



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:58 PM UTC

PDB ID : 7MPI / pdb_00007mpi
EMDB ID : EMD-23934
Title : Stm1 bound vacant 80S structure isolated from cbf5-D95A
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-05-04
Resolution : 3.05 Å (reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

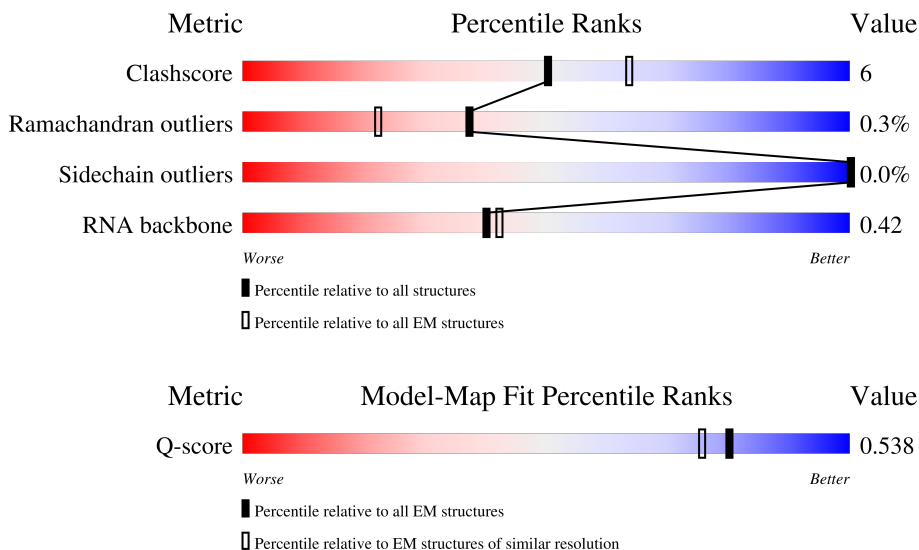
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.05 Å.

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





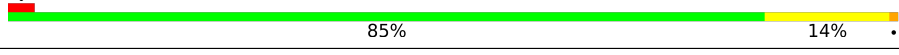




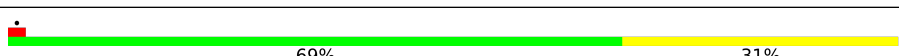
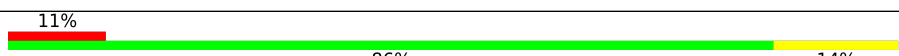

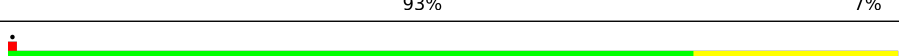
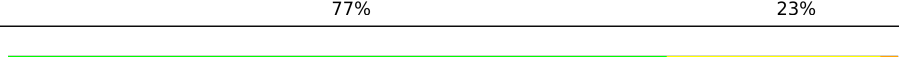
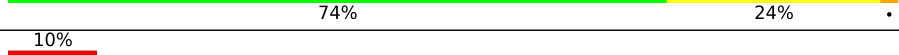



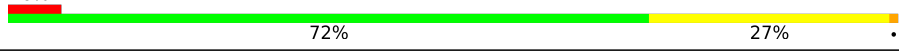



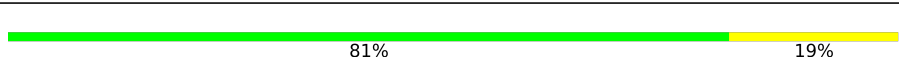

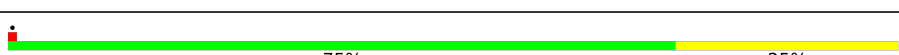
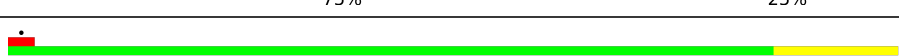

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13971 (2.55 - 3.55)

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

Mol	Chain	Length	Quality of chain
1	BA	206	
2	BB	214	
3	BC	217	



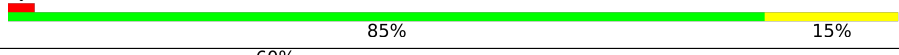
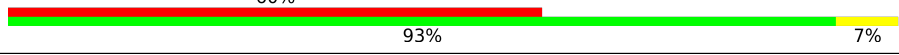

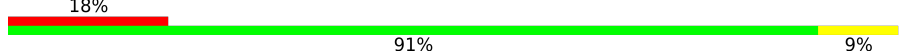
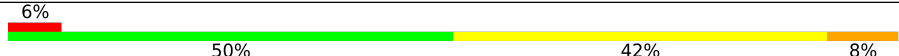
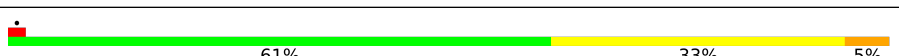
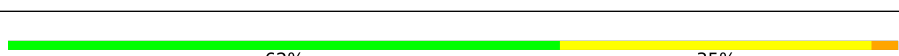

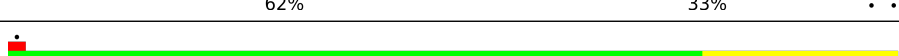
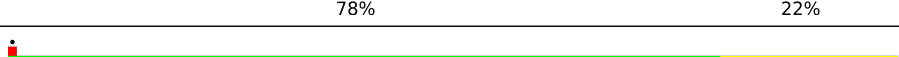
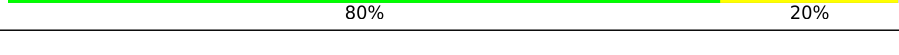



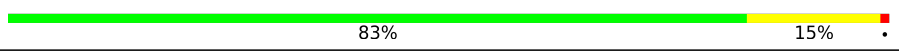



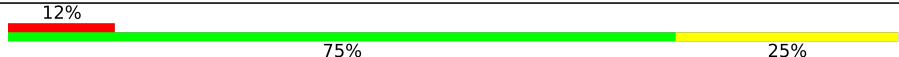

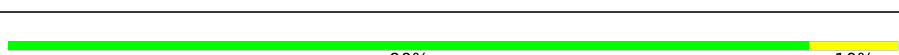
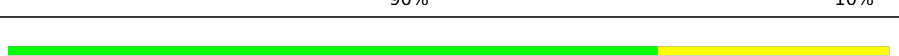

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Mol	Chain	Length	Quality of chain
4	BD	223	 84% 16%
5	BE	260	 78% 21%
6	BF	206	 85% 14%
7	BG	226	 83% 16%
8	BH	184	 5% 82% 17%
9	BI	188	 69% 31%
10	BJ	185	 77% 23%
11	BK	96	 69% 31%
12	BL	155	 11% 86% 14%
13	BM	121	 85% 93% 7%
14	BN	150	 77% 23%
15	BO	127	 74% 24%
16	BP	124	 10% 77% 22%
17	BQ	141	 74% 24%
18	BR	121	 81% 19%
19	BS	145	 6% 72% 27%
20	BT	141	 74% 26%
21	BU	107	 7% 76% 24%
22	BV	87	 75% 25%
23	BW	129	 81% 19%
24	BX	144	 80% 17%
25	BY	134	 75% 25%
26	BZ	69	 86% 14%
27	Ba	97	 70% 28%
28	Bb	81	 89% 11%

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Mol	Chain	Length	Quality of chain
29	Bc	63	 83% 17%
30	Bd	53	 79% 21%
31	Be	60	 85% 15%
32	Bf	57	 60% 93% 7%
33	Bg	312	 82% 18%
34	Bh	89	 18% 91% 9%
35	B5	1781	 6% 50% 42% 8%
36	A1	3137	 61% 33% 5%
37	A3	121	 62% 35% .
38	A4	158	 62% 33% . .
39	AA	247	 78% 22%
40	AB	386	 80% 20%
41	AC	361	 88% 11% .
42	AD	292	 85% 15%
43	AE	156	 86% 13% .
44	AF	222	 83% 15% .
45	AG	230	 84% 16%
46	AH	190	 85% 15%
47	AI	205	 85% 15%
48	AJ	169	 12% 75% 25%
49	AL	193	 86% 13% .
50	AM	136	 90% 10%
51	AN	203	 73% 26%
52	AO	197	 89% 11%
53	AP	175	 88% 12%


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Mol	Chain	Length	Quality of chain
54	AQ	185	88% 12%
55	AR	188	13% 86% 14%
56	AS	172	88% 11%
57	AT	159	84% 16%
58	AU	100	88% 12%
59	AV	136	88% 12%
60	AW	63	83% 17%
61	AX	121	90% 10%
62	AY	126	86% 14%
63	AZ	135	73% 26%
64	Aa	148	84% 14%
65	Ab	58	5% 98%
66	Ac	97	78% 22%
67	Ad	109	91% 9%
68	Ae	127	87% 13%
69	Af	106	92% 8%
70	Ag	112	84% 16%
71	Ah	119	87% 12%
72	Ai	99	92% 8%
73	Aj	87	83% 17%
74	Ak	77	8% 87% 13%
75	Al	50	82% 18%
76	Am	52	73% 27%
77	An	25	64% 68% 32%
78	Ao	105	7% 93% 7%

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Mol	Chain	Length	Quality of chain
79	Ap	91	 79% 20%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
35	3AU	B5	1191	X	-	-	-
35	G7M	B5	1575	X	-	-	-

2 Entry composition [i](#)

There are 81 unique types of molecules in this entry. The entry contains 199433 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	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 3 is a protein called 40S ribosomal protein S2.

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

- Molecule 4 is a protein called 40S ribosomal protein S3.

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

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S5.

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

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

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

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	ASN	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	THR	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	ALA	deletion	UNP P0CX39

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S12.

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

- Molecule 14 is a protein called 40S ribosomal protein S13.

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

- Molecule 15 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S15.

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

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BR	?	-	SER	deletion	UNP P02407
BR	?	-	ASN	deletion	UNP P02407
BR	?	-	GLY	deletion	UNP P02407
BR	?	-	VAL	deletion	UNP P02407

- Molecule 19 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S20.

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

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S28-A.

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 40S ribosomal protein S29-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

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

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

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bf	97	ALA	LYS	conflict	UNP P05759
Bf	?	-	CYS	deletion	UNP P05759
Bf	?	-	GLY	deletion	UNP P05759
Bf	?	-	ALA	deletion	UNP P05759

- Molecule 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 34 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
34	Bh	89	675	391	137	147	0	0

- Molecule 35 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	B5	1781	37849	16931	6657	12480	1781	1	0

- Molecule 36 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	A1	3137	67139	30012	12094	21896	3137	0	0

- Molecule 37 is a RNA chain called 5s rRNA.

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

- Molecule 38 is a RNA chain called 5.8 S rRNA.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	AB	386	3078	1953	584	533	8	0	0

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L5.

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

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

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

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	THR	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326

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Chain	Residue	Modelled	Actual	Comment	Reference
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	ALA	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	PHE	deletion	UNP Q02326
AE	?	-	PRO	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326

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

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

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

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

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

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

- Molecule 47 is a protein called 60S ribosomal protein L10.

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

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	?	-	MET	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	SER	deletion	UNP P41805
AI	?	-	CYS	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	GLY	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	ASP	deletion	UNP P41805
AI	?	-	ARG	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805

- Molecule 48 is a protein called 60S ribosomal protein L11-A.

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

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

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

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

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

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

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

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

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

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

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

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	VAL	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	GLU	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- Molecule 68 is a protein called 60S ribosomal protein L32.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 74 is a protein called 60S ribosomal protein L38.

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

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

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

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

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

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

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

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

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

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

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

- Molecule 80 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	BD	1	Total	Mg	0
			1	1	
80	BJ	1	Total	Mg	0
			1	1	
80	BL	1	Total	Mg	0
			1	1	
80	B5	91	Total	Mg	0
			91	91	
80	A1	242	Total	Mg	0
			242	242	
80	A3	2	Total	Mg	0
			2	2	
80	A4	9	Total	Mg	0
			9	9	
80	AB	3	Total	Mg	0
			3	3	
80	AG	1	Total	Mg	0
			1	1	
80	AL	1	Total	Mg	0
			1	1	
80	AN	2	Total	Mg	0
			2	2	
80	AO	1	Total	Mg	0
			1	1	
80	AP	1	Total	Mg	0
			1	1	
80	AR	1	Total	Mg	0
			1	1	
80	AX	1	Total	Mg	0
			1	1	
80	Ae	4	Total	Mg	0
			4	4	
80	Af	2	Total	Mg	0
			2	2	
80	Aj	2	Total	Mg	0
			2	2	

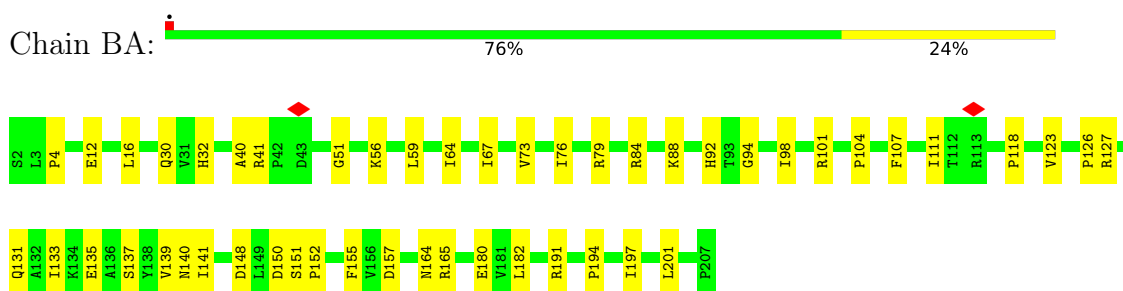
- Molecule 81 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
81	Bb	1	Total 1	Zn 1	0
81	Ao	1	Total 1	Zn 1	0

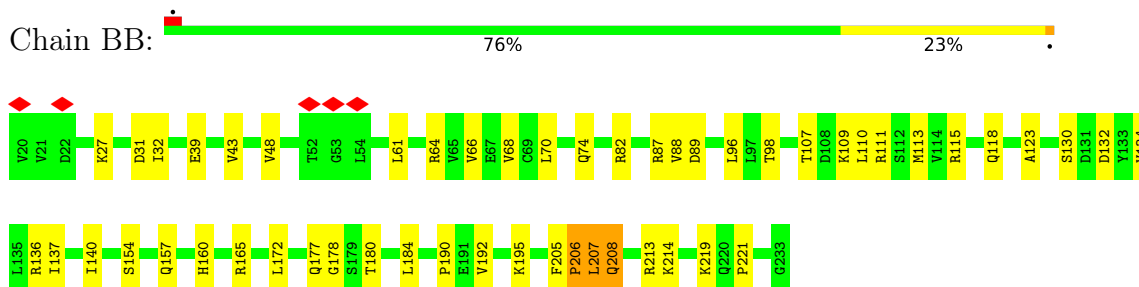
3 Residue-property plots

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

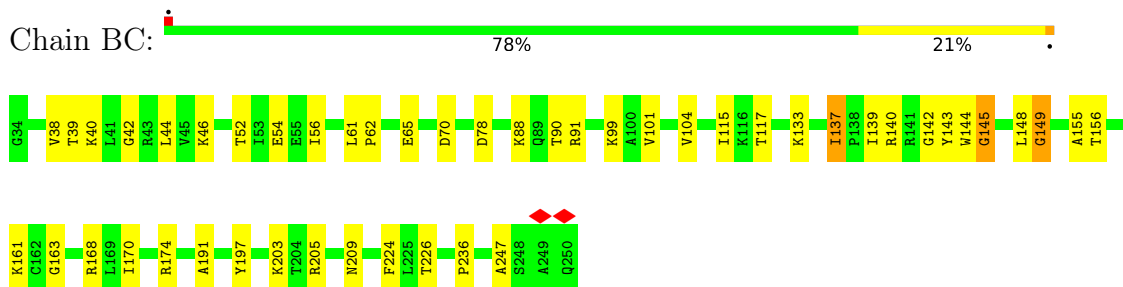
- Molecule 1: 40S ribosomal protein S0-A



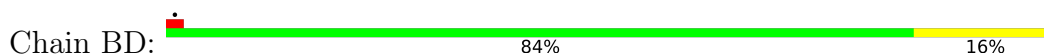
- Molecule 2: 40S ribosomal protein S1-A



- Molecule 3: 40S ribosomal protein S2

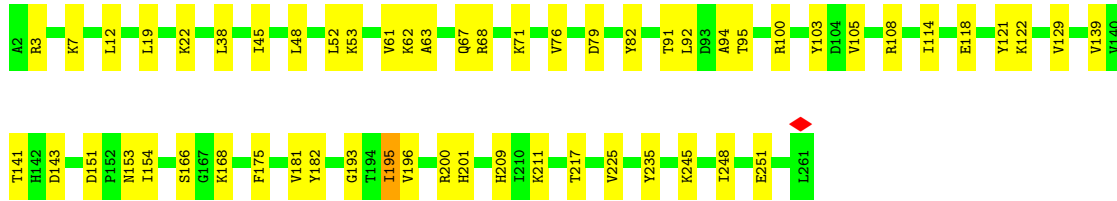
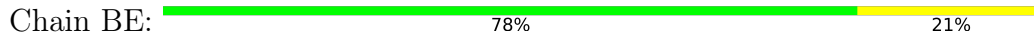


