S9-A

Chain BJ:



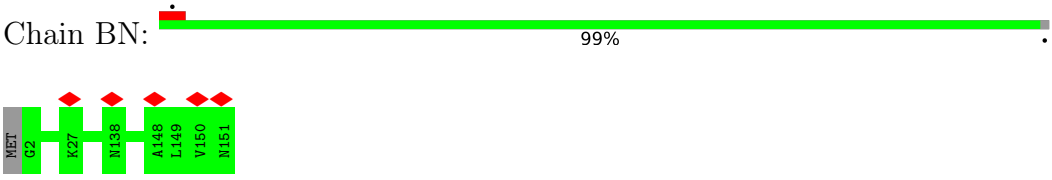
• Molecule 9: 40S ribosomal protein S11-A

Chain BL:



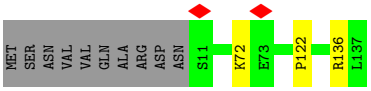
• Molecule 10: 40S ribosomal protein S13

Chain BN:



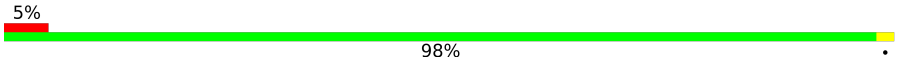
• Molecule 11: 40S ribosomal protein S14-A

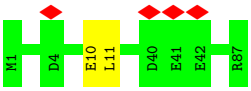
Chain BO:



• Molecule 12: 40S ribosomal protein S21-A

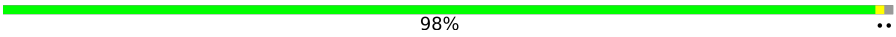
Chain BV:

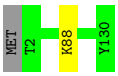




• Molecule 13: RPS22A isoform 1

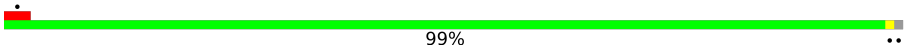
Chain BW:

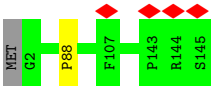




• Molecule 14: 40S ribosomal protein S23-A

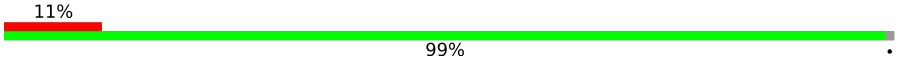
Chain BX:

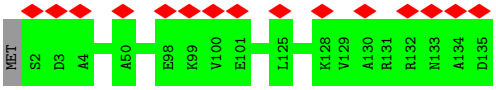




• Molecule 15: 40S ribosomal protein S24-A

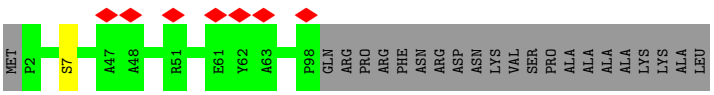
Chain BY:





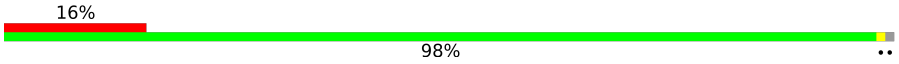
• Molecule 16: RPS26B isoform 1

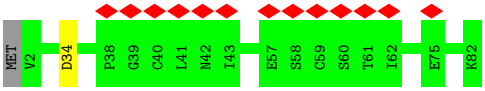
Chain Ba:



• Molecule 17: 40S ribosomal protein S27-A

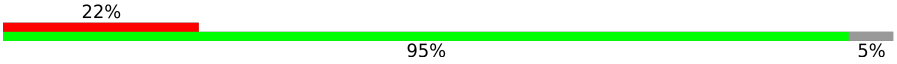
Chain Bb:

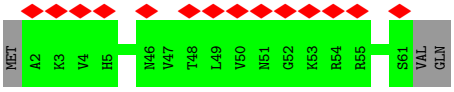




• Molecule 18: 40S ribosomal protein S30-A

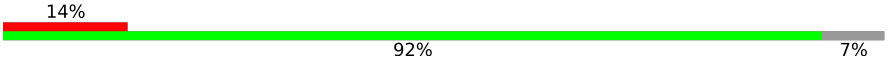
Chain Be:

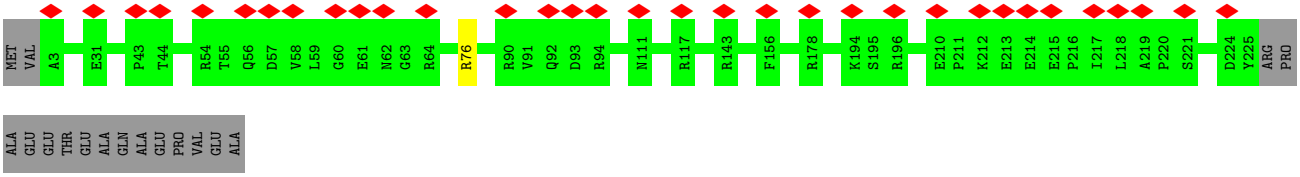




• Molecule 19: RPS3 isoform 1

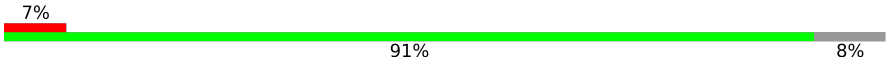
Chain BD:

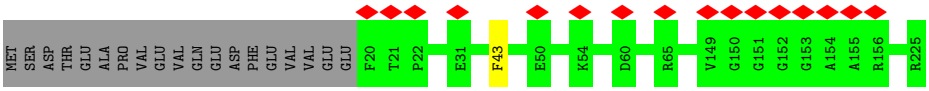




• Molecule 20: Rps5p

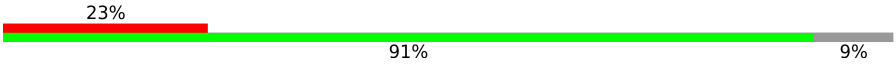
Chain BF:

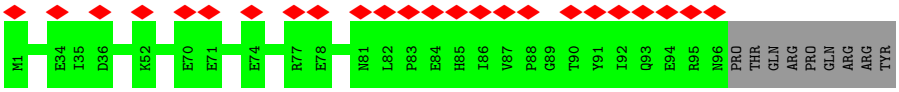




• Molecule 21: 40S ribosomal protein S10-A

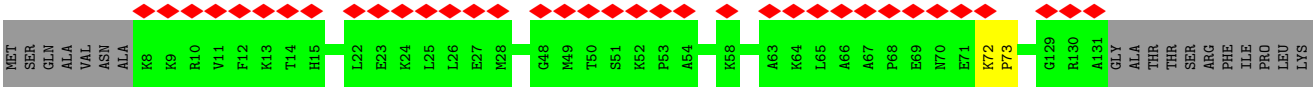
Chain BK:





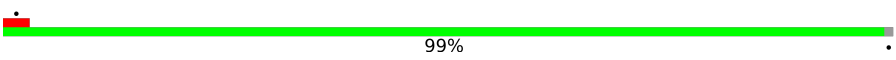
• Molecule 22: RPS15 isoform 1

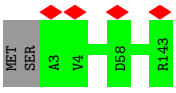
Chain BP:



• Molecule 23: 40S ribosomal protein S16-A

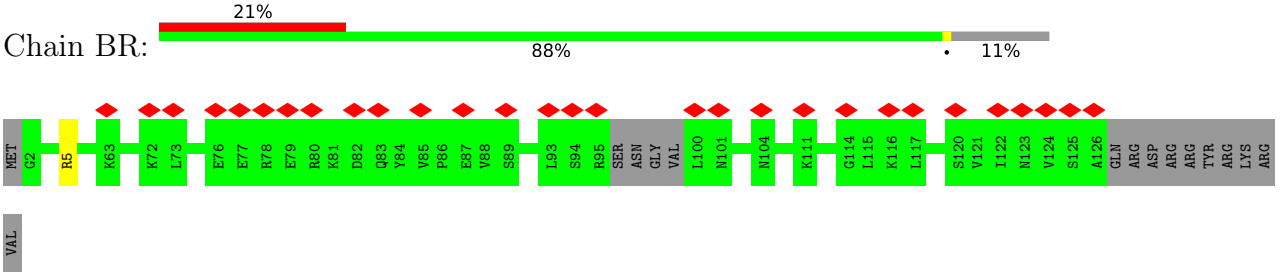
Chain BQ:





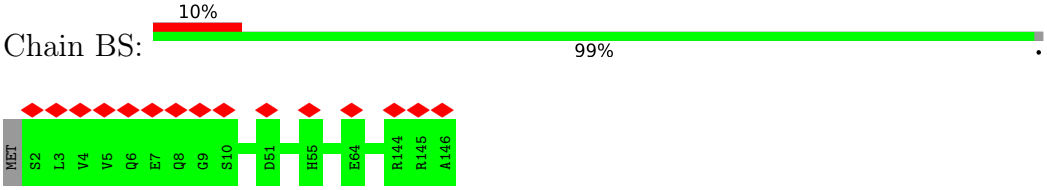
• Molecule 24: 40S ribosomal protein S17-A

Chain BR:



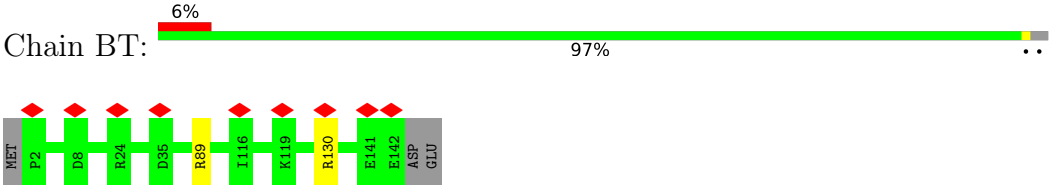
• Molecule 25: 40S ribosomal protein S18-A

Chain BS:



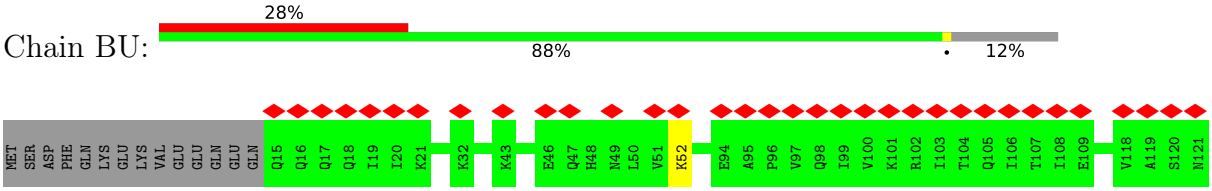
• Molecule 26: 40S ribosomal protein S19-A

Chain BT:



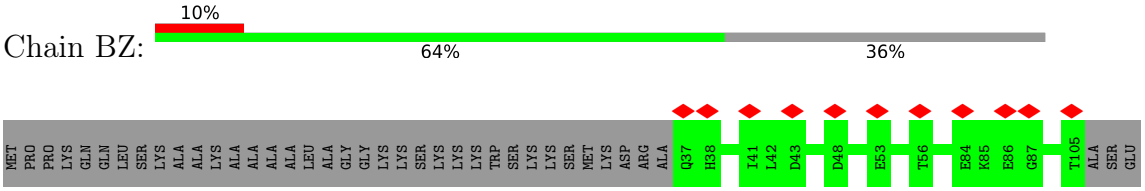
• Molecule 27: RPS20 isoform 1

Chain BU:



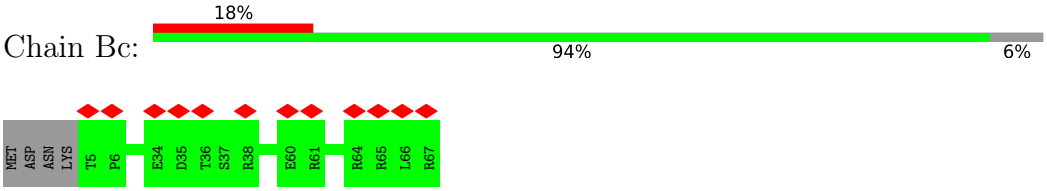
• Molecule 28: RPS25A isoform 1

Chain BZ:



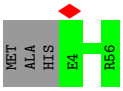
• Molecule 29: RPS28A isoform 1

Chain Bc:



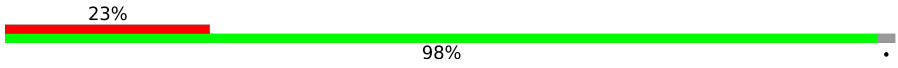
• Molecule 30: RPS29A isoform 1

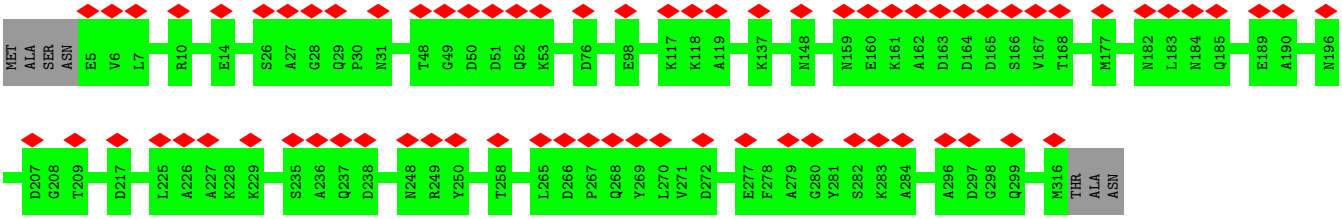
Chain Bd:



