



Full wwPDB EM Validation Report ⓘ

Oct 13, 2024 – 01:20 AM EDT

PDB ID : 9AXT
EMDB ID : EMD-43972
Title : Non-translating *S. pombe* ribosome
Authors : Gluc, M.; Gemin, O.; Purdy, M.; Mattei, S.; Jomaa, A.
Deposited on : 2024-03-06
Resolution : 2.40 Å (reported)

This is a Full wwPDB EM Validation 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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

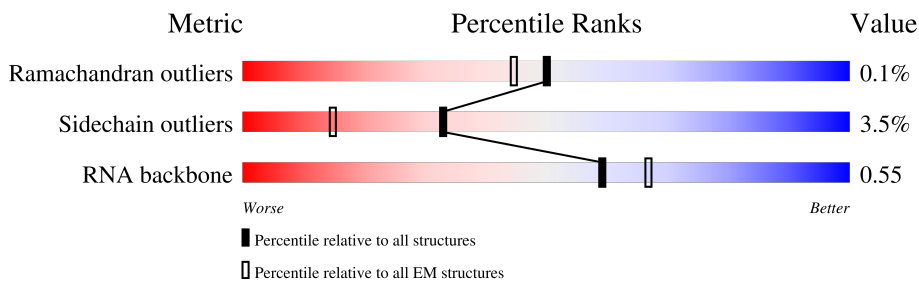
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	AA	1842	52% (Poor fit) 69% (0 outliers), 23% (1 outlier), 7% (2+ outliers), 2% (Not modelled)
2	AD	292	27% (0 outliers), 67% (1 outlier), 30% (2+ outliers), 5% (Not modelled)
3	AE	252	54% (0 outliers), 81% (1 outlier), 5% (2+ outliers), 14% (Not modelled)
4	AF	253	24% (0 outliers), 81% (1 outlier), 15% (2+ outliers), 5% (Not modelled)
5	AG	249	87% (0 outliers), 82% (1 outlier), 5% (2+ outliers), 13% (Not modelled)
6	AH	262	24% (0 outliers), 94% (1 outlier), 5% (2+ outliers), 5% (Not modelled)
7	AI	203	99% (0 outliers), 97% (1 outlier), 5% (2+ outliers), 5% (Not modelled)
8	AJ	239	90% (0 outliers), 89% (1 outlier), 8% (2+ outliers), 5% (Not modelled)

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Mol	Chain	Length	Quality of chain
9	AK	195	79% 93% 6%
10	AL	200	46% 92% 6%
11	AM	192	49% 89% 7%
12	AN	147	63% 62% 37%
13	AO	152	27% 90% 6%
14	AP	145	83% 78% 6% 17%
15	AQ	151	44% 97%
16	AR	139	53% 88% 8%
17	AS	154	77% 75% 23%
18	AT	140	99% 99%
19	AU	131	87% 85% 5% 10%
20	AV	152	93% 91% 7%
21	AW	144	99% 95%
22	Aa	118	85% 84% 14%
23	Ab	87	32% 94% 6%
24	Ac	130	98%
25	Ad	143	82% 96%
26	Ae	134	82% 96%
27	Af	89	78% 74% 22%
28	Ag	119	27% 77% 18%
29	Ah	83	67% 94%
30	Ai	68	88% 88% 7%
31	Aj	56	93% 93% 5%
32	Ak	61	98% 92% 7%
33	B0	106	8% 86% 12%



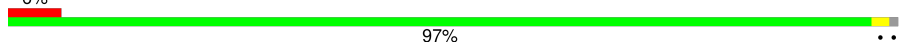
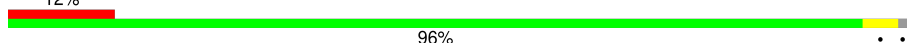
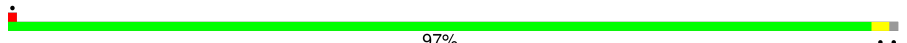
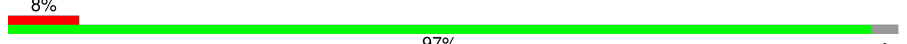


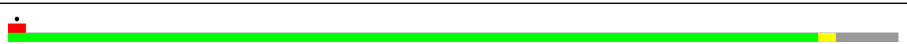

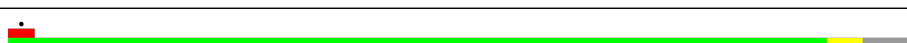

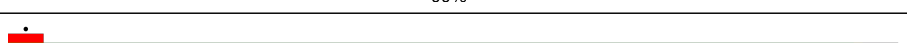
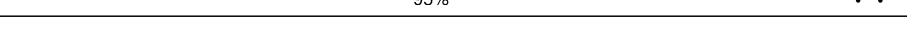
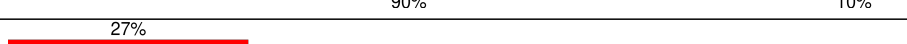
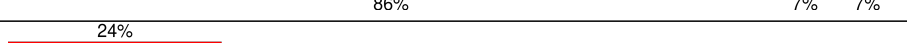
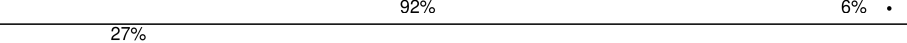
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Mol	Chain	Length	Quality of chain
34	B1	94	19% 96%
35	B2	3498	16% 73% 19% 8%
36	B3	246	41% 7% 52%
37	B4	165	7% 79% 16% 5%
38	BN	253	98%
39	BO	388	97%
40	BP	363	98%
41	BQ	294	20% 95%
42	BR	195	15% 81% 17%
43	BS	251	9% 92% 7%
44	BT	259	15% 86% 12%
45	BU	189	87% 86% 11%
46	BV	221	79% 83% 14%
47	BW	174	61% 89% 7%
48	BX	208	17% 99%
49	BY	134	7% 96%
50	BZ	201	97%
51	Ba	197	98%
52	Bb	187	78% 19%
53	Bc	187	98%
54	Bd	193	7% 79% 19%
55	Be	176	10% 98%
56	Bf	160	19% 98%
57	Bg	117	22% 82% 15%
58	Bh	139	7% 94%

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Mol	Chain	Length	Quality of chain
59	Bi	149	
60	Bj	141	
61	Bk	126	
62	Bl	136	
63	Bm	148	
64	Bn	61	
65	Bo	109	
66	Bp	113	
67	Bq	127	
68	Br	108	
69	Bs	111	
70	Bt	122	
71	Bu	99	
72	Bv	91	
73	Bw	74	
74	Bx	51	
75	By	134	

2 Entry composition

There are 76 unique types of molecules in this entry. The entry contains 194719 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	1705	36359	16255	6470	11929	1705	0	0

- Molecule 2 is a protein called Small ribosomal subunit protein uS2A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	AD	205	1602	1016	294	287	5	0	0

- Molecule 3 is a protein called Small ribosomal subunit protein eS1B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	AE	216	1733	1093	319	316	5	0	0

- Molecule 4 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	AF	216	1660	1072	289	292	7	0	0

- Molecule 5 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	AG	216	1701	1080	308	305	8	0	0

- Molecule 6 is a protein called Small ribosomal subunit protein eS4C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	AH	261	2083	1330	391	356	6	0	0

- Molecule 7 is a protein called Small ribosomal subunit protein uS7A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	AI	203	1559	972	291	290	6	0	0

- Molecule 8 is a protein called Small ribosomal subunit protein eS6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	AJ	221	1784	1123	352	302	7	0	0

- Molecule 9 is a protein called Small ribosomal subunit protein eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	AK	193	1530	967	284	276	3	0	0

- Molecule 10 is a protein called Small ribosomal subunit protein eS8B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	AL	188	1506	936	303	264	3	0	0

- Molecule 11 is a protein called Small ribosomal subunit protein uS4B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	AM	178	1462	928	291	241	2	0	0

- Molecule 12 is a protein called Small ribosomal subunit protein eS10B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	AN	92	748	484	132	130	2	0	0

- Molecule 13 is a protein called Small ribosomal subunit protein uS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	AO	143	1164	743	222	196	3	0	0

- Molecule 14 is a protein called Small ribosomal subunit protein eS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	AP	121	884	549	151	177	7	0	0

- Molecule 15 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	AQ	150	1184	754	222	204	4	0	0

- Molecule 16 is a protein called Small ribosomal subunit protein uS11B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	AR	128	949	587	184	174	4	0	0

- Molecule 17 is a protein called Small ribosomal subunit protein uS19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	AS	119	954	608	179	163	4	0	0

- Molecule 18 is a protein called Small ribosomal subunit protein uS9A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	AT	140	1082	688	203	186	5	0	0

- Molecule 19 is a protein called Small ribosomal subunit protein eS17A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	AU	118	972	606	185	179	2	0	0

- Molecule 20 is a protein called Small ribosomal subunit protein uS13B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	AV	141	1144	714	222	204	4	0	0

- Molecule 21 is a protein called Small ribosomal subunit protein eS19A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	AW	142	1119	699	212	205	3	0	0

- Molecule 22 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	Aa	101	815	511	156	146	2	0	0

- Molecule 23 is a protein called Small ribosomal subunit protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	Ab	87	672	411	122	135	4	0	0

- Molecule 24 is a protein called Small ribosomal subunit protein uS8A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Ac	129	1028	649	196	179	4	0	0

- Molecule 25 is a protein called Small ribosomal subunit protein uS12A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	Ad	142	1095	692	214	187	2	0	0

- Molecule 26 is a protein called Small ribosomal subunit protein eS24A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	Ae	133	1078	672	217	185	4	0	0

- Molecule 27 is a protein called Small ribosomal subunit protein eS25A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	Af	69	551	350	103	97	1	0	0

- Molecule 28 is a protein called Small ribosomal subunit protein eS26B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ag	97	Total	C	N	O	S	0	0
			795	491	167	132	5		

- Molecule 29 is a protein called Small ribosomal subunit protein eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ah	81	Total	C	N	O	S	0	0
			619	388	114	108	9		

- Molecule 30 is a protein called Small ribosomal subunit protein eS28A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ai	63	Total	C	N	O	S	0	0
			498	308	99	90	1		

- Molecule 31 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Aj	53	Total	C	N	O	S	0	0
			447	282	91	73	1		

- Molecule 32 is a protein called Small ribosomal subunit protein eS30B.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ak	60	Total	C	N	O	S	0	0
			475	296	99	78	2		

- Molecule 33 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	B0	93	Total	C	N	O	S	0	0
			758	479	152	122	5		

- Molecule 34 is a protein called Large ribosomal subunit protein eL43A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	B1	93	Total	C	N	O	S	0	0
			718	442	147	123	6		

- Molecule 35 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	B2	3212	68676	30687	12377	22400	3212	0	0

- Molecule 36 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	B3	119	2539	1133	454	833	119	0	0

- Molecule 37 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	B4	157	3332	1491	583	1101	157	0	0

- Molecule 38 is a protein called Large ribosomal subunit protein uL2C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	BN	248	1872	1166	377	324	5	0	0

- Molecule 39 is a protein called Large ribosomal subunit protein uL3A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	BO	384	3050	1929	576	535	10	0	0

- Molecule 40 is a protein called Large ribosomal subunit protein uL4A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
40	BP	362	2799	1768	538	490	3	0	0

- Molecule 41 is a protein called Large ribosomal subunit protein uL18B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
41	BQ	287	2312	1461	410	437	4	0	0

- Molecule 42 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
42	BR	162	1251	802	231	215	3	0	0

- Molecule 43 is a protein called Large ribosomal subunit protein uL30C.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	BS	233	1897	1211	349	334	3	0	0

- Molecule 44 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	BT	229	1772	1135	325	309	3	0	0

- Molecule 45 is a protein called Large ribosomal subunit protein uL6B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	BU	168	1319	828	244	242	5	0	0

- Molecule 46 is a protein called Large ribosomal subunit protein uL16A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
46	BV	191	1549	982	291	270	6	0	0

- Molecule 47 is a protein called Large ribosomal subunit protein uL5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	BW	167	1346	854	252	235	5	0	0

- Molecule 48 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
48	BX	207	1654	1034	329	290	1	0	0

- Molecule 49 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
49	BY	130	1038	662	198	174	4	0	0

- Molecule 50 is a protein called Large ribosomal subunit protein eL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
50	BZ	200	1676	1050	348	275	3	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein uL13A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
51	Ba	196	1545	991	294	256	4	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein uL22A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
52	Bb	152	1212	770	229	210	3	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein eL18B.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
53	Bc	186	1487	937	300	250	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein eL19B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
54	Bd	157	1301	809	275	212	5	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein eL20A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
55	Be	173	1423	916	268	234	5	0	0

- Molecule 56 is a protein called Large ribosomal subunit protein eL21B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
56	Bf	159	1286	810	247	226	3	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	Bg	99	798	518	138	142		0	0

- Molecule 58 is a protein called Large ribosomal subunit protein uL14B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
58	Bh	134	999	630	184	177	8	0	0

- Molecule 59 is a protein called Large ribosomal subunit protein eL24B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
59	Bi	63	523	336	102	82	3	0	0

- Molecule 60 is a protein called Large ribosomal subunit protein uL23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
60	Bj	118	947	605	175	166	1	0	0

- Molecule 61 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
61	Bk	125	998	622	201	173	2	0	0

- Molecule 62 is a protein called Large ribosomal subunit protein eL27A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
62	Bl	135	1078	698	200	178	2	0	0

- Molecule 63 is a protein called Large ribosomal subunit protein uL15B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
63	Bm	147	1171	740	235	194	2	0	0

- Molecule 64 is a protein called Large ribosomal subunit protein eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
64	Bn	59	495	299	112	84		0	0

- Molecule 65 is a protein called Large ribosomal subunit protein eL30A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	Bo	94	705	450	121	130	4	0	0

- Molecule 66 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
66	Bp	103	857	538	167	149	3	0	0

- Molecule 67 is a protein called Large ribosomal subunit protein eL32A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
67	Bq	118	944	591	191	157	5	0	0

- Molecule 68 is a protein called Large ribosomal subunit protein eL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
68	Br	104	831	531	160	137	3	0	0

- Molecule 69 is a protein called Large ribosomal subunit protein eL34B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
69	Bs	106	858	538	176	142	2	0	0

- Molecule 70 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
70	Bt	121	Total	C	N	O	0	0
			999	629	194	176		

- Molecule 71 is a protein called Large ribosomal subunit protein eL36B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Bu	95	Total	C	N	O	S	0	0
			759	472	159	127	1		

- Molecule 72 is a protein called Large ribosomal subunit protein eL37B.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bv	82	Total	C	N	O	S	0	0
			652	399	140	106	7		

- Molecule 73 is a protein called Large ribosomal subunit protein eL38A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bw	69	Total	C	N	O	S	0	0
			560	355	103	101	1		

- Molecule 74 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bx	50	Total	C	N	O	S	0	0
			436	273	98	64	1		

- Molecule 75 is a protein called Large ribosomal subunit protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	By	134	Total	C	N	O	S	0	0
			1039	646	204	187	2		

- Molecule 76 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
76	Ag	1	Total	Zn	0
			1	1	
76	Ah	1	Total	Zn	0
			1	1	
76	Aj	1	Total	Zn	0
			1	1	