- Molecule 4: 40S ribosomal protein S3

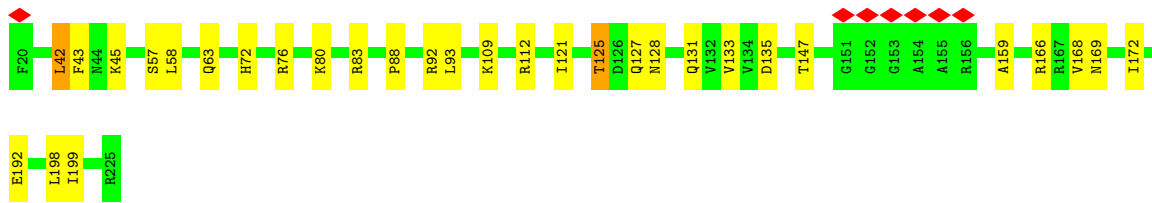
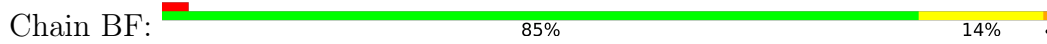




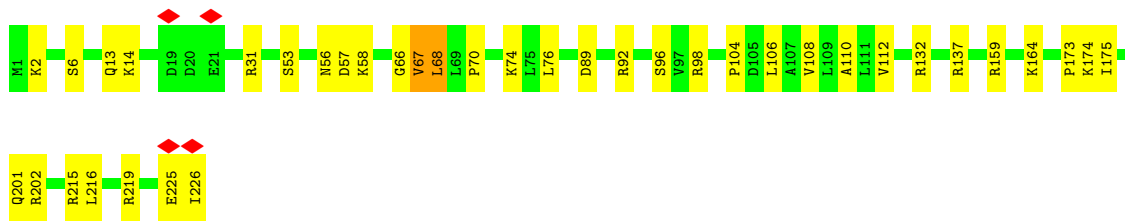
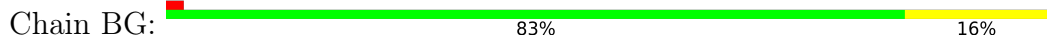
• Molecule 5: 40S ribosomal protein S4-A



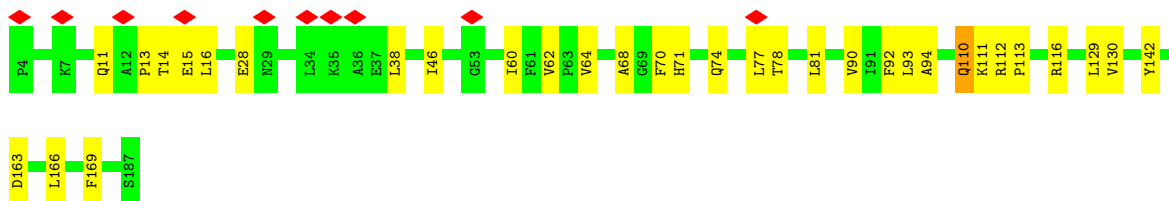
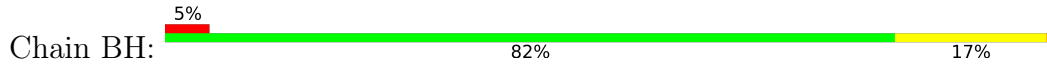
• Molecule 6: 40S ribosomal protein S5



• Molecule 7: 40S ribosomal protein S6-A

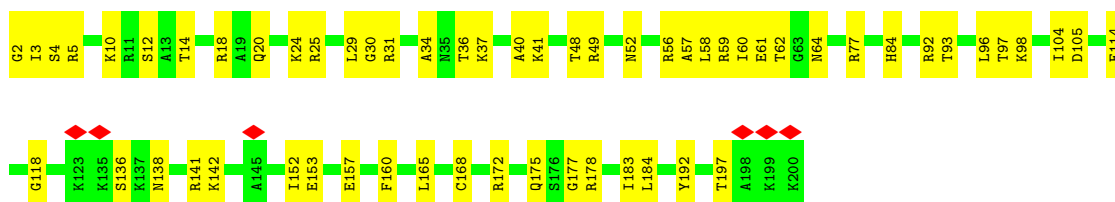


• Molecule 8: 40S ribosomal protein S7-A




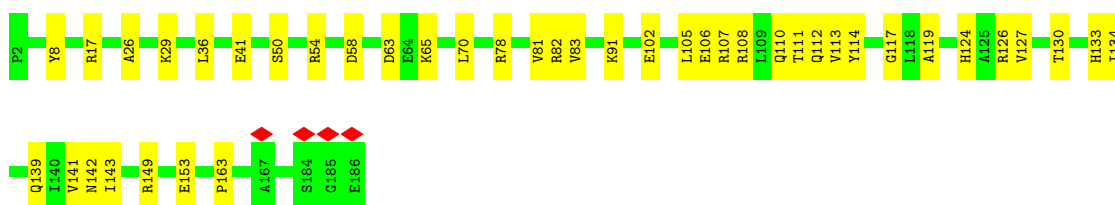
- Molecule 9: 40S ribosomal protein S8-A

Chain BI:  69% 31%



- Molecule 10: 40S ribosomal protein S9-A

Chain BJ:  77% 23%

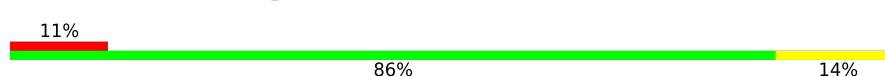


- Molecule 11: 40S ribosomal protein S10-A

Chain BK:  69% 31%

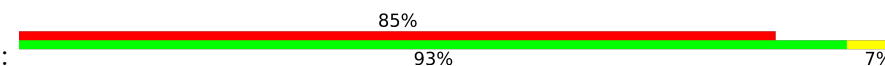


- Molecule 12: 40S ribosomal protein S11-A

Chain BL:  11% 86% 14%

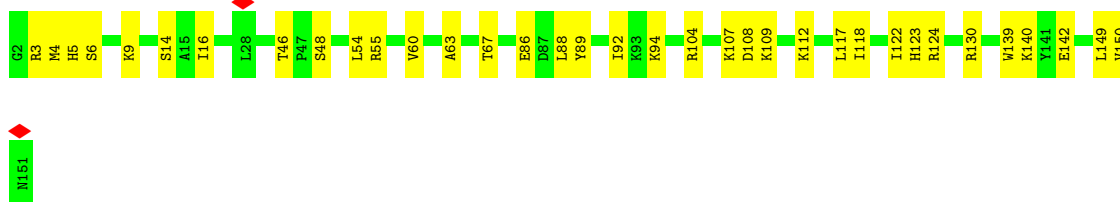
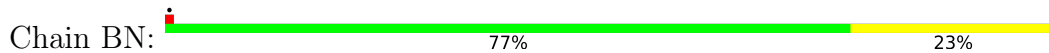


- Molecule 13: 40S ribosomal protein S12

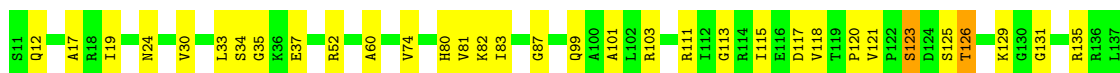
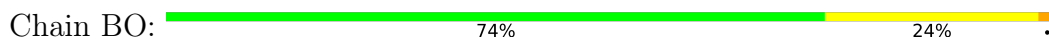
Chain BM:  85% 93% 7%



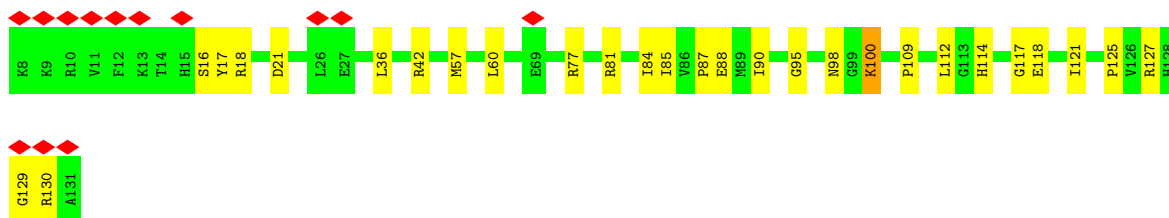
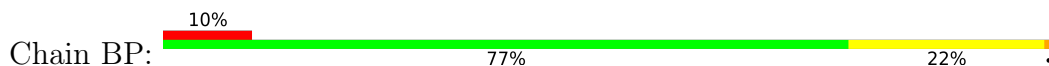
- Molecule 14: 40S ribosomal protein S13



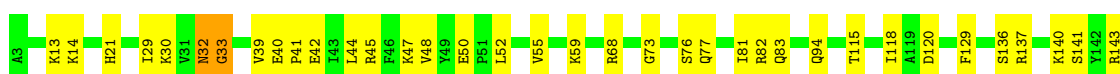
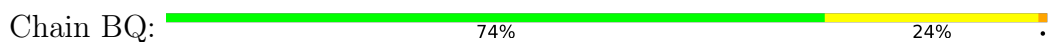
- Molecule 15: 40S ribosomal protein S14-A



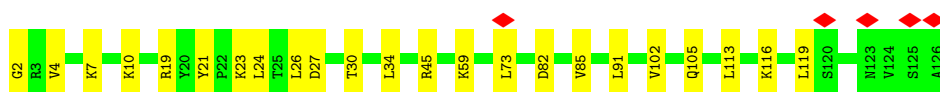
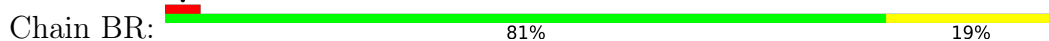
- Molecule 16: 40S ribosomal protein S15



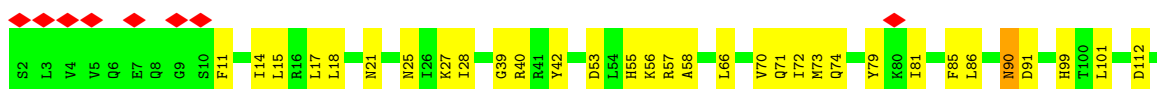
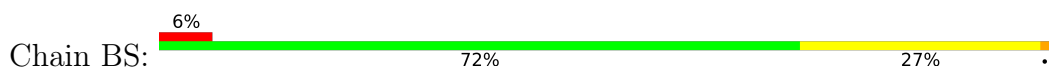
- Molecule 17: 40S ribosomal protein S16-A

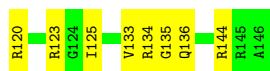


- Molecule 18: 40S ribosomal protein S17-A

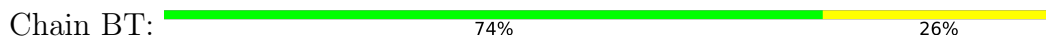


- Molecule 19: 40S ribosomal protein S18-A

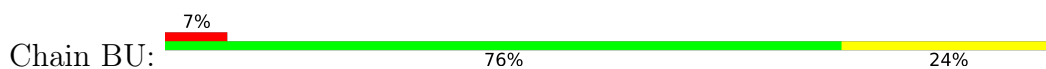




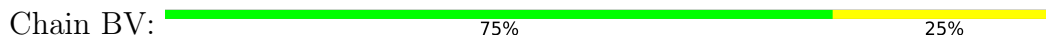
- Molecule 20: 40S ribosomal protein S19-A



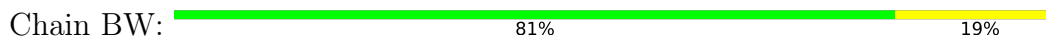
- Molecule 21: 40S ribosomal protein S20



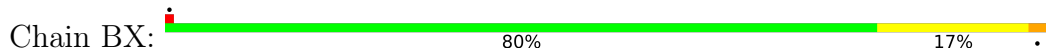
- Molecule 22: 40S ribosomal protein S21-A



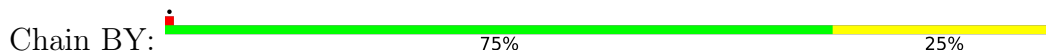
- Molecule 23: 40S ribosomal protein S22-A



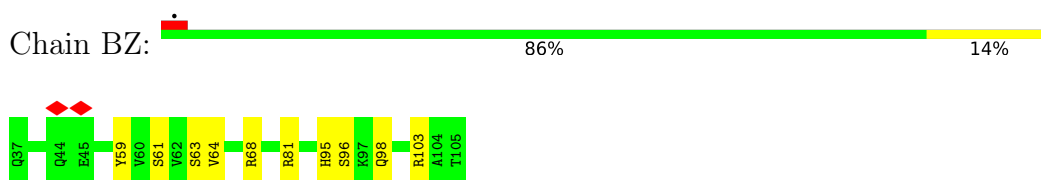
- Molecule 24: 40S ribosomal protein S23-A



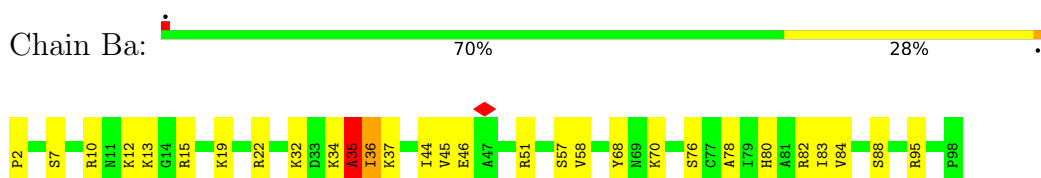
- Molecule 25: 40S ribosomal protein S24-A



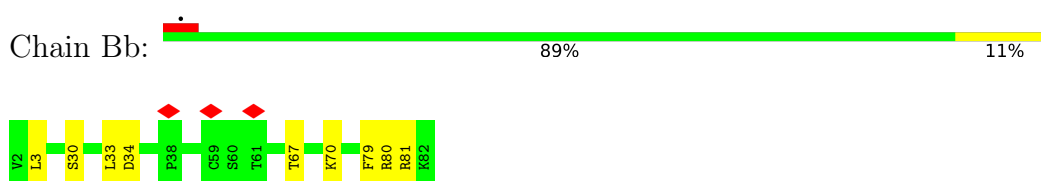
- Molecule 26: 40S ribosomal protein S25-A



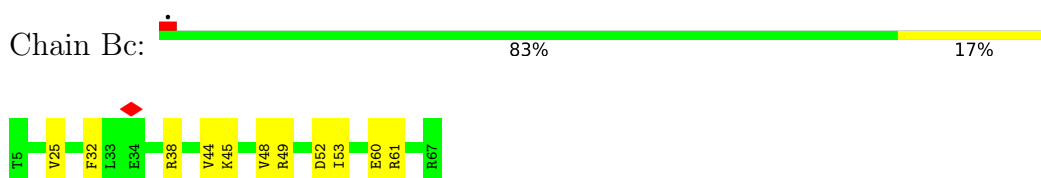
- Molecule 27: 40S ribosomal protein S26-B



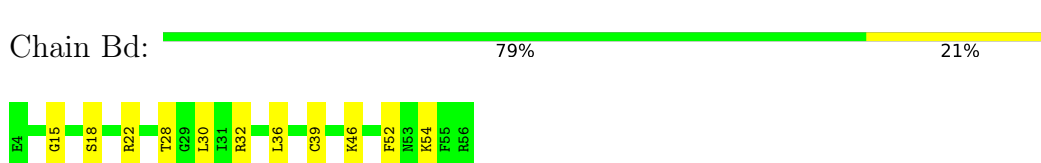
- Molecule 28: 40S ribosomal protein S27-A



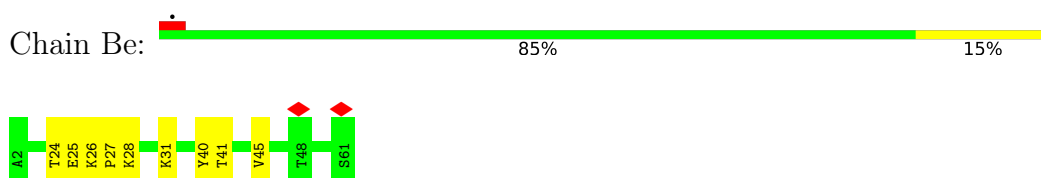
- Molecule 29: 40S ribosomal protein S28-A



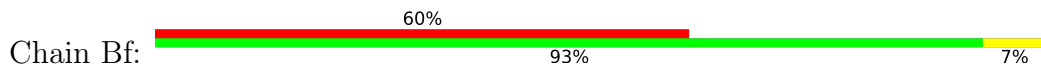
- Molecule 30: 40S ribosomal protein S29-A

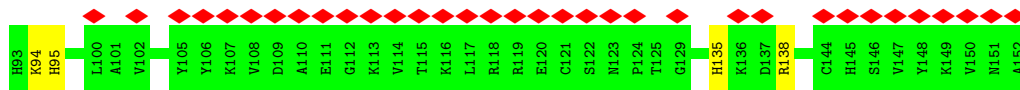


- Molecule 31: 40S ribosomal protein S30-A

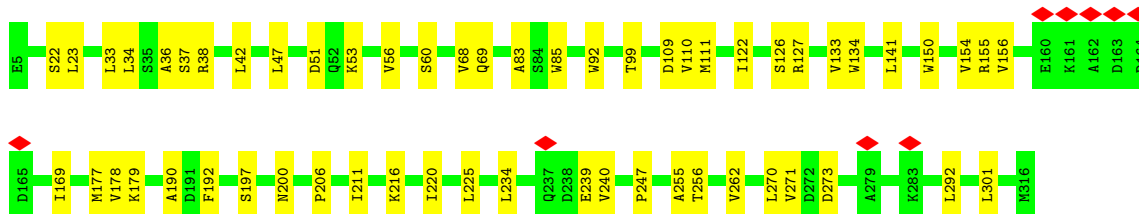
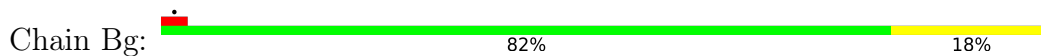