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

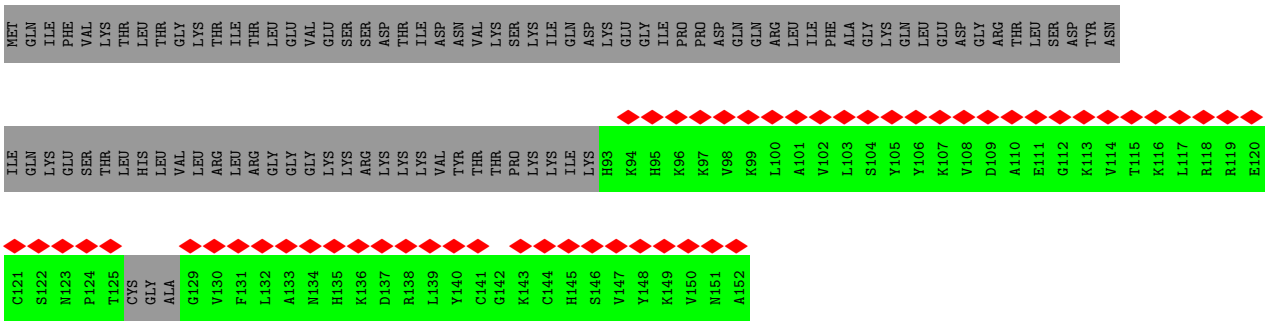
Chain Bg:





• Molecule 32: Ubiquitin-40S ribosomal protein S31

Chain Bf:

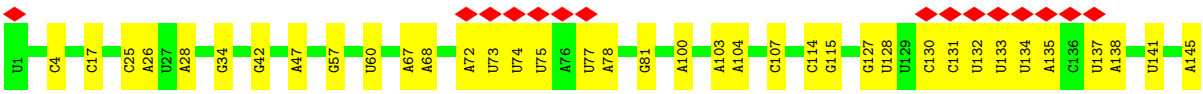


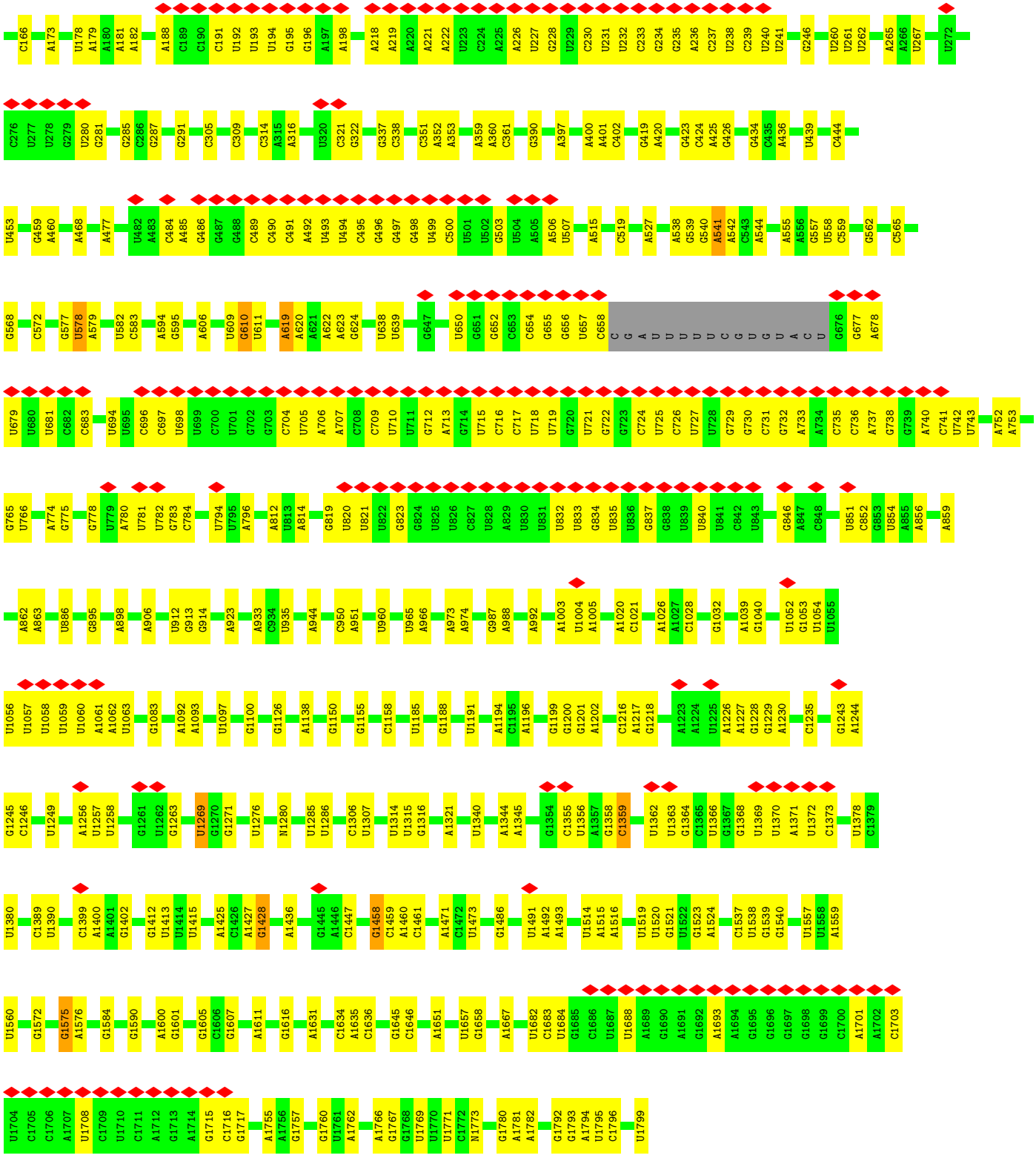
• Molecule 33: 40S ribosomal protein S12

Chain BM:

• Molecule 34: 18S rRNA

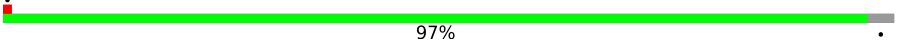
Chain B5:

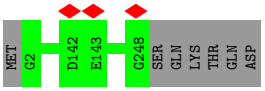




• Molecule 35: 60S ribosomal protein L2-A

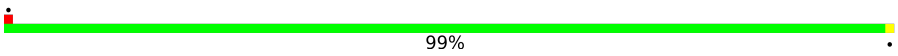
Chain AA:

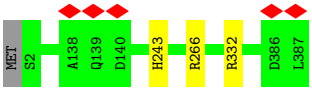




• Molecule 36: 60S ribosomal protein L3

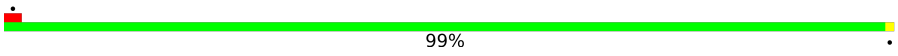
Chain AB:

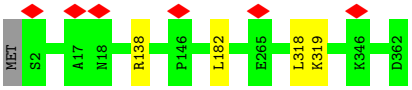




• Molecule 37: RPL4A isoform 1

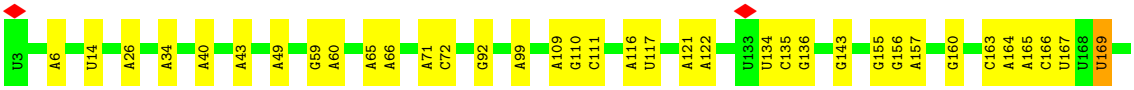
Chain AC:

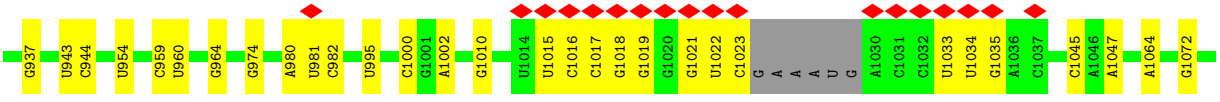


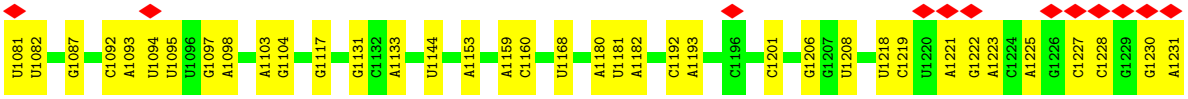


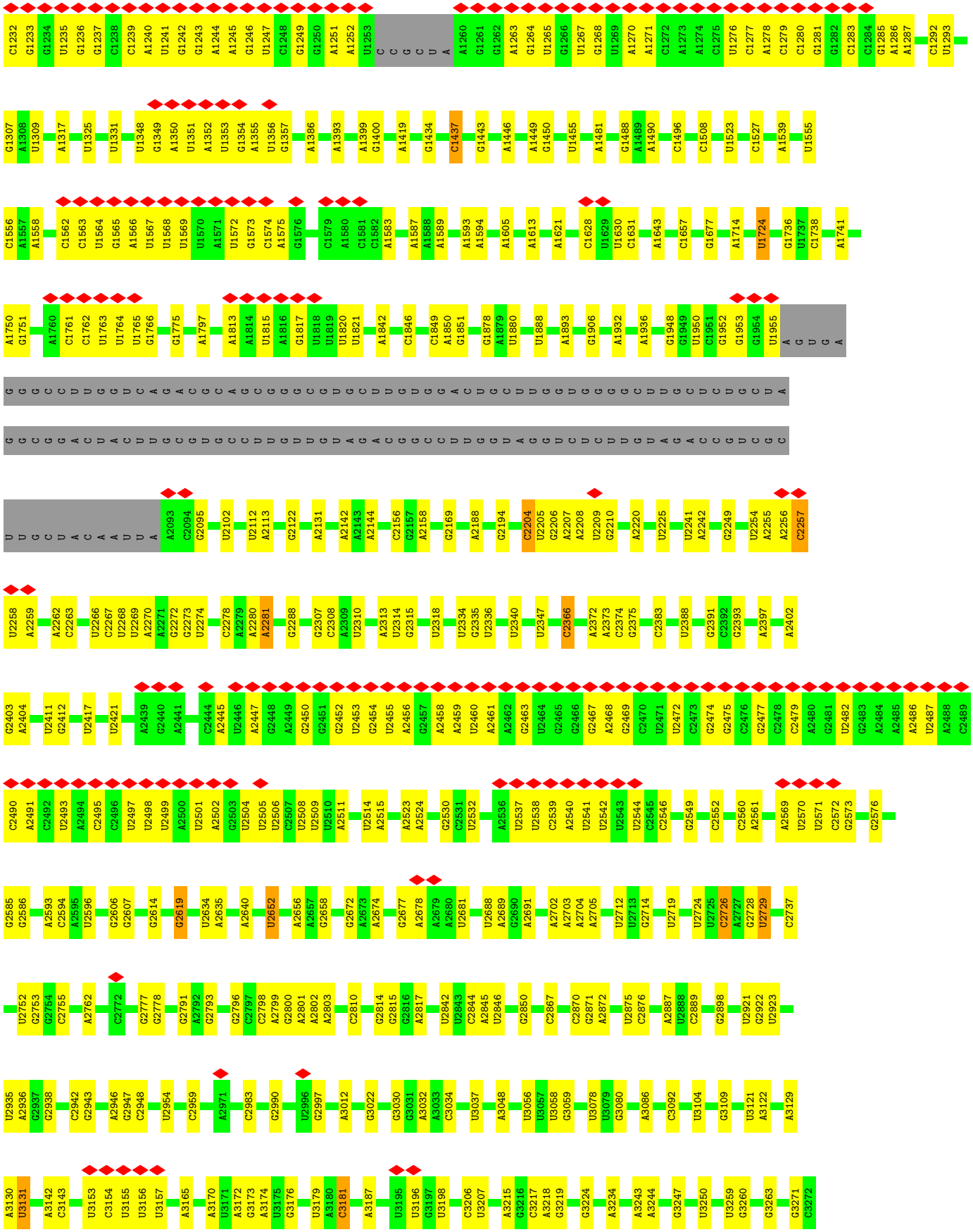
• Molecule 38: 25S rRNA

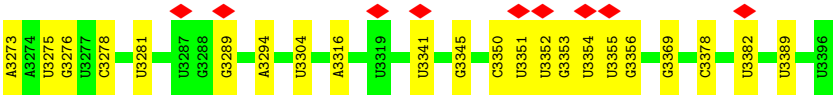
Chain A1:





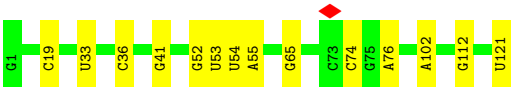






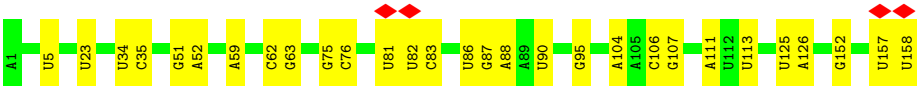
• Molecule 39: 5s rRNA

Chain A3:



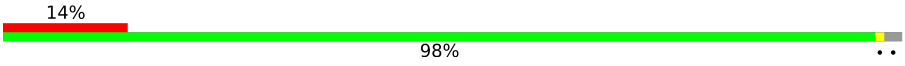
• Molecule 40: 5.8 S rRNA

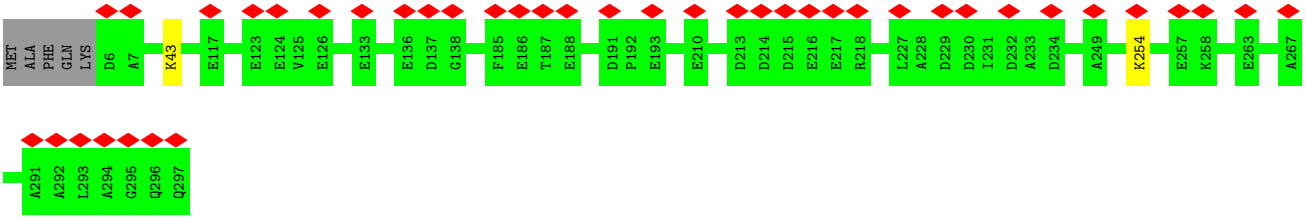
Chain A4:



• Molecule 41: RPL5 isoform 1

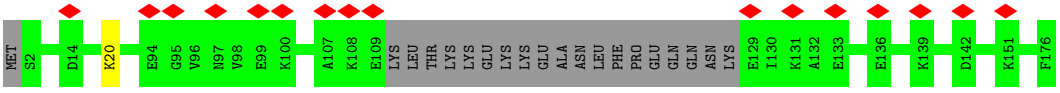
Chain AD:





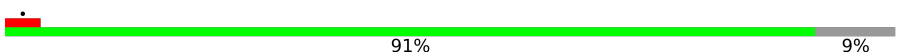
• Molecule 42: 60S ribosomal protein L6-A

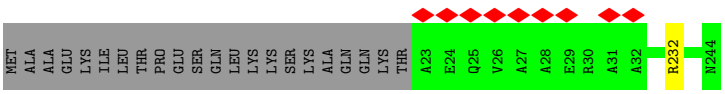
Chain AE:



• Molecule 43: 60S ribosomal protein L7-A

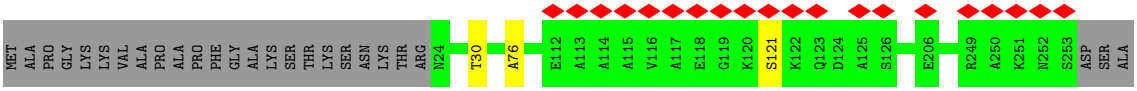
Chain AF:





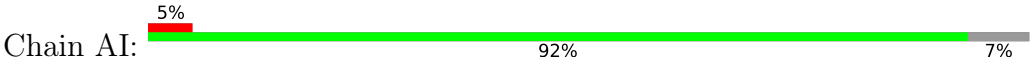
• Molecule 44: 60S ribosomal protein L8-A

Chain AG:

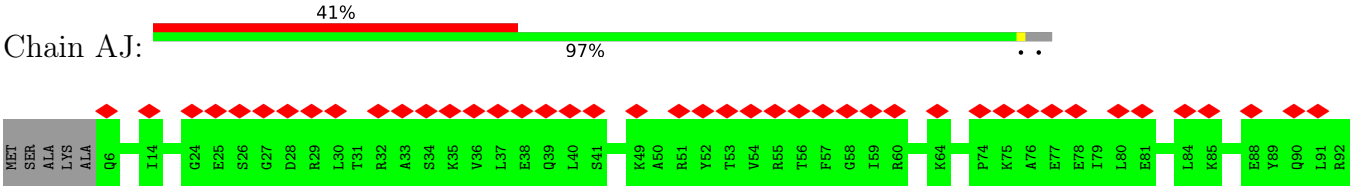


• Molecule 45: 60S ribosomal protein L9-A

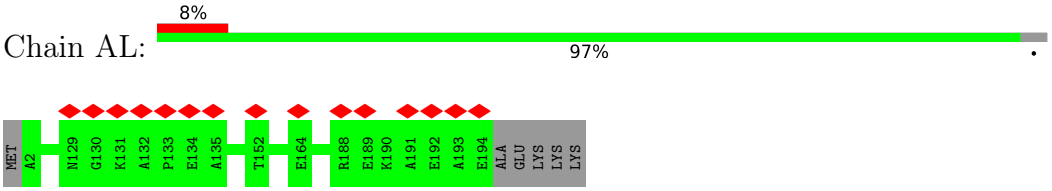
• Molecule 46: RPL10 isoform 1



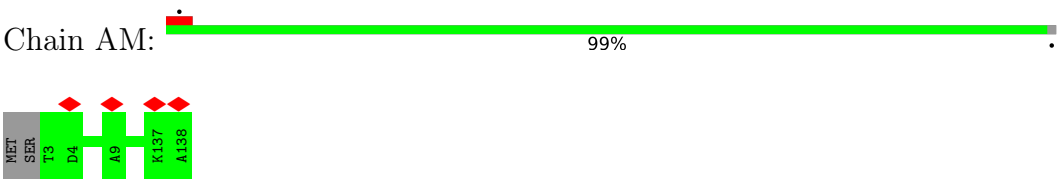
• Molecule 47: RPL11A isoform 1



• Molecule 48: 60S ribosomal protein L13-A



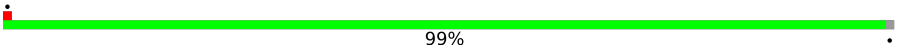
• Molecule 49: 60S ribosomal protein L14-A

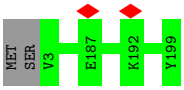


• Molecule 50: 60S ribosomal protein L15-A

• Molecule 51: 60S ribosomal protein L16-A

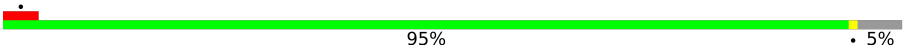
Chain AO:

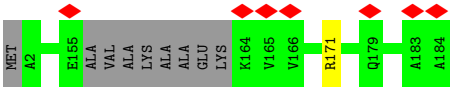




• Molecule 52: 60S ribosomal protein L17-A

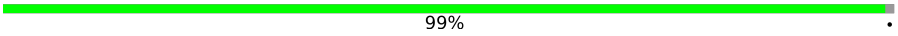
Chain AP:





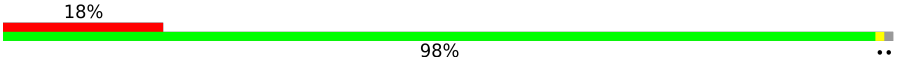
• Molecule 53: 60S ribosomal protein L18-A

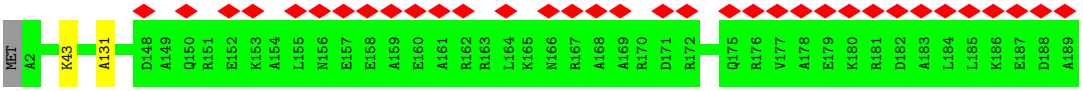
Chain AQ:



• Molecule 54: 60S ribosomal protein L19-A

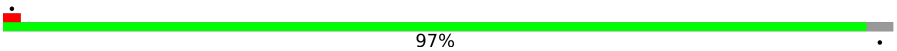
Chain AR:

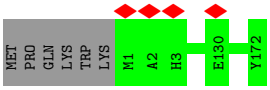




• Molecule 55: 60S ribosomal protein L20

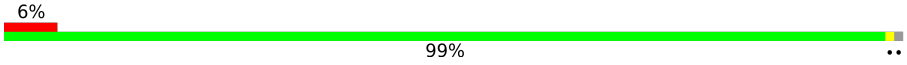
Chain AS:

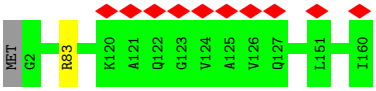




• Molecule 56: 60S ribosomal protein L21-A

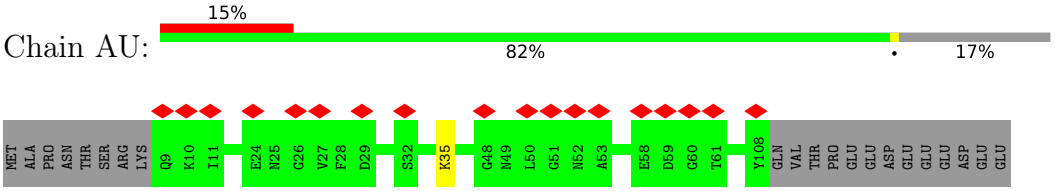
Chain AT:





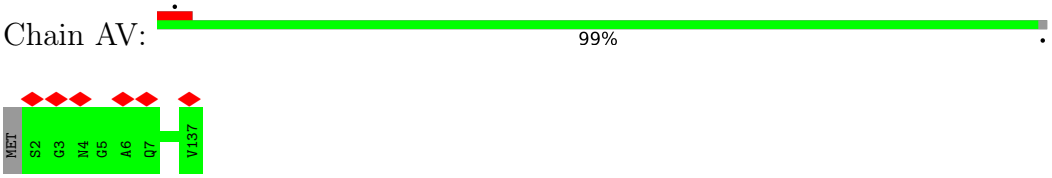
• Molecule 57: 60S ribosomal protein L22-A

Chain AU:



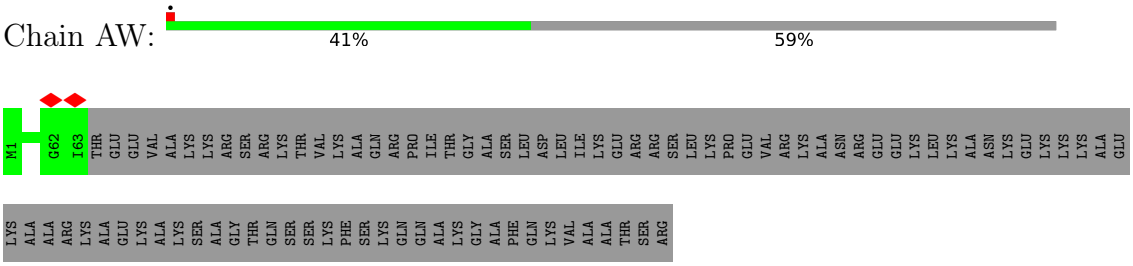
• Molecule 58: 60S ribosomal protein L23-A

Chain AV:



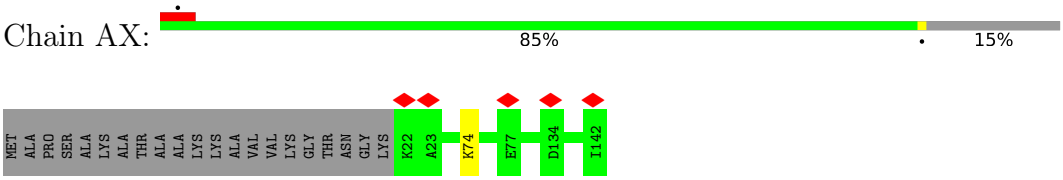
• Molecule 59: RPL24A isoform 1

Chain AW:



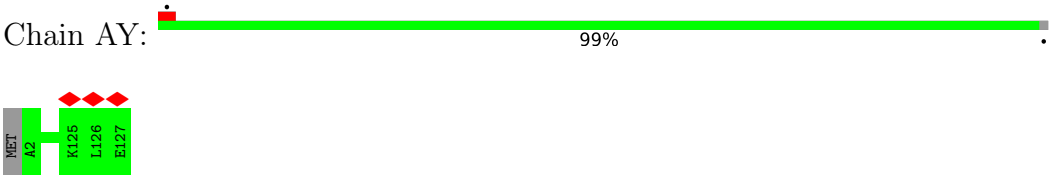
• Molecule 60: 60S ribosomal protein L25

Chain AX:



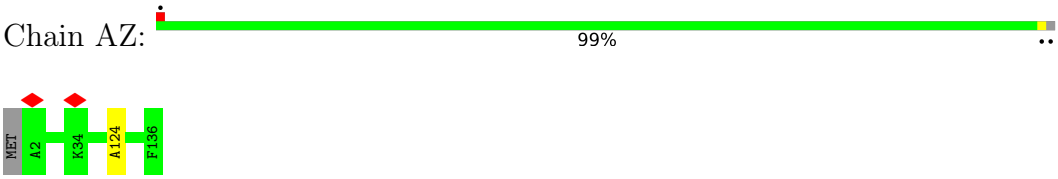
• Molecule 61: 60S ribosomal protein L26-A

Chain AY:



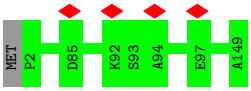
• Molecule 62: 60S ribosomal protein L27-A

Chain AZ:



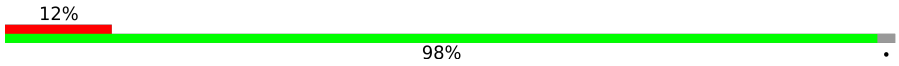
• Molecule 63: 60S ribosomal protein L28

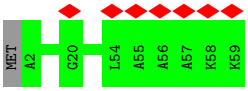
Chain Aa:



• Molecule 64: RPL29 isoform 1

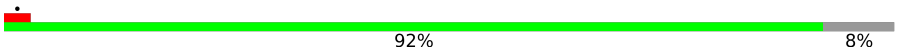
Chain Ab:

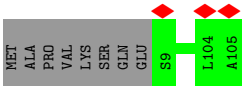




• Molecule 65: 60S ribosomal protein L30

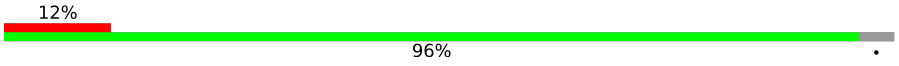
Chain Ac:

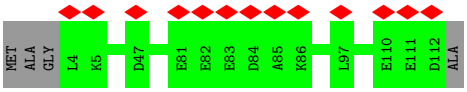




• Molecule 66: 60S ribosomal protein L31-A

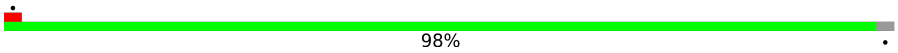
Chain Ad:

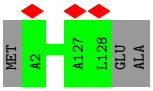




• Molecule 67: RPL32 isoform 1

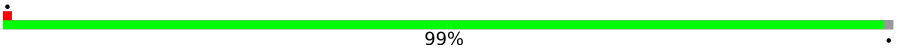
Chain Ae:





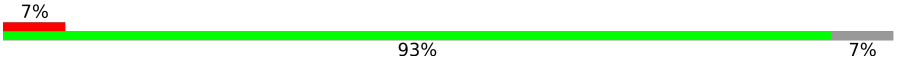
• Molecule 68: 60S ribosomal protein L33-A