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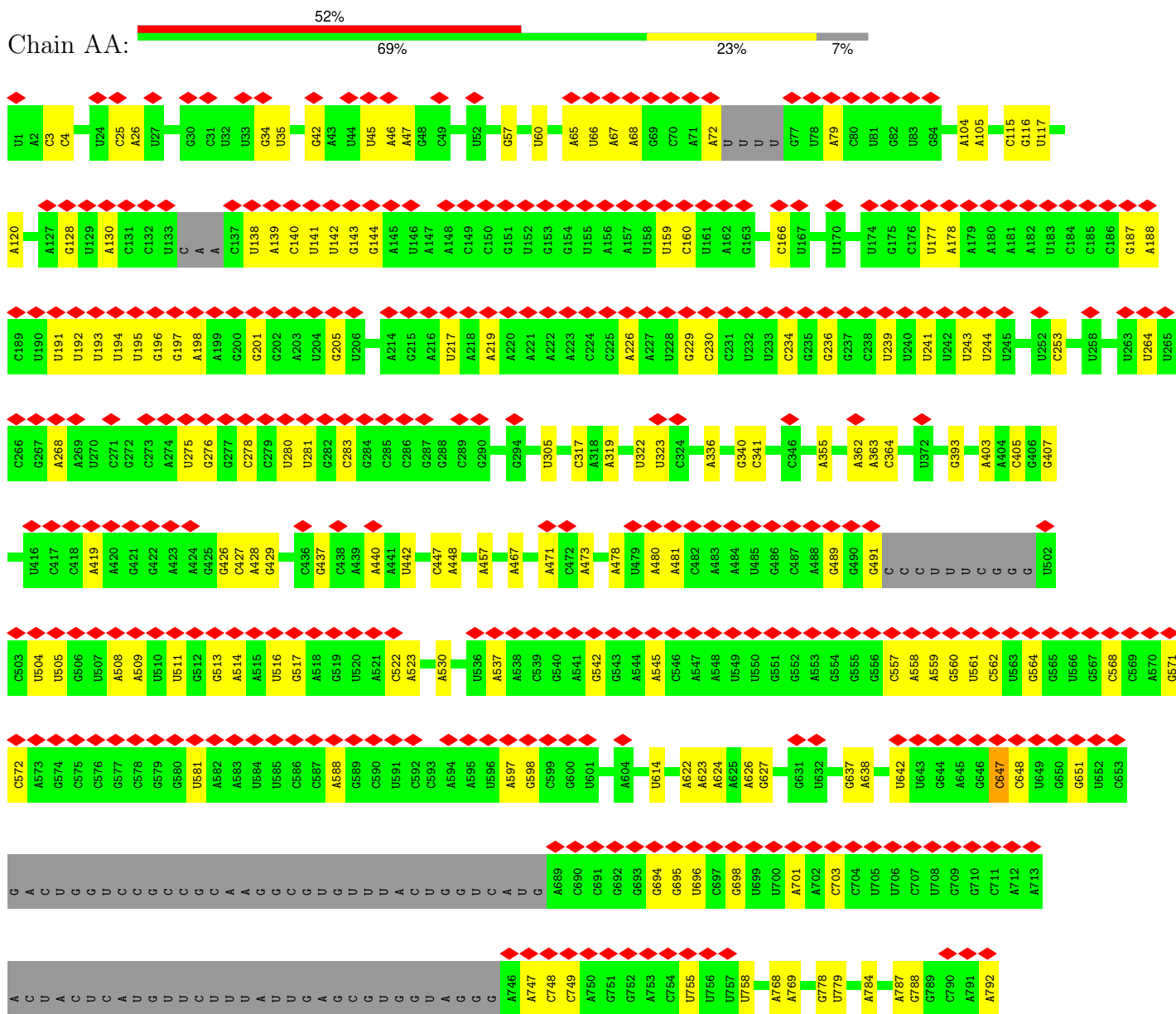
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Mol	Chain	Residues	Atoms		AltConf
76	B0	1	Total 1	Zn 1	0
76	B1	1	Total 1	Zn 1	0
76	Bv	1	Total 1	Zn 1	0

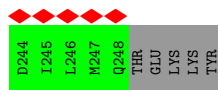
3 Residue-property plots i

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

- Molecule 1: 18S ribosomal RNA

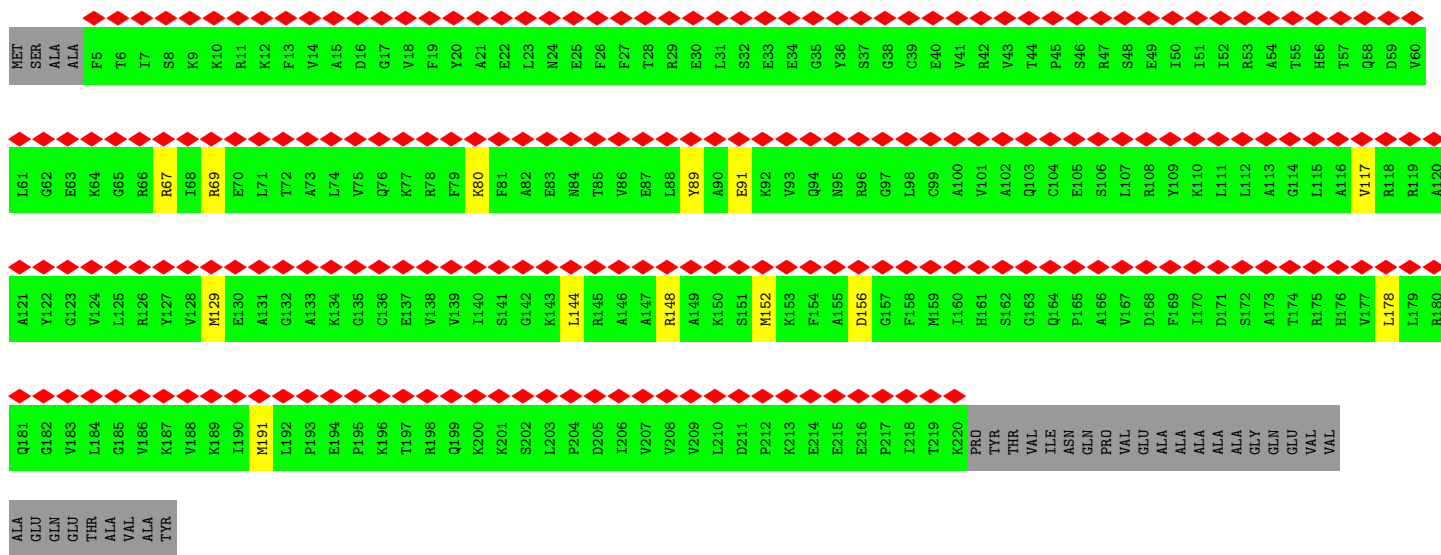


G	G1663	U1601	C1481	A1361	G1281	A1221	C1003	U802	G793
C	C1664	U1602	G1482	A1362	G1282	C1222	A1007	G802	U794
A	A1675	G1603	C1483	A1363	U1283	U1223	A1008	A803	U795
A	C1676	C1604	G1484	U1364	G1284	C1224	A1009	A804	U796
C	A1677	U1605	C1485	A1366	U1285	A1225	A1010	C807	U797
C	C1678	C1606	G1486	A1367	U1286	C1226	A1011	U808	U798
G	C1681	U1607	U1487	U1368	G1287	U1227	A1012	A807	G802
G	A1682	G1608	U1488	U1369	U1288	A1228	A1013	A808	A803
A	G1683	C1609	A1489	G1370	G1289	G1229	A1014	A809	A804
A	U1684	U1610	A1490	A1371	U1290	U1230	C1011	C807	C807
A	C1685	A1611	A1491	U1372	C1291	U1231	G1012	A808	A808
C	G1686	G1612	C1492	U1373	A1292	C1232	A1013	U809	U809
U	C1687	G1613	U1493	C1373	U1293	U1233	U1014	U810	U810
U	U1688	A1614	U1494	A1374	G1294	A1234	A1176	U823	U823
U	A1689	G1615	A1495	G1375	G1295	G1235	A1177	A824	A824
U	C1690	G1616	C1496	C1376	U1296	A1236	A1178	A825	A825
U	U1691	A1617	A1497	C1377	C1297	C1237	U1179	A826	A826
U	G1692	A1618	G1498	A1378	G1298	A1238	U1180	A827	A827
U	C1693	U1619	A1499	U1379	U1299	U1239	U1019	A828	A828
U	A1694	U1620	G1500	U1380	U1300	A1240	A1020	A829	A829
U	G1695	C1621	C1501	U1381	C1301	G1241	U1027	A830	A830
U	A1696	U1622	A1503	U1382	U1302	U1242	A1028	G831	G831
U	U1697	G1623	A1504	G1383	U1303	A1243	C1036	A832	A832
U	U1698	A1624	U1505	A1384	A1304	G1244	A1041	C833	C833
U	G1699	C1625	G1506	C1385	G1305	A1245	A1042	G834	G834
U	A1700	U1626	A1507	G1386	G1308	U1247	C1043	U835	U835
U	U1701	A1627	A1508	G1387	U1322	U1248	A1054	G836	G836
U	U1702	C1628	G1509	A1388	C1323	U1249	U1067	U837	U837
U	G1703	U1629	U1510	U1389	U1324	U1250	U1068	G838	G838
U	U1704	G1631	G	U1390	G1325	A1251	U1069	G839	G839
U	C1705	C1632	A	A1391	C1326	C1252	U1070	U841	U841
U	U1706	A1633	A	U1392	U1327	A1253	C1072	C842	C842
U	U1707	U1636	A	U1393	U1328	G1254	A	A844	A844
U	C1708	C1637	A	G1394	A1329	A1255	U	U845	U845
U	U1709	A1638	A	U1395	U1330	U1256	U	U846	U846
U	U1710	C1639	C	C1396	A1331	U1257	A	U847	U847
U	U1711	U1640	U	U1397	U1332	G1258	U1078	U848	U848
U	U1719	A1641	U	C1398	G1333	A1259	C1079	U849	U849
U	G1720	G1642	U	U1399	C1334	G1260	A	U850	U850
U	C1721	C1643	U	C1400	G1335	A1261	U	G852	G852
U	A1722	U1644	U	U1401	A1336	U1262	U	G853	G853
U	U1723	G1645	G	U1402	A1337	C1263	U	U854	U854
U	U1724	U1646	A	G1403	U1338	U1264	U	U855	U855
U	G1725	C1647	U	A1404	A1338	U1265	U	U856	U856
U	C1727	U1650	U	G1405	A1342	U1266	U	C957	C957
U	U	G1651	U	U1406	C1349	U1267	U	U858	U858
U	U	A1652	U	G1407	C1350	U1268	U	U859	U859
U	U	C1653	U	A1408	U1351	C1269	U	G860	G860
U	U	A1654	U	C1409	U1352	U1271	U	G861	G861
U	U	U1655	U	A1411	A1353	C1272	U	A862	A862
U	U	U1656	U	U1412	A1354	A1273	U	G863	G863
U	U	A1657	U	U1413	C1355	U1274	U	G864	G864
U	U	U1658	U	G1414	G1356	U1275	U	G865	G865
U	U	G1659	U	U1415	U1357	C1276	U	C966	C966
U	U	C1660	U	C1416	G1358	U1277	U		
U	U	U1661	U	U1417	C1359	A1278	U		
U	U	U1662	U	A1418	U1360	U1279	U		
U	U		U	A1419			U		
U	U		U	A1420			U		



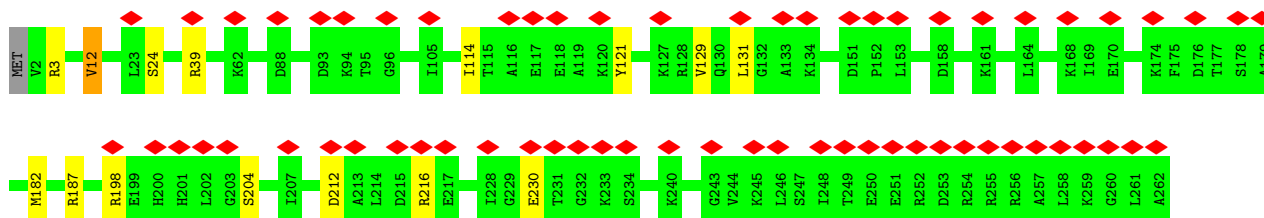
- Molecule 5: Small ribosomal subunit protein uS3

Chain AG:



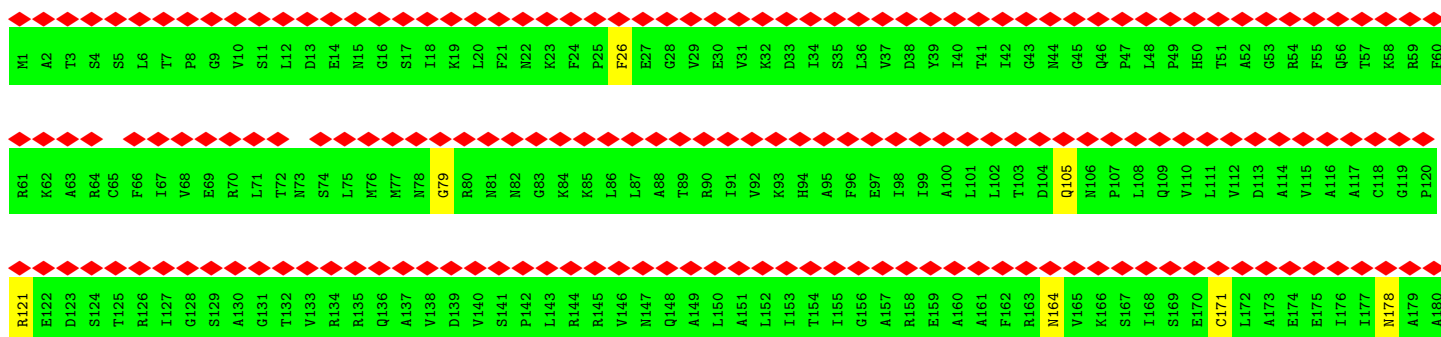
- Molecule 6: Small ribosomal subunit protein eS4C

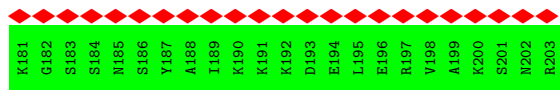
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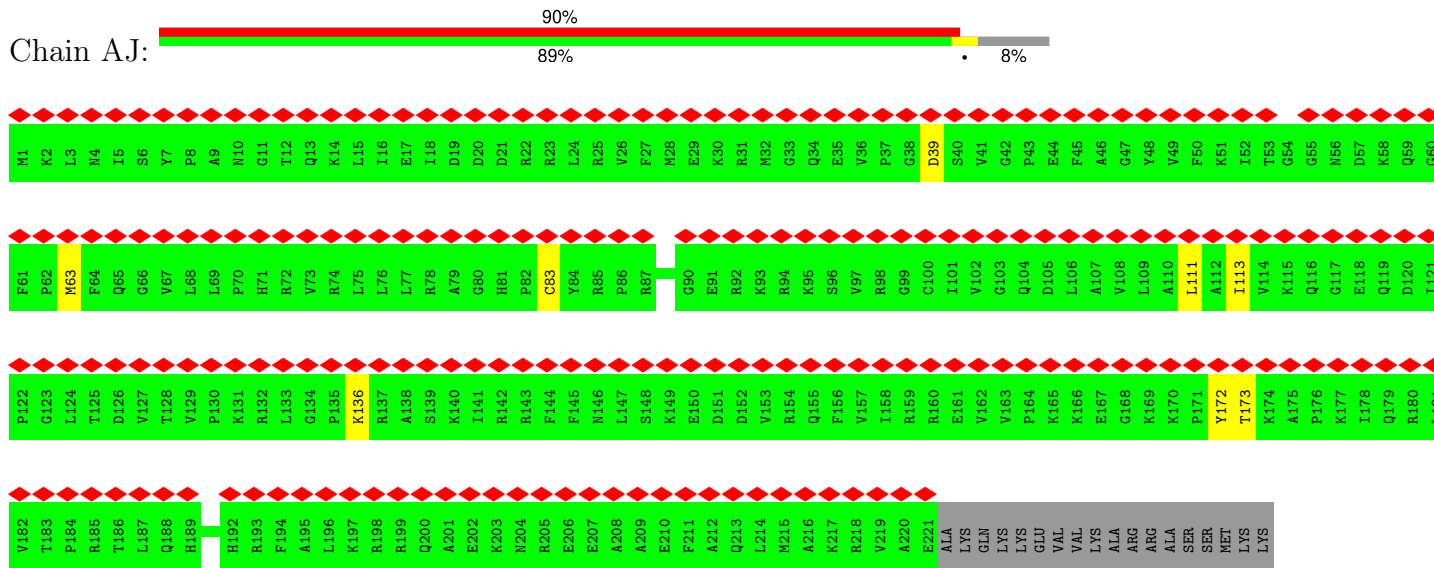
- Molecule 7: Small ribosomal subunit protein uS7A

Chain AI:

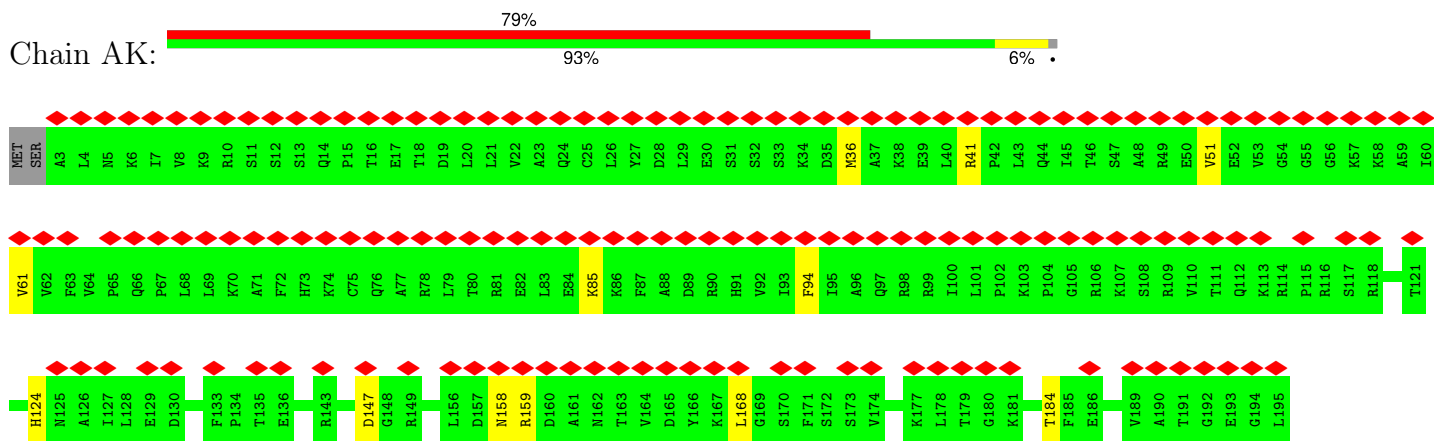




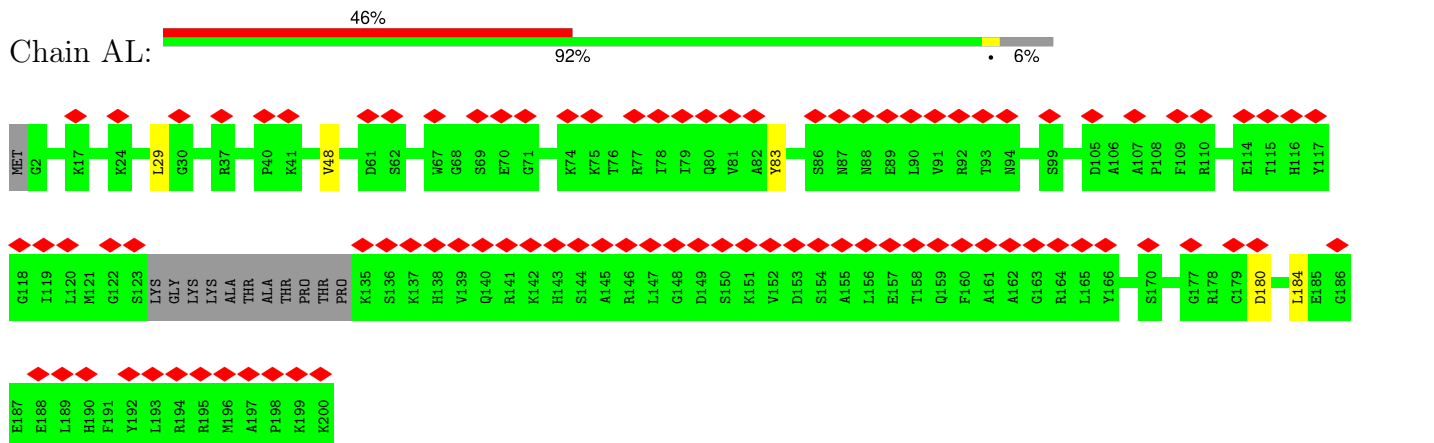
• Molecule 8: Small ribosomal subunit protein eS6B

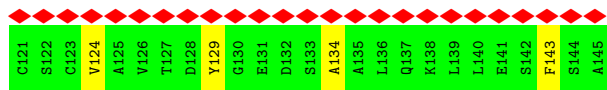


• Molecule 9: Small ribosomal subunit protein eS7

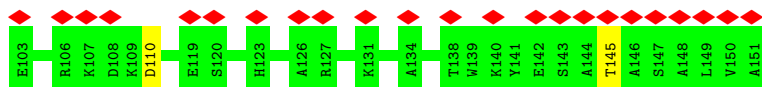
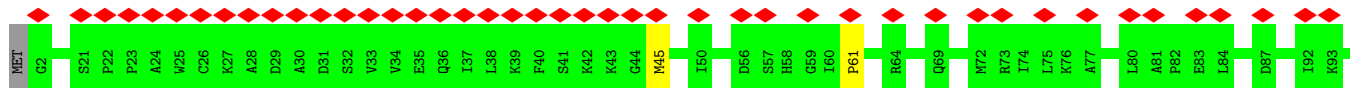


• Molecule 10: Small ribosomal subunit protein eS8B

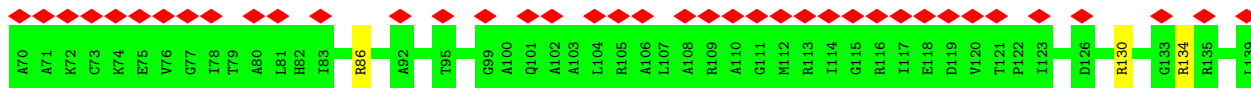
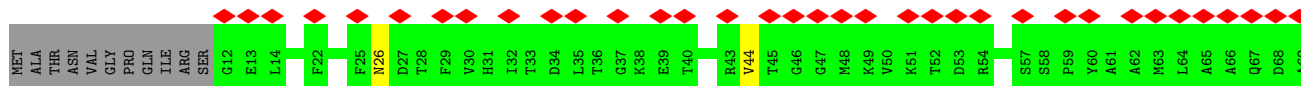
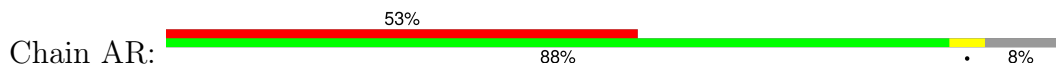




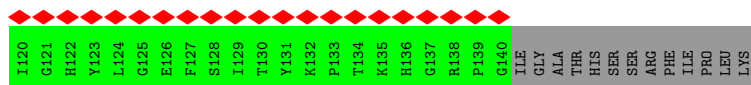
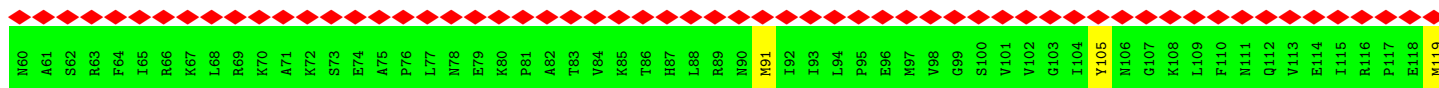
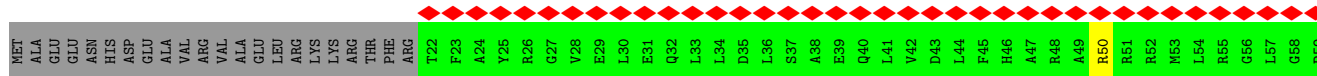
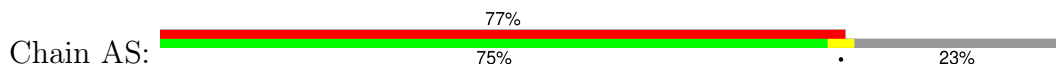
• Molecule 15: Small ribosomal subunit protein uS15



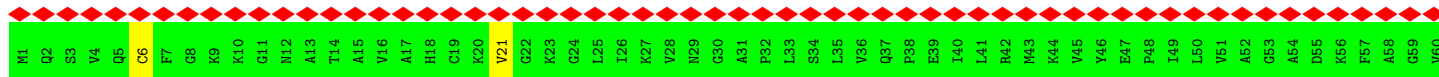
• Molecule 16: Small ribosomal subunit protein uS11B

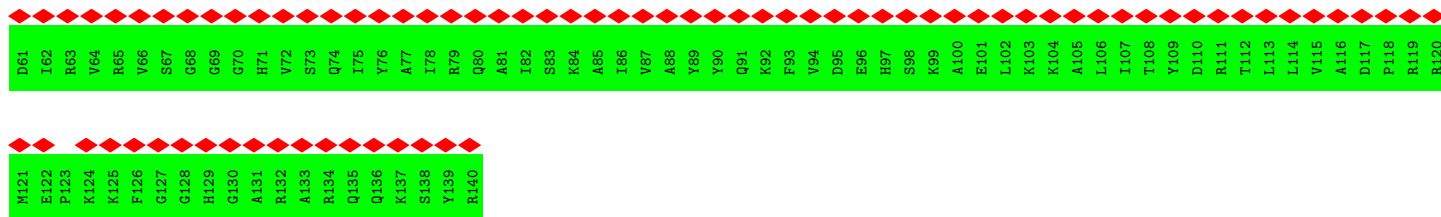


• Molecule 17: Small ribosomal subunit protein uS19B

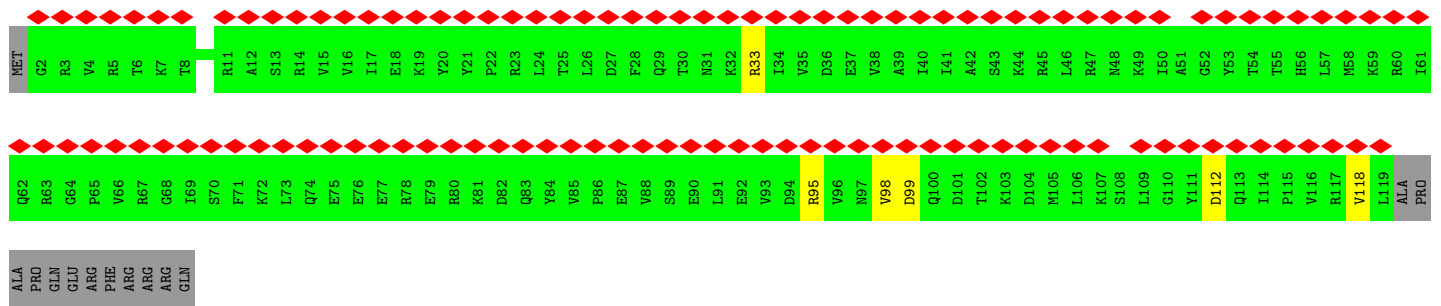
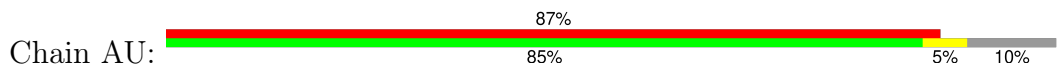


• Molecule 18: Small ribosomal subunit protein uS9A

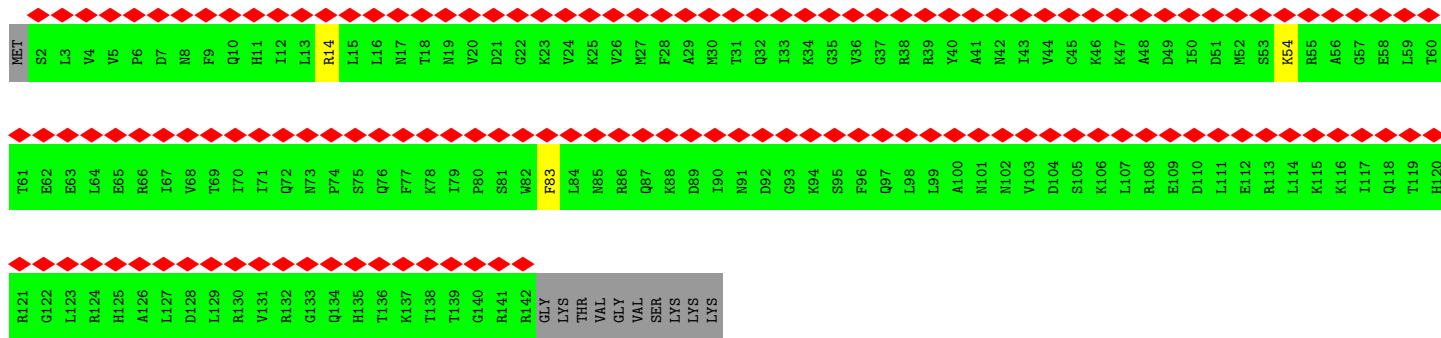
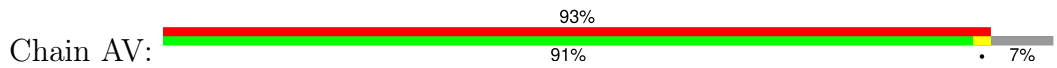




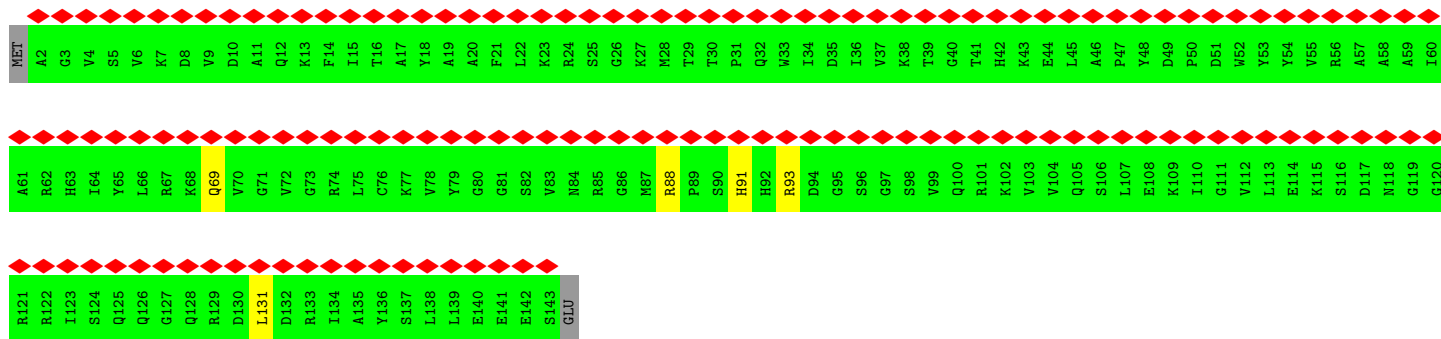
• Molecule 19: Small ribosomal subunit protein eS17A



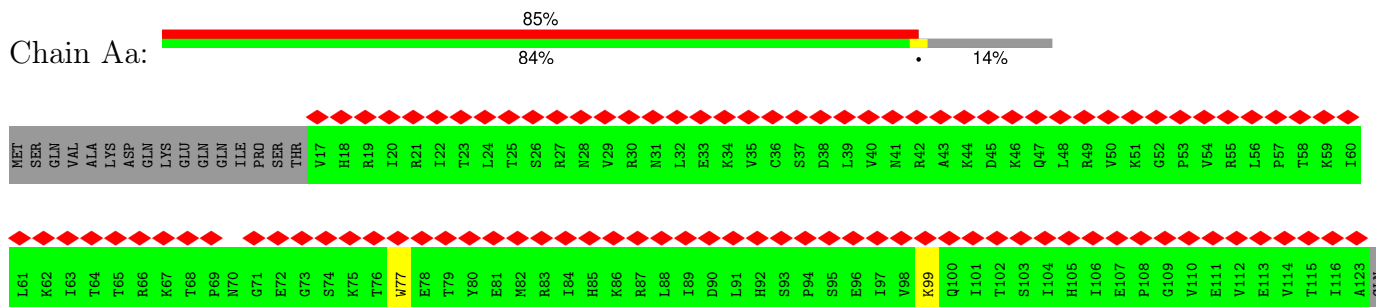
• Molecule 20: Small ribosomal subunit protein uS13B