- Molecule 32: 40S ribosomal protein S31

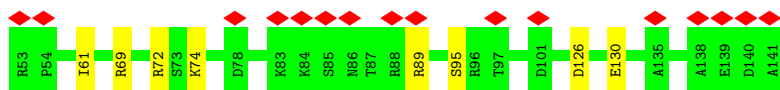




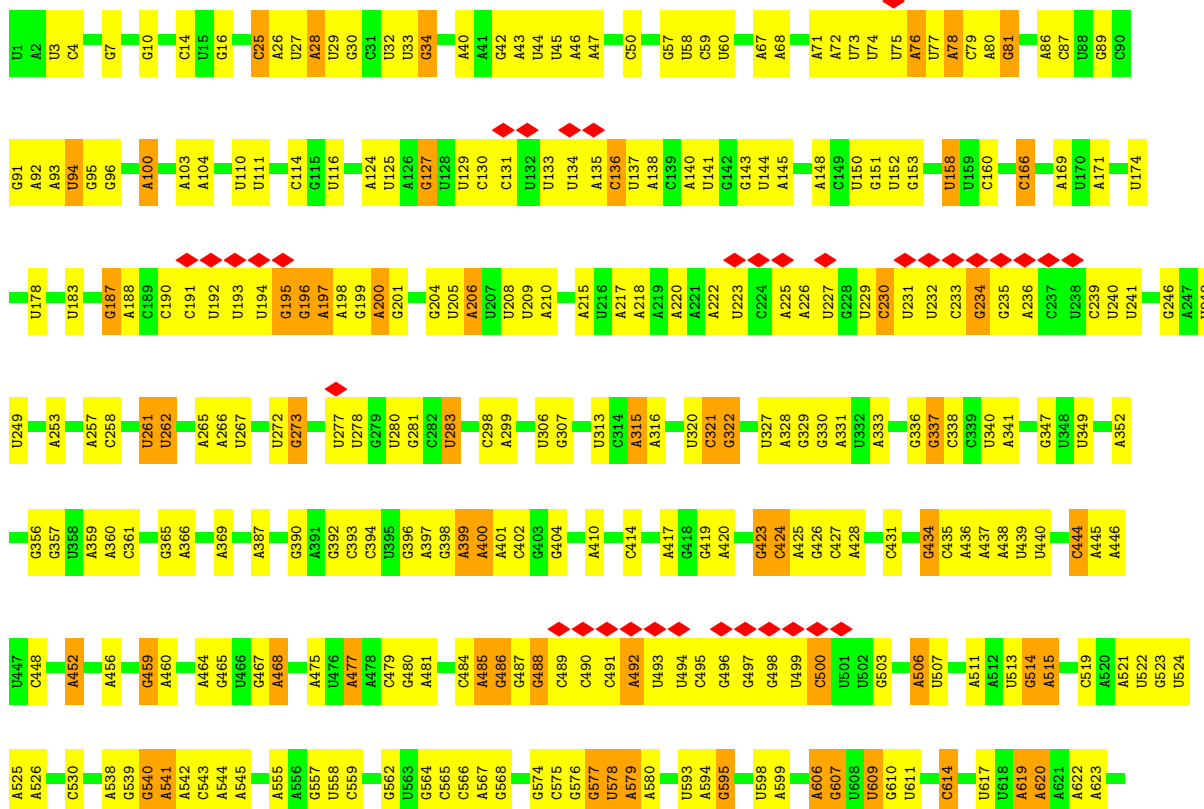
• Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

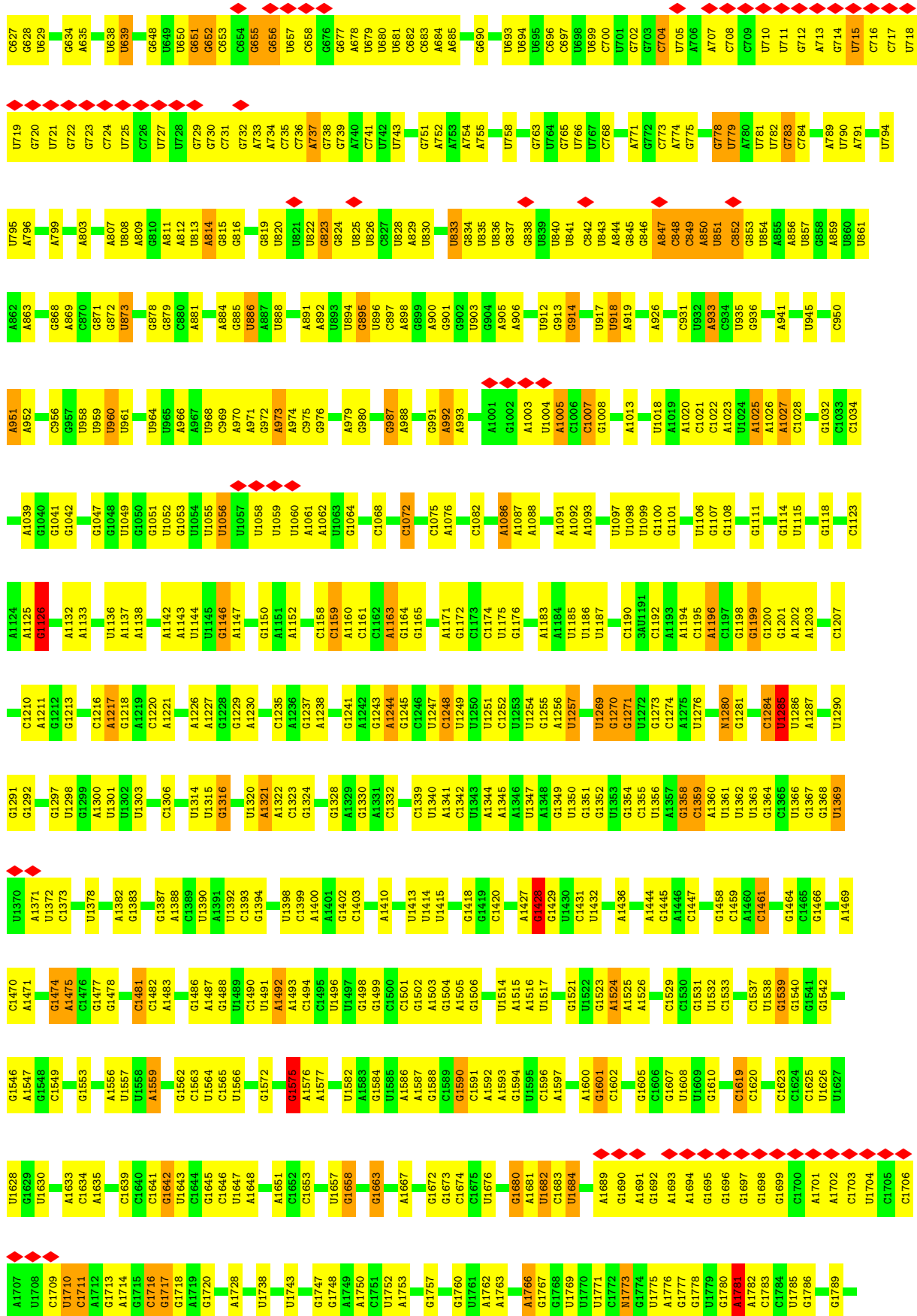


• Molecule 34: Suppressor protein STM1



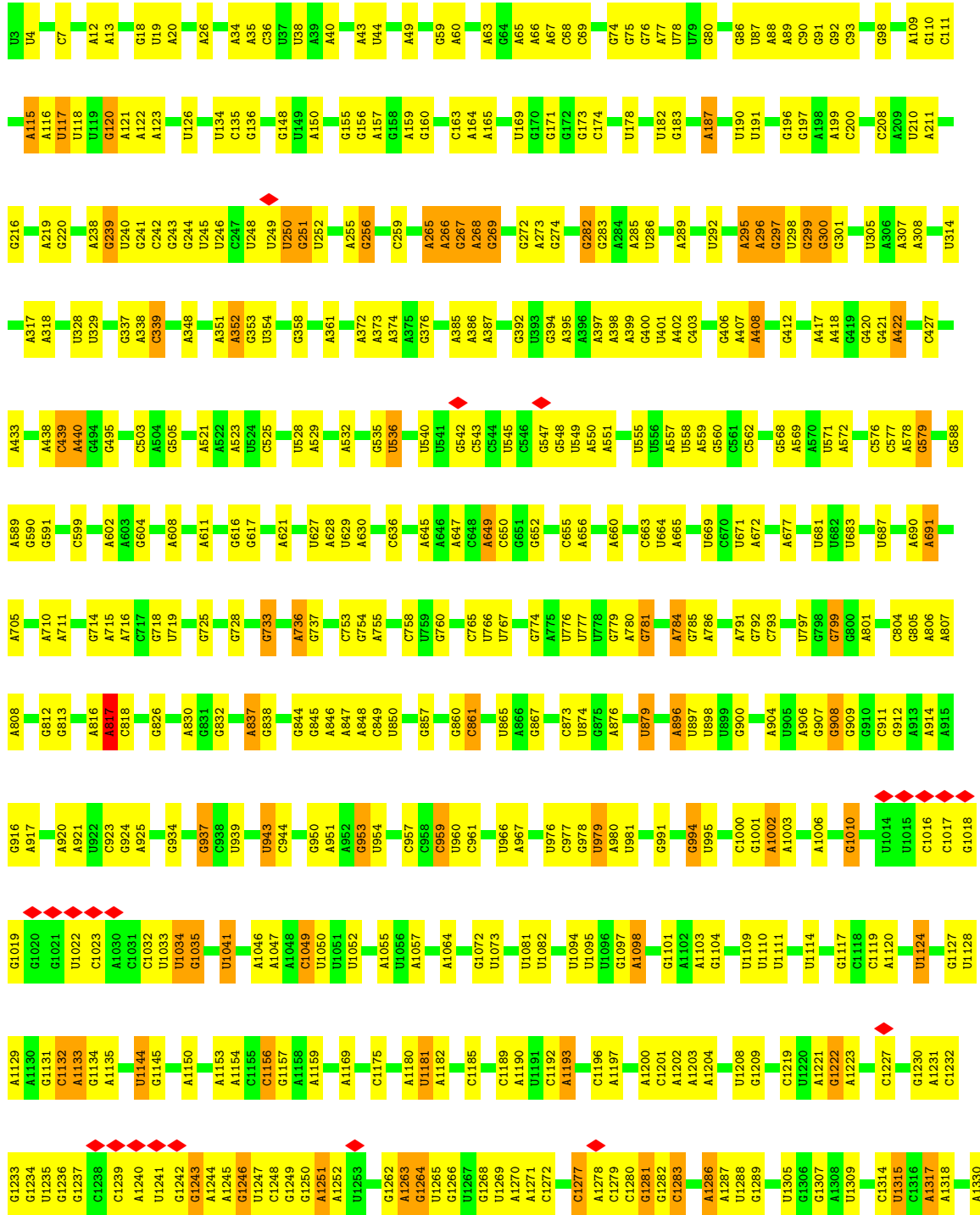
• Molecule 35: 18S rRNA



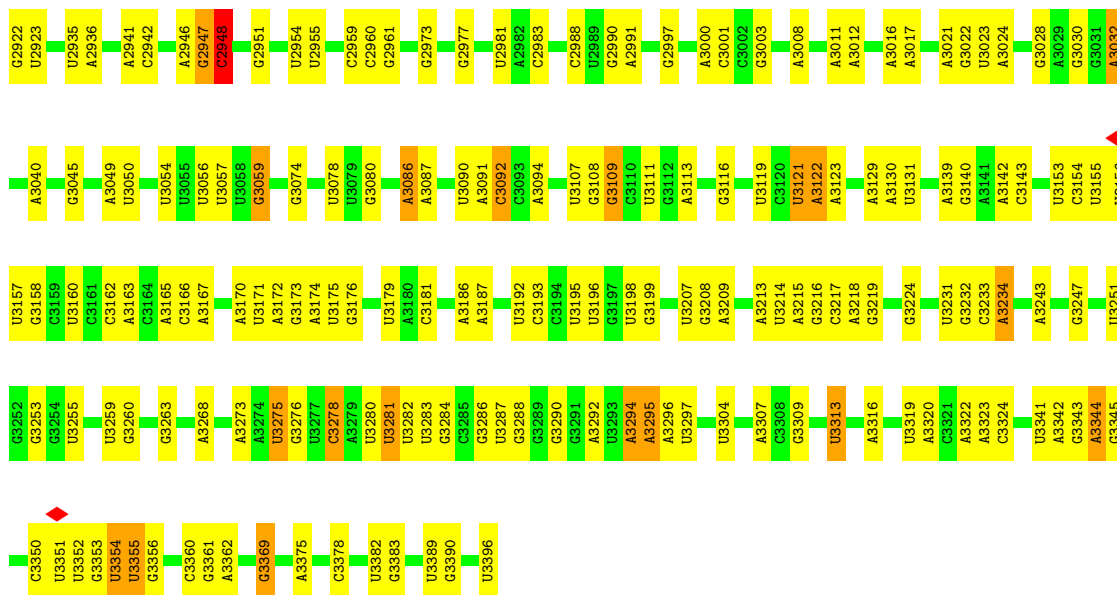




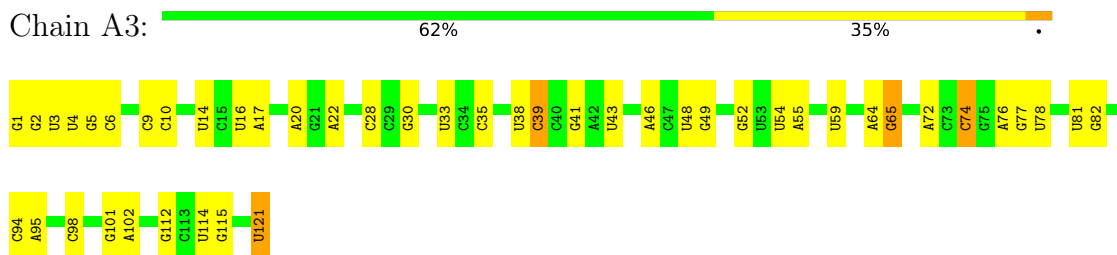
• Molecule 36: 25S rRNA



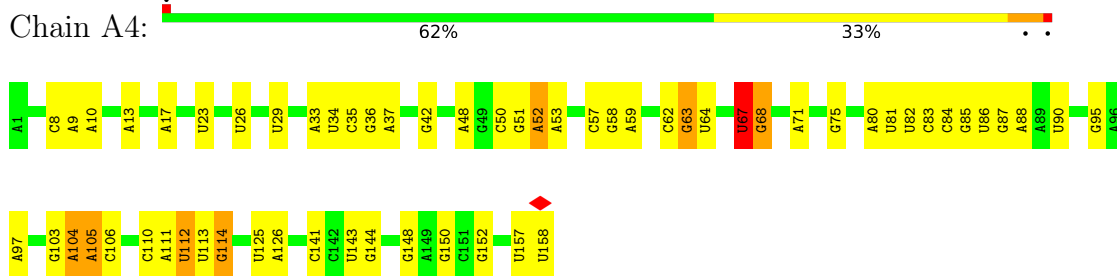
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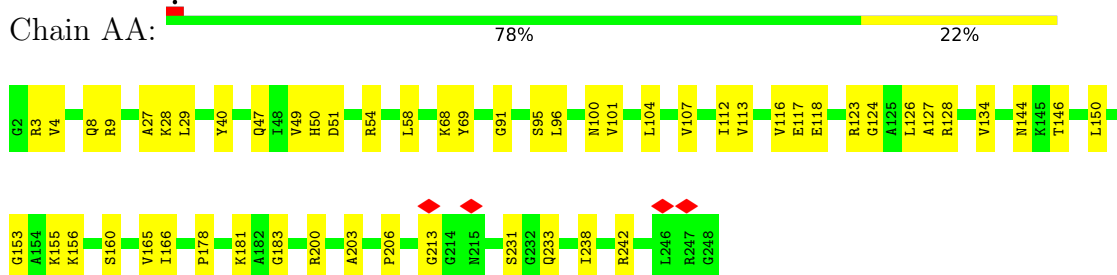
• Molecule 37: 5s rRNA



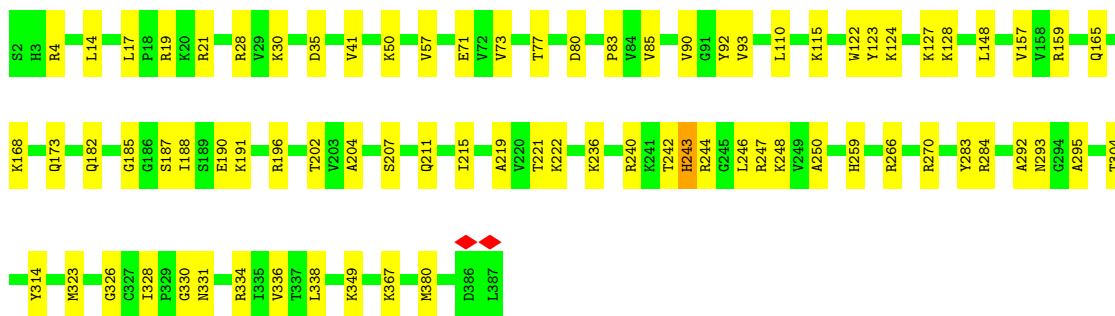
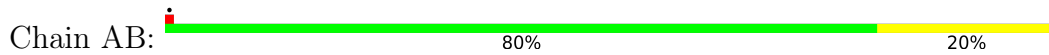
• Molecule 38: 5.8 S rRNA