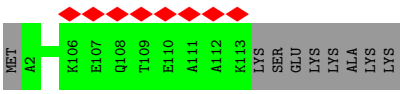
Chain Af:



• Molecule 69: 60S ribosomal protein L34-A

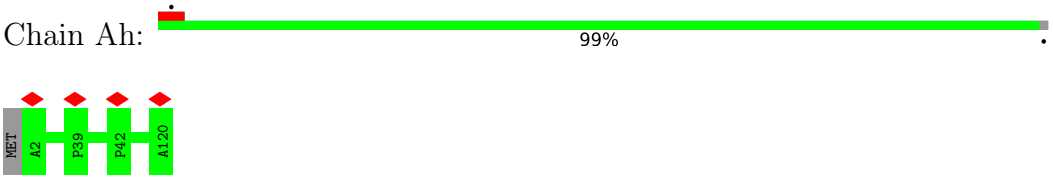
Chain Ag:





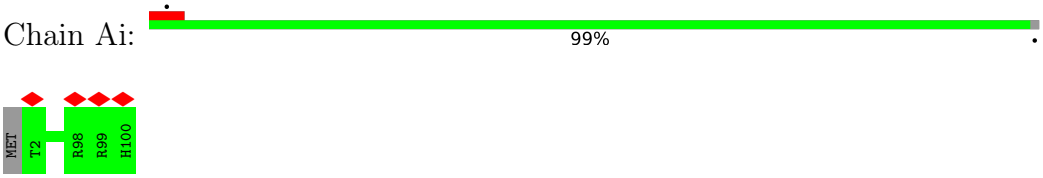
• Molecule 70: 60S ribosomal protein L35-A

Chain Ah:



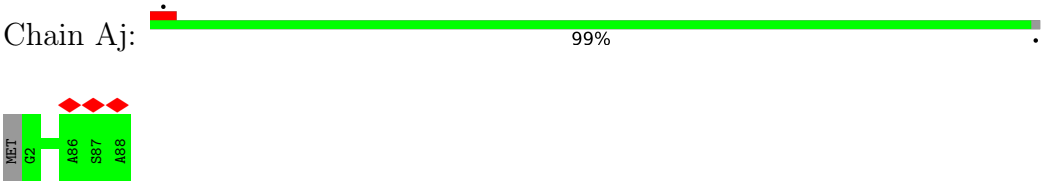
• Molecule 71: 60S ribosomal protein L36-A

Chain Ai:



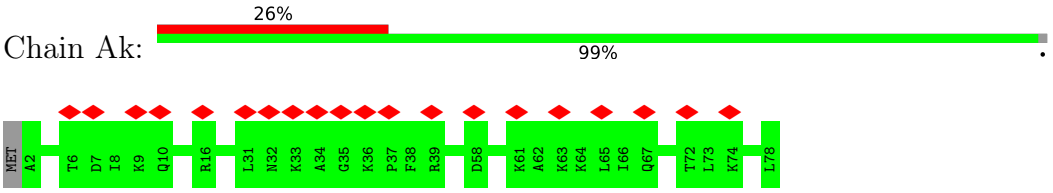
• Molecule 72: 60S ribosomal protein L37-A

Chain Aj:



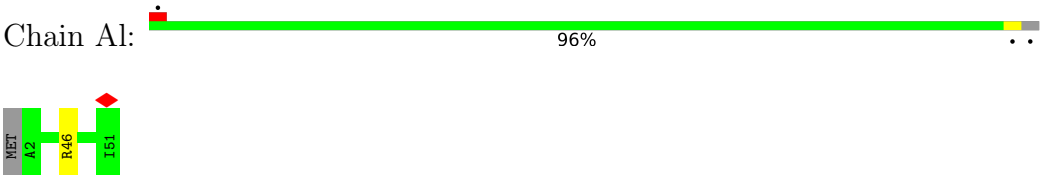
• Molecule 73: RPL38 isoform 1

Chain Ak:



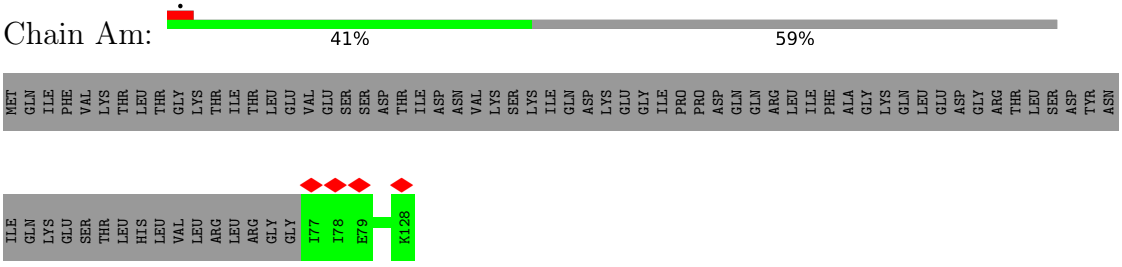
• Molecule 74: 60S ribosomal protein L39

Chain Al:



• Molecule 75: Ubiquitin-60S ribosomal protein L40

Chain Am:

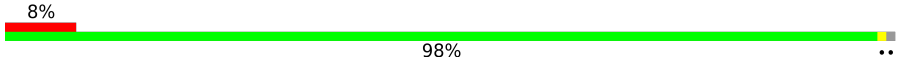


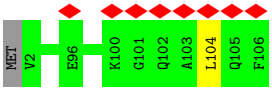
• Molecule 76: 60S ribosomal protein L41-A

Chain An:

• Molecule 77: 60S ribosomal protein L42-A

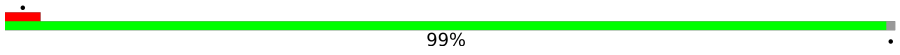
Chain Ao:

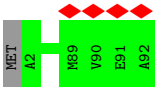




• Molecule 78: 60S ribosomal protein L43-A

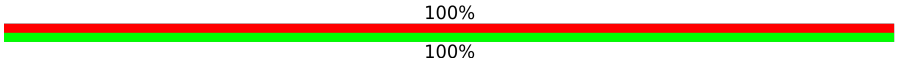
Chain Ap:

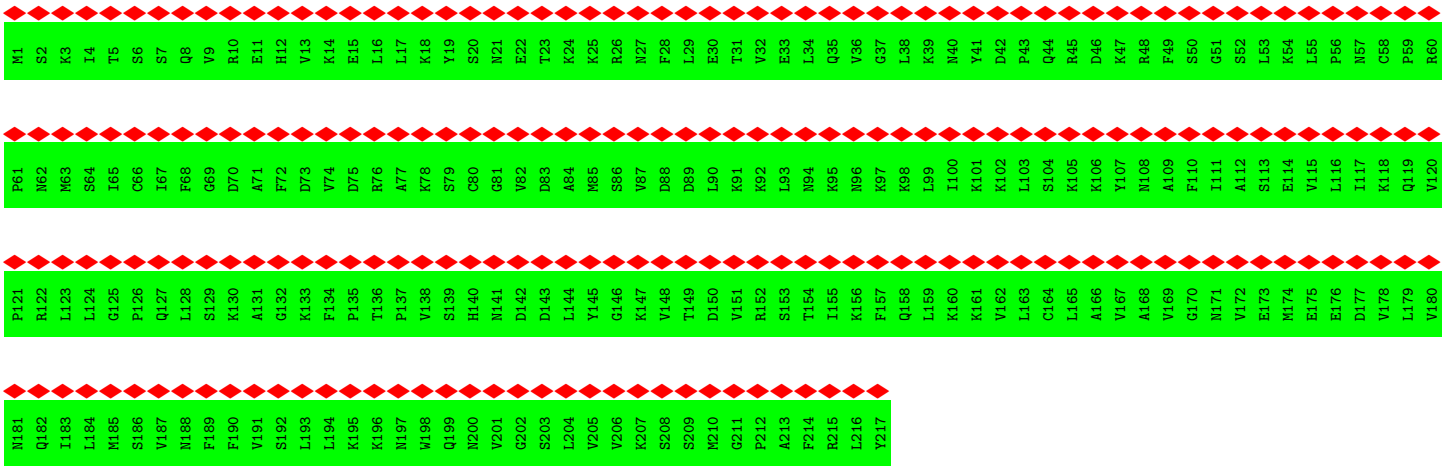




• Molecule 79: RPL1A isoform 1

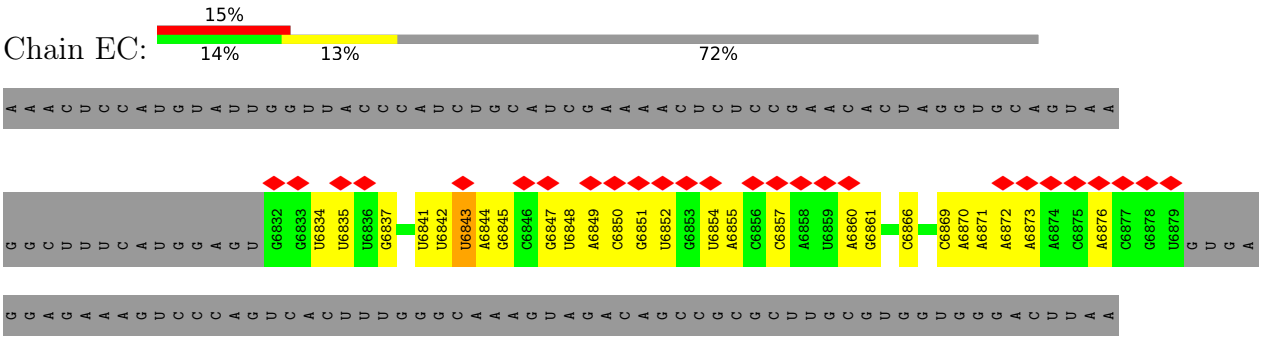
Chain E:

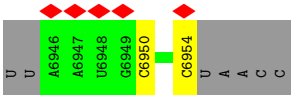




• Molecule 80: TSV IRES

Chain EC:




U
U
A6946
A6947
U6948
G6949
C6950
C6954
U
A
A
C
C

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	300118	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	10.371	Depositor
Minimum map value	-0.362	Depositor
Average map value	0.144	Depositor
Map value standard deviation	0.326	Depositor
Recommended contour level	1.1	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: MG, UR3, XSX, 1MA, MA6, OMC, OMU, A2M, HIC, OMG, 4AC, 5MC, ZN, 7MG

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	0.27	0/1653	0.54	0/2261
2	BB	0.26	0/1735	0.56	0/2335
3	BC	0.28	0/1665	0.51	0/2263
4	BE	0.28	0/2109	0.57	0/2839
5	BG	0.26	0/1844	0.56	0/2464
6	BH	0.28	0/1506	0.58	0/2028
7	BI	0.28	0/1514	0.61	0/2021
8	BJ	0.86	2/1519 (0.1%)	0.65	2/2035 (0.1%)
9	BL	0.29	0/1272	0.54	0/1712
10	BN	0.27	0/1215	0.53	0/1638
11	BO	0.29	0/952	0.62	0/1279
12	BV	0.53	0/693	0.68	2/935 (0.2%)
13	BW	0.30	0/1038	0.55	0/1395
14	BX	0.27	0/1139	0.57	0/1518
15	BY	0.29	0/1087	0.58	0/1449
16	Ba	0.27	0/782	0.63	0/1047
17	Bb	0.26	0/620	0.61	1/838 (0.1%)
18	Be	0.28	0/483	0.57	0/643
19	BD	0.28	0/1759	0.56	0/2368
20	BF	0.28	0/1629	0.55	0/2202
21	BK	0.30	0/837	0.53	0/1131
22	BP	0.95	4/1012 (0.4%)	1.08	5/1356 (0.4%)
23	BQ	0.28	0/1125	0.54	0/1510
24	BR	0.26	0/984	0.57	0/1318
25	BS	0.28	0/1211	0.61	0/1628
26	BT	0.30	0/1113	0.58	1/1494 (0.1%)
27	BU	0.27	0/865	0.54	0/1169
28	BZ	0.26	0/566	0.53	0/761
29	Bc	0.27	0/499	0.64	0/670
30	Bd	0.29	0/453	0.63	0/602
31	Bg	0.26	0/2454	0.53	0/3340
32	Bf	0.24	0/462	0.54	0/617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	BM	0.24	0/921	0.52	0/1245
34	B5	0.36	0/41880	0.85	21/65248 (0.0%)
35	AA	0.29	0/1912	0.59	0/2569
36	AB	0.28	0/3138	0.57	0/4217
37	AC	0.28	0/2800	0.55	1/3790 (0.0%)
38	A1	0.38	0/75445	0.85	37/117621 (0.0%)
39	A3	0.33	0/2883	0.82	0/4491
40	A4	0.37	0/3746	0.82	1/5832 (0.0%)
41	AD	0.27	0/2390	0.53	0/3225
42	AE	0.27	0/1260	0.52	0/1694
43	AF	0.27	0/1821	0.51	0/2451
44	AG	0.27	0/1830	0.52	0/2469
45	AH	0.30	0/1531	0.55	0/2062
46	AI	0.29	0/1708	0.54	0/2290
47	AJ	0.26	0/1374	0.57	0/1842
48	AL	0.27	0/1568	0.58	0/2106
49	AM	0.26	0/1068	0.51	0/1438
50	AN	0.28	0/1757	0.60	0/2354
51	AO	0.28	0/1585	0.53	0/2128
52	AP	0.29	0/1410	0.56	0/1893
53	AQ	0.26	0/1465	0.57	0/1965
54	AR	0.25	0/1538	0.57	0/2050
55	AS	0.31	0/1481	0.59	0/1990
56	AT	0.28	0/1300	0.54	0/1743
57	AU	0.30	0/812	0.55	0/1099
58	AV	0.33	0/1018	0.63	0/1369
59	AW	0.28	0/533	0.54	0/707
60	AX	0.28	0/983	0.52	0/1325
61	AY	0.27	0/1004	0.57	0/1341
62	AZ	0.27	0/1118	0.51	0/1497
63	Aa	0.28	0/1204	0.55	0/1612
64	Ab	0.25	0/473	0.53	0/629
65	Ac	0.30	0/751	0.53	0/1008
66	Ad	0.27	0/904	0.54	0/1213
67	Ae	0.26	0/1041	0.53	0/1394
68	Af	0.31	0/868	0.57	0/1168
69	Ag	0.28	0/890	0.60	0/1189
70	Ah	0.26	0/978	0.51	0/1301
71	Ai	0.27	0/778	0.60	0/1034
72	Aj	0.29	0/696	0.60	0/923
73	Ak	0.28	0/618	0.58	0/826
74	Al	0.25	0/443	0.60	0/588
75	Am	0.27	0/423	0.56	0/562