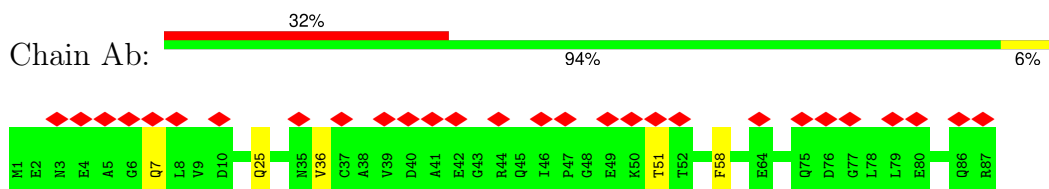
• Molecule 21: Small ribosomal subunit protein eS19A



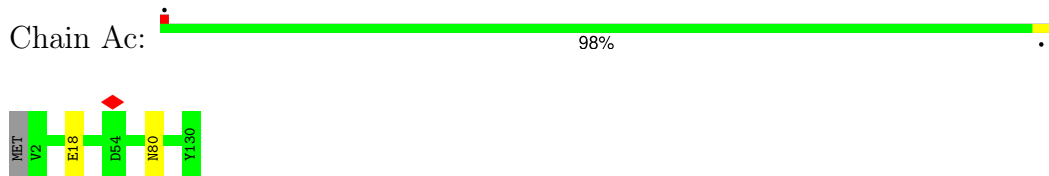
• Molecule 22: Small ribosomal subunit protein uS10



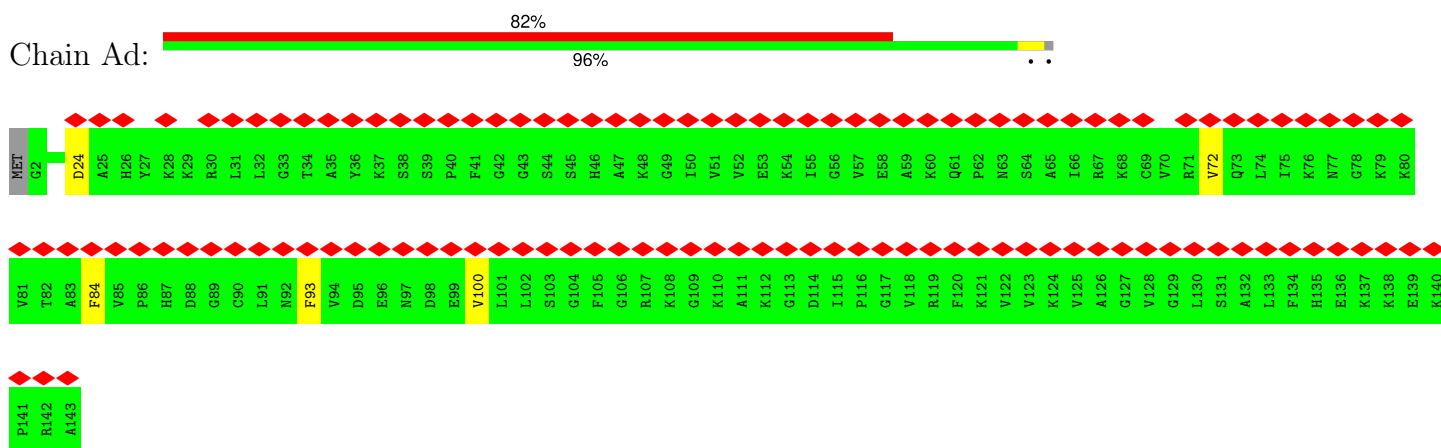
• Molecule 23: Small ribosomal subunit protein eS21



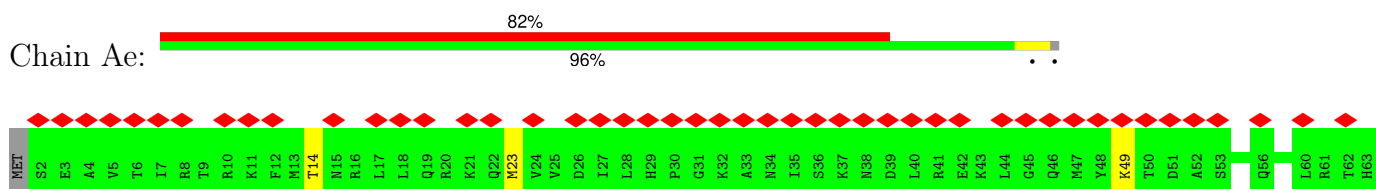
• Molecule 24: Small ribosomal subunit protein uS8A

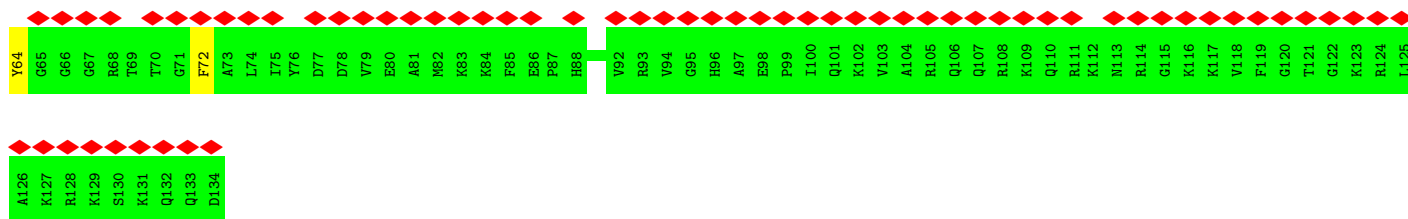


• Molecule 25: Small ribosomal subunit protein uS12A

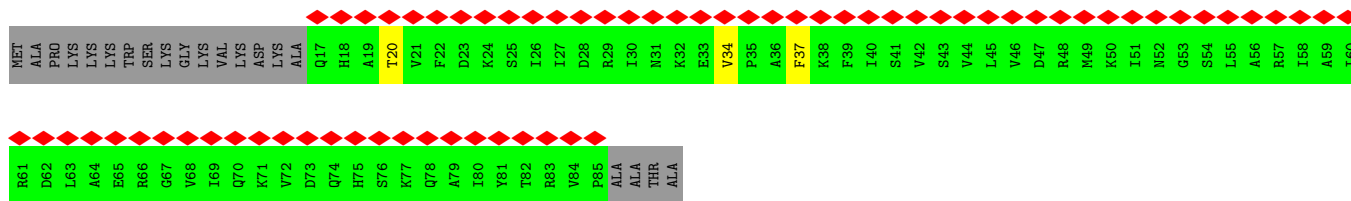
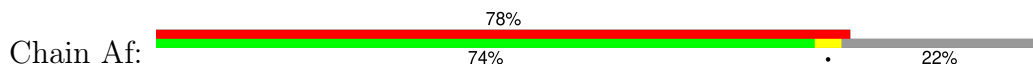


• Molecule 26: Small ribosomal subunit protein eS24A

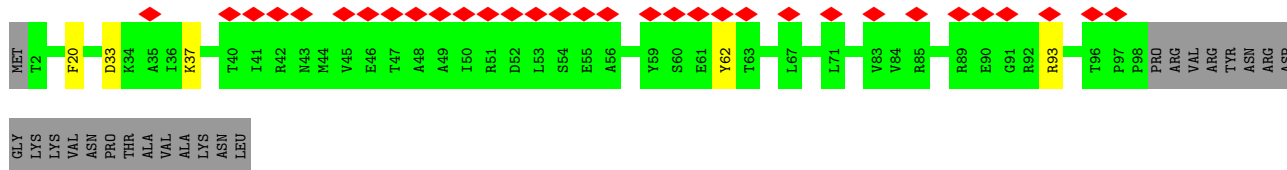
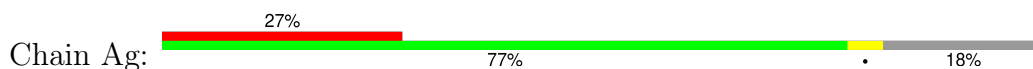




• Molecule 27: Small ribosomal subunit protein eS25A



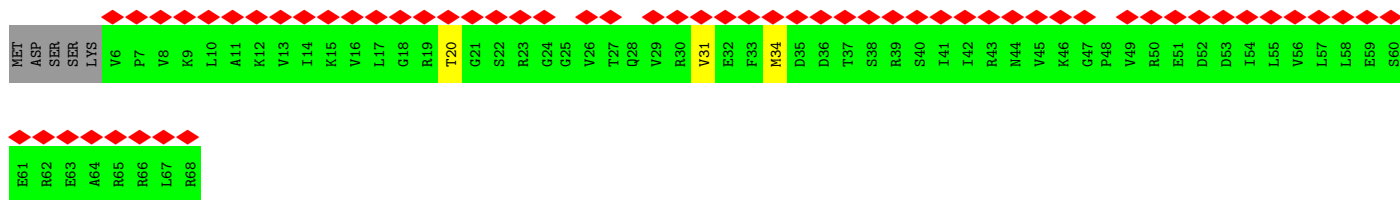
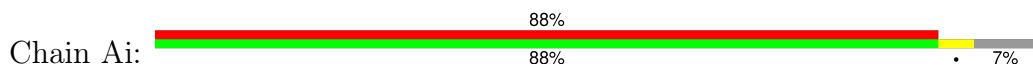
• Molecule 28: Small ribosomal subunit protein eS26B



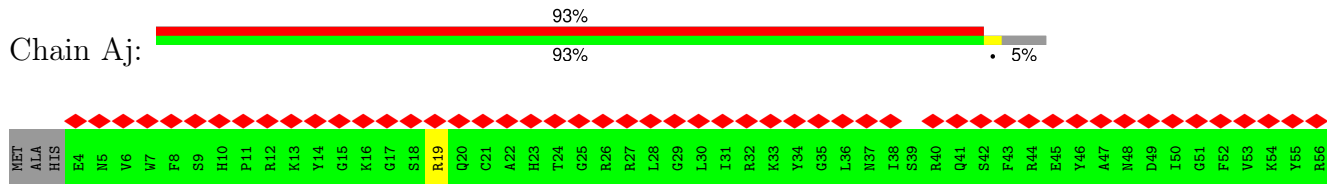
• Molecule 29: Small ribosomal subunit protein eS27



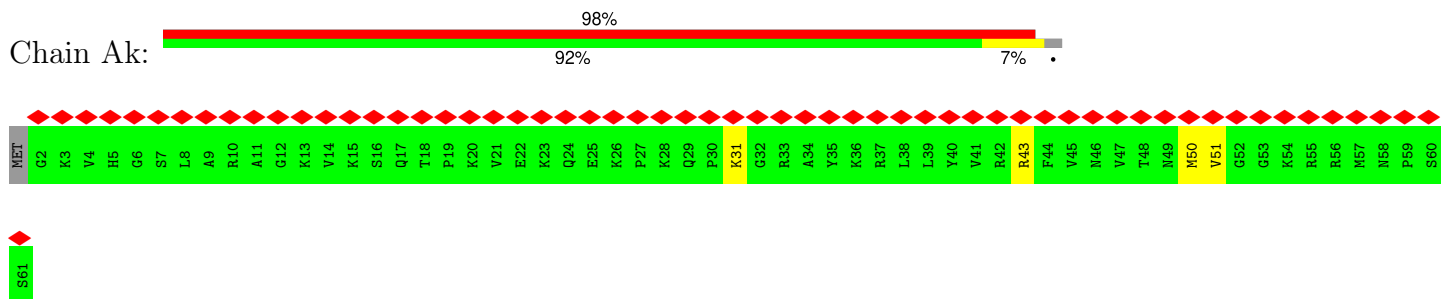
• Molecule 30: Small ribosomal subunit protein eS28A



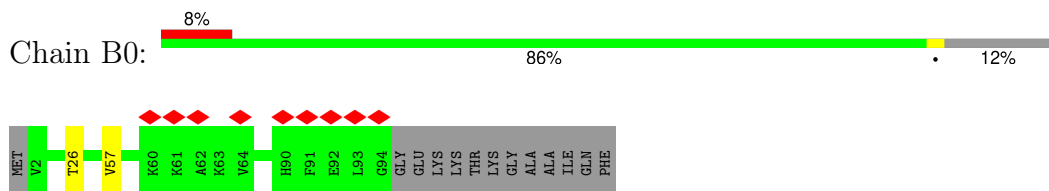
- Molecule 31: Small ribosomal subunit protein uS14



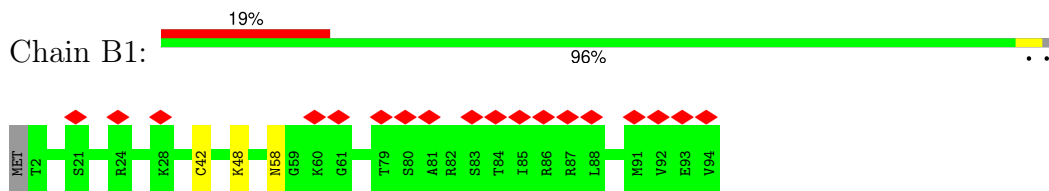
- Molecule 32: Small ribosomal subunit protein eS30B



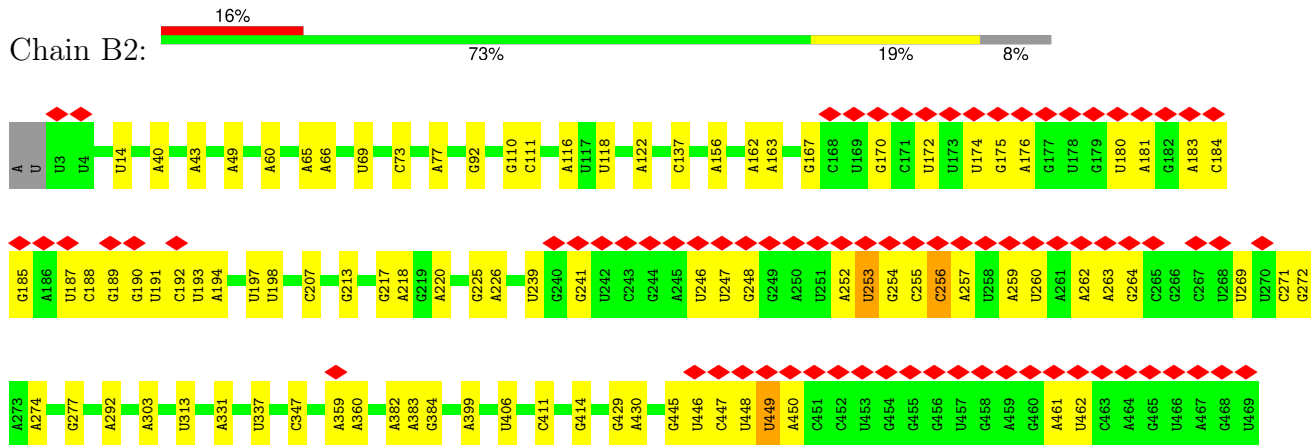
- Molecule 33: Large ribosomal subunit protein eL42