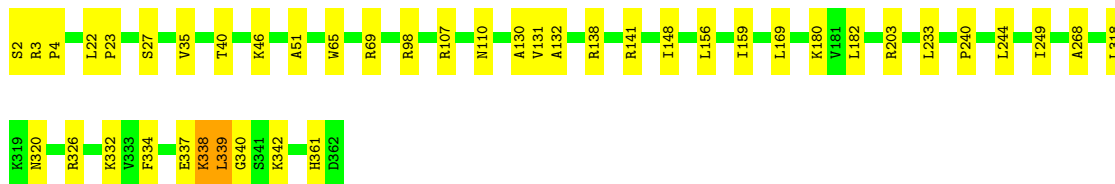
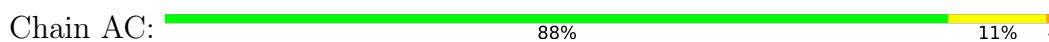
• Molecule 39: 60S ribosomal protein L2-A



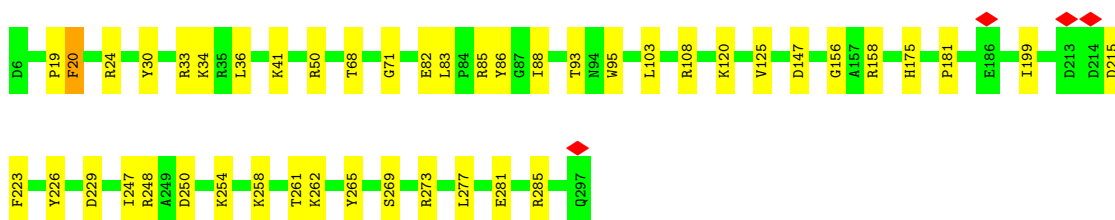
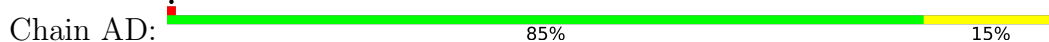
• Molecule 40: 60S ribosomal protein L3



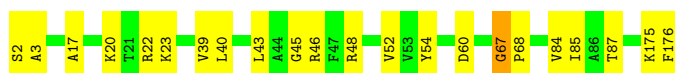
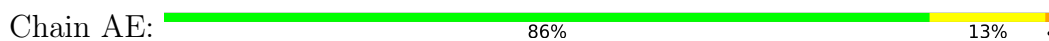
• Molecule 41: 60S ribosomal protein L4-A



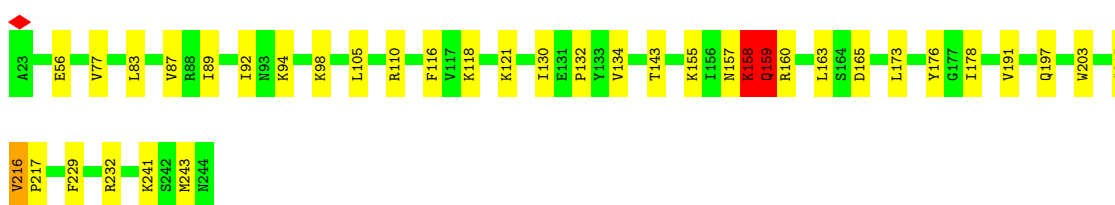
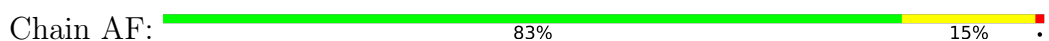
• Molecule 42: 60S ribosomal protein L5



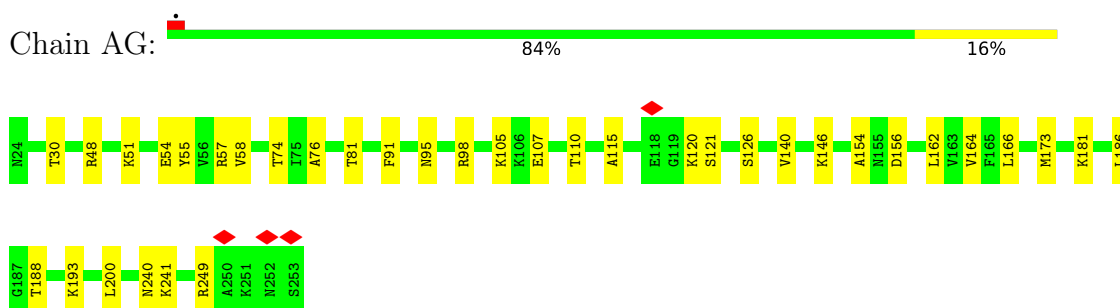
• Molecule 43: 60S ribosomal protein L6-A



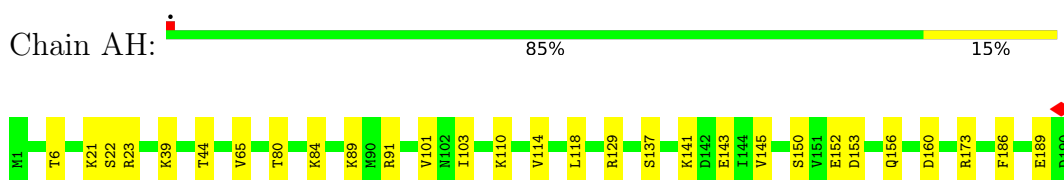
• Molecule 44: 60S ribosomal protein L7-A



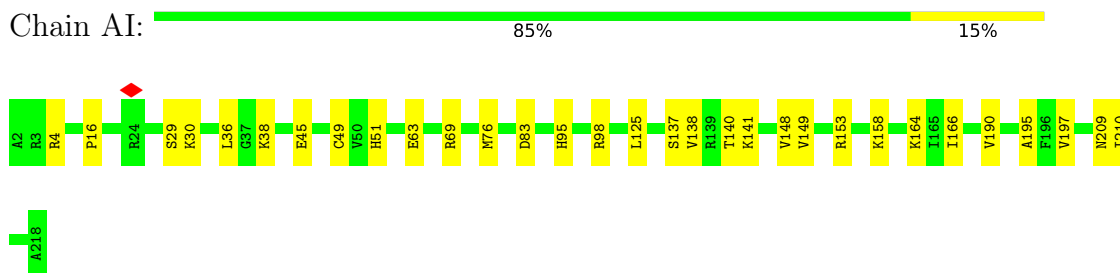
- Molecule 45: 60S ribosomal protein L8-A



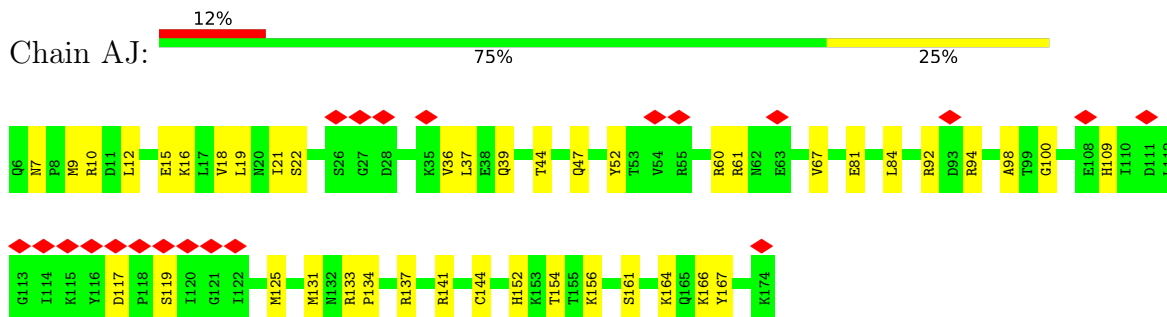
- Molecule 46: 60S ribosomal protein L9-A



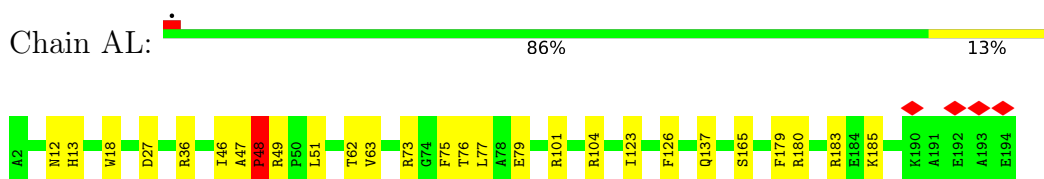
- Molecule 47: 60S ribosomal protein L10



- Molecule 48: 60S ribosomal protein L11-A

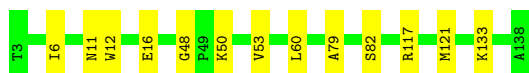


- Molecule 49: 60S ribosomal protein L13-A




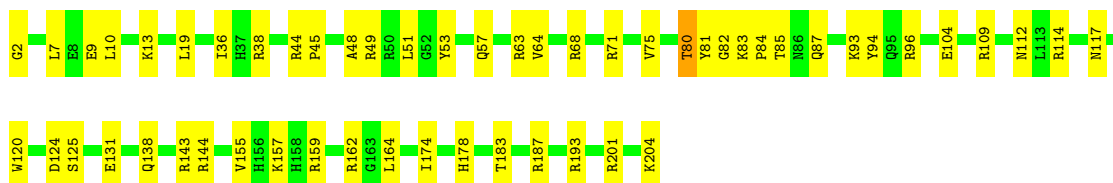
- Molecule 50: 60S ribosomal protein L14-A

Chain AM:  90% 10%



- Molecule 51: 60S ribosomal protein L15-A

Chain AN:  73% 26%




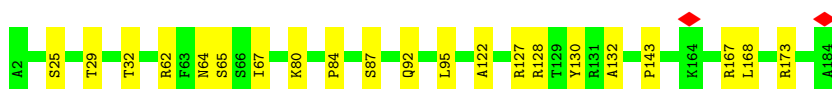
- Molecule 52: 60S ribosomal protein L16-A

Chain AO:  89% 11%




- Molecule 53: 60S ribosomal protein L17-A

Chain AP:  88% 12%




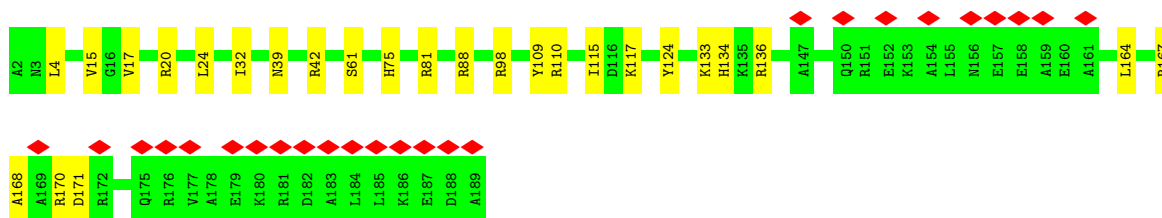
- Molecule 54: 60S ribosomal protein L18-A

Chain AQ:  88% 12%




- Molecule 55: 60S ribosomal protein L19-A

Chain AR:  13% 86% 14%




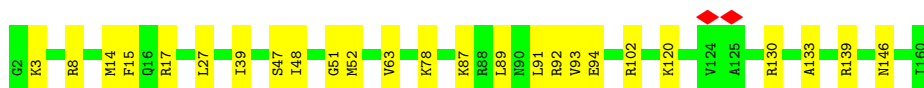
- Molecule 56: 60S ribosomal protein L20-A

Chain AS:  88% 11%




- Molecule 57: 60S ribosomal protein L21-A

Chain AT:  84% 16%




- Molecule 58: 60S ribosomal protein L22-A

Chain AU:  88% 12%




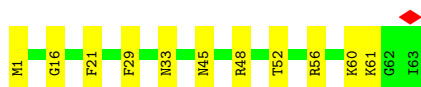
- Molecule 59: 60S ribosomal protein L23-A

Chain AV:  88% 12%



- Molecule 60: 60S ribosomal protein L24-A

Chain AW:  83% 17%



- Molecule 61: 60S ribosomal protein L25

Chain AX:  90% 10%

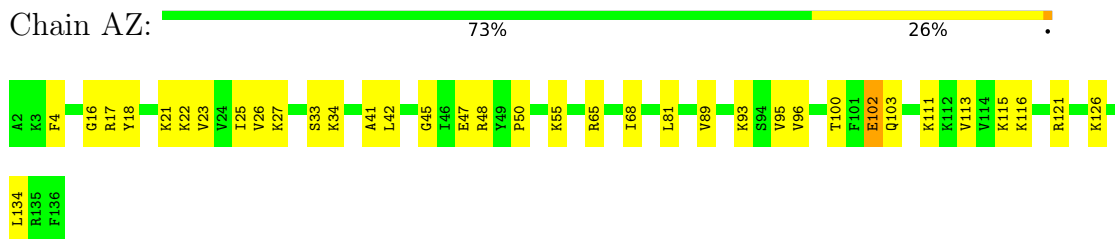


- Molecule 62: 60S ribosomal protein L26-A

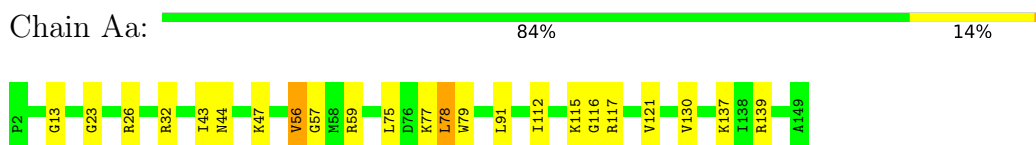
Chain AY:  86% 14%



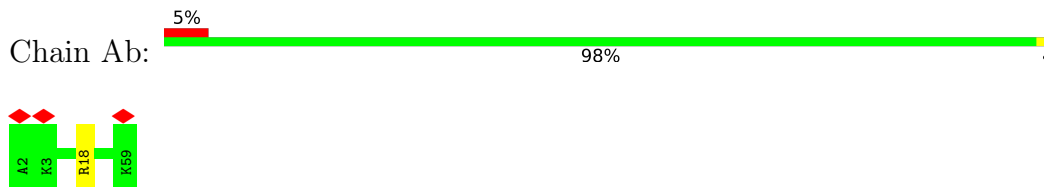
- Molecule 63: 60S ribosomal protein L27-A



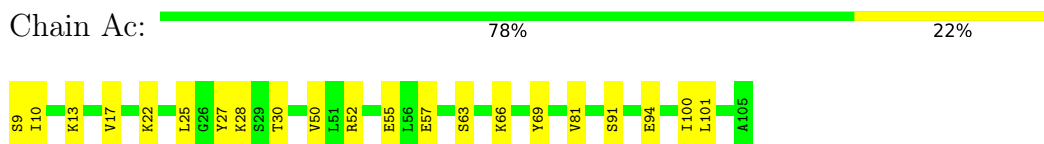
- Molecule 64: 60S ribosomal protein L28



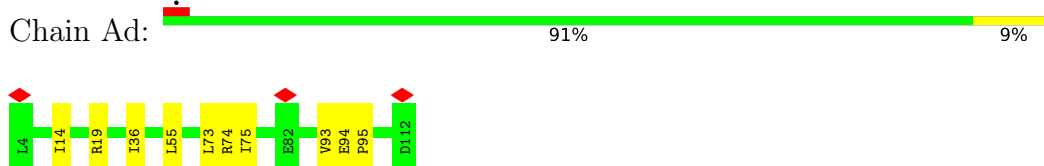
- Molecule 65: 60S ribosomal protein L29



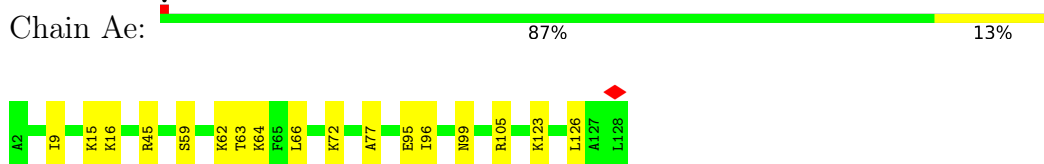
- Molecule 66: 60S ribosomal protein L30



- Molecule 67: 60S ribosomal protein L31-A



- Molecule 68: 60S ribosomal protein L32

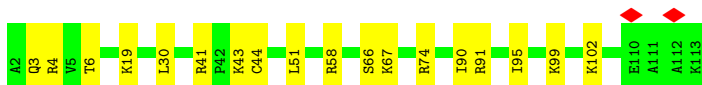
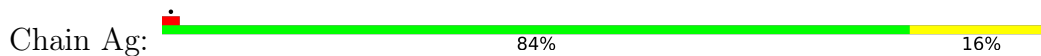


- Molecule 69: 60S ribosomal protein L33-A

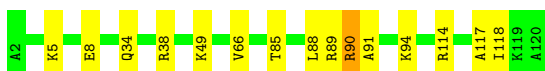
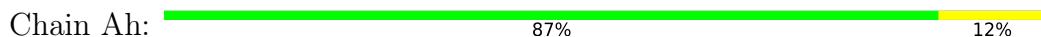




- Molecule 70: 60S ribosomal protein L34-A



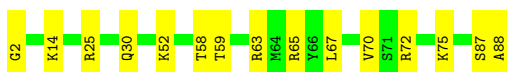
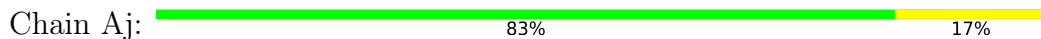
- Molecule 71: 60S ribosomal protein L35-A



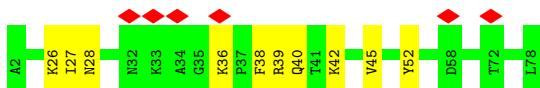
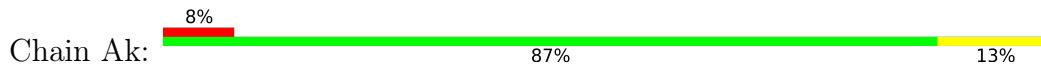
- Molecule 72: 60S ribosomal protein L36-A