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	An	0.23	0/234	0.73	0/300
77	Ao	0.33	0/860	0.61	1/1136 (0.1%)
78	Ap	0.27	0/701	0.61	0/934
79	E	0.27	0/1745	0.51	0/2342
80	EC	0.32	2/1349 (0.1%)	0.88	1/2096 (0.0%)
All	All	0.35	8/216030 (0.0%)	0.76	73/317172 (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
6	BH	0	1
11	BO	0	1
14	BX	0	1
16	Ba	0	1
20	BF	0	1
36	AB	0	1
37	AC	0	1
41	AD	0	1
43	AF	0	1
44	AG	0	3
54	AR	0	1
62	AZ	0	1
All	All	0	14

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	BJ	169	PRO	N-CD	-28.38	1.08	1.47
22	BP	73	PRO	CB-CG	21.14	2.55	1.50
22	BP	73	PRO	CG-CD	-16.85	0.95	1.50
8	BJ	169	PRO	CG-CD	-13.29	1.06	1.50
22	BP	73	PRO	N-CD	6.41	1.56	1.47

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
22	BP	73	PRO	CB-CG-CD	-27.30	0.05	106.50
34	B5	1575	7MG	OP1-P-O3'	-16.73	68.40	105.20
22	BP	73	PRO	CA-N-CD	-13.64	92.40	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	B5	1575	7MG	O3'-P-O5'	9.66	122.35	104.00
38	A1	406	G	O4'-C1'-N9	9.31	115.64	108.20

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
20	BF	43	PHE	Peptide
6	BH	64	VAL	Peptide
11	BO	122	PRO	Peptide
14	BX	88	PRO	Peptide
16	Ba	7	SER	Peptide

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/252 (81%)	185 (91%)	19 (9%)	0	100	100
2	BB	212/255 (83%)	185 (87%)	27 (13%)	0	100	100
3	BC	215/254 (85%)	208 (97%)	7 (3%)	0	100	100
4	BE	258/261 (99%)	241 (93%)	17 (7%)	0	100	100
5	BG	224/236 (95%)	215 (96%)	9 (4%)	0	100	100
6	BH	182/190 (96%)	163 (90%)	19 (10%)	0	100	100
7	BI	184/200 (92%)	165 (90%)	19 (10%)	0	100	100
8	BJ	183/197 (93%)	172 (94%)	11 (6%)	0	100	100
9	BL	153/156 (98%)	141 (92%)	12 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	BN	148/151 (98%)	139 (94%)	9 (6%)	0	100	100
11	BO	125/137 (91%)	109 (87%)	16 (13%)	0	100	100
12	BV	85/87 (98%)	75 (88%)	10 (12%)	0	100	100
13	BW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
14	BX	142/145 (98%)	127 (89%)	15 (11%)	0	100	100
15	BY	132/135 (98%)	125 (95%)	7 (5%)	0	100	100
16	Ba	95/119 (80%)	79 (83%)	16 (17%)	0	100	100
17	Bb	79/82 (96%)	63 (80%)	16 (20%)	0	100	100
18	Be	58/63 (92%)	54 (93%)	4 (7%)	0	100	100
19	BD	221/240 (92%)	208 (94%)	13 (6%)	0	100	100
20	BF	204/225 (91%)	183 (90%)	21 (10%)	0	100	100
21	BK	94/105 (90%)	82 (87%)	12 (13%)	0	100	100
22	BP	122/142 (86%)	108 (88%)	14 (12%)	0	100	100
23	BQ	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
24	BR	117/136 (86%)	117 (100%)	0	0	100	100
25	BS	143/146 (98%)	133 (93%)	10 (7%)	0	100	100
26	BT	139/144 (96%)	122 (88%)	17 (12%)	0	100	100
27	BU	105/121 (87%)	100 (95%)	5 (5%)	0	100	100
28	BZ	67/108 (62%)	65 (97%)	2 (3%)	0	100	100
29	Bc	61/67 (91%)	57 (93%)	4 (7%)	0	100	100
30	Bd	51/56 (91%)	51 (100%)	0	0	100	100
31	Bg	310/319 (97%)	272 (88%)	38 (12%)	0	100	100
32	Bf	53/152 (35%)	41 (77%)	12 (23%)	0	100	100
33	BM	119/143 (83%)	90 (76%)	29 (24%)	0	100	100
35	AA	245/254 (96%)	231 (94%)	14 (6%)	0	100	100
36	AB	383/387 (99%)	366 (96%)	17 (4%)	0	100	100
37	AC	359/362 (99%)	337 (94%)	22 (6%)	0	100	100
41	AD	290/297 (98%)	277 (96%)	13 (4%)	0	100	100
42	AE	152/176 (86%)	140 (92%)	12 (8%)	0	100	100
43	AF	220/244 (90%)	213 (97%)	7 (3%)	0	100	100
44	AG	228/256 (89%)	211 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	AH	188/191 (98%)	172 (92%)	16 (8%)	0	100	100
46	AI	201/221 (91%)	188 (94%)	13 (6%)	0	100	100
47	AJ	167/174 (96%)	148 (89%)	19 (11%)	0	100	100
48	AL	191/199 (96%)	175 (92%)	16 (8%)	0	100	100
49	AM	134/138 (97%)	130 (97%)	4 (3%)	0	100	100
50	AN	201/204 (98%)	188 (94%)	13 (6%)	0	100	100
51	AO	195/199 (98%)	192 (98%)	3 (2%)	0	100	100
52	AP	171/184 (93%)	165 (96%)	6 (4%)	0	100	100
53	AQ	183/186 (98%)	176 (96%)	7 (4%)	0	100	100
54	AR	186/189 (98%)	178 (96%)	8 (4%)	0	100	100
55	AS	170/178 (96%)	162 (95%)	8 (5%)	0	100	100
56	AT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
57	AU	98/121 (81%)	95 (97%)	3 (3%)	0	100	100
58	AV	134/137 (98%)	131 (98%)	3 (2%)	0	100	100
59	AW	61/155 (39%)	60 (98%)	1 (2%)	0	100	100
60	AX	119/142 (84%)	118 (99%)	1 (1%)	0	100	100
61	AY	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
62	AZ	133/136 (98%)	126 (95%)	7 (5%)	0	100	100
63	Aa	146/149 (98%)	133 (91%)	13 (9%)	0	100	100
64	Ab	56/59 (95%)	48 (86%)	8 (14%)	0	100	100
65	Ac	95/105 (90%)	90 (95%)	5 (5%)	0	100	100
66	Ad	107/113 (95%)	102 (95%)	5 (5%)	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%)	108 (98%)	2 (2%)	0	100	100
70	Ah	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
71	Ai	97/100 (97%)	92 (95%)	5 (5%)	0	100	100
72	Aj	85/88 (97%)	79 (93%)	6 (7%)	0	100	100
73	Ak	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
74	Al	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
75	Am	50/128 (39%)	48 (96%)	2 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
76	An	23/25 (92%)	23 (100%)	0	0	100	100
77	Ao	103/106 (97%)	91 (88%)	12 (12%)	0	100	100
78	Ap	89/92 (97%)	82 (92%)	7 (8%)	0	100	100
79	E	215/217 (99%)	207 (96%)	8 (4%)	0	100	100
All	All	11086/12103 (92%)	10325 (93%)	761 (7%)	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%)	172 (99%)	1 (1%)	86	93
2	BB	191/224 (85%)	190 (100%)	1 (0%)	88	94
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%)	132 (97%)	4 (3%)	42	54
10	BN	127/128 (99%)	127 (100%)	0	100	100
11	BO	96/105 (91%)	94 (98%)	2 (2%)	53	67
12	BV	74/74 (100%)	74 (100%)	0	100	100
13	BW	110/111 (99%)	109 (99%)	1 (1%)	78	88
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	Be	51/54 (94%)	51 (100%)	0	100	100
19	BD	182/195 (93%)	181 (100%)	1 (0%)	88	94
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%)	109 (99%)	1 (1%)	78	88
25	BS	128/129 (99%)	128 (100%)	0	100	100
26	BT	113/116 (97%)	112 (99%)	1 (1%)	78	88
27	BU	100/114 (88%)	99 (99%)	1 (1%)	76	86
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
35	AA	189/196 (96%)	189 (100%)	0	100	100
36	AB	321/322 (100%)	320 (100%)	1 (0%)	92	97
37	AC	288/289 (100%)	286 (99%)	2 (1%)	84	91
41	AD	241/245 (98%)	240 (100%)	1 (0%)	91	96
42	AE	134/153 (88%)	133 (99%)	1 (1%)	84	91
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%)	169 (99%)	1 (1%)	86	93
46	AI	176/187 (94%)	175 (99%)	1 (1%)	86	93
47	AJ	147/150 (98%)	146 (99%)	1 (1%)	84	91
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%)	140 (99%)	1 (1%)	84	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
53	AQ	150/151 (99%)	150 (100%)	0	100 100
54	AR	153/154 (99%)	152 (99%)	1 (1%)	84 91
55	AS	156/162 (96%)	156 (100%)	0	100 100
56	AT	136/137 (99%)	135 (99%)	1 (1%)	84 91
57	AU	87/107 (81%)	86 (99%)	1 (1%)	73 85
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%)	104 (99%)	1 (1%)	76 86
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
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%)	44 (98%)	1 (2%)	52 65
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%)	9441 (100%)	27 (0%)	92 97

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	AC	138	ARG

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Mol	Chain	Res	Type
42	AE	20	LYS
57	AU	35	LYS
41	AD	254	LYS
45	AH	106	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
45	AH	162	GLN
58	AV	98	ASN
47	AJ	90	GLN
53	AQ	45	ASN
62	AZ	128	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	B5	1775/1798 (98%)	416 (23%)	18 (1%)
38	A1	3186/3360 (94%)	612 (19%)	34 (1%)
39	A3	120/121 (99%)	13 (10%)	1 (0%)
40	A4	157/158 (99%)	28 (17%)	0
80	EC	55/202 (27%)	25 (45%)	1 (1%)
All	All	5293/5639 (93%)	1094 (20%)	54 (1%)

5 of 1094 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
34	B5	4	C
34	B5	17	C
34	B5	25	C
34	B5	26	A
34	B5	34	G

5 of 54 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
38	A1	873	C
38	A1	1354	G
38	A1	2801	A
38	A1	916	G

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Mol	Chain	Res	Type
38	A1	1218	U