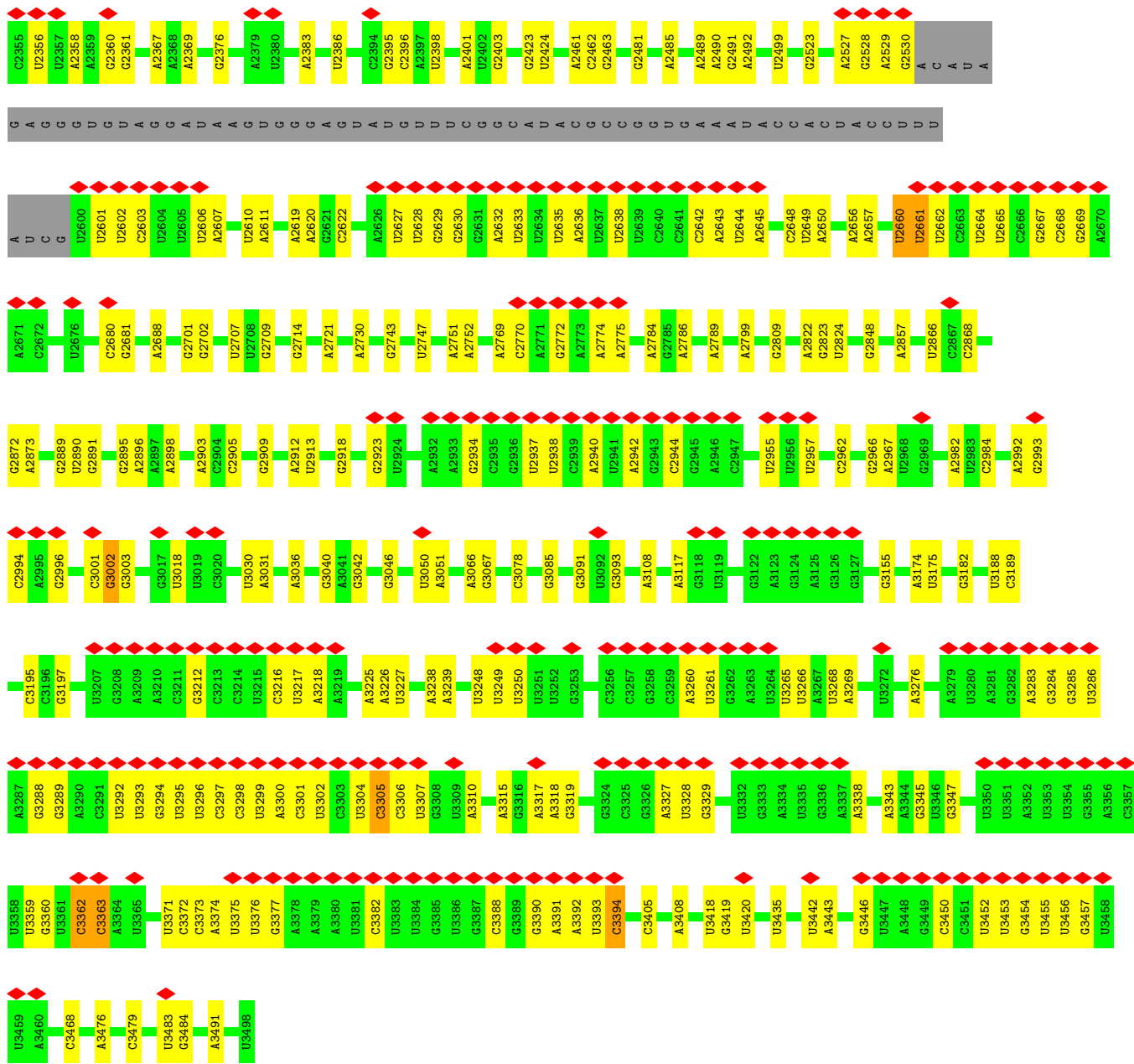


- Molecule 34: Large ribosomal subunit protein eL43A

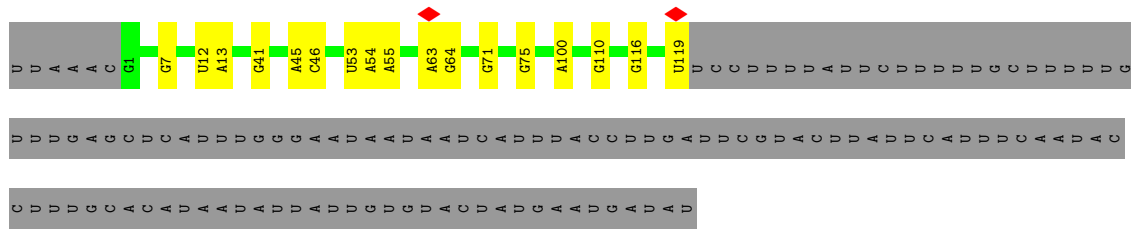
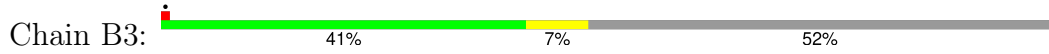


- Molecule 35: 28S ribosomal RNA




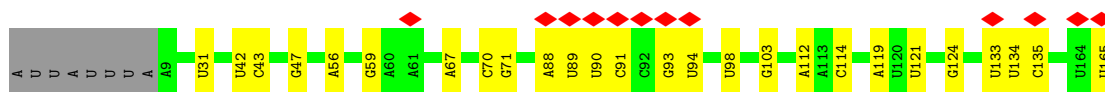


• Molecule 36: 5S ribosomal RNA



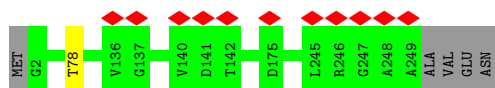
• Molecule 37: 5.8S ribosomal RNA

Chain B4: 



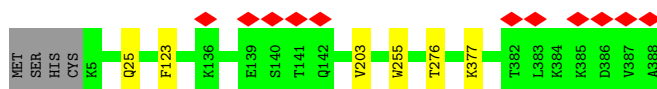
- Molecule 38: Large ribosomal subunit protein uL2C

Chain BN: 



- Molecule 39: Large ribosomal subunit protein uL3A

Chain BO: 



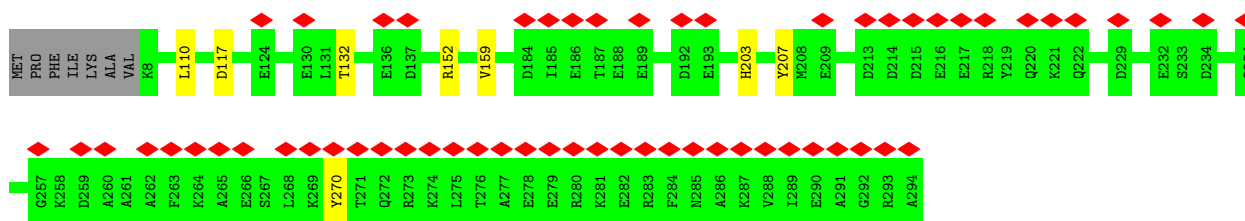
- Molecule 40: Large ribosomal subunit protein uL4A

Chain BP: 




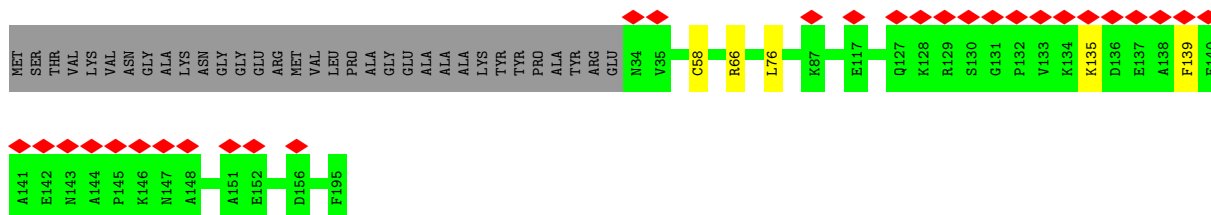
- Molecule 41: Large ribosomal subunit protein uL18B

Chain BQ: 

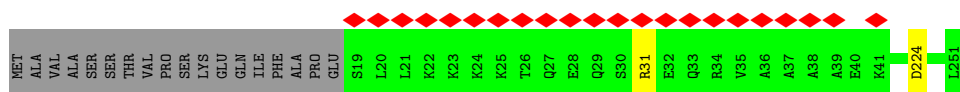


- Molecule 42: Large ribosomal subunit protein eL6

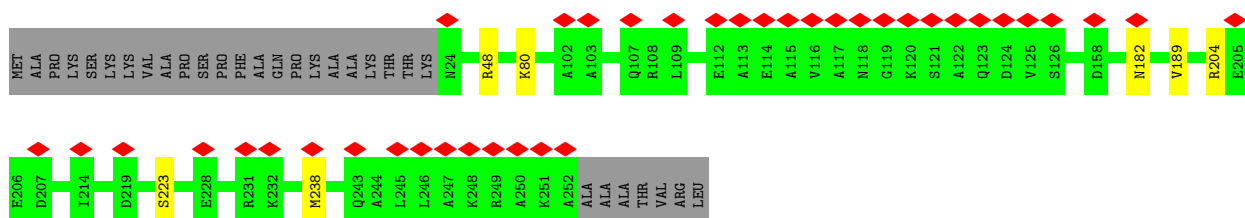
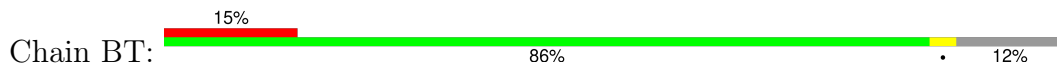
Chain BR: 



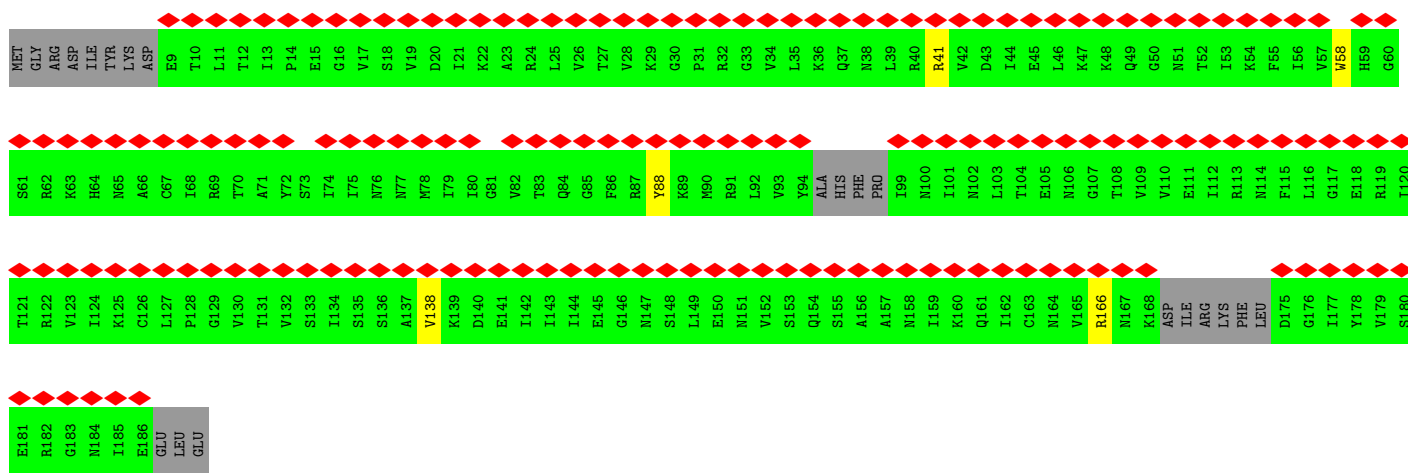
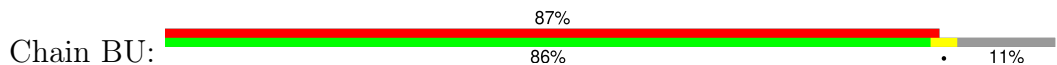
• Molecule 43: Large ribosomal subunit protein uL30C



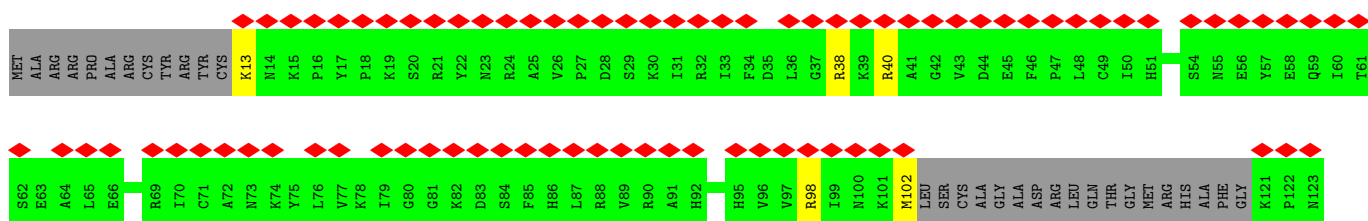
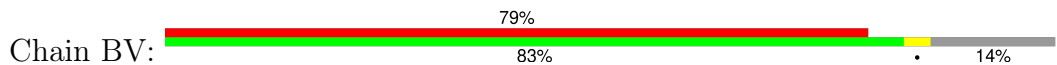
• Molecule 44: Large ribosomal subunit protein eL8

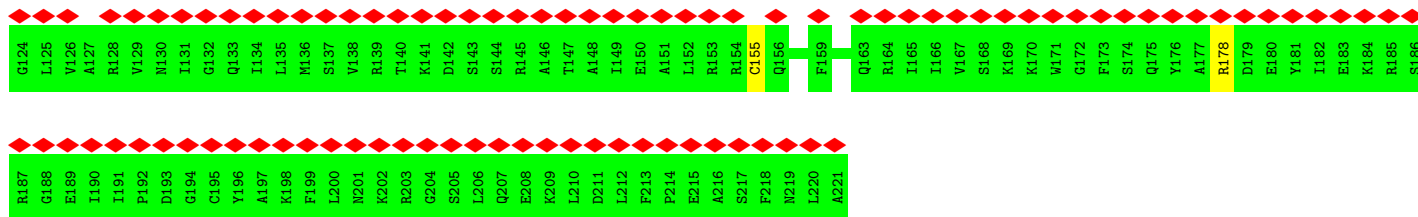


• Molecule 45: Large ribosomal subunit protein uL6B

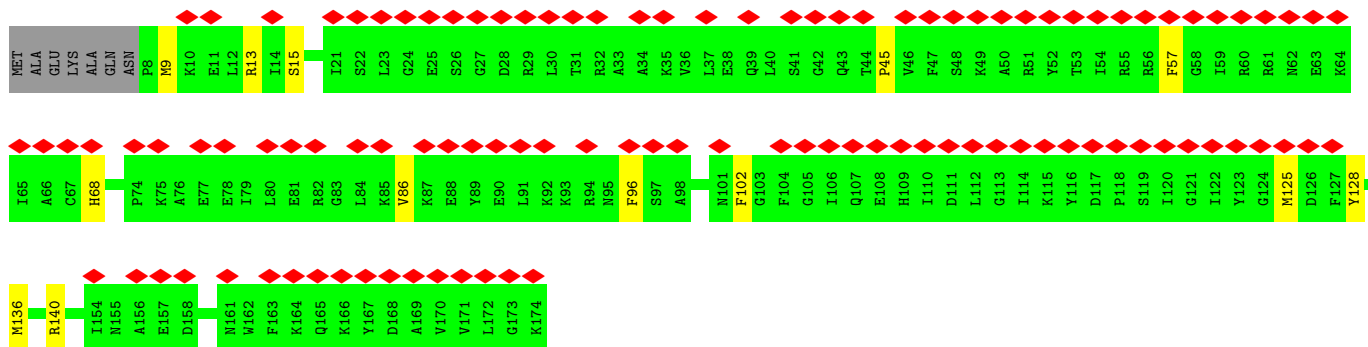
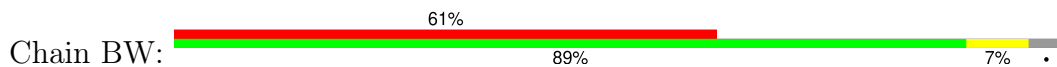


• Molecule 46: Large ribosomal subunit protein uL16A

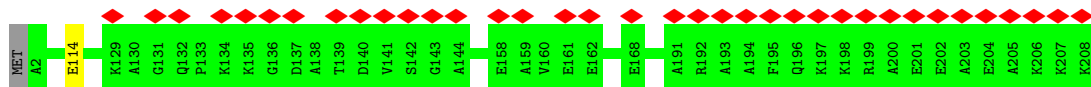




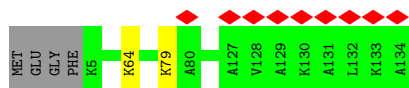
• Molecule 47: Large ribosomal subunit protein uL5A



• Molecule 48: Large ribosomal subunit protein eL13



• Molecule 49: Large ribosomal subunit protein eL14



• Molecule 50: Large ribosomal subunit protein eL15B

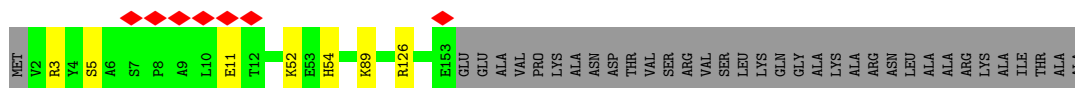
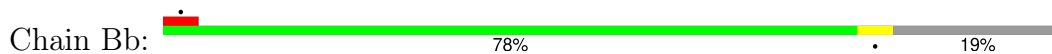