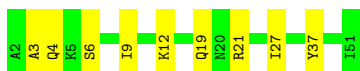
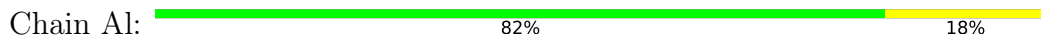
- Molecule 73: 60S ribosomal protein L37-A



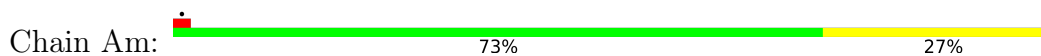
- Molecule 74: 60S ribosomal protein L38



- Molecule 75: 60S ribosomal protein L39

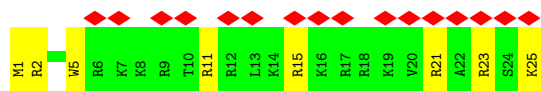


- Molecule 76: 60S ribosomal protein L40-A

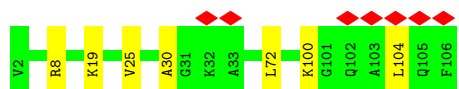




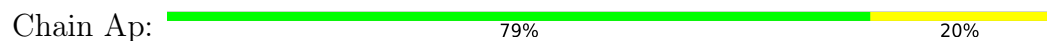
- Molecule 77: 60S ribosomal protein L41-A



- Molecule 78: 60S ribosomal protein L42-A



- Molecule 79: 60S ribosomal protein L43-A



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	404065	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.062	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0065	Depositor
Map size (Å)	463.968, 463.968, 463.968	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	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: UR3, MG, 5MC, 1MA, G7M, OMC, HIC, MA6, OMU, 3AU, OMG, 4AC, A2M, ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BA	0.39	0/1653	0.67	0/2261
2	BB	0.41	0/1735	0.86	3/2335 (0.1%)
3	BC	0.39	0/1665	0.74	3/2263 (0.1%)
4	BD	0.34	0/1759	0.60	0/2368
5	BE	0.38	0/2109	0.71	4/2839 (0.1%)
6	BF	0.36	0/1629	0.71	0/2202
7	BG	0.34	0/1844	0.71	3/2464 (0.1%)
8	BH	0.36	0/1506	0.75	0/2028
9	BI	0.40	0/1514	0.78	0/2021
10	BJ	0.39	0/1519	0.74	0/2035
11	BK	0.59	2/837 (0.2%)	1.11	4/1131 (0.4%)
12	BL	0.38	0/1272	0.62	0/1712
13	BM	0.28	0/921	0.78	0/1245
14	BN	0.37	0/1215	0.67	0/1638
15	BO	0.40	0/952	0.82	1/1279 (0.1%)
16	BP	0.38	0/1012	0.74	0/1356
17	BQ	0.42	0/1125	0.73	0/1510
18	BR	0.30	0/984	0.72	0/1318
19	BS	0.42	0/1211	0.77	0/1628
20	BT	0.42	0/1113	0.76	0/1494
21	BU	0.34	0/865	0.69	1/1169 (0.1%)
22	BV	0.45	0/692	0.67	2/932 (0.2%)
23	BW	0.48	0/1038	0.73	0/1395
24	BX	0.42	0/1139	0.89	5/1518 (0.3%)
25	BY	0.39	0/1087	0.72	0/1449
26	BZ	0.37	0/566	0.81	0/761
27	Ba	0.45	0/782	0.90	2/1047 (0.2%)
28	Bb	0.35	0/620	0.65	0/838
29	Bc	0.33	0/499	0.64	0/670
30	Bd	0.39	0/452	0.74	0/600
31	Be	0.28	0/483	0.56	0/643
32	Bf	0.24	0/462	0.69	0/617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bg	0.37	0/2454	0.70	0/3340
34	Bh	0.28	0/678	0.65	0/905
35	B5	0.40	2/41700 (0.0%)	0.48	2/64963 (0.0%)
36	A1	0.50	2/74123 (0.0%)	0.47	15/115559 (0.0%)
37	A3	0.41	0/2883	0.41	0/4491
38	A4	0.56	0/3745	0.48	1/5828 (0.0%)
39	AA	0.39	0/1912	0.58	0/2569
40	AB	0.51	0/3136	0.65	4/4213 (0.1%)
41	AC	0.50	0/2800	0.73	3/3790 (0.1%)
42	AD	0.30	0/2390	0.65	3/3225 (0.1%)
43	AE	0.46	0/1260	0.65	0/1694
44	AF	0.51	0/1821	0.73	5/2451 (0.2%)
45	AG	0.40	0/1830	0.69	0/2469
46	AH	0.40	0/1531	0.65	0/2062
47	AI	0.31	0/1708	0.61	0/2290
48	AJ	0.31	0/1374	0.73	0/1842
49	AL	0.48	0/1568	0.74	3/2106 (0.1%)
50	AM	0.46	0/1068	0.57	0/1438
51	AN	0.52	0/1757	0.69	0/2354
52	AO	0.53	0/1585	0.65	0/2128
53	AP	0.51	0/1410	0.62	0/1893
54	AQ	0.45	0/1465	0.58	0/1965
55	AR	0.41	0/1538	0.60	0/2050
56	AS	0.52	0/1481	0.69	0/1990
57	AT	0.40	0/1300	0.67	0/1743
58	AU	0.37	0/812	0.69	0/1099
59	AV	0.47	0/1018	0.64	0/1369
60	AW	0.47	0/533	0.60	0/707
61	AX	0.47	0/983	0.63	0/1325
62	AY	0.50	0/1004	0.63	0/1341
63	AZ	0.38	0/1118	0.69	2/1497 (0.1%)
64	Aa	0.46	0/1204	0.73	3/1612 (0.2%)
65	Ab	0.29	0/473	0.63	0/629
66	Ac	0.36	0/751	0.59	0/1008
67	Ad	0.50	0/904	0.56	0/1213
68	Ae	0.51	0/1041	0.61	0/1394
69	Af	0.57	0/868	0.60	0/1168
70	Ag	0.47	0/890	0.63	0/1189
71	Ah	0.42	0/978	0.63	0/1301
72	Ai	0.38	0/778	0.79	0/1034
73	Aj	0.51	0/696	0.67	0/923
74	Ak	0.33	0/618	0.60	0/826
75	Al	0.48	0/443	0.61	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Am	0.42	0/423	0.72	2/562 (0.4%)
77	An	0.29	0/234	0.64	0/300
78	Ao	0.27	0/860	0.63	0/1136
79	Ap	0.41	0/701	0.74	2/934 (0.2%)
All	All	0.45	6/212107 (0.0%)	0.57	73/311279 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	BA	0	1
2	BB	0	5
3	BC	0	2
5	BE	0	1
6	BF	0	2
7	BG	0	1
8	BH	0	2
9	BI	0	1
10	BJ	0	3
11	BK	0	2
15	BO	0	1
16	BP	0	1
17	BQ	0	3
19	BS	0	2
20	BT	0	1
24	BX	0	5
26	BZ	0	1
27	Ba	0	2
35	B5	4	0
40	AB	0	1
41	AC	0	4
42	AD	0	1
43	AE	0	1
44	AF	0	3
45	AG	0	3
46	AH	0	1
48	AJ	0	3
49	AL	0	2
51	AN	0	2
52	AO	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	AS	0	1
63	AZ	0	1
71	Ah	0	1
72	Ai	0	1
All	All	4	62

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	BK	88	PRO	CG-CD	-11.68	1.11	1.50
11	BK	88	PRO	CB-CG	-6.46	1.17	1.49
35	B5	578	OMU	O3'-P	5.42	1.61	1.56
36	A1	2946	A2M	O3'-P	5.31	1.61	1.56
35	B5	619	A2M	O3'-P	5.05	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	BK	88	PRO	N-CD-CG	-18.33	75.71	103.20
36	A1	266	A	OP1-P-OP2	-13.61	78.76	119.60
11	BK	88	PRO	CB-CG-CD	13.57	149.52	106.10
11	BK	88	PRO	CA-CB-CG	-12.73	80.30	104.50
36	A1	266	A	O5'-P-OP1	-11.82	72.53	108.00

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	B5	1191	3AU	C12
35	B5	1575	G7M	C4',C2',C3'

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BA	94	GLY	Peptide
2	BB	177	GLN	Peptide
2	BB	205	PHE	Peptide
2	BB	206	PRO	Peptide
2	BB	27	LYS	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BA	1612	0	1623	36	0
2	BB	1709	0	1784	33	0
3	BC	1635	0	1723	31	0
4	BD	1734	0	1817	26	0
5	BE	2068	0	2154	39	0
6	BF	1609	0	1675	26	0
7	BG	1820	0	1918	28	0
8	BH	1481	0	1572	19	0
9	BI	1489	0	1525	44	0
10	BJ	1494	0	1573	29	0
11	BK	817	0	804	18	0
12	BL	1244	0	1314	12	0
13	BM	913	0	955	6	0
14	BN	1192	0	1255	27	0
15	BO	941	0	979	24	0
16	BP	991	0	1035	18	0
17	BQ	1105	0	1166	26	0
18	BR	975	0	1039	24	0
19	BS	1192	0	1222	28	0
20	BT	1095	0	1114	27	0
21	BU	855	0	917	18	0
22	BV	684	0	671	17	0
23	BW	1021	0	1060	18	0
24	BX	1121	0	1196	15	0
25	BY	1073	0	1132	30	0
26	BZ	558	0	598	6	0
27	Ba	769	0	818	25	0
28	Bb	610	0	631	8	0
29	Bc	497	0	535	8	0
30	Bd	442	0	432	8	0
31	Be	475	0	525	7	0
32	Bf	454	0	468	3	0
33	Bg	2401	0	2356	38	0
34	Bh	675	0	654	10	0
35	B5	37849	0	19076	421	0
36	A1	67139	0	33792	500	0
37	A3	2579	0	1304	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	A4	3353	0	1695	27	0
39	AA	1878	0	1946	39	0
40	AB	3078	0	3149	51	0
41	AC	2748	0	2859	28	0
42	AD	2341	0	2290	30	0
43	AE	1239	0	1326	16	0
44	AF	1784	0	1862	24	0
45	AG	1798	0	1894	26	0
46	AH	1510	0	1576	18	0
47	AI	1672	0	1711	22	0
48	AJ	1353	0	1383	28	0
49	AL	1543	0	1608	21	0
50	AM	1053	0	1149	11	0
51	AN	1720	0	1779	38	0
52	AO	1555	0	1659	14	0
53	AP	1388	0	1423	15	0
54	AQ	1441	0	1543	16	0
55	AR	1521	0	1617	18	0
56	AS	1445	0	1487	15	0
57	AT	1276	0	1323	19	0
58	AU	796	0	812	8	0
59	AV	1003	0	1048	12	0
60	AW	521	0	551	8	0
61	AX	968	0	1036	8	0
62	AY	993	0	1081	13	0
63	AZ	1092	0	1155	22	0
64	Aa	1173	0	1215	19	0
65	Ab	462	0	491	1	0
66	Ac	743	0	797	14	0
67	Ad	890	0	938	6	0
68	Ae	1020	0	1089	12	0
69	Af	850	0	880	6	0
70	Ag	880	0	945	13	0
71	Ah	969	0	1078	11	0
72	Ai	771	0	849	5	0
73	Aj	681	0	686	11	0
74	Ak	612	0	682	7	0
75	Al	436	0	475	7	0
76	Am	417	0	459	11	0
77	An	233	0	284	11	0
78	Ao	847	0	914	6	0
79	Ap	694	0	738	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	A1	242	0	0	0	0
80	A3	2	0	0	0	0
80	A4	9	0	0	0	0
80	AB	3	0	0	0	0
80	AG	1	0	0	0	0
80	AL	1	0	0	0	0
80	AN	2	0	0	0	0
80	AO	1	0	0	0	0
80	AP	1	0	0	0	0
80	AR	1	0	0	0	0
80	AX	1	0	0	0	0
80	Ae	4	0	0	0	0
80	Af	2	0	0	0	0
80	Aj	2	0	0	0	0
80	B5	91	0	0	0	0
80	BD	1	0	0	0	0
80	BJ	1	0	0	0	0
80	BL	1	0	0	0	0
81	Ao	1	0	0	0	0
81	Bb	1	0	0	0	0
All	All	199433	0	147894	1872	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

The worst 5 of 1872 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:B5:1354:G:O6	35:B5:1369:U:C4	2.07	1.08
35:B5:868:G:H1	35:B5:960:U:H3	1.06	1.02
35:B5:1354:G:O6	35:B5:1369:U:N3	1.91	1.02
36:A1:1222:G:H21	36:A1:1286:A:N6	1.60	0.98
35:B5:1356:U:H3	35:B5:1367:G:H1	1.12	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BA	204/206 (99%)	181 (89%)	22 (11%)	1 (0%)	24	52
2	BB	212/214 (99%)	176 (83%)	34 (16%)	2 (1%)	14	39
3	BC	215/217 (99%)	199 (93%)	15 (7%)	1 (0%)	24	52
4	BD	221/223 (99%)	207 (94%)	14 (6%)	0	100	100
5	BE	258/260 (99%)	228 (88%)	30 (12%)	0	100	100
6	BF	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	24	52
7	BG	224/226 (99%)	205 (92%)	16 (7%)	3 (1%)	9	31
8	BH	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	24	52
9	BI	184/188 (98%)	149 (81%)	35 (19%)	0	100	100
10	BJ	183/185 (99%)	165 (90%)	17 (9%)	1 (0%)	24	52
11	BK	94/96 (98%)	77 (82%)	17 (18%)	0	100	100
12	BL	153/155 (99%)	138 (90%)	15 (10%)	0	100	100
13	BM	119/121 (98%)	85 (71%)	34 (29%)	0	100	100
14	BN	148/150 (99%)	139 (94%)	9 (6%)	0	100	100
15	BO	125/127 (98%)	109 (87%)	15 (12%)	1 (1%)	16	42
16	BP	122/124 (98%)	100 (82%)	21 (17%)	1 (1%)	16	42
17	BQ	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	18	45
18	BR	117/121 (97%)	111 (95%)	6 (5%)	0	100	100
19	BS	143/145 (99%)	129 (90%)	13 (9%)	1 (1%)	18	45
20	BT	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
21	BU	105/107 (98%)	98 (93%)	7 (7%)	0	100	100
22	BV	83/87 (95%)	72 (87%)	11 (13%)	0	100	100
23	BW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
24	BX	142/144 (99%)	118 (83%)	21 (15%)	3 (2%)	5	21
25	BY	132/134 (98%)	124 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	BZ	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
27	Ba	95/97 (98%)	74 (78%)	19 (20%)	2 (2%)	5	21
28	Bb	79/81 (98%)	68 (86%)	11 (14%)	0	100	100
29	Bc	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
30	Bd	51/53 (96%)	51 (100%)	0	0	100	100
31	Be	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
32	Bf	53/57 (93%)	36 (68%)	17 (32%)	0	100	100
33	Bg	310/312 (99%)	276 (89%)	34 (11%)	0	100	100
34	Bh	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
39	AA	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
40	AB	383/386 (99%)	368 (96%)	14 (4%)	1 (0%)	36	63
41	AC	359/361 (99%)	321 (89%)	36 (10%)	2 (1%)	21	48
42	AD	290/292 (99%)	267 (92%)	22 (8%)	1 (0%)	36	63
43	AE	152/156 (97%)	142 (93%)	10 (7%)	0	100	100
44	AF	220/222 (99%)	206 (94%)	12 (6%)	2 (1%)	14	39
45	AG	228/230 (99%)	210 (92%)	18 (8%)	0	100	100
46	AH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
47	AI	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
48	AJ	167/169 (99%)	146 (87%)	21 (13%)	0	100	100
49	AL	191/193 (99%)	171 (90%)	17 (9%)	3 (2%)	7	26
50	AM	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
51	AN	201/203 (99%)	185 (92%)	15 (8%)	1 (0%)	24	52
52	AO	195/197 (99%)	188 (96%)	6 (3%)	1 (0%)	24	52
53	AP	171/175 (98%)	164 (96%)	7 (4%)	0	100	100
54	AQ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
55	AR	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
56	AS	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
57	AT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
58	AU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	AV	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
60	AW	61/63 (97%)	59 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	AX	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
62	AY	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
63	AZ	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	42
64	Aa	146/148 (99%)	129 (88%)	16 (11%)	1 (1%)	18	45
65	Ab	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Ac	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
67	Ad	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
68	Ae	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Af	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
70	Ag	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
71	Ah	117/119 (98%)	109 (93%)	7 (6%)	1 (1%)	14	39
72	Ai	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
73	Aj	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
74	Ak	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
75	Al	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
76	Am	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
77	An	23/25 (92%)	23 (100%)	0	0	100	100
78	Ao	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
79	Ap	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
All	All	10956/11121 (98%)	10008 (91%)	915 (8%)	33 (0%)	37	63

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	BX	97	ASP
41	AC	339	LEU
44	AF	159	GLN
49	AL	48	PRO
51	AN	81	TYR