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

66 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	OMG	A1	2793	38	18,26,27	0.96	1 (5%)	19,38,41	1.16	2 (10%)
38	5MC	A1	2870	38	18,22,23	1.03	2 (11%)	26,32,35	1.26	2 (7%)
34	OMG	B5	562	34	18,26,27	0.92	1 (5%)	19,38,41	1.13	2 (10%)
34	4AC	B5	1773	34	21,24,25	0.99	1 (4%)	29,34,37	2.09	6 (20%)
34	A2M	B5	436	34	18,25,26	1.00	1 (5%)	18,36,39	1.27	2 (11%)
34	OMC	B5	1007	34	19,22,23	0.79	0	26,31,34	0.81	0
38	1MA	A1	645	81,38	16,25,26	1.47	2 (12%)	18,37,40	1.02	2 (11%)
38	A2M	A1	807	38	18,25,26	1.00	1 (5%)	18,36,39	1.28	2 (11%)
34	A2M	B5	28	34,81	18,25,26	1.00	1 (5%)	18,36,39	1.26	2 (11%)
34	OMG	B5	1271	34	18,26,27	0.94	1 (5%)	19,38,41	1.07	2 (10%)
38	A2M	A1	2640	38	18,25,26	0.99	1 (5%)	18,36,39	1.18	2 (11%)
34	A2M	B5	420	34	18,25,26	1.04	1 (5%)	18,36,39	1.20	2 (11%)
38	OMG	A1	867	38	18,26,27	0.87	1 (5%)	19,38,41	1.16	2 (10%)
38	OMU	A1	2421	38	19,22,23	1.20	3 (15%)	26,31,34	1.73	5 (19%)
38	A2M	A1	2946	81,38	18,25,26	0.99	1 (5%)	18,36,39	1.25	2 (11%)
34	A2M	B5	796	34	18,25,26	1.01	1 (5%)	18,36,39	1.20	2 (11%)
38	OMU	A1	2729	38	19,22,23	1.24	4 (21%)	26,31,34	1.75	4 (15%)
34	MA6	B5	1781	34	19,26,27	0.94	1 (5%)	18,38,41	1.31	2 (11%)
38	UR3	A1	2634	38	19,22,23	0.97	0	26,32,35	1.44	2 (7%)
34	OMG	B5	1428	34,81	18,26,27	0.93	1 (5%)	19,38,41	1.05	2 (10%)
38	OMG	A1	2815	38	18,26,27	0.92	1 (5%)	19,38,41	1.14	2 (10%)
34	OMU	B5	578	34	19,22,23	1.17	2 (10%)	26,31,34	1.75	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
38	OMG	A1	2619	38	18,26,27	0.92	1 (5%)	19,38,41	1.02	2 (10%)
38	OMC	A1	2959	38	19,22,23	0.83	0	26,31,34	0.88	1 (3%)
38	OMU	A1	2724	38	19,22,23	1.19	3 (15%)	26,31,34	1.79	6 (23%)
38	A2M	A1	2281	38	18,25,26	0.91	1 (5%)	18,36,39	1.34	2 (11%)
34	A2M	B5	974	34	18,25,26	0.94	1 (5%)	18,36,39	1.39	3 (16%)
34	A2M	B5	100	34,81	18,25,26	1.01	1 (5%)	18,36,39	1.15	2 (11%)
38	A2M	A1	1449	81,38	18,25,26	1.00	1 (5%)	18,36,39	1.27	2 (11%)
38	A2M	A1	817	81,38	18,25,26	1.02	1 (5%)	18,36,39	1.39	2 (11%)
34	A2M	B5	541	34	18,25,26	0.99	1 (5%)	18,36,39	1.23	2 (11%)
38	OMC	A1	1437	81,38	19,22,23	0.80	0	26,31,34	1.00	2 (7%)
38	OMC	A1	663	38	19,22,23	0.82	0	26,31,34	0.80	0
38	A2M	A1	2220	38	18,25,26	1.00	1 (5%)	18,36,39	1.30	3 (16%)
38	OMU	A1	898	38	19,22,23	1.23	3 (15%)	26,31,34	1.73	5 (19%)
38	OMG	A1	2922	38	18,26,27	0.93	1 (5%)	19,38,41	1.07	2 (10%)
38	OMU	A1	2921	38	19,22,23	1.20	2 (10%)	26,31,34	1.73	5 (19%)
38	5MC	A1	2278	81,38	18,22,23	0.95	2 (11%)	26,32,35	1.12	3 (11%)
34	OMU	B5	1269	34	19,22,23	1.25	4 (21%)	26,31,34	1.76	5 (19%)
34	MA6	B5	1782	34	19,26,27	0.92	1 (5%)	18,38,41	1.37	2 (11%)
38	A2M	A1	2280	38	18,25,26	1.00	1 (5%)	18,36,39	1.29	2 (11%)
38	OMC	A1	2948	38	19,22,23	0.81	0	26,31,34	0.88	1 (3%)
34	OMC	B5	414	34	19,22,23	0.82	0	26,31,34	0.81	0
38	OMC	A1	650	38	19,22,23	0.83	0	26,31,34	0.95	1 (3%)
38	OMG	A1	908	38	18,26,27	0.95	1 (5%)	19,38,41	1.12	2 (10%)
34	OMC	B5	1639	34	19,22,23	0.79	0	26,31,34	0.79	0
38	1MA	A1	2142	81,38	16,25,26	1.47	2 (12%)	18,37,40	1.06	2 (11%)
34	7MG	B5	1575	34	22,26,27	5.88	5 (22%)	29,39,42	3.42	8 (27%)
34	4AC	B5	1280	34	21,24,25	1.00	1 (4%)	29,34,37	1.11	4 (13%)
36	HIC	AB	243	36	8,11,12	1.62	2 (25%)	6,14,16	1.00	0
38	A2M	A1	649	38	18,25,26	1.02	1 (5%)	18,36,39	1.17	2 (11%)
38	OMU	A1	1888	38	19,22,23	1.24	2 (10%)	26,31,34	1.80	5 (19%)
34	OMG	B5	1572	34	18,26,27	0.96	1 (5%)	19,38,41	1.13	2 (10%)
38	OMC	A1	2337	38	19,22,23	0.78	0	26,31,34	0.81	0
38	OMG	A1	1450	38	18,26,27	0.94	1 (5%)	19,38,41	1.10	2 (10%)
38	OMG	A1	2288	38	18,26,27	0.91	1 (5%)	19,38,41	1.13	2 (10%)
38	OMU	A1	2347	38	19,22,23	1.23	2 (10%)	26,31,34	1.65	5 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
38	A2M	A1	876	38	18,25,26	1.06	2 (11%)	18,36,39	1.22	2 (11%)
38	OMG	A1	2791	38	18,26,27	0.92	1 (5%)	19,38,41	1.13	2 (10%)
38	OMC	A1	2197	38	19,22,23	0.78	0	26,31,34	0.84	0
34	A2M	B5	619	34,81	18,25,26	0.91	1 (5%)	18,36,39	1.27	2 (11%)
38	A2M	A1	1133	38	18,25,26	1.03	1 (5%)	18,36,39	1.30	2 (11%)
34	XSX	B5	1191	34	24,28,29	0.98	0	33,40,43	2.04	4 (12%)
38	OMG	A1	805	38	18,26,27	0.91	1 (5%)	19,38,41	1.17	2 (10%)
38	OMU	A1	2417	38	19,22,23	1.21	3 (15%)	26,31,34	1.73	5 (19%)
34	OMG	B5	1126	34	18,26,27	0.90	1 (5%)	19,38,41	1.15	2 (10%)

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	OMG	A1	2793	38	-	1/5/27/28	0/3/3/3
38	5MC	A1	2870	38	-	4/7/25/26	0/2/2/2
34	OMG	B5	562	34	-	0/5/27/28	0/3/3/3
34	4AC	B5	1773	34	-	4/11/29/30	0/2/2/2
34	A2M	B5	436	34	-	0/5/27/28	0/3/3/3
34	OMC	B5	1007	34	-	1/9/27/28	0/2/2/2
38	1MA	A1	645	81,38	-	0/3/25/26	0/3/3/3
38	A2M	A1	807	38	-	0/5/27/28	0/3/3/3
34	A2M	B5	28	34,81	-	1/5/27/28	0/3/3/3
34	OMG	B5	1271	34	-	1/5/27/28	0/3/3/3
38	A2M	A1	2640	38	-	0/5/27/28	0/3/3/3
34	A2M	B5	420	34	-	0/5/27/28	0/3/3/3
38	OMG	A1	867	38	-	1/5/27/28	0/3/3/3
38	OMU	A1	2421	38	-	1/9/27/28	0/2/2/2
38	A2M	A1	2946	81,38	-	1/5/27/28	0/3/3/3
34	A2M	B5	796	34	-	1/5/27/28	0/3/3/3
38	OMU	A1	2729	38	-	3/9/27/28	0/2/2/2
34	MA6	B5	1781	34	-	0/7/29/30	0/3/3/3
38	UR3	A1	2634	38	-	0/7/25/26	0/2/2/2
34	OMG	B5	1428	34,81	-	2/5/27/28	0/3/3/3
38	OMG	A1	2815	38	-	0/5/27/28	0/3/3/3
34	OMU	B5	578	34	-	0/9/27/28	0/2/2/2
38	OMG	A1	2619	38	-	1/5/27/28	0/3/3/3
38	OMC	A1	2959	38	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	2724	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2281	38	-	1/5/27/28	0/3/3/3
34	A2M	B5	974	34	-	1/5/27/28	0/3/3/3
34	A2M	B5	100	34,81	-	1/5/27/28	0/3/3/3
38	A2M	A1	1449	81,38	-	0/5/27/28	0/3/3/3
38	A2M	A1	817	81,38	-	2/5/27/28	0/3/3/3
34	A2M	B5	541	34	-	3/5/27/28	0/3/3/3
38	OMC	A1	1437	81,38	-	4/9/27/28	0/2/2/2
38	OMC	A1	663	38	-	0/9/27/28	0/2/2/2
38	A2M	A1	2220	38	-	1/5/27/28	0/3/3/3
38	OMU	A1	898	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	2922	38	-	0/5/27/28	0/3/3/3
38	OMU	A1	2921	38	-	0/9/27/28	0/2/2/2
38	5MC	A1	2278	81,38	-	0/7/25/26	0/2/2/2
34	OMU	B5	1269	34	-	4/9/27/28	0/2/2/2
34	MA6	B5	1782	34	-	3/7/29/30	0/3/3/3
38	A2M	A1	2280	38	-	1/5/27/28	0/3/3/3
38	OMC	A1	2948	38	-	0/9/27/28	0/2/2/2
34	OMC	B5	414	34	-	1/9/27/28	0/2/2/2
38	OMC	A1	650	38	-	0/9/27/28	0/2/2/2
38	OMG	A1	908	38	-	0/5/27/28	0/3/3/3
34	OMC	B5	1639	34	-	0/9/27/28	0/2/2/2
38	1MA	A1	2142	81,38	-	0/3/25/26	0/3/3/3
34	7MG	B5	1575	34	-	0/7/37/38	0/3/3/3
34	4AC	B5	1280	34	-	0/11/29/30	0/2/2/2
36	HIC	AB	243	36	-	0/5/6/8	0/1/1/1
38	A2M	A1	649	38	-	1/5/27/28	0/3/3/3
38	OMU	A1	1888	38	-	0/9/27/28	0/2/2/2
34	OMG	B5	1572	34	-	0/5/27/28	0/3/3/3
38	OMC	A1	2337	38	-	1/9/27/28	0/2/2/2
38	OMG	A1	1450	38	-	0/5/27/28	0/3/3/3
38	OMG	A1	2288	38	-	0/5/27/28	0/3/3/3
38	OMU	A1	2347	38	-	2/9/27/28	0/2/2/2
38	A2M	A1	876	38	-	0/5/27/28	0/3/3/3
38	OMG	A1	2791	38	-	0/5/27/28	0/3/3/3
38	OMC	A1	2197	38	-	6/9/27/28	0/2/2/2
34	A2M	B5	619	34,81	-	2/5/27/28	0/3/3/3
38	A2M	A1	1133	38	-	0/5/27/28	0/3/3/3
34	XSX	B5	1191	34	-	5/16/34/35	0/2/2/2
38	OMG	A1	805	38	-	1/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
38	OMU	A1	2417	38	-	1/9/27/28	0/2/2/2
34	OMG	B5	1126	34	-	1/5/27/28	0/3/3/3

The worst 5 of 82 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	B5	1575	7MG	C1'-N9	-26.80	0.97	1.46
38	A1	2142	1MA	C2-N3	4.47	1.34	1.29
38	A1	645	1MA	C2-N3	4.41	1.34	1.29
36	AB	243	HIC	CD2-CG	3.42	1.41	1.36
38	A1	645	1MA	C6-N6	3.11	1.35	1.27

The worst 5 of 162 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
34	B5	1575	7MG	O4'-C1'-N9	-12.60	92.13	109.30
34	B5	1575	7MG	N9-C4-N3	9.01	138.95	125.47
34	B5	1191	XSX	C3-C1-N3	8.74	128.38	112.00
34	B5	1773	4AC	N4-C4-N3	7.63	126.65	113.85
38	A1	2634	UR3	C4-N3-C2	-5.98	118.93	124.56

There are no chirality outliers.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
34	B5	28	A2M	C1'-C2'-O2'-CM'
34	B5	100	A2M	C1'-C2'-O2'-CM'
34	B5	414	OMC	C1'-C2'-O2'-CM2
34	B5	619	A2M	O4'-C4'-C5'-O5'
34	B5	796	A2M	C1'-C2'-O2'-CM'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 273 ligands modelled in this entry, 273 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
38	A1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	2439:A	O3'	2440:G	P	6.91

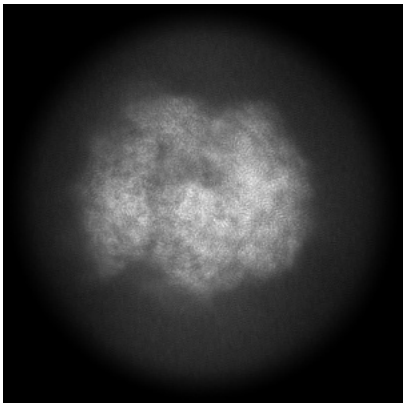
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-28636. These allow visual inspection of the internal detail of the map and identification of artifacts.

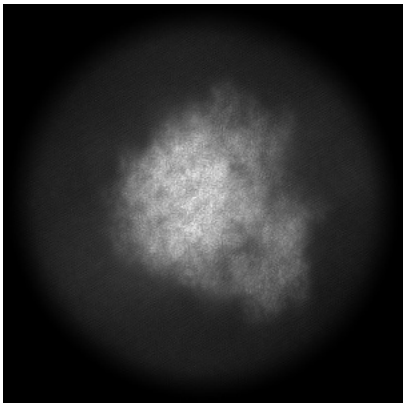
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

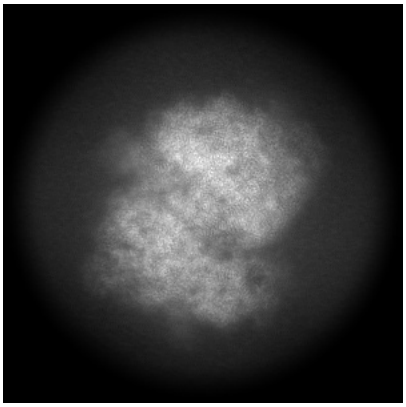
6.1.1 Primary map



X



Y

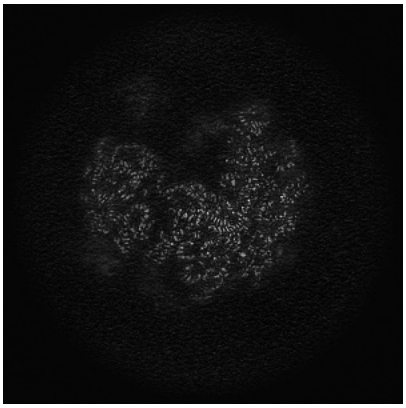


Z

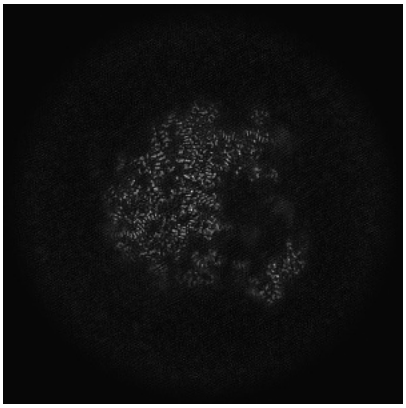
The images above show the map projected in three orthogonal directions.