• Molecule 51: Large ribosomal subunit protein uL13A





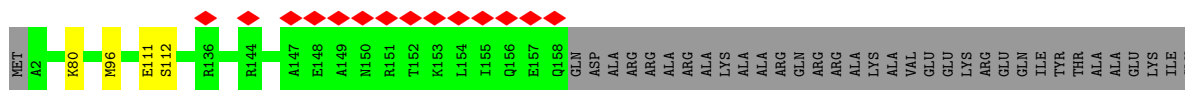
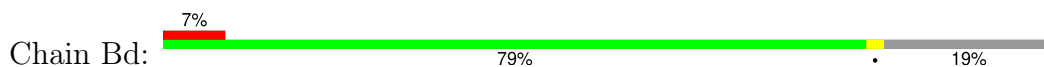
- Molecule 52: Large ribosomal subunit protein uL22A



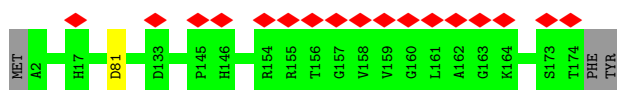
- Molecule 53: Large ribosomal subunit protein eL18B



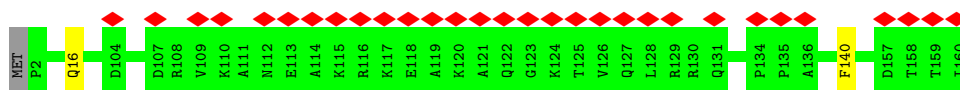
- Molecule 54: Large ribosomal subunit protein eL19B



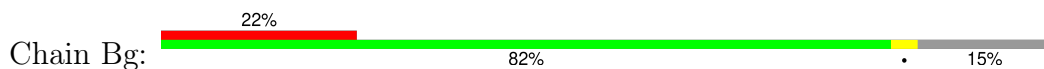
- Molecule 55: Large ribosomal subunit protein eL20A

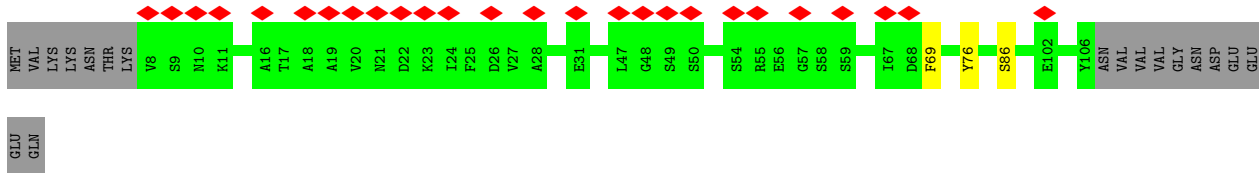


- Molecule 56: Large ribosomal subunit protein eL21B



- Molecule 57: Large ribosomal subunit protein eL22

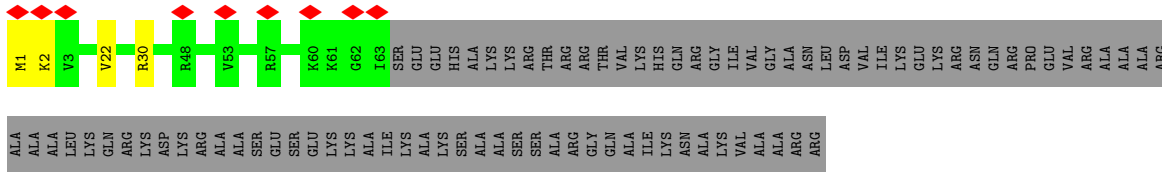




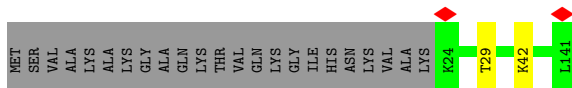
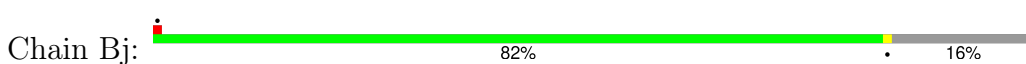
● Molecule 58: Large ribosomal subunit protein uL14B



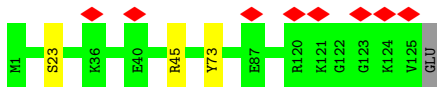
● Molecule 59: Large ribosomal subunit protein eL24B



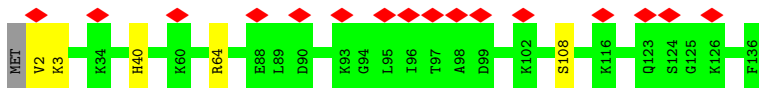
● Molecule 60: Large ribosomal subunit protein uL23A



● Molecule 61: Large ribosomal subunit protein uL24



● Molecule 62: Large ribosomal subunit protein eL27A

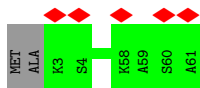


● Molecule 63: Large ribosomal subunit protein uL15B

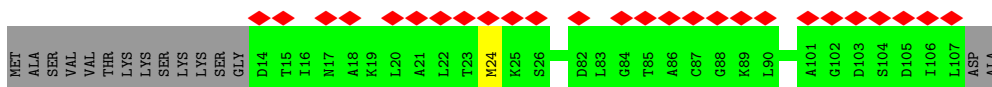
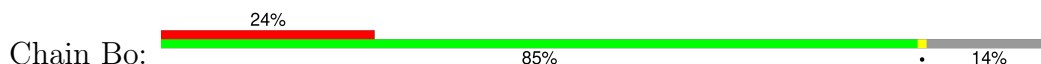




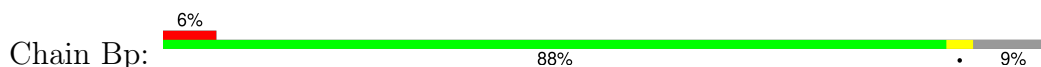
- Molecule 64: Large ribosomal subunit protein eL29



- Molecule 65: Large ribosomal subunit protein eL30A



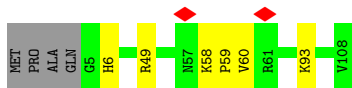
- Molecule 66: Large ribosomal subunit protein eL31



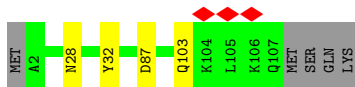
- Molecule 67: Large ribosomal subunit protein eL32A



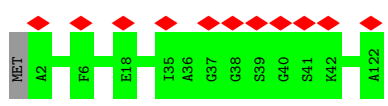
- Molecule 68: Large ribosomal subunit protein eL33A



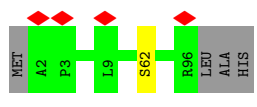
- Molecule 69: Large ribosomal subunit protein eL34B



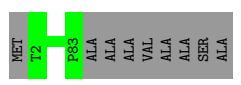
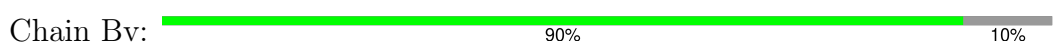
- Molecule 70: Large ribosomal subunit protein uL29



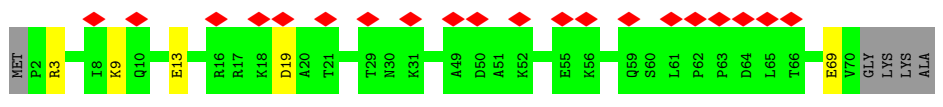
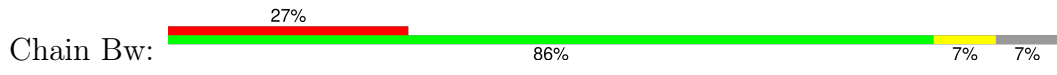
• Molecule 71: Large ribosomal subunit protein eL36B



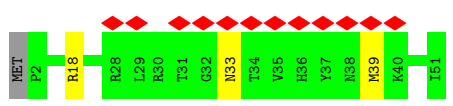
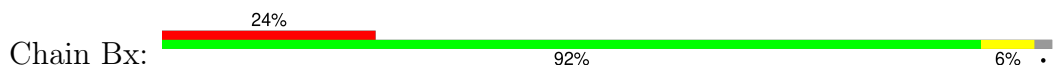
• Molecule 72: Large ribosomal subunit protein eL37B



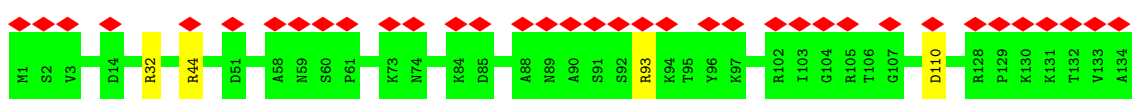
• Molecule 73: Large ribosomal subunit protein eL38A



• Molecule 74: Large ribosomal subunit protein eL39



• Molecule 75: Large ribosomal subunit protein eL28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73376	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1600	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.236	Depositor
Minimum map value	-1.145	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.26	Depositor
Map size (\AA)	424.96, 424.96, 424.96	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.83, 0.83, 0.83	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.17	0/40661	0.77	22/63326 (0.0%)
2	AD	0.25	0/1635	0.53	0/2228
3	AE	0.24	0/1756	0.52	0/2358
4	AF	0.26	0/1695	0.51	1/2297 (0.0%)
5	AG	0.24	0/1726	0.51	0/2316
6	AH	0.25	0/2125	0.55	0/2858
7	AI	0.24	0/1577	0.49	0/2123
8	AJ	0.25	0/1815	0.56	0/2428
9	AK	0.25	0/1554	0.54	0/2091
10	AL	0.24	0/1534	0.55	0/2050
11	AM	0.25	0/1487	0.58	0/1990
12	AN	0.24	0/769	0.48	0/1043
13	AO	0.24	0/1190	0.52	0/1602
14	AP	0.23	0/892	0.48	0/1208
15	AQ	0.83	2/1208 (0.2%)	1.04	5/1624 (0.3%)
16	AR	0.25	0/961	0.56	0/1293
17	AS	0.25	0/973	0.56	0/1307
18	AT	0.24	0/1100	0.49	0/1474
19	AU	0.23	0/983	0.55	0/1318
20	AV	0.23	0/1158	0.51	0/1552
21	AW	0.23	0/1139	0.47	0/1531
22	Aa	0.22	0/826	0.53	0/1114
23	Ab	0.23	0/680	0.49	0/918
24	Ac	0.23	0/1042	0.49	0/1399
25	Ad	0.25	0/1115	0.52	0/1489
26	Ae	0.24	0/1093	0.54	0/1453
27	Af	0.23	0/558	0.55	0/750
28	Ag	0.23	0/808	0.57	0/1083
29	Ah	0.41	1/630 (0.2%)	0.66	1/845 (0.1%)
30	Ai	0.24	0/500	0.63	0/669
31	Aj	0.24	0/458	0.56	0/610
32	Ak	0.23	0/482	0.55	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B0	0.24	0/772	0.51	0/1025
34	B1	0.23	0/727	0.58	0/973
35	B2	0.19	0/76871	0.79	41/119827 (0.0%)
36	B3	0.18	0/2838	0.77	0/4422
37	B4	0.18	0/3723	0.76	0/5796
38	BN	0.24	0/1910	0.54	0/2575
39	BO	0.24	0/3116	0.51	0/4190
40	BP	0.24	0/2852	0.49	0/3850
41	BQ	0.24	0/2361	0.50	0/3173
42	BR	0.25	0/1275	0.50	0/1719
43	BS	0.24	0/1929	0.47	0/2583
44	BT	0.24	0/1801	0.45	0/2430
45	BU	0.23	0/1330	0.50	0/1789
46	BV	0.24	0/1579	0.49	0/2115
47	BW	0.58	2/1369 (0.1%)	0.74	4/1830 (0.2%)
48	BX	0.24	0/1686	0.51	0/2267
49	BY	0.23	0/1054	0.48	0/1413
50	BZ	0.23	0/1717	0.54	0/2306
51	Ba	0.25	0/1575	0.48	0/2109
52	Bb	0.25	0/1237	0.49	0/1661
53	Bc	0.24	0/1511	0.55	0/2021
54	Bd	0.23	0/1320	0.51	0/1757
55	Be	0.25	0/1458	0.51	0/1961
56	Bf	0.24	0/1314	0.49	0/1771
57	Bg	0.24	0/812	0.48	0/1090
58	Bh	0.25	0/1015	0.52	0/1369
59	Bi	0.25	0/534	0.50	0/709
60	Bj	0.24	0/963	0.49	0/1296
61	Bk	0.23	0/1008	0.54	0/1341
62	Bl	0.24	0/1101	0.49	0/1477
63	Bm	0.23	0/1200	0.52	0/1611
64	Bn	0.23	0/503	0.51	0/664
65	Bo	0.25	0/714	0.52	0/961
66	Bp	0.23	0/872	0.52	0/1172
67	Bq	0.24	0/958	0.53	0/1278
68	Br	0.53	2/853 (0.2%)	1.03	3/1146 (0.3%)
69	Bs	0.25	0/870	0.56	0/1165
70	Bt	0.23	0/1008	0.49	0/1340
71	Bu	0.23	0/766	0.53	0/1017
72	Bv	0.24	0/666	0.56	0/881
73	Bw	0.26	0/566	0.54	0/757
74	Bx	0.23	0/447	0.58	0/597
75	By	0.23	0/1053	0.51	0/1414

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.23	7/209364 (0.0%)	0.70	77/307834 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	AQ	61	PRO	CG-CD	-24.71	0.69	1.50
47	BW	45	PRO	CG-CD	-18.24	0.90	1.50
68	Br	59	PRO	CB-CG	-11.28	0.93	1.50
15	AQ	61	PRO	CB-CG	11.14	2.05	1.50
29	Ah	10	PRO	CG-CD	-6.76	1.28	1.50
68	Br	59	PRO	CG-CD	-5.89	1.31	1.50
47	BW	45	PRO	N-CD	5.09	1.54	1.47