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	173/173 (100%)	173 (100%)	0	100	100
2	BB	191/191 (100%)	191 (100%)	0	100	100
3	BC	176/176 (100%)	176 (100%)	0	100	100
4	BD	182/182 (100%)	182 (100%)	0	100	100
5	BE	221/221 (100%)	221 (100%)	0	100	100
6	BF	173/173 (100%)	173 (100%)	0	100	100
7	BG	193/193 (100%)	193 (100%)	0	100	100
8	BH	165/165 (100%)	165 (100%)	0	100	100
9	BI	150/150 (100%)	150 (100%)	0	100	100
10	BJ	158/158 (100%)	158 (100%)	0	100	100
11	BK	89/89 (100%)	89 (100%)	0	100	100
12	BL	136/136 (100%)	136 (100%)	0	100	100
13	BM	98/98 (100%)	98 (100%)	0	100	100
14	BN	127/127 (100%)	127 (100%)	0	100	100
15	BO	96/96 (100%)	96 (100%)	0	100	100
16	BP	104/104 (100%)	104 (100%)	0	100	100
17	BQ	117/117 (100%)	117 (100%)	0	100	100
18	BR	110/110 (100%)	110 (100%)	0	100	100
19	BS	128/128 (100%)	128 (100%)	0	100	100
20	BT	113/113 (100%)	113 (100%)	0	100	100
21	BU	100/100 (100%)	100 (100%)	0	100	100
22	BV	74/74 (100%)	74 (100%)	0	100	100
23	BW	110/110 (100%)	110 (100%)	0	100	100
24	BX	119/119 (100%)	119 (100%)	0	100	100
25	BY	112/112 (100%)	112 (100%)	0	100	100
26	BZ	61/61 (100%)	61 (100%)	0	100	100
27	Ba	83/83 (100%)	83 (100%)	0	100	100
28	Bb	70/70 (100%)	70 (100%)	0	100	100
29	Bc	56/56 (100%)	56 (100%)	0	100	100
30	Bd	47/47 (100%)	46 (98%)	1 (2%)	47	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	Be	51/51 (100%)	51 (100%)	0	100	100
32	Bf	49/49 (100%)	49 (100%)	0	100	100
33	Bg	256/257 (100%)	256 (100%)	0	100	100
34	Bh	68/68 (100%)	68 (100%)	0	100	100
39	AA	189/189 (100%)	189 (100%)	0	100	100
40	AB	321/321 (100%)	319 (99%)	2 (1%)	78	81
41	AC	288/288 (100%)	288 (100%)	0	100	100
42	AD	241/241 (100%)	241 (100%)	0	100	100
43	AE	134/134 (100%)	134 (100%)	0	100	100
44	AF	186/186 (100%)	186 (100%)	0	100	100
45	AG	189/189 (100%)	189 (100%)	0	100	100
46	AH	170/170 (100%)	170 (100%)	0	100	100
47	AI	176/176 (100%)	176 (100%)	0	100	100
48	AJ	147/147 (100%)	147 (100%)	0	100	100
49	AL	154/154 (100%)	154 (100%)	0	100	100
50	AM	107/107 (100%)	107 (100%)	0	100	100
51	AN	175/175 (100%)	175 (100%)	0	100	100
52	AO	160/160 (100%)	160 (100%)	0	100	100
53	AP	141/141 (100%)	141 (100%)	0	100	100
54	AQ	150/150 (100%)	150 (100%)	0	100	100
55	AR	153/153 (100%)	153 (100%)	0	100	100
56	AS	156/156 (100%)	156 (100%)	0	100	100
57	AT	136/136 (100%)	136 (100%)	0	100	100
58	AU	87/87 (100%)	87 (100%)	0	100	100
59	AV	104/104 (100%)	104 (100%)	0	100	100
60	AW	55/55 (100%)	55 (100%)	0	100	100
61	AX	105/105 (100%)	105 (100%)	0	100	100
62	AY	109/109 (100%)	109 (100%)	0	100	100
63	AZ	115/115 (100%)	115 (100%)	0	100	100
64	Aa	118/118 (100%)	118 (100%)	0	100	100
65	Ab	46/46 (100%)	46 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	Ac	81/81 (100%)	81 (100%)	0	100	100
67	Ad	96/96 (100%)	96 (100%)	0	100	100
68	Ae	109/109 (100%)	109 (100%)	0	100	100
69	Af	90/90 (100%)	90 (100%)	0	100	100
70	Ag	95/95 (100%)	95 (100%)	0	100	100
71	Ah	104/104 (100%)	104 (100%)	0	100	100
72	Ai	81/81 (100%)	81 (100%)	0	100	100
73	Aj	70/70 (100%)	70 (100%)	0	100	100
74	Ak	68/68 (100%)	68 (100%)	0	100	100
75	Al	45/45 (100%)	45 (100%)	0	100	100
76	Am	47/47 (100%)	47 (100%)	0	100	100
77	An	23/23 (100%)	23 (100%)	0	100	100
78	Ao	90/90 (100%)	90 (100%)	0	100	100
79	Ap	71/71 (100%)	71 (100%)	0	100	100
All	All	9338/9339 (100%)	9335 (100%)	3 (0%)	100	100

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

Mol	Chain	Res	Type
30	Bd	28	THR
40	AB	90	VAL
40	AB	93	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
52	AO	182[A]	ASN
63	AZ	36	HIS
53	AP	55	GLN
57	AT	5	HIS
65	Ab	43	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	B5	1779/1781 (99%)	525 (29%)	11 (0%)
36	A1	3131/3137 (99%)	727 (23%)	17 (0%)
37	A3	120/121 (99%)	19 (15%)	0
38	A4	156/158 (98%)	34 (21%)	1 (0%)
All	All	5186/5197 (99%)	1305 (25%)	29 (0%)

5 of 1305 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	B5	4	C
35	B5	25	C
35	B5	26	A
35	B5	34	G
35	B5	42	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	A1	439	C
36	A1	3121	U
36	A1	916	G
36	A1	2111	G
36	A1	873	C

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	$\# Z > 2$
36	OMG	A1	2619	36	23,26,27	1.17	3 (13%)	32,38,41	2.01	6 (18%)
36	OMC	A1	2337	36	19,22,23	0.87	2 (10%)	25,31,34	1.19	2 (8%)
36	5MC	A1	2278	36,80	19,22,23	1.55	3 (15%)	26,32,35	1.35	5 (19%)
36	OMU	A1	2421	36	19,22,23	1.27	4 (21%)	25,31,34	1.74	5 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	OMU	A1	1888	36	19,22,23	1.42	4 (21%)	25,31,34	2.00	5 (20%)
35	A2M	B5	796	35	22,25,26	1.59	5 (22%)	30,36,39	2.12	9 (30%)
35	OMC	B5	1639	35	19,22,23	0.79	1 (5%)	25,31,34	0.89	1 (4%)
35	OMG	B5	1271	35	23,26,27	1.22	4 (17%)	32,38,41	1.96	6 (18%)
36	OMG	A1	805	36	23,26,27	1.24	4 (17%)	32,38,41	2.00	8 (25%)
35	OMG	B5	1572	35	23,26,27	1.21	3 (13%)	32,38,41	1.99	6 (18%)
36	OMU	A1	2729	36	19,22,23	1.41	4 (21%)	25,31,34	1.82	6 (24%)
36	OMU	A1	2921	36	19,22,23	1.23	3 (15%)	25,31,34	1.89	6 (24%)
36	A2M	A1	2280	36	22,25,26	1.47	4 (18%)	30,36,39	2.09	9 (30%)
36	OMU	A1	2417	36	19,22,23	1.30	4 (21%)	25,31,34	1.78	4 (16%)
35	4AC	B5	1773	35	21,24,25	1.17	3 (14%)	28,34,37	2.89	6 (21%)
36	A2M	A1	649	36	22,25,26	1.36	3 (13%)	30,36,39	2.10	7 (23%)
35	A2M	B5	100	35,80	22,25,26	1.50	5 (22%)	30,36,39	2.25	10 (33%)
36	A2M	A1	876	36	22,25,26	1.46	5 (22%)	30,36,39	2.12	8 (26%)
35	MA6	B5	1782	35	23,26,27	1.57	4 (17%)	33,38,41	1.98	8 (24%)
35	G7M	B5	1575	35	23,26,27	2.39	5 (21%)	34,39,42	3.05	12 (35%)
36	A2M	A1	1133	36	22,25,26	1.53	5 (22%)	30,36,39	2.11	8 (26%)
35	OMG	B5	1126	35	23,26,27	1.19	4 (17%)	32,38,41	1.93	6 (18%)
35	OMC	B5	414	35	19,22,23	0.89	2 (10%)	25,31,34	0.89	1 (4%)
35	A2M	B5	541	35	22,25,26	1.47	3 (13%)	30,36,39	2.22	6 (20%)
36	OMC	A1	2959	36	19,22,23	0.83	1 (5%)	25,31,34	1.01	1 (4%)
36	OMC	A1	1437	36,80	19,22,23	0.95	1 (5%)	25,31,34	1.55	5 (20%)
36	UR3	A1	2634	36,80	19,22,23	0.98	1 (5%)	26,32,35	1.62	3 (11%)
35	A2M	B5	28	35,80	22,25,26	1.47	5 (22%)	30,36,39	2.15	10 (33%)
35	OMU	B5	578	35	19,22,23	1.29	4 (21%)	25,31,34	1.82	4 (16%)
35	OMC	B5	1007	35	19,22,23	0.82	0	25,31,34	0.87	1 (4%)
36	A2M	A1	807	36	22,25,26	1.47	3 (13%)	30,36,39	2.21	8 (26%)
35	OMG	B5	1428	35,80	23,26,27	1.22	3 (13%)	32,38,41	2.02	6 (18%)
36	OMC	A1	650	36	19,22,23	0.88	2 (10%)	25,31,34	0.81	0
35	A2M	B5	974	35	22,25,26	1.49	5 (22%)	30,36,39	2.16	10 (33%)
35	OMG	B5	562	35	23,26,27	1.27	4 (17%)	32,38,41	2.05	7 (21%)
35	3AU	B5	1191	35	24,28,29	0.48	0	30,40,43	0.70	0
36	A2M	A1	2281	36	22,25,26	1.44	6 (27%)	30,36,39	2.29	10 (33%)
35	A2M	B5	436	35	22,25,26	1.53	5 (22%)	30,36,39	1.90	7 (23%)
40	HIC	AB	243	40	10,11,12	1.28	1 (10%)	9,14,16	3.48	3 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
35	4AC	B5	1280	35	21,24,25	1.10	1 (4%)	28,34,37	1.60	6 (21%)
36	OMC	A1	663	36	19,22,23	0.97	2 (10%)	25,31,34	0.88	0
36	OMU	A1	898	36	19,22,23	1.41	4 (21%)	25,31,34	1.89	5 (20%)
36	A2M	A1	2220	36	22,25,26	1.52	5 (22%)	30,36,39	1.95	10 (33%)
36	OMG	A1	2791	36	23,26,27	1.18	3 (13%)	32,38,41	2.04	6 (18%)
36	1MA	A1	645	36,80	21,25,26	1.35	4 (19%)	30,37,40	1.72	6 (20%)
36	OMG	A1	2815	36	23,26,27	1.21	4 (17%)	32,38,41	2.05	7 (21%)
36	5MC	A1	2870	36	19,22,23	1.35	2 (10%)	26,32,35	1.17	3 (11%)
36	OMU	A1	2724	36	19,22,23	1.28	4 (21%)	25,31,34	1.88	5 (20%)
35	A2M	B5	619	35,80	22,25,26	1.49	6 (27%)	30,36,39	2.11	10 (33%)
36	OMG	A1	2922	36	23,26,27	1.19	3 (13%)	32,38,41	1.95	6 (18%)
36	OMG	A1	2793	36	23,26,27	1.20	4 (17%)	32,38,41	2.01	7 (21%)
36	OMC	A1	2948	36	19,22,23	0.86	1 (5%)	25,31,34	1.18	3 (12%)
36	OMG	A1	2288	36	23,26,27	1.22	3 (13%)	32,38,41	2.12	7 (21%)
36	OMC	A1	2197	36	19,22,23	0.78	0	25,31,34	0.77	0
36	A2M	A1	2640	36	22,25,26	1.47	5 (22%)	30,36,39	1.99	6 (20%)
36	A2M	A1	817	36,80	22,25,26	1.53	4 (18%)	30,36,39	2.14	7 (23%)
36	OMG	A1	1450	36	23,26,27	1.32	4 (17%)	32,38,41	1.95	6 (18%)
36	OMG	A1	908	36,80	23,26,27	1.21	3 (13%)	32,38,41	2.25	7 (21%)
36	A2M	A1	2946	36,80	22,25,26	1.48	4 (18%)	30,36,39	2.03	10 (33%)
36	A2M	A1	1449	36,80	22,25,26	1.55	5 (22%)	30,36,39	2.09	8 (26%)
36	OMG	A1	867	36,80	23,26,27	1.23	4 (17%)	32,38,41	2.06	8 (25%)
36	OMU	A1	2347	36	19,22,23	1.42	4 (21%)	25,31,34	1.93	6 (24%)
35	A2M	B5	420	35	22,25,26	1.51	4 (18%)	30,36,39	1.98	9 (30%)
35	MA6	B5	1781	35	23,26,27	1.45	4 (17%)	33,38,41	2.12	11 (33%)
35	OMU	B5	1269	35,80	19,22,23	1.31	4 (21%)	25,31,34	1.96	7 (28%)
36	1MA	A1	2142	36	21,25,26	1.30	5 (23%)	30,37,40	1.75	5 (16%)

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
36	OMG	A1	2619	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	2337	36	-	0/9/27/28	0/2/2/2
36	5MC	A1	2278	36,80	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	OMU	A1	2421	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	1888	36	-	0/9/27/28	0/2/2/2
35	A2M	B5	796	35	-	0/9/27/28	0/3/3/3
35	OMC	B5	1639	35	-	0/9/27/28	0/2/2/2
35	OMG	B5	1271	35	-	0/9/27/28	0/3/3/3
36	OMG	A1	805	36	-	1/9/27/28	0/3/3/3
35	OMG	B5	1572	35	-	0/9/27/28	0/3/3/3
36	OMU	A1	2729	36	-	3/9/27/28	0/2/2/2
36	OMU	A1	2921	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	2280	36	-	0/9/27/28	0/3/3/3
36	OMU	A1	2417	36	-	1/9/27/28	0/2/2/2
35	4AC	B5	1773	35	-	3/11/29/30	0/2/2/2
36	A2M	A1	649	36	-	2/9/27/28	0/3/3/3
35	A2M	B5	100	35,80	-	2/9/27/28	0/3/3/3
36	A2M	A1	876	36	-	0/9/27/28	0/3/3/3
35	MA6	B5	1782	35	-	3/11/29/30	0/3/3/3
35	G7M	B5	1575	35	3/3/5/5	3/7/25/26	0/3/3/3
36	A2M	A1	1133	36	-	0/9/27/28	0/3/3/3
35	OMG	B5	1126	35	-	1/9/27/28	0/3/3/3
35	OMC	B5	414	35	-	0/9/27/28	0/2/2/2
35	A2M	B5	541	35	-	4/9/27/28	0/3/3/3
36	OMC	A1	2959	36	-	0/9/27/28	0/2/2/2
36	OMC	A1	1437	36,80	-	2/9/27/28	0/2/2/2
36	UR3	A1	2634	36,80	-	0/7/25/26	0/2/2/2
35	A2M	B5	28	35,80	-	1/9/27/28	0/3/3/3
35	OMU	B5	578	35	-	3/9/27/28	0/2/2/2
35	OMC	B5	1007	35	-	0/9/27/28	0/2/2/2
36	A2M	A1	807	36	-	2/9/27/28	0/3/3/3
35	OMG	B5	1428	35,80	-	4/9/27/28	0/3/3/3
36	OMC	A1	650	36	-	0/9/27/28	0/2/2/2
35	A2M	B5	974	35	-	0/9/27/28	0/3/3/3
35	3AU	B5	1191	35	1/1/7/7	2/16/34/35	0/2/2/2
35	OMG	B5	562	35	-	0/9/27/28	0/3/3/3
36	A2M	A1	2281	36	-	1/9/27/28	0/3/3/3
35	A2M	B5	436	35	-	0/9/27/28	0/3/3/3
40	HIC	AB	243	40	-	0/5/6/8	0/1/1/1
35	4AC	B5	1280	35	-	4/11/29/30	0/2/2/2
36	OMC	A1	663	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	898	36	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	A2M	A1	2220	36	-	1/9/27/28	0/3/3/3
36	OMG	A1	2791	36	-	0/9/27/28	0/3/3/3
36	1MA	A1	645	36,80	-	1/7/25/26	0/3/3/3
36	OMG	A1	2815	36	-	0/9/27/28	0/3/3/3
36	5MC	A1	2870	36	-	4/7/25/26	0/2/2/2
36	OMU	A1	2724	36	-	0/9/27/28	0/2/2/2
35	A2M	B5	619	35,80	-	2/9/27/28	0/3/3/3
36	OMG	A1	2922	36	-	0/9/27/28	0/3/3/3
36	OMG	A1	2793	36	-	0/9/27/28	0/3/3/3
36	OMC	A1	2948	36	-	0/9/27/28	0/2/2/2
36	OMG	A1	2288	36	-	2/9/27/28	0/3/3/3
36	OMC	A1	2197	36	-	6/9/27/28	0/2/2/2
36	A2M	A1	2640	36	-	0/9/27/28	0/3/3/3
36	A2M	A1	817	36,80	-	1/9/27/28	0/3/3/3
36	OMG	A1	1450	36	-	2/9/27/28	0/3/3/3
36	OMG	A1	908	36,80	-	3/9/27/28	0/3/3/3
36	A2M	A1	2946	36,80	-	1/9/27/28	0/3/3/3
36	A2M	A1	1449	36,80	-	0/9/27/28	0/3/3/3
36	OMG	A1	867	36,80	-	1/9/27/28	0/3/3/3
36	OMU	A1	2347	36	-	2/9/27/28	0/2/2/2
35	A2M	B5	420	35	-	0/9/27/28	0/3/3/3
35	MA6	B5	1781	35	-	6/11/29/30	0/3/3/3
35	OMU	B5	1269	35,80	-	3/9/27/28	0/2/2/2
36	1MA	A1	2142	36	-	2/7/25/26	0/3/3/3

The worst 5 of 224 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	B5	1575	G7M	C8-N7	6.80	1.44	1.33
35	B5	1575	G7M	C5-N7	-5.93	1.32	1.39
36	A1	2278	5MC	C5-C4	5.45	1.48	1.44
35	B5	1782	MA6	C5-C4	5.19	1.48	1.39
36	A1	2870	5MC	C5-C4	4.53	1.47	1.44

The worst 5 of 396 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B5	1773	4AC	N4-C4-N3	11.03	131.77	113.87
40	AB	243	HIC	NE2-CE1-ND1	-9.07	109.19	112.66
35	B5	1575	G7M	CN7-N7-C8	-8.62	111.74	124.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B5	1773	4AC	C5-C4-N4	-8.28	108.99	122.94
36	A1	908	OMG	C5-C4-N3	-7.08	117.12	128.39

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
35	B5	1191	3AU	C12
35	B5	1575	G7M	C4'
35	B5	1575	G7M	C2'
35	B5	1575	G7M	C3'

5 of 79 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	B5	28	A2M	C1'-C2'-O2'-CM'
35	B5	619	A2M	O4'-C4'-C5'-O5'
35	B5	1280	4AC	N3-C4-N4-C7
35	B5	1280	4AC	C5-C4-N4-C7
35	B5	1280	4AC	O7-C7-N4-C4

There are no ring outliers.