6.2 Central slices

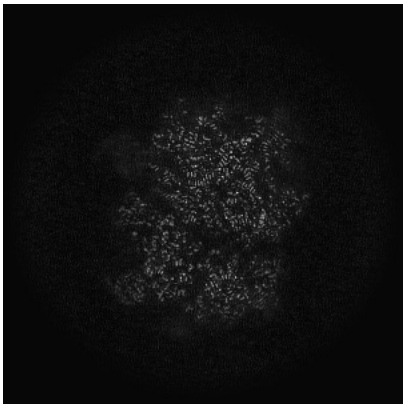
6.2.1 Primary map



X Index: 200



Y Index: 200

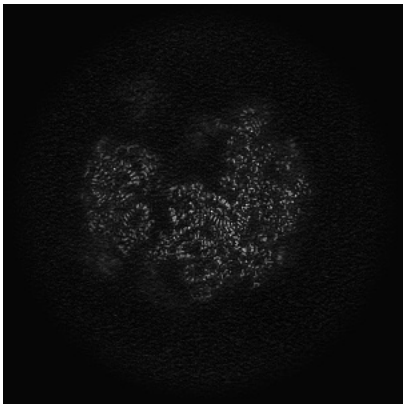


Z Index: 200

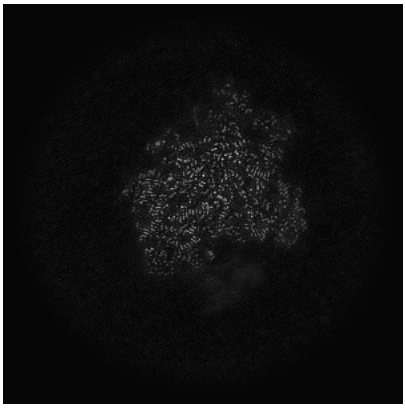
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

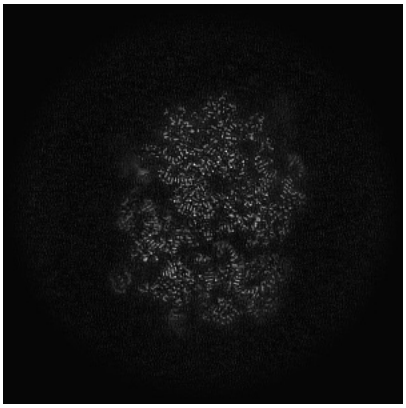
6.3.1 Primary map



X Index: 201



Y Index: 246

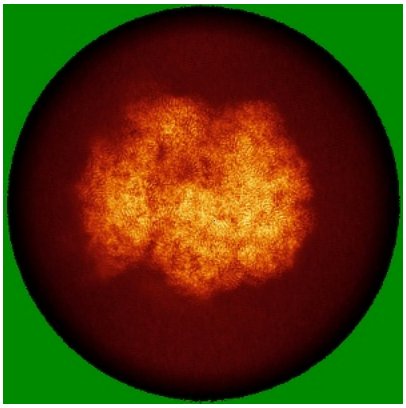


Z Index: 191

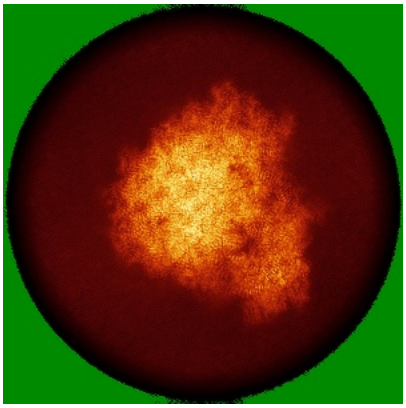
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

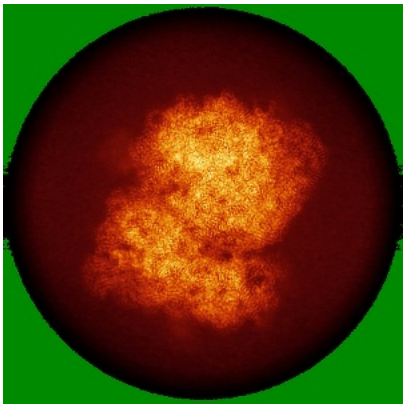
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

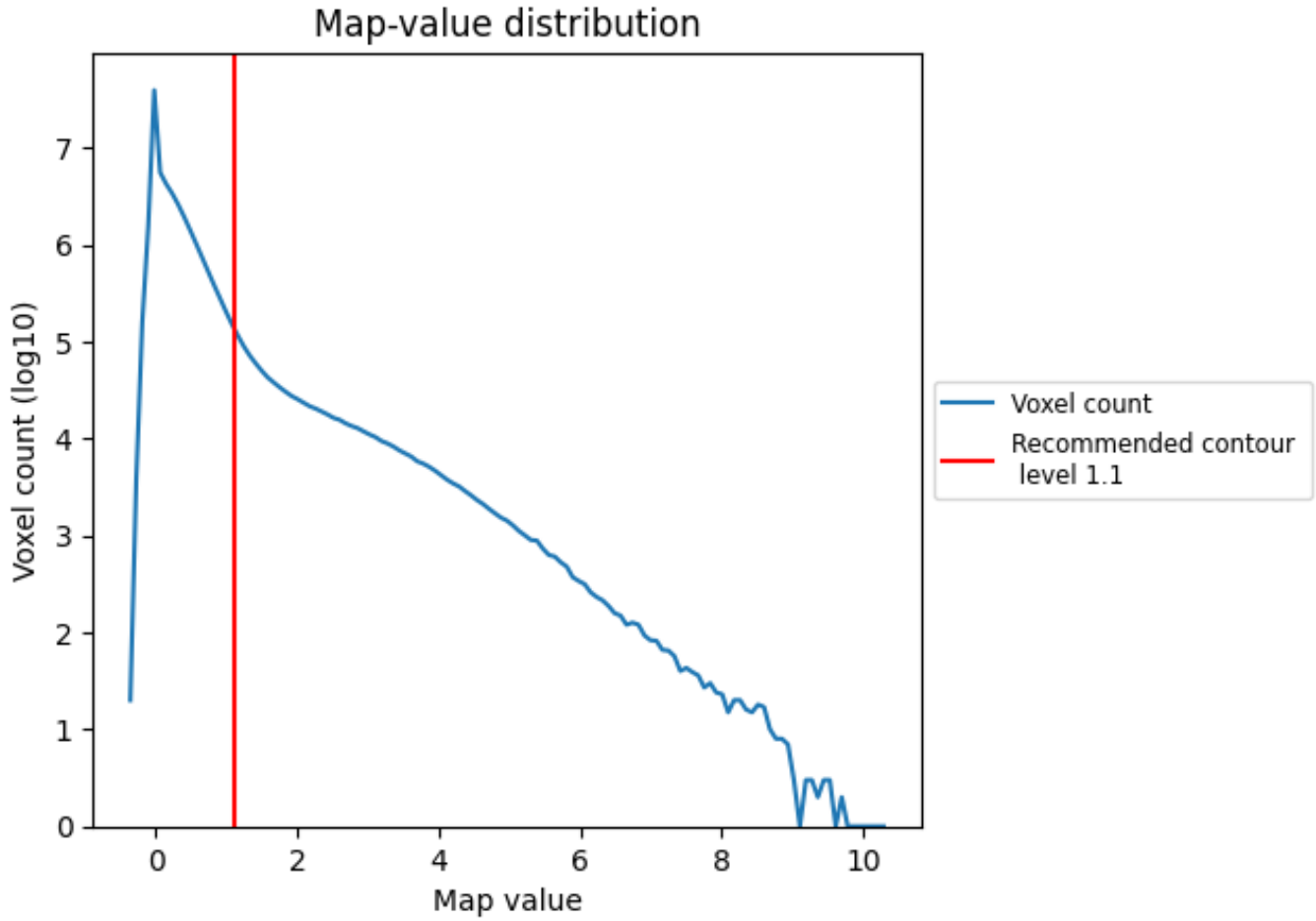
6.6 Mask visualisation (i)

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

7 Map analysis

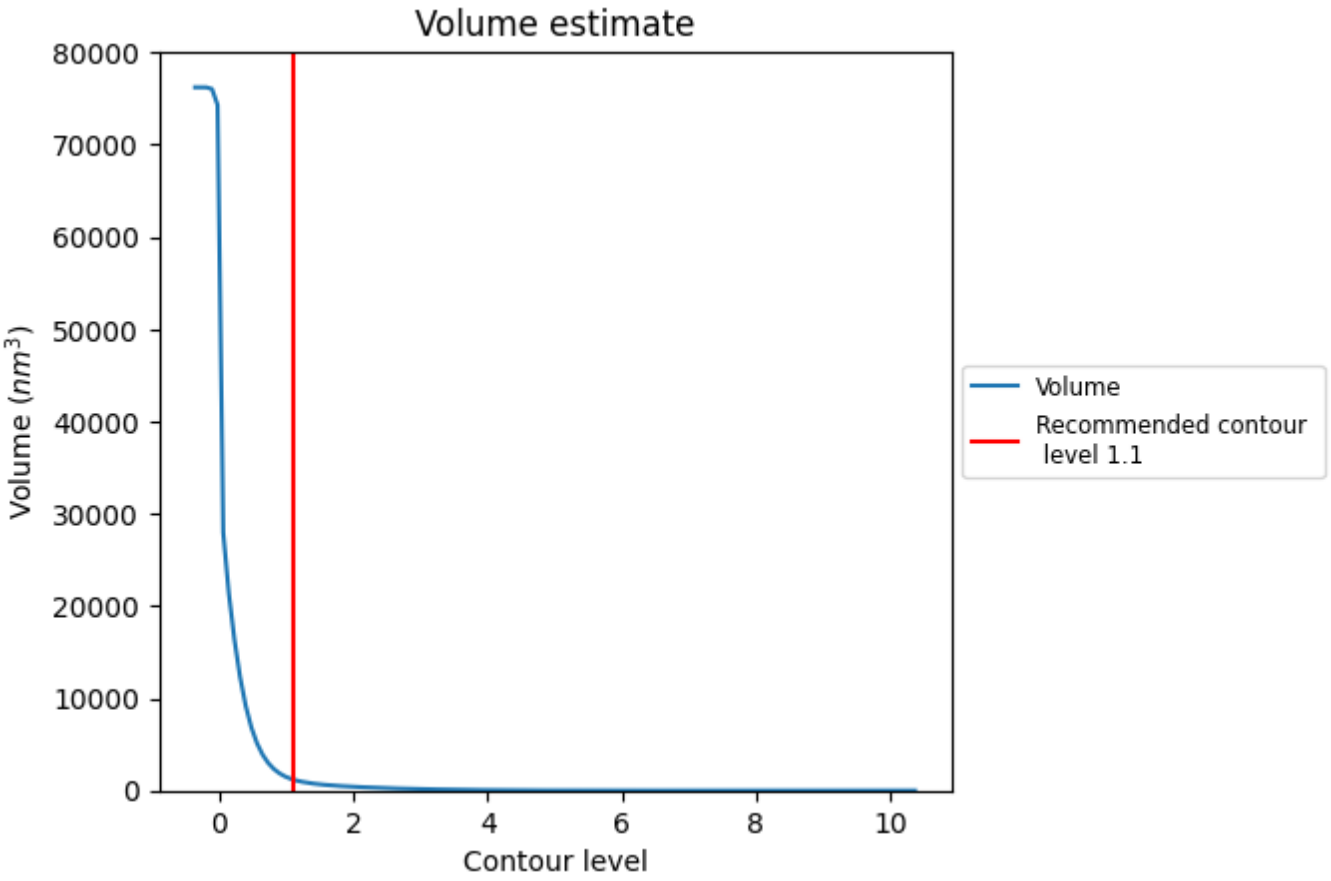
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