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AQ	61	PRO	N-CD-CG	-26.75	63.07	103.20
35	B2	3363	C	O5'-P-OP1	-24.73	81.02	110.70
15	AQ	61	PRO	CA-CB-CG	-19.05	67.80	104.00
68	Br	59	PRO	CB-CG-CD	18.84	179.98	106.50
47	BW	45	PRO	N-CD-CG	-17.52	76.92	103.20
68	Br	59	PRO	N-CD-CG	-17.04	77.63	103.20
35	B2	3363	C	OP1-P-OP2	16.66	144.59	119.60
68	Br	59	PRO	CA-CB-CG	-15.73	74.11	104.00
35	B2	3363	C	O5'-P-OP2	-15.27	91.95	105.70
35	B2	3362	C	OP1-P-O3'	-14.61	73.06	105.20
35	B2	3362	C	OP2-P-O3'	-12.79	77.07	105.20
15	AQ	61	PRO	N-CA-CB	-11.36	89.67	103.30
29	Ah	10	PRO	N-CD-CG	-10.37	87.65	103.20
47	BW	45	PRO	CA-CB-CG	-8.46	87.93	104.00
35	B2	1639	U	C2-N1-C1'	8.31	127.67	117.70
1	AA	1476	C	C2-N1-C1'	7.83	127.41	118.80
35	B2	1311	C	N3-C2-O2	-7.82	116.42	121.90
35	B2	1639	U	N1-C2-O2	7.71	128.20	122.80
1	AA	1476	C	N1-C2-O2	7.65	123.49	118.90
35	B2	3394	C	N1-C2-O2	7.59	123.46	118.90
1	AA	648	C	N3-C2-O2	-7.47	116.67	121.90
35	B2	3394	C	C2-N1-C1'	7.41	126.95	118.80
35	B2	1529	U	C2-N1-C1'	7.01	126.12	117.70
35	B2	1639	U	N3-C2-O2	-6.96	117.33	122.20
1	AA	749	C	N3-C2-O2	-6.94	117.04	121.90
47	BW	45	PRO	CA-N-CD	-6.93	101.80	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	AQ	61	PRO	CB-CG-CD	-6.89	79.64	106.50
35	B2	3002	G	C4-N9-C1'	6.68	135.19	126.50
1	AA	1409	C	C2-N1-C1'	6.66	126.12	118.80
1	AA	647	C	N1-C2-O2	6.56	122.83	118.90
1	AA	1555	U	C2-N1-C1'	6.49	125.49	117.70
35	B2	3305	C	N1-C2-O2	6.44	122.76	118.90
35	B2	3305	C	C2-N1-C1'	6.37	125.81	118.80
1	AA	1410	U	C2-N1-C1'	6.29	125.24	117.70
35	B2	137	C	C2-N1-C1'	6.21	125.64	118.80
35	B2	137	C	N1-C2-O2	6.20	122.62	118.90
35	B2	3002	G	C8-N9-C1'	-6.20	118.94	127.00
47	BW	45	PRO	N-CA-CB	-6.20	95.78	102.60
1	AA	1409	C	N1-C2-O2	6.20	122.62	118.90
1	AA	1476	C	N3-C2-O2	-6.16	117.59	121.90
15	AQ	61	PRO	CA-N-CD	-6.12	102.93	111.50
35	B2	256	C	C2-N1-C1'	6.09	125.50	118.80
35	B2	3002	G	N3-C4-N9	6.07	129.64	126.00
35	B2	3394	C	N3-C2-O2	-6.04	117.67	121.90
35	B2	1311	C	N1-C2-O2	6.03	122.52	118.90
35	B2	760	C	C2-N1-C1'	5.97	125.37	118.80
1	AA	1555	U	N1-C2-O2	5.69	126.78	122.80
4	AF	219	LEU	CA-CB-CG	5.68	128.36	115.30
35	B2	2660	U	C2-N1-C1'	5.65	124.48	117.70
35	B2	1639	U	C6-N1-C1'	-5.52	113.48	121.20
1	AA	695	G	N1-C2-N2	-5.50	111.25	116.20
35	B2	1529	U	N1-C2-O2	5.43	126.60	122.80
35	B2	2660	U	N1-C2-O2	5.40	126.58	122.80
1	AA	1476	C	C6-N1-C1'	-5.37	114.36	120.80
35	B2	2661	U	C2-N1-C1'	5.37	124.14	117.70
1	AA	1263	C	C2-N1-C1'	5.36	124.69	118.80
35	B2	137	C	N3-C2-O2	-5.35	118.16	121.90
1	AA	1410	U	N1-C2-O2	5.33	126.53	122.80
35	B2	3305	C	N3-C2-O2	-5.29	118.19	121.90
1	AA	695	G	N3-C2-N2	5.29	123.60	119.90
1	AA	1476	C	C6-N1-C2	-5.22	118.21	120.30
35	B2	1063	C	N1-C2-O2	5.17	122.00	118.90
1	AA	1555	U	N3-C2-O2	-5.17	118.58	122.20
35	B2	414	G	O4'-C1'-N9	5.17	112.33	108.20
1	AA	1409	C	N3-C2-O2	-5.16	118.29	121.90
1	AA	980	U	C2-N1-C1'	5.16	123.89	117.70
35	B2	253	U	N1-C2-O2	5.16	126.41	122.80
35	B2	583	C	N1-C2-O2	5.15	121.99	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B2	2660	U	N3-C2-O2	-5.14	118.60	122.20
35	B2	1529	U	N3-C2-O2	-5.13	118.61	122.20
35	B2	1062	U	C2-N1-C1'	5.12	123.85	117.70
35	B2	3394	C	C6-N1-C2	-5.08	118.27	120.30
35	B2	3394	C	C6-N1-C1'	-5.05	114.73	120.80
1	AA	1242	U	C2-N1-C1'	5.05	123.76	117.70
35	B2	449	U	N1-C2-O2	5.05	126.34	122.80
1	AA	1263	C	N1-C2-O2	5.03	121.92	118.90
35	B2	253	U	C2-N1-C1'	5.00	123.70	117.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AD	203/292 (70%)	183 (90%)	20 (10%)	0	100	100
3	AE	214/252 (85%)	197 (92%)	16 (8%)	1 (0%)	25	38
4	AF	214/253 (85%)	205 (96%)	8 (4%)	1 (0%)	25	38
5	AG	214/249 (86%)	201 (94%)	13 (6%)	0	100	100
6	AH	259/262 (99%)	249 (96%)	9 (4%)	1 (0%)	30	44
7	AI	201/203 (99%)	187 (93%)	13 (6%)	1 (0%)	25	38
8	AJ	219/239 (92%)	210 (96%)	9 (4%)	0	100	100
9	AK	191/195 (98%)	181 (95%)	10 (5%)	0	100	100
10	AL	184/200 (92%)	179 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	AM	176/192 (92%)	166 (94%)	9 (5%)	1 (1%)	22	33
12	AN	90/147 (61%)	77 (86%)	12 (13%)	1 (1%)	12	18
13	AO	141/152 (93%)	126 (89%)	15 (11%)	0	100	100
14	AP	119/145 (82%)	103 (87%)	14 (12%)	2 (2%)	7	10
15	AQ	148/151 (98%)	143 (97%)	5 (3%)	0	100	100
16	AR	126/139 (91%)	117 (93%)	9 (7%)	0	100	100
17	AS	117/154 (76%)	102 (87%)	15 (13%)	0	100	100
18	AT	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
19	AU	116/131 (88%)	107 (92%)	7 (6%)	2 (2%)	7	10
20	AV	139/152 (91%)	129 (93%)	10 (7%)	0	100	100
21	AW	140/144 (97%)	131 (94%)	9 (6%)	0	100	100
22	Aa	99/118 (84%)	97 (98%)	2 (2%)	0	100	100
23	Ab	85/87 (98%)	81 (95%)	4 (5%)	0	100	100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Ad	140/143 (98%)	135 (96%)	5 (4%)	0	100	100
26	Ae	131/134 (98%)	126 (96%)	5 (4%)	0	100	100
27	Af	67/89 (75%)	66 (98%)	1 (2%)	0	100	100
28	Ag	95/119 (80%)	91 (96%)	4 (4%)	0	100	100
29	Ah	79/83 (95%)	75 (95%)	4 (5%)	0	100	100
30	Ai	61/68 (90%)	57 (93%)	4 (7%)	0	100	100
31	Aj	51/56 (91%)	45 (88%)	6 (12%)	0	100	100
32	Ak	58/61 (95%)	52 (90%)	5 (9%)	1 (2%)	7	10
33	B0	91/106 (86%)	88 (97%)	3 (3%)	0	100	100
34	B1	91/94 (97%)	84 (92%)	7 (8%)	0	100	100
38	BN	246/253 (97%)	231 (94%)	15 (6%)	0	100	100
39	BO	382/388 (98%)	369 (97%)	13 (3%)	0	100	100
40	BP	360/363 (99%)	346 (96%)	14 (4%)	0	100	100
41	BQ	285/294 (97%)	279 (98%)	6 (2%)	0	100	100
42	BR	160/195 (82%)	143 (89%)	17 (11%)	0	100	100
43	BS	231/251 (92%)	226 (98%)	5 (2%)	0	100	100
44	BT	227/259 (88%)	222 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	BU	162/189 (86%)	157 (97%)	5 (3%)	0	100	100
46	BV	187/221 (85%)	183 (98%)	4 (2%)	0	100	100
47	BW	165/174 (95%)	157 (95%)	8 (5%)	0	100	100
48	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100
49	BY	128/134 (96%)	126 (98%)	2 (2%)	0	100	100
50	BZ	198/201 (98%)	191 (96%)	6 (3%)	1 (0%)	25	38
51	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
52	Bb	150/187 (80%)	145 (97%)	5 (3%)	0	100	100
53	Bc	184/187 (98%)	178 (97%)	6 (3%)	0	100	100
54	Bd	155/193 (80%)	151 (97%)	4 (3%)	0	100	100
55	Be	171/176 (97%)	168 (98%)	3 (2%)	0	100	100
56	Bf	157/160 (98%)	151 (96%)	6 (4%)	0	100	100
57	Bg	97/117 (83%)	87 (90%)	10 (10%)	0	100	100
58	Bh	132/139 (95%)	127 (96%)	5 (4%)	0	100	100
59	Bi	61/149 (41%)	60 (98%)	1 (2%)	0	100	100
60	Bj	116/141 (82%)	109 (94%)	7 (6%)	0	100	100
61	Bk	123/126 (98%)	121 (98%)	2 (2%)	0	100	100
62	Bl	133/136 (98%)	124 (93%)	9 (7%)	0	100	100
63	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
64	Bn	57/61 (93%)	55 (96%)	2 (4%)	0	100	100
65	Bo	92/109 (84%)	91 (99%)	1 (1%)	0	100	100
66	Bp	101/113 (89%)	98 (97%)	3 (3%)	0	100	100
67	Bq	116/127 (91%)	114 (98%)	2 (2%)	0	100	100
68	Br	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
69	Bs	104/111 (94%)	101 (97%)	3 (3%)	0	100	100
70	Bt	119/122 (98%)	116 (98%)	3 (2%)	0	100	100
71	Bu	93/99 (94%)	91 (98%)	2 (2%)	0	100	100
72	Bv	80/91 (88%)	74 (92%)	6 (8%)	0	100	100
73	Bw	67/74 (90%)	65 (97%)	2 (3%)	0	100	100
74	Bx	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
75	By	132/134 (98%)	126 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	10389/11466 (91%)	9904 (95%)	473 (5%)	12 (0%)	50	65

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AH	12	VAL
19	AU	118	VAL
3	AE	147	ALA
7	AI	79	GLY
50	BZ	183	SER
11	AM	147	VAL
14	AP	134	ALA
4	AF	237	THR
14	AP	110	ASP
32	Ak	51	VAL
12	AN	37	VAL
19	AU	98	VAL

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	
2	AD	170/228 (75%)	161 (95%)	9 (5%)	19	33
3	AE	193/223 (86%)	181 (94%)	12 (6%)	15	26
4	AF	175/199 (88%)	167 (95%)	8 (5%)	23	39
5	AG	181/203 (89%)	168 (93%)	13 (7%)	12	20
6	AH	226/227 (100%)	211 (93%)	15 (7%)	14	23
7	AI	169/169 (100%)	163 (96%)	6 (4%)	30	49
8	AJ	188/204 (92%)	180 (96%)	8 (4%)	25	42
9	AK	169/171 (99%)	157 (93%)	12 (7%)	12	20
10	AL	157/166 (95%)	152 (97%)	5 (3%)	34	54
11	AM	155/165 (94%)	149 (96%)	6 (4%)	27	46

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	AN	77/116 (66%)	77 (100%)	0	100	100
13	AO	124/131 (95%)	118 (95%)	6 (5%)	21	37
14	AP	92/118 (78%)	86 (94%)	6 (6%)	14	24
15	AQ	127/128 (99%)	124 (98%)	3 (2%)	44	64
16	AR	95/104 (91%)	90 (95%)	5 (5%)	19	33
17	AS	101/131 (77%)	97 (96%)	4 (4%)	27	45
18	AT	111/111 (100%)	109 (98%)	2 (2%)	54	73
19	AU	107/120 (89%)	103 (96%)	4 (4%)	29	48
20	AV	127/136 (93%)	124 (98%)	3 (2%)	44	64
21	AW	117/119 (98%)	112 (96%)	5 (4%)	25	42
22	Aa	95/111 (86%)	93 (98%)	2 (2%)	48	69
23	Ab	73/73 (100%)	68 (93%)	5 (7%)	13	22
24	Ac	114/115 (99%)	112 (98%)	2 (2%)	54	73
25	Ad	112/113 (99%)	107 (96%)	5 (4%)	23	40
26	Ae	112/113 (99%)	107 (96%)	5 (4%)	23	40
27	Af	61/75 (81%)	58 (95%)	3 (5%)	21	36
28	Ag	87/106 (82%)	82 (94%)	5 (6%)	17	29
29	Ah	71/73 (97%)	69 (97%)	2 (3%)	38	59
30	Ai	56/61 (92%)	53 (95%)	3 (5%)	18	32
31	Aj	45/47 (96%)	44 (98%)	1 (2%)	47	67
32	Ak	51/52 (98%)	48 (94%)	3 (6%)	16	28
33	B0	84/93 (90%)	82 (98%)	2 (2%)	44	64
34	B1	74/75 (99%)	71 (96%)	3 (4%)	26	44
38	BN	188/192 (98%)	187 (100%)	1 (0%)	86	94
39	BO	318/326 (98%)	312 (98%)	6 (2%)	52	72
40	BP	293/294 (100%)	288 (98%)	5 (2%)	56	75
41	BQ	235/241 (98%)	227 (97%)	8 (3%)	32	52
42	BR	132/155 (85%)	127 (96%)	5 (4%)	28	47
43	BS	198/213 (93%)	196 (99%)	2 (1%)	73	86
44	BT	182/212 (86%)	175 (96%)	7 (4%)	28	47
45	BU	149/168 (89%)	144 (97%)	5 (3%)	32	52

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	BV	165/187 (88%)	158 (96%)	7 (4%)	25	43
47	BW	141/146 (97%)	129 (92%)	12 (8%)	8	14
48	BX	166/167 (99%)	165 (99%)	1 (1%)	84	92
49	BY	110/113 (97%)	108 (98%)	2 (2%)	54	73
50	BZ	175/176 (99%)	171 (98%)	4 (2%)	45	66
51	Ba	159/160 (99%)	156 (98%)	3 (2%)	52	72
52	Bb	124/149 (83%)	117 (94%)	7 (6%)	17	30
53	Bc	157/158 (99%)	154 (98%)	3 (2%)	52	72
54	Bd	136/163 (83%)	132 (97%)	4 (3%)	37	58
55	Be	151/154 (98%)	150 (99%)	1 (1%)	81	91
56	Bf	138/139 (99%)	136 (99%)	2 (1%)	62	79
57	Bg	86/103 (84%)	83 (96%)	3 (4%)	31	51
58	Bh	103/107 (96%)	99 (96%)	4 (4%)	27	46
59	Bi	57/121 (47%)	53 (93%)	4 (7%)	12	21
60	Bj	105/122 (86%)	103 (98%)	2 (2%)	52	72
61	Bk	110/111 (99%)	107 (97%)	3 (3%)	40	60
62	Bl	114/115 (99%)	109 (96%)	5 (4%)	24	41
63	Bm	122/123 (99%)	119 (98%)	3 (2%)	42	63
64	Bn	50/51 (98%)	50 (100%)	0	100	100
65	Bo	75/87 (86%)	74 (99%)	1 (1%)	65	81
66	Bp	94/102 (92%)	91 (97%)	3 (3%)	34	54
67	Bq	100/107 (94%)	98 (98%)	2 (2%)	50	70
68	Br	91/94 (97%)	86 (94%)	5 (6%)	18	31
69	Bs	91/96 (95%)	87 (96%)	4 (4%)	24	41
70	Bt	106/107 (99%)	106 (100%)	0	100	100
71	Bu	81/84 (96%)	80 (99%)	1 (1%)	67	82
72	Bv	68/71 (96%)	68 (100%)	0	100	100
73	Bw	63/66 (96%)	58 (92%)	5 (8%)	10	16
74	Bx	46/47 (98%)	43 (94%)	3 (6%)	14	24
75	By	113/113 (100%)	109 (96%)	4 (4%)	31	51
All	All	8888/9616 (92%)	8578 (96%)	310 (4%)	33	51

All (310) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AD	10	LEU
2	AD	21	LEU
2	AD	87	ARG
2	AD	113	TYR
2	AD	137	LYS
2	AD	153	ASP
2	AD	160	ASP
2	AD	170	ARG
2	AD	171	LYS
3	AE	64	ARG
3	AE	77	GLU
3	AE	81	PHE
3	AE	111	ARG
3	AE	115	ARG
3	AE	119	THR
3	AE	146	ARG
3	AE	152	LYS
3	AE	178	SER
3	AE	182	ARG
3	AE	205	PHE
3	AE	222	LYS
4	AF	48	LYS
4	AF	85	VAL
4	AF	96	ARG
4	AF	110	VAL
4	AF	122	THR
4	AF	125	ARG
4	AF	182	VAL
4	AF	209	PHE
5	AG	67	ARG
5	AG	69	ARG
5	AG	80	LYS
5	AG	89	TYR
5	AG	91	GLU
5	AG	117	VAL
5	AG	129	MET
5	AG	144	LEU
5	AG	148	ARG
5	AG	152	MET
5	AG	156	ASP
5	AG	178	LEU
5	AG	191	MET