20 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A1	2278	5MC	1	0
36	A1	1888	OMU	1	0
35	B5	1271	OMG	1	0
36	A1	2729	OMU	1	0
35	B5	1773	4AC	1	0
36	A1	1133	A2M	1	0
35	B5	1126	OMG	2	0
35	B5	28	A2M	1	0
35	B5	1007	OMC	1	0
35	B5	1428	OMG	2	0
40	AB	243	HIC	1	0
35	B5	1280	4AC	3	0
36	A1	2220	A2M	1	0
36	A1	2724	OMU	2	0
36	A1	2948	OMC	2	0
36	A1	2197	OMC	1	0
36	A1	2640	A2M	1	0
36	A1	817	A2M	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A1	1449	A2M	1	0
35	B5	1781	MA6	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 368 ligands modelled in this entry, 368 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
36	A1	5
53	AP	1
9	BI	1
35	B5	1
43	AE	1
47	AI	1
32	Bf	1
18	BR	1
38	A4	1
22	BV	1

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Mol	Chain	Number of breaks
49	AL	1
40	AB	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1253:U	O3'	1260:A	P	26.01
1	AP	155:GLU	C	164:LYS	N	23.68
1	A1	1955:U	O3'	2093:A	P	22.93
1	BI	123:LYS	C	135:LYS	N	19.36
1	A1	1023:C	O3'	1030:A	P	17.87

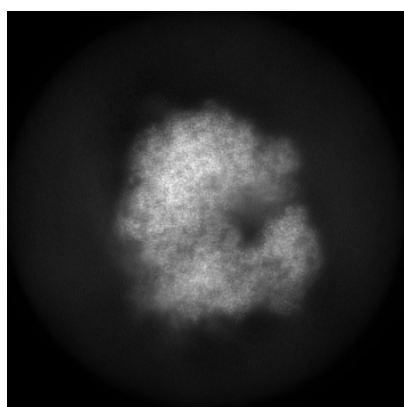
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23934. These allow visual inspection of the internal detail of the map and identification of artifacts.

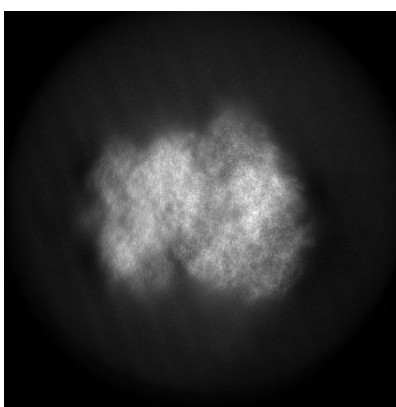
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

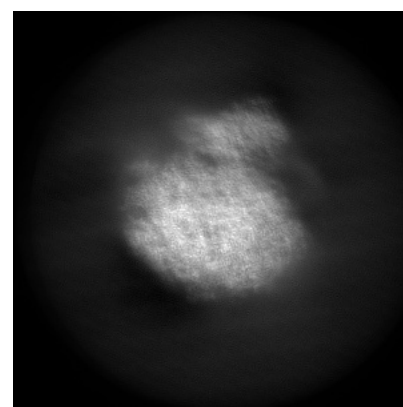
6.1.1 Primary map



X



Y

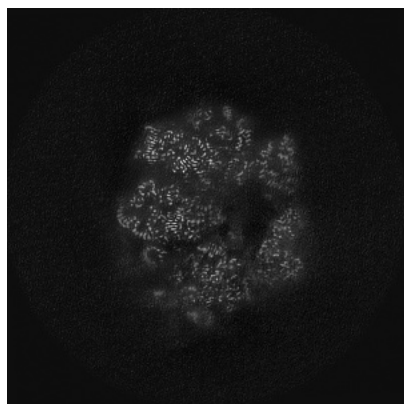


Z

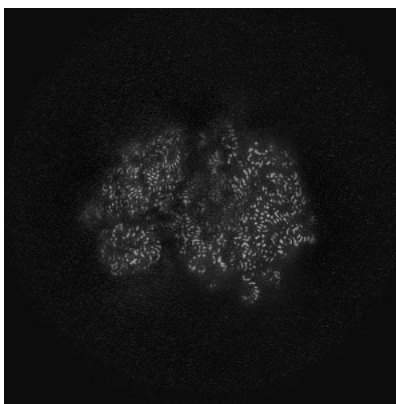
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

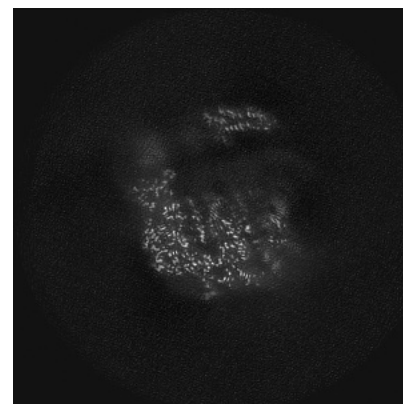
6.2.1 Primary map



X Index: 216



Y Index: 216

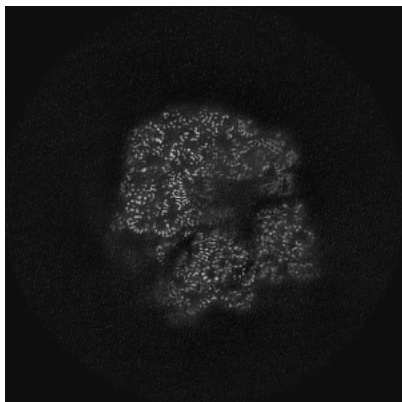


Z Index: 216

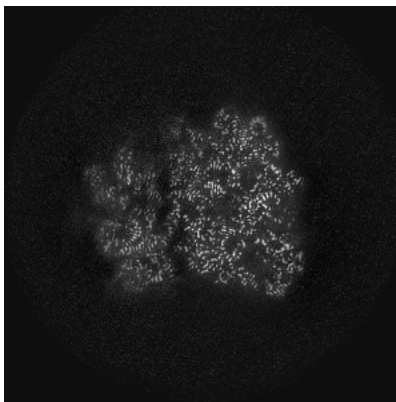
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

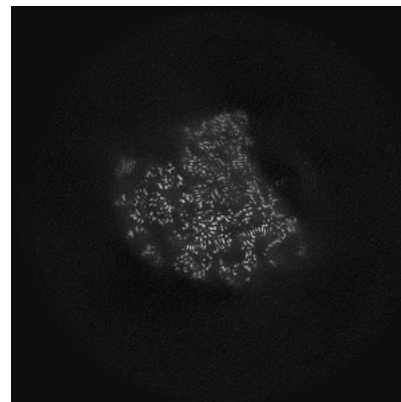
6.3.1 Primary map



X Index: 236



Y Index: 192

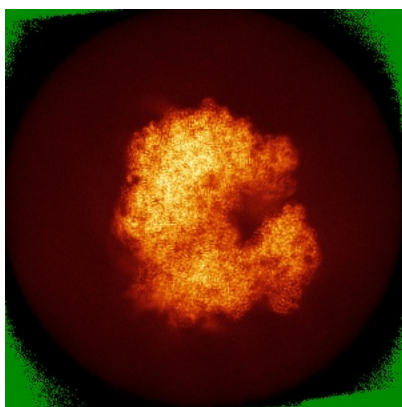


Z Index: 266

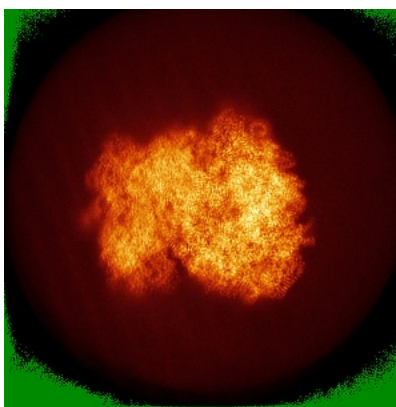
The images above show the largest variance slices of the map in three orthogonal directions.

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

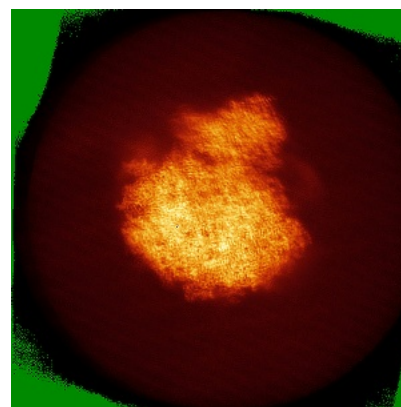
6.4.1 Primary map



X



Y

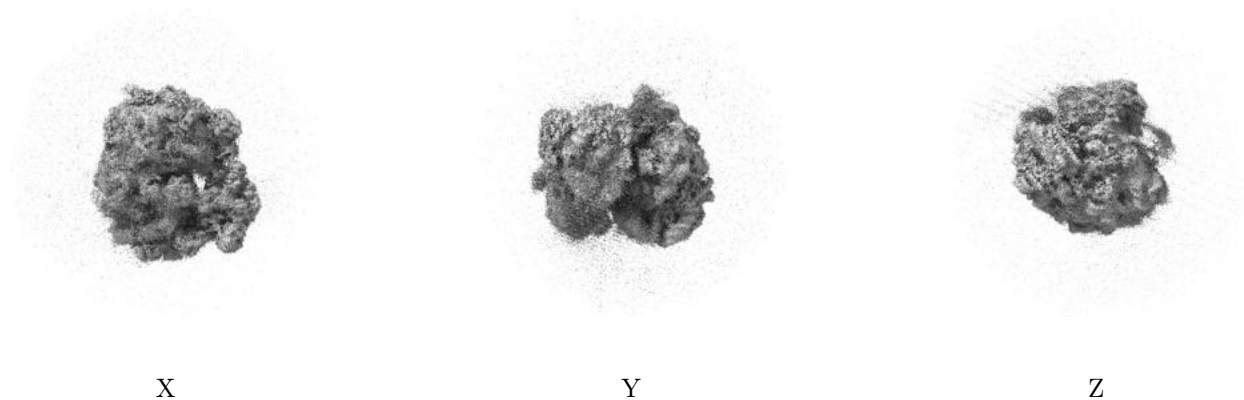


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.0065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

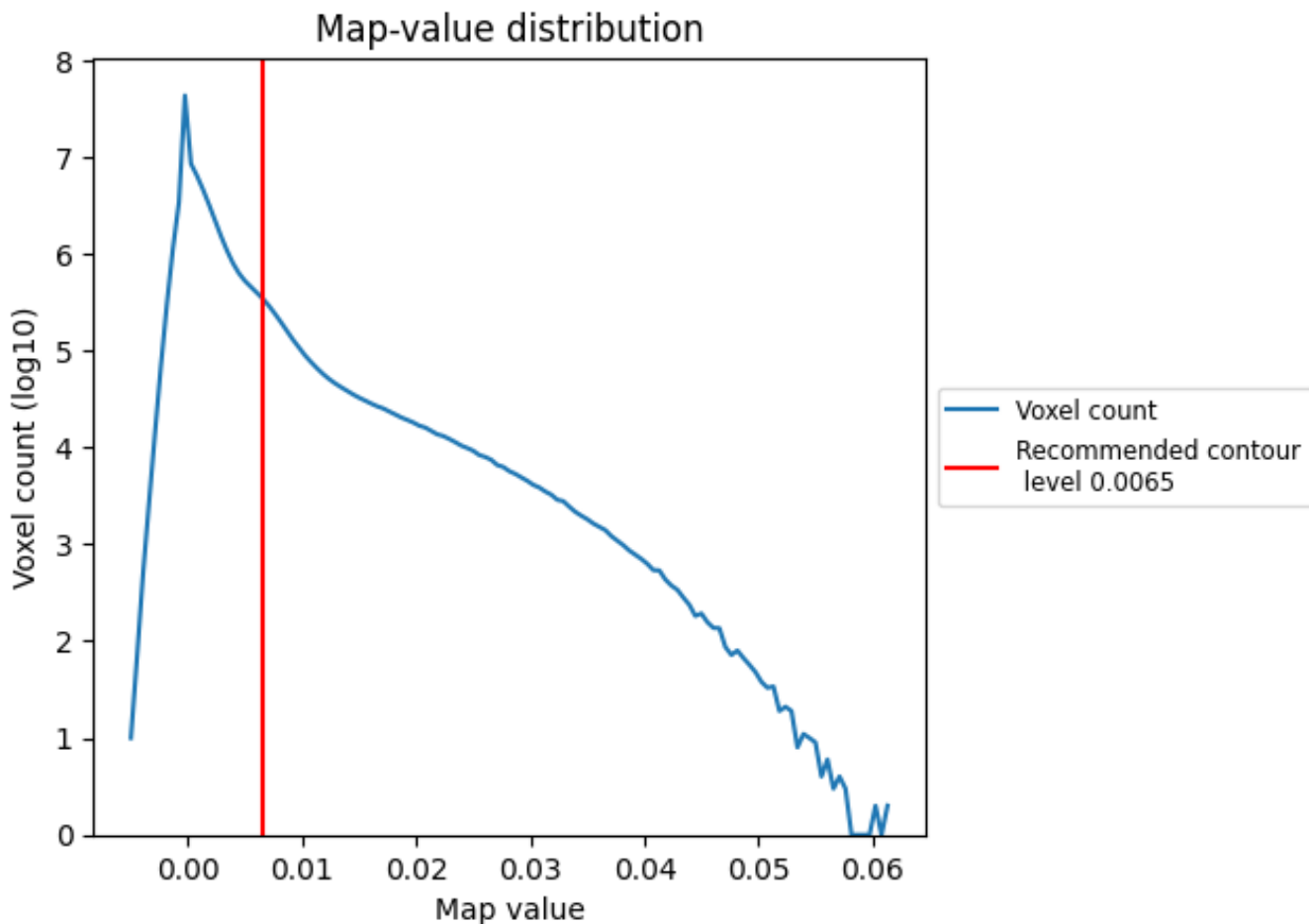
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

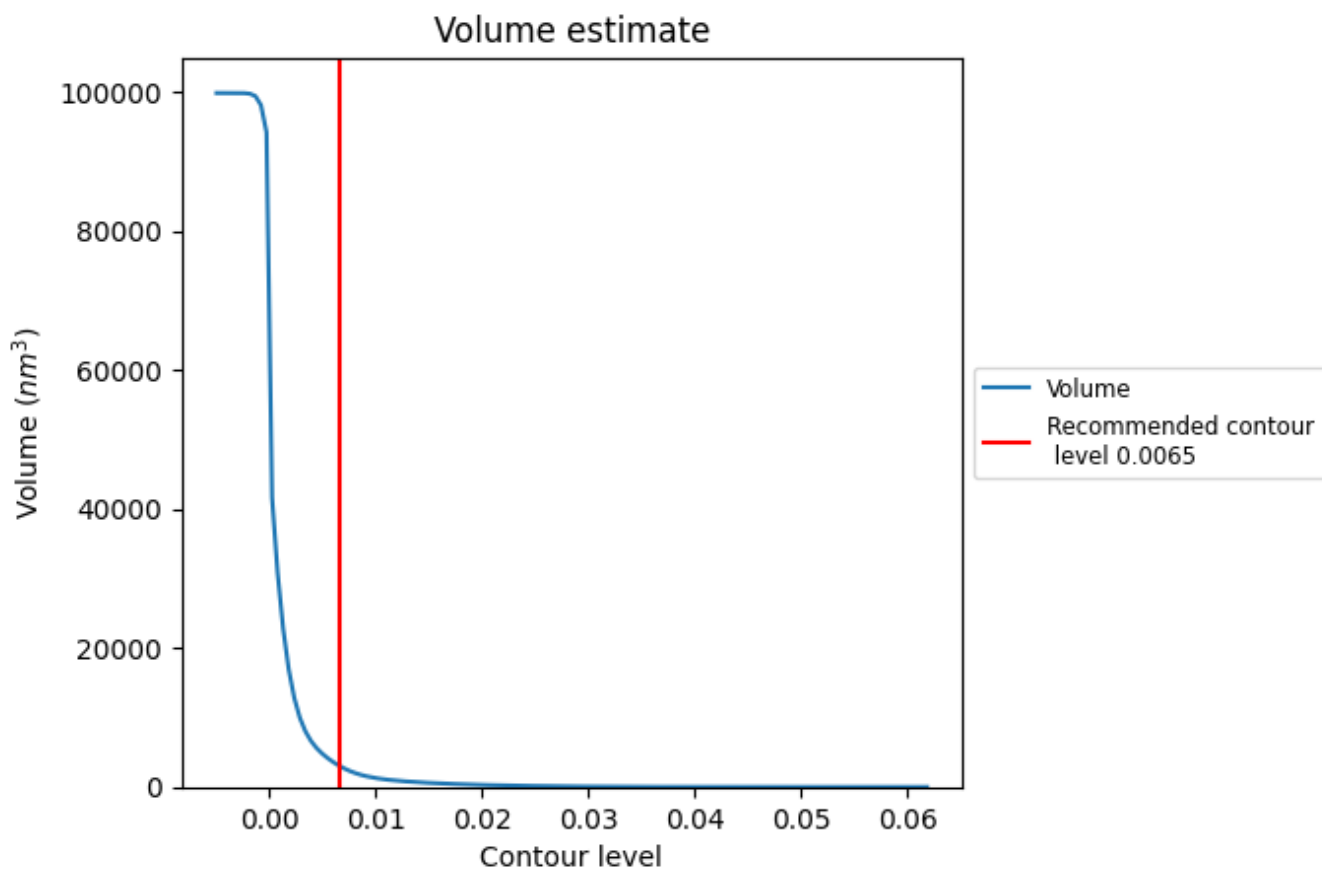
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