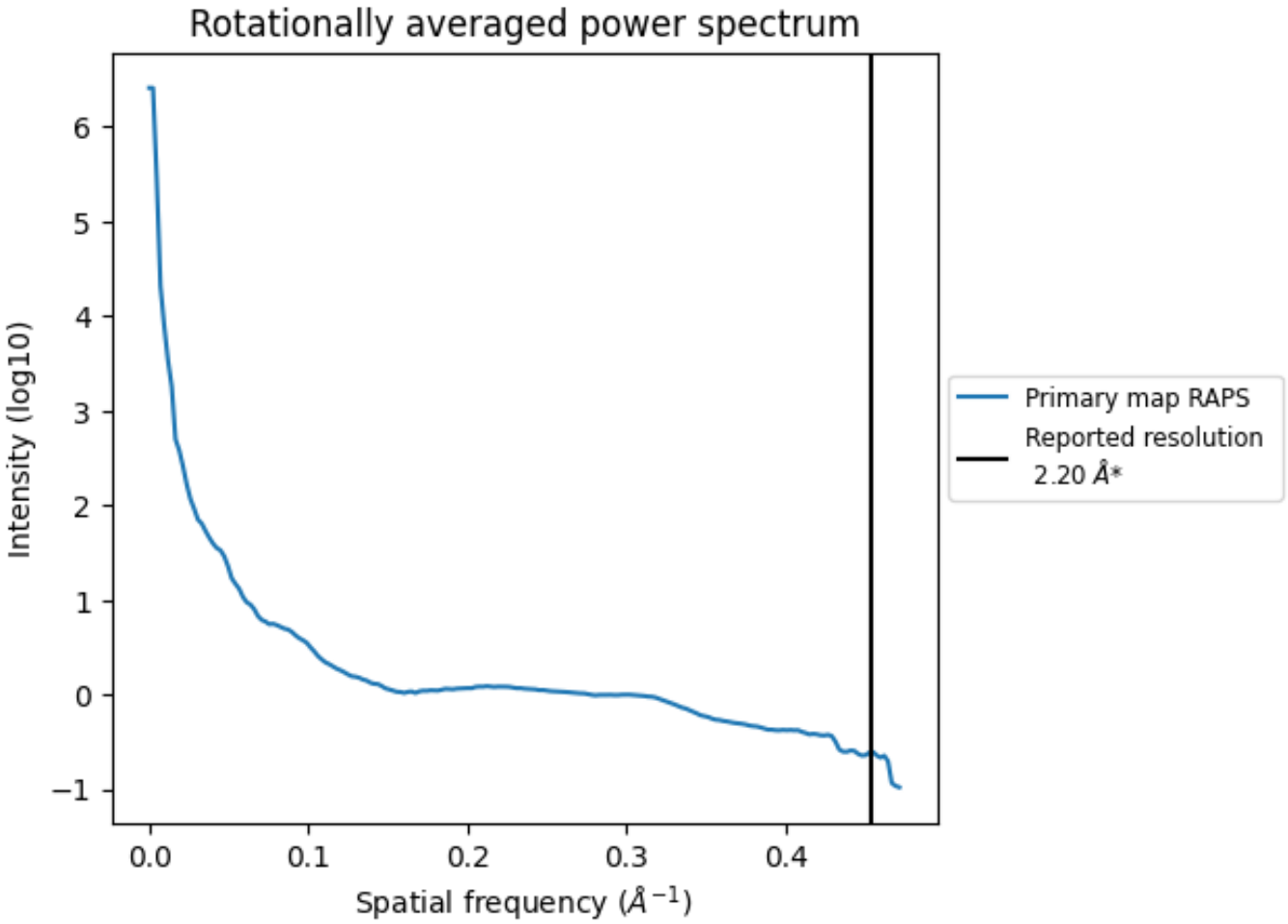
7.2 Volume estimate (i)



The volume at the recommended contour level is 1196 nm^3; this corresponds to an approximate mass of 1081 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 0.455 Å^{-1}

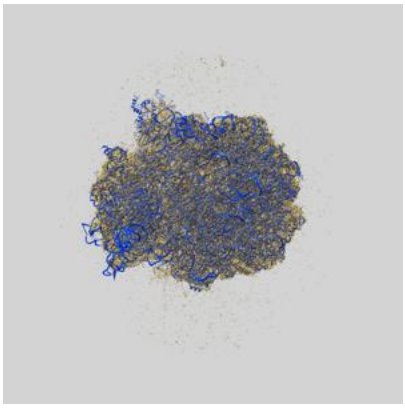
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

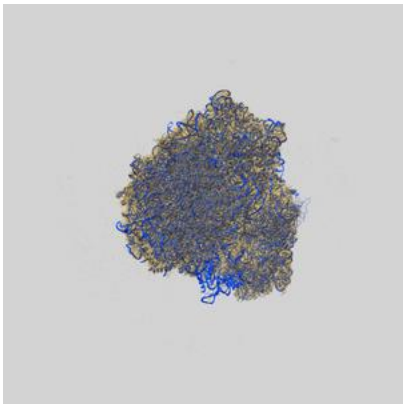
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-28636 and PDB model 8EVT. Per-residue inclusion information can be found in section 3 on page 19.

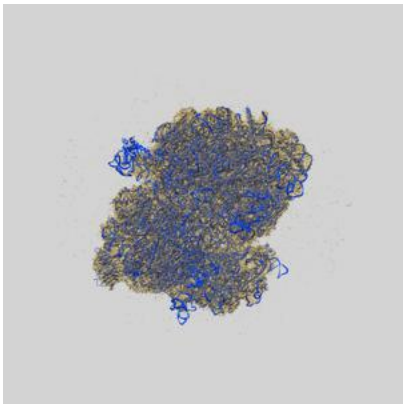
9.1 Map-model overlay



X



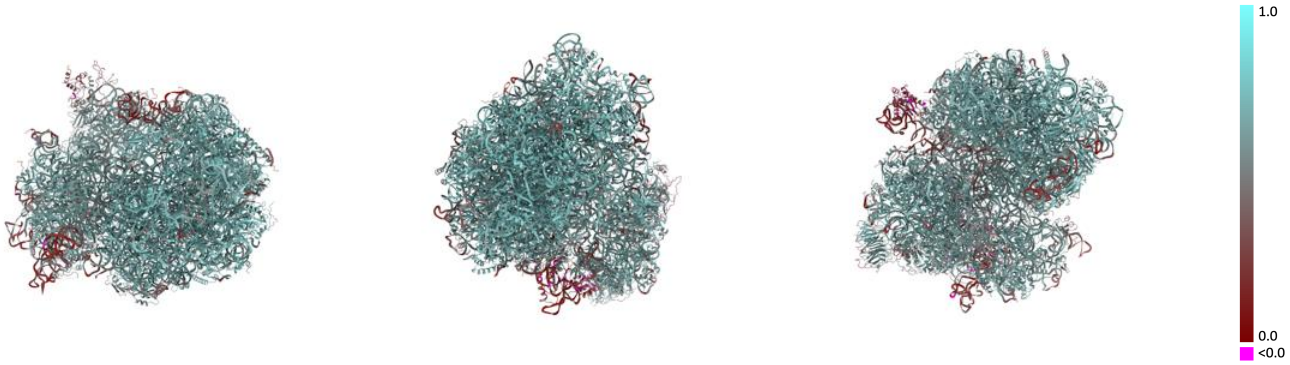
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.1 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.

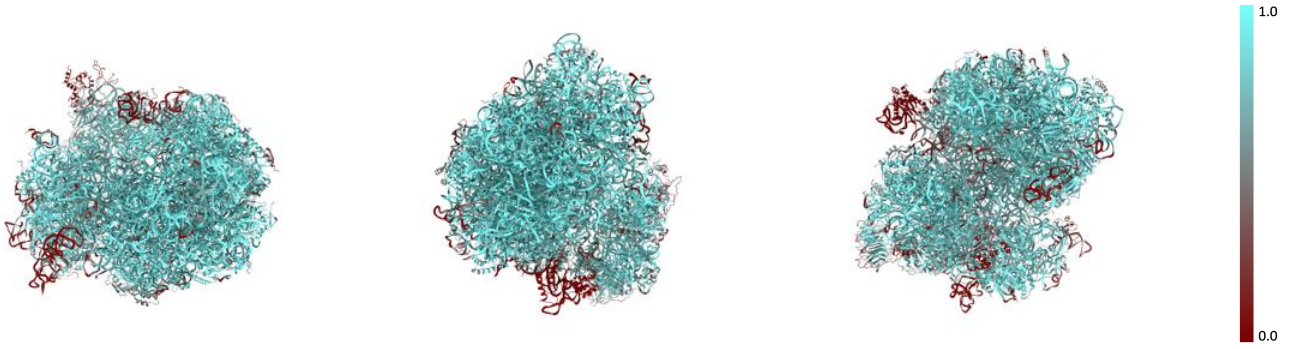
9.2 Q-score mapped to coordinate model



X Y Z

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

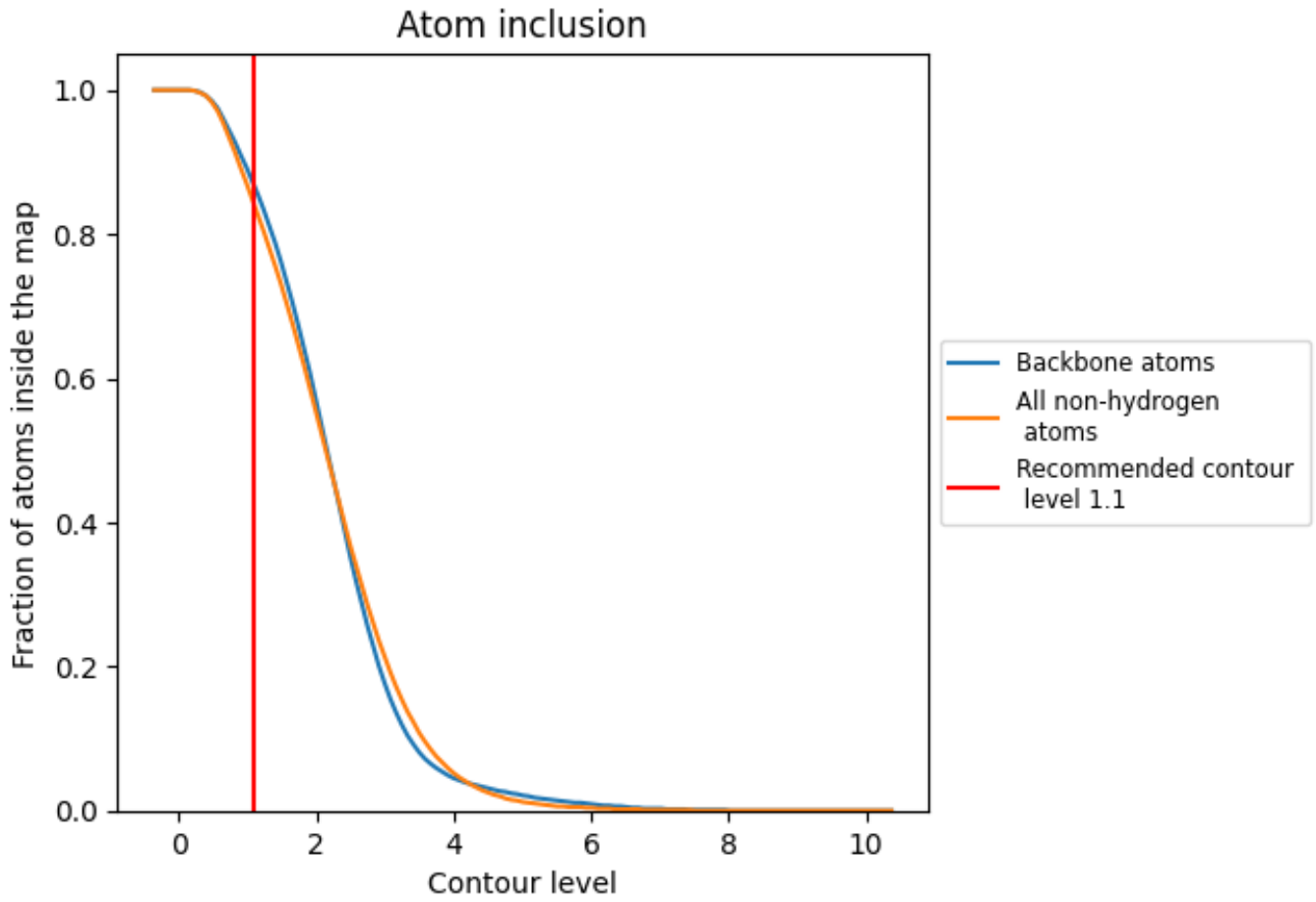
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (1.1).

9.4 Atom inclusion (i)



At the recommended contour level, 87% of all backbone atoms, 84% 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 (1.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8390	0.6260
A1	0.8920	0.6480
A3	0.9400	0.6580
A4	0.9490	0.6850
AA	0.9610	0.7190
AB	0.9250	0.6990
AC	0.9200	0.7070
AD	0.7360	0.5960
AE	0.7680	0.6210
AF	0.9130	0.7040
AG	0.8180	0.6430
AH	0.8330	0.6540
AI	0.8560	0.6670
AJ	0.5090	0.4710
AL	0.8800	0.6800
AM	0.8630	0.6640
AN	0.9820	0.7440
AO	0.9300	0.7110
AP	0.9020	0.7050
AQ	0.9570	0.7340
AR	0.7830	0.6120
AS	0.8990	0.6900
AT	0.8810	0.6790
AU	0.6570	0.5680
AV	0.9000	0.6860
AW	0.8990	0.6860
AX	0.8930	0.6890
AY	0.8930	0.6870
AZ	0.8560	0.6440
Aa	0.9330	0.7150
Ab	0.8140	0.6190
Ac	0.8610	0.6390
Ad	0.8260	0.6540
Ae	0.9310	0.7200
Af	0.9560	0.7220

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Chain	Atom inclusion	Q-score
Ag	0.8840	0.6760
Ah	0.8740	0.6830
Ai	0.8590	0.6430
Aj	0.9620	0.7320
Ak	0.6130	0.5660
Al	0.9570	0.7100
Am	0.8690	0.6650
An	0.7970	0.6160
Ao	0.8490	0.6660
Ap	0.9030	0.6920
B5	0.8330	0.5860
BA	0.8020	0.6140
BB	0.7640	0.5900
BC	0.8840	0.6550
BD	0.6770	0.5700
BE	0.8910	0.6450
BF	0.8140	0.6200
BG	0.6330	0.5420
BH	0.5790	0.5120
BI	0.8180	0.6070
BJ	0.8540	0.6330
BK	0.6040	0.5160
BL	0.8000	0.5940
BM	0.0530	0.2660
BN	0.8880	0.6450
BO	0.8490	0.6000
BP	0.6210	0.5310
BQ	0.8970	0.6700
BR	0.6670	0.5590
BS	0.7630	0.5830
BT	0.8220	0.6210
BU	0.5750	0.5300
BV	0.8510	0.6330
BW	0.9640	0.7000
BX	0.8900	0.6430
BY	0.7570	0.5990
BZ	0.7600	0.6010
Ba	0.8490	0.6000
Bb	0.7800	0.6020
Bc	0.6750	0.5490
Bd	0.9100	0.6460
Be	0.7040	0.5640

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Chain	Atom inclusion	Q-score
Bf	0.0900	0.2390
Bg	0.6440	0.5650
E	0.0120	0.1830
EC	0.4360	0.3750