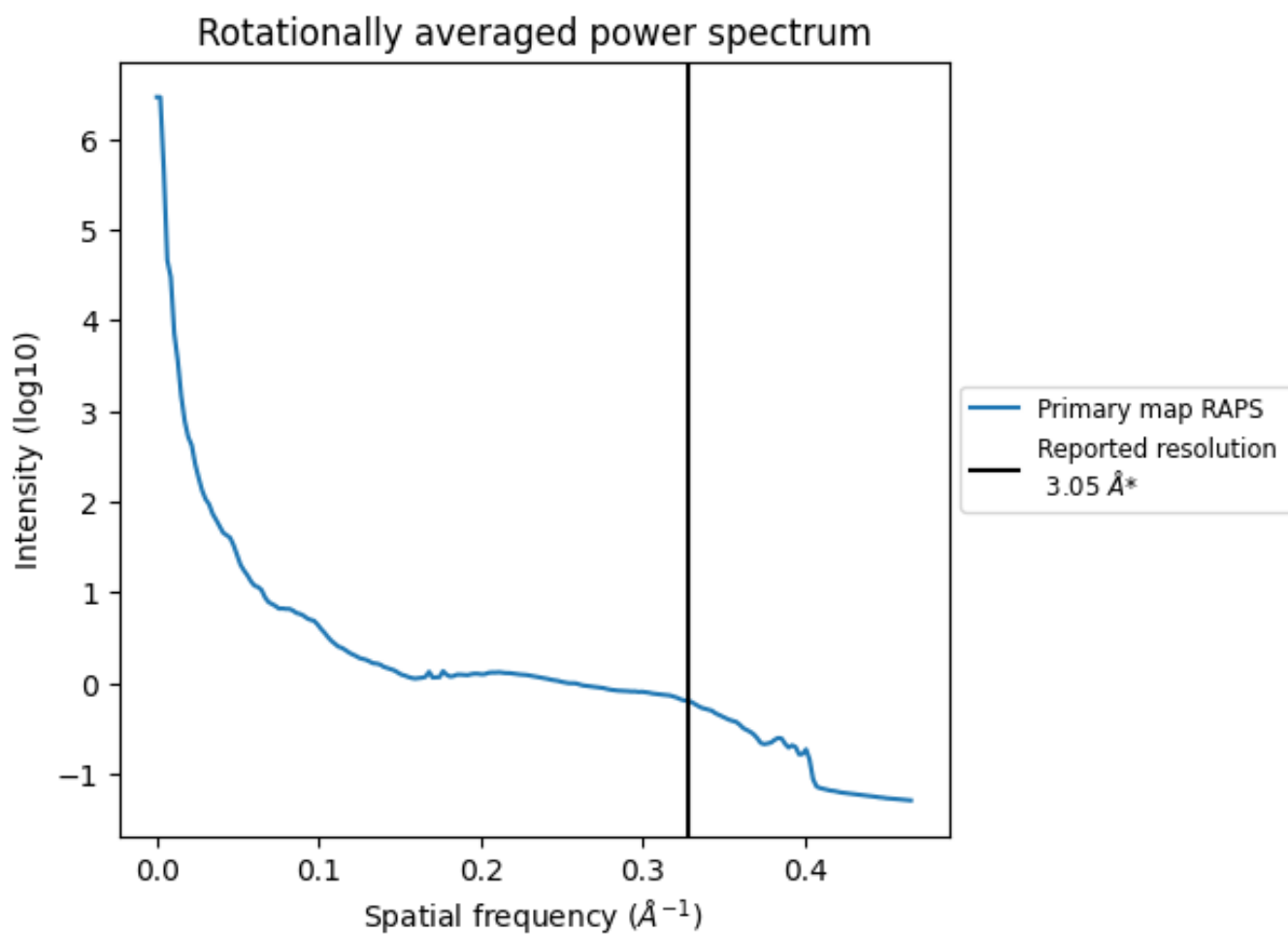
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3102 nm³; this corresponds to an approximate mass of 2802 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 0.328 Å⁻¹

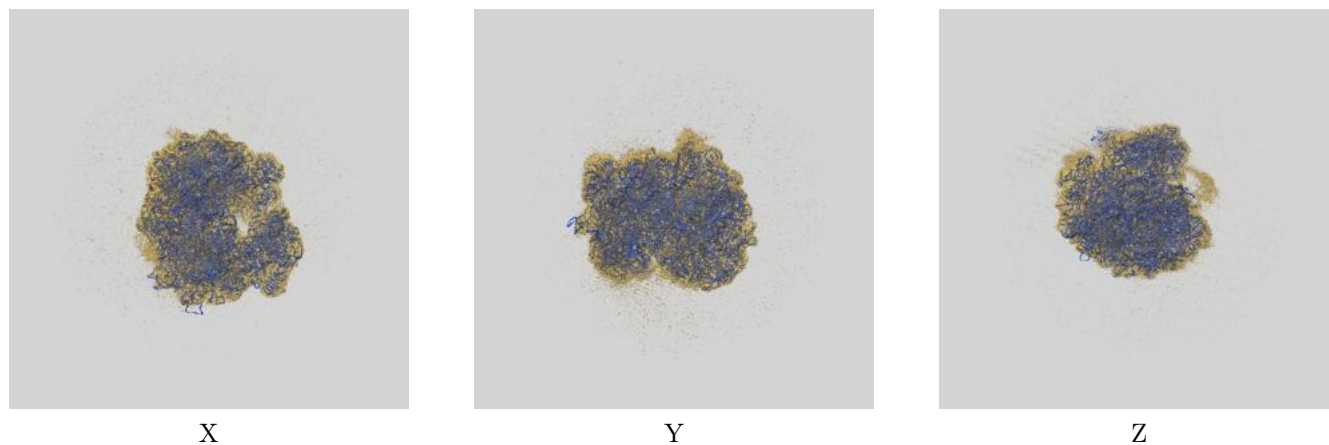
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

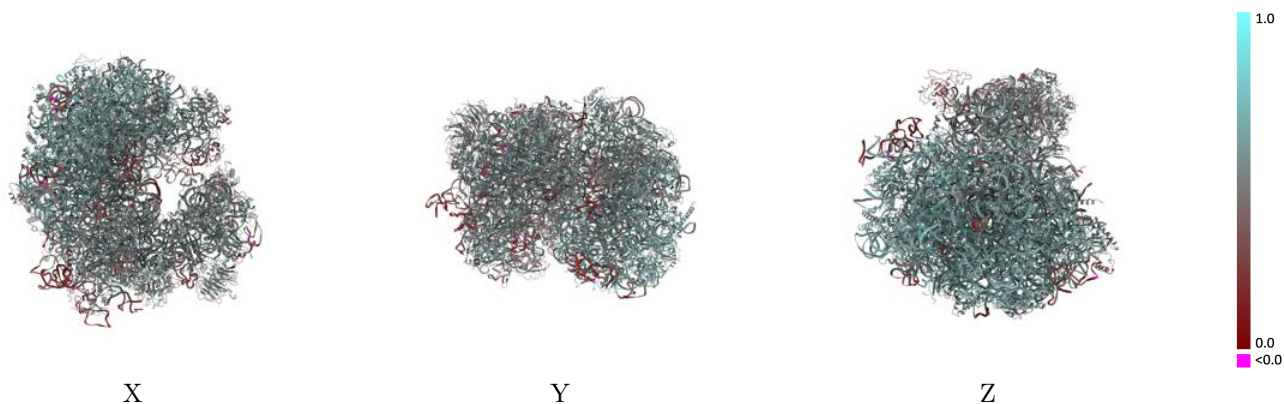
This section contains information regarding the fit between EMDB map EMD-23934 and PDB model 7MPI. Per-residue inclusion information can be found in section 3 on page 22.

9.1 Map-model overlay [i](#)



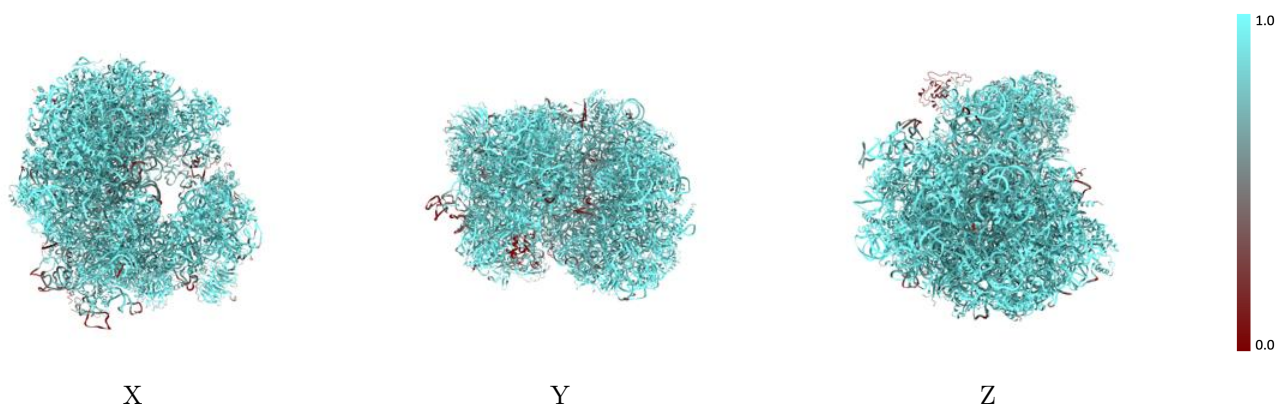
The images above show the 3D surface view of the map at the recommended contour level 0.0065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



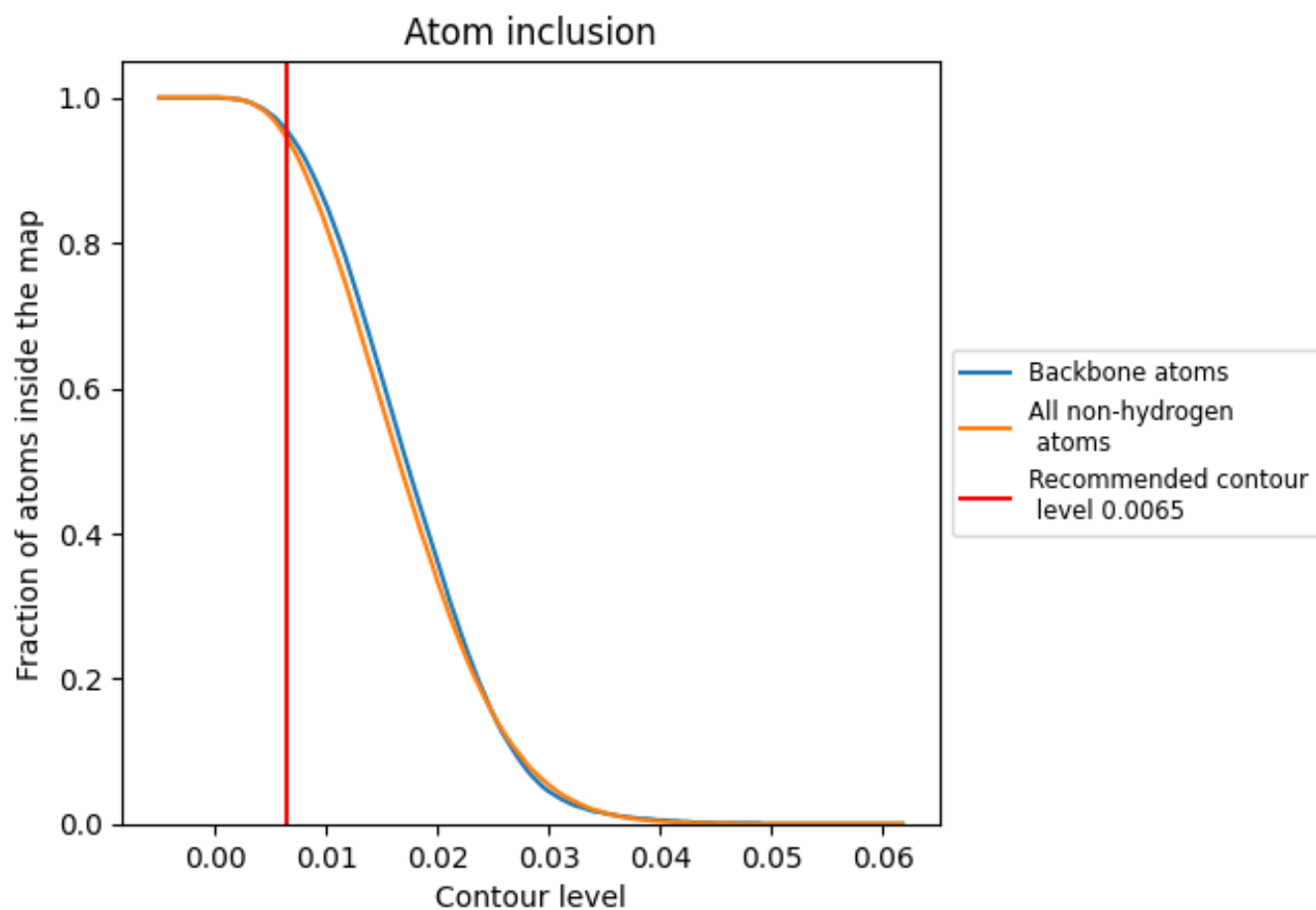
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0065).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary





















































































The table lists the average atom inclusion at the recommended contour level (0.0065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.5380
A1	 0.9690	 0.5660
A3	 0.9990	 0.5510
A4	 0.9910	 0.6160
AA	 0.9470	 0.5690
AB	 0.9820	 0.6220
AC	 0.9770	 0.6070
AD	 0.9240	 0.4860
AE	 0.9620	 0.5840
AF	 0.9800	 0.6140
AG	 0.9630	 0.5480
AH	 0.9660	 0.5790
AI	 0.9510	 0.4970
AJ	 0.7920	 0.3910
AL	 0.9510	 0.5870
AM	 0.9810	 0.6080
AN	 0.9880	 0.6150
AO	 0.9880	 0.6260
AP	 0.9750	 0.6280
AQ	 0.9890	 0.6130
AR	 0.8470	 0.5280
AS	 0.9830	 0.6170
AT	 0.9630	 0.5730
AU	 0.9080	 0.5180
AV	 0.9520	 0.6040
AW	 0.9430	 0.6020
AX	 0.9700	 0.5920
AY	 0.9760	 0.6000
AZ	 0.9800	 0.5340
Aa	 0.9890	 0.6040
Ab	 0.9160	 0.5150
Ac	 0.9770	 0.5290
Ad	 0.9430	 0.5940
Ae	 0.9860	 0.6280
Af	 0.9950	 0.6500









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Chain	Atom inclusion	Q-score
Ag	 0.9680	 0.5780
Ah	 0.9780	 0.5920
Ai	 0.9340	 0.5470
Aj	 0.9970	 0.6350
Ak	 0.8350	 0.4790
Al	 0.9930	 0.6250
Am	 0.9650	 0.5860
An	 0.3630	 0.3240
Ao	 0.8770	 0.4870
Ap	 0.9580	 0.5750
B5	 0.9270	 0.4810
BA	 0.9310	 0.5120
BB	 0.9320	 0.4700
BC	 0.9540	 0.5270
BD	 0.9460	 0.4950
BE	 0.9800	 0.5210
BF	 0.9410	 0.4940
BG	 0.8930	 0.4890
BH	 0.8310	 0.4440
BI	 0.9340	 0.5110
BJ	 0.9670	 0.5120
BK	 0.9480	 0.4480
BL	 0.8760	 0.5080
BM	 0.1450	 0.2070
BN	 0.9450	 0.5220
BO	 0.9640	 0.4950
BP	 0.8480	 0.4610
BQ	 0.9690	 0.5320
BR	 0.7970	 0.4450
BS	 0.8920	 0.4910
BT	 0.9360	 0.5340
BU	 0.8760	 0.4500
BV	 0.9340	 0.5380
BW	 0.9860	 0.5530
BX	 0.9530	 0.5330
BY	 0.9500	 0.5150
BZ	 0.8710	 0.4960
Ba	 0.9660	 0.5260
Bb	 0.9070	 0.5020
Bc	 0.9370	 0.5010
Bd	 0.9930	 0.5480
Be	 0.9170	 0.4960

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Chain	Atom inclusion	Q-score
Bf	 0.3650	 0.2290
Bg	 0.9080	 0.4920
Bh	 0.6980	 0.3680