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Mol	Chain	Res	Type
6	AH	3	ARG
6	AH	12	VAL
6	AH	24	SER
6	AH	39	ARG
6	AH	114	ILE
6	AH	121	TYR
6	AH	129	VAL
6	AH	131	LEU
6	AH	182	MET
6	AH	187	ARG
6	AH	198	ARG
6	AH	204	SER
6	AH	212	ASP
6	AH	216	ARG
6	AH	230	GLU
7	AI	26	PHE
7	AI	105	GLN
7	AI	121	ARG
7	AI	164	ASN
7	AI	171	CYS
7	AI	178	ASN
8	AJ	39	ASP
8	AJ	63	MET
8	AJ	83	CYS
8	AJ	111	LEU
8	AJ	113	ILE
8	AJ	136	LYS
8	AJ	172	TYR
8	AJ	173	THR
9	AK	36	MET
9	AK	41	ARG
9	AK	51	VAL
9	AK	61	VAL
9	AK	85	LYS
9	AK	94	PHE
9	AK	124	HIS
9	AK	147	ASP
9	AK	158	ASN
9	AK	159	ARG
9	AK	168	LEU
9	AK	184	THR
10	AL	29	LEU

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Mol	Chain	Res	Type
10	AL	48	VAL
10	AL	83	TYR
10	AL	180	ASP
10	AL	184	LEU
11	AM	29	LYS
11	AM	89	SER
11	AM	114	PHE
11	AM	135	ARG
11	AM	154	LYS
11	AM	158	PHE
13	AO	41	THR
13	AO	52	ASP
13	AO	64	ARG
13	AO	71	THR
13	AO	115	ASN
13	AO	120	VAL
14	AP	43	HIS
14	AP	48	ARG
14	AP	67	LEU
14	AP	124	VAL
14	AP	129	TYR
14	AP	143	PHE
15	AQ	45	MET
15	AQ	110	ASP
15	AQ	145	THR
16	AR	26	ASN
16	AR	44	VAL
16	AR	86	ARG
16	AR	130	ARG
16	AR	134	ARG
17	AS	50	ARG
17	AS	91	MET
17	AS	105	TYR
17	AS	119	MET
18	AT	6	CYS
18	AT	21	VAL
19	AU	33	ARG
19	AU	95	ARG
19	AU	99	ASP
19	AU	112	ASP
20	AV	14	ARG
20	AV	54	LYS

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Mol	Chain	Res	Type
20	AV	83	PHE
21	AW	69	GLN
21	AW	88	ARG
21	AW	91	HIS
21	AW	93	ARG
21	AW	131	LEU
22	Aa	77	TRP
22	Aa	99	LYS
23	Ab	7	GLN
23	Ab	25	GLN
23	Ab	36	VAL
23	Ab	51	THR
23	Ab	58	PHE
24	Ac	18	GLU
24	Ac	80	ASN
25	Ad	24	ASP
25	Ad	72	VAL
25	Ad	84	PHE
25	Ad	93	PHE
25	Ad	100	VAL
26	Ae	14	THR
26	Ae	23	MET
26	Ae	49	LYS
26	Ae	64	TYR
26	Ae	72	PHE
27	Af	20	THR
27	Af	34	VAL
27	Af	37	PHE
28	Ag	20	PHE
28	Ag	33	ASP
28	Ag	37	LYS
28	Ag	62	TYR
28	Ag	93	ARG
29	Ah	33	MET
29	Ah	46	VAL
30	Ai	20	THR
30	Ai	31	VAL
30	Ai	34	MET
31	Aj	19	ARG
32	Ak	31	LYS
32	Ak	43	ARG
32	Ak	50	MET

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Mol	Chain	Res	Type
33	B0	26	THR
33	B0	57	VAL
34	B1	42	CYS
34	B1	48	LYS
34	B1	58	ASN
38	BN	78	THR
39	BO	25	GLN
39	BO	123	PHE
39	BO	203	VAL
39	BO	255	TRP
39	BO	276	THR
39	BO	377	LYS
40	BP	5	ARG
40	BP	95	MET
40	BP	122	TYR
40	BP	268	THR
40	BP	291	ARG
41	BQ	110	LEU
41	BQ	117	ASP
41	BQ	132	THR
41	BQ	152	ARG
41	BQ	159	VAL
41	BQ	203	HIS
41	BQ	207	TYR
41	BQ	270	TYR
42	BR	58	CYS
42	BR	66	ARG
42	BR	76	LEU
42	BR	135	LYS
42	BR	139	PHE
43	BS	31	ARG
43	BS	224	ASP
44	BT	48	ARG
44	BT	80	LYS
44	BT	182	ASN
44	BT	189	VAL
44	BT	204	ARG
44	BT	223	SER
44	BT	238	MET
45	BU	41	ARG
45	BU	58	TRP
45	BU	88	TYR

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Mol	Chain	Res	Type
45	BU	138	VAL
45	BU	166	ARG
46	BV	13	LYS
46	BV	38	ARG
46	BV	40	ARG
46	BV	98	ARG
46	BV	102	MET
46	BV	155	CYS
46	BV	178	ARG
47	BW	9	MET
47	BW	13	ARG
47	BW	15	SER
47	BW	57	PHE
47	BW	68	HIS
47	BW	86	VAL
47	BW	96	PHE
47	BW	102	PHE
47	BW	125	MET
47	BW	128	TYR
47	BW	136	MET
47	BW	140	ARG
48	BX	114	GLU
49	BY	64	LYS
49	BY	79	LYS
50	BZ	96	ARG
50	BZ	140	LYS
50	BZ	155	VAL
50	BZ	201	ARG
51	Ba	101	GLU
51	Ba	111	PRO
51	Ba	175	LYS
52	Bb	3	ARG
52	Bb	5	SER
52	Bb	11	GLU
52	Bb	52	LYS
52	Bb	54	HIS
52	Bb	89	LYS
52	Bb	126	ARG
53	Bc	6	GLU
53	Bc	148	ARG
53	Bc	169	GLU
54	Bd	80	LYS

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Mol	Chain	Res	Type
54	Bd	96	MET
54	Bd	111	GLU
54	Bd	112	SER
55	Be	81	ASP
56	Bf	16	GLN
56	Bf	140	PHE
57	Bg	69	PHE
57	Bg	76	TYR
57	Bg	86	SER
58	Bh	40	SER
58	Bh	47	ARG
58	Bh	58	ASP
58	Bh	117	THR
59	Bi	1	MET
59	Bi	2	LYS
59	Bi	22	VAL
59	Bi	30	ARG
60	Bj	29	THR
60	Bj	42	LYS
61	Bk	23	SER
61	Bk	45	ARG
61	Bk	73	TYR
62	Bl	2	VAL
62	Bl	3	LYS
62	Bl	40	HIS
62	Bl	64	ARG
62	Bl	108	SER
63	Bm	15	VAL
63	Bm	82	VAL
63	Bm	120	THR
65	Bo	24	MET
66	Bp	36	ARG
66	Bp	52	LYS
66	Bp	63	GLU
67	Bq	27	GLU
67	Bq	88	THR
68	Br	6	HIS
68	Br	49	ARG
68	Br	58	LYS
68	Br	60	VAL
68	Br	93	LYS
69	Bs	28	ASN

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Mol	Chain	Res	Type
69	Bs	32	TYR
69	Bs	87	ASP
69	Bs	103	GLN
71	Bu	62	SER
73	Bw	3	ARG
73	Bw	9	LYS
73	Bw	13	GLU
73	Bw	19	ASP
73	Bw	69	GLU
74	Bx	18	ARG
74	Bx	33	ASN
74	Bx	39	MET
75	By	32	ARG
75	By	44	ARG
75	By	93	ARG
75	By	110	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
2	AD	24	ASN
2	AD	167	ASN
4	AF	227	ASN
5	AG	95	ASN
5	AG	176	HIS
6	AH	36	HIS
6	AH	157	ASN
6	AH	167	ASN
7	AI	15	ASN
7	AI	109	GLN
8	AJ	34	GLN
9	AK	66	GLN
9	AK	144	GLN
10	AL	103	GLN
11	AM	139	GLN
11	AM	155	HIS
13	AO	78	HIS
13	AO	135	ASN
15	AQ	58	HIS
18	AT	135	GLN
21	AW	125	GLN
23	Ab	35	ASN

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Mol	Chain	Res	Type
25	Ad	46	HIS
26	Ae	29	HIS
29	Ah	26	GLN
32	Ak	29	GLN
33	B0	81	ASN
39	BO	259	ASN
39	BO	293	ASN
40	BP	212	ASN
41	BQ	63	GLN
41	BQ	203	HIS
41	BQ	220	GLN
43	BS	27	GLN
43	BS	46	GLN
43	BS	194	HIS
44	BT	38	GLN
44	BT	131	ASN
44	BT	182	ASN
45	BU	77	ASN
50	BZ	19	ASN
51	Ba	116	GLN
51	Ba	189	ASN
53	Bc	14	GLN
54	Bd	130	ASN
54	Bd	150	ASN
55	Be	48	ASN
58	Bh	134	ASN
62	Bl	27	GLN
62	Bl	40	HIS
62	Bl	78	ASN
65	Bo	74	HIS
66	Bp	103	ASN
70	Bt	15	ASN
70	Bt	33	GLN
70	Bt	84	GLN
71	Bu	19	GLN
72	Bv	76	ASN
75	By	29	GLN
75	By	41	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1687/1842 (91%)	413 (24%)	16 (0%)
35	B2	3204/3498 (91%)	644 (20%)	26 (0%)
36	B3	118/246 (47%)	17 (14%)	1 (0%)
37	B4	156/165 (94%)	26 (16%)	1 (0%)
All	All	5165/5751 (89%)	1100 (21%)	44 (0%)

All (1100) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	3	C
1	AA	4	C
1	AA	25	C
1	AA	26	A
1	AA	34	G
1	AA	35	U
1	AA	42	G
1	AA	45	U
1	AA	46	A
1	AA	47	A
1	AA	57	G
1	AA	60	U
1	AA	65	A
1	AA	66	U
1	AA	67	A
1	AA	68	A
1	AA	72	A
1	AA	79	A
1	AA	105	A
1	AA	115	C
1	AA	116	G
1	AA	117	U
1	AA	120	A
1	AA	128	G
1	AA	130	A
1	AA	138	U
1	AA	139	A
1	AA	141	U
1	AA	142	U
1	AA	143	G
1	AA	144	G
1	AA	159	U
1	AA	160	C
1	AA	166	C

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Mol	Chain	Res	Type
1	AA	177	U
1	AA	178	A
1	AA	188	A
1	AA	191	U
1	AA	192	U
1	AA	193	U
1	AA	194	U
1	AA	195	U
1	AA	196	G
1	AA	197	G
1	AA	198	A
1	AA	201	G
1	AA	205	G
1	AA	217	U
1	AA	219	A
1	AA	226	A
1	AA	229	G
1	AA	230	C
1	AA	234	C
1	AA	236	G
1	AA	239	U
1	AA	241	U
1	AA	243	U
1	AA	244	U
1	AA	253	C
1	AA	264	U
1	AA	268	A
1	AA	275	U
1	AA	276	G
1	AA	278	C
1	AA	280	U
1	AA	281	U
1	AA	283	C
1	AA	305	U
1	AA	317	C
1	AA	319	A
1	AA	322	U
1	AA	323	U
1	AA	336	A
1	AA	340	G
1	AA	341	C
1	AA	355	A

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Mol	Chain	Res	Type
1	AA	362	A
1	AA	363	A
1	AA	364	C
1	AA	393	G
1	AA	403	A
1	AA	405	C
1	AA	407	G
1	AA	419	A
1	AA	426	G
1	AA	427	C
1	AA	428	A
1	AA	429	G
1	AA	437	G
1	AA	440	A
1	AA	442	U
1	AA	447	C
1	AA	448	A
1	AA	457	A
1	AA	467	A
1	AA	471	A
1	AA	473	A
1	AA	478	A
1	AA	480	A
1	AA	481	A
1	AA	489	G
1	AA	491	G
1	AA	504	U
1	AA	505	U
1	AA	508	A
1	AA	509	A
1	AA	511	U
1	AA	513	G
1	AA	514	A
1	AA	516	U
1	AA	517	G
1	AA	522	C
1	AA	523	A
1	AA	530	A
1	AA	537	A
1	AA	542	G
1	AA	545	A
1	AA	557	C

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Mol	Chain	Res	Type
1	AA	558	A
1	AA	559	A
1	AA	560	G
1	AA	561	U
1	AA	562	C
1	AA	564	G
1	AA	568	C
1	AA	571	G
1	AA	572	C
1	AA	581	U
1	AA	588	A
1	AA	597	A
1	AA	598	G
1	AA	614	U
1	AA	622	A
1	AA	623	A
1	AA	624	A
1	AA	626	A
1	AA	627	G
1	AA	637	G
1	AA	638	A
1	AA	642	U
1	AA	647	C
1	AA	651	G
1	AA	694	G
1	AA	696	U
1	AA	698	G
1	AA	701	A
1	AA	703	C
1	AA	747	A
1	AA	748	C
1	AA	755	U
1	AA	758	U
1	AA	768	A
1	AA	769	A
1	AA	778	G
1	AA	779	U
1	AA	784	A
1	AA	787	A
1	AA	788	G
1	AA	792	A
1	AA	793	G

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Mol	Chain	Res	Type
1	AA	795	U
1	AA	797	U
1	AA	798	G
1	AA	802	G
1	AA	804	A
1	AA	808	A
1	AA	810	U
1	AA	826	A
1	AA	827	A
1	AA	828	U
1	AA	831	G
1	AA	833	C
1	AA	834	G
1	AA	835	U
1	AA	838	G
1	AA	841	U
1	AA	844	A
1	AA	845	U
1	AA	846	U
1	AA	848	U
1	AA	849	G
1	AA	850	U
1	AA	865	G
1	AA	868	G
1	AA	869	U
1	AA	878	A
1	AA	888	U
1	AA	891	G
1	AA	910	G
1	AA	912	C
1	AA	913	A
1	AA	921	A
1	AA	926	U
1	AA	928	G
1	AA	929	G
1	AA	947	U
1	AA	948	A
1	AA	950	U
1	AA	974	U
1	AA	975	U
1	AA	981	A
1	AA	984	C

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Mol	Chain	Res	Type
1	AA	985	A
1	AA	998	A
1	AA	1003	A
1	AA	1007	A
1	AA	1011	C
1	AA	1014	U
1	AA	1015	C
1	AA	1018	A
1	AA	1019	U
1	AA	1036	C
1	AA	1041	A
1	AA	1043	C
1	AA	1054	A
1	AA	1067	U
1	AA	1068	G
1	AA	1072	C
1	AA	1092	A
1	AA	1098	C
1	AA	1108	A
1	AA	1112	C
1	AA	1113	U
1	AA	1114	U
1	AA	1116	G
1	AA	1129	A
1	AA	1154	A
1	AA	1166	G
1	AA	1171	G
1	AA	1174	C
1	AA	1176	A
1	AA	1179	A
1	AA	1180	U
1	AA	1181	G
1	AA	1182	G
1	AA	1184	G
1	AA	1187	G
1	AA	1190	C
1	AA	1201	A
1	AA	1202	U
1	AA	1203	U
1	AA	1210	A
1	AA	1211	A
1	AA	1213	A

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Mol	Chain	Res	Type
1	AA	1214	C
1	AA	1215	G
1	AA	1216	G
1	AA	1217	G
1	AA	1219	A
1	AA	1224	C
1	AA	1233	C
1	AA	1235	G
1	AA	1242	U
1	AA	1243	A
1	AA	1244	A
1	AA	1245	G
1	AA	1246	G
1	AA	1247	A
1	AA	1248	U
1	AA	1257	U
1	AA	1260	G
1	AA	1261	A
1	AA	1262	G
1	AA	1263	C
1	AA	1266	U
1	AA	1268	U
1	AA	1269	C
1	AA	1272	G
1	AA	1273	A
1	AA	1274	U
1	AA	1275	U
1	AA	1277	U
1	AA	1284	G
1	AA	1301	C
1	AA	1303	U
1	AA	1304	A
1	AA	1305	G
1	AA	1308	G
1	AA	1324	U
1	AA	1331	U
1	AA	1332	U
1	AA	1335	G
1	AA	1336	A
1	AA	1338	A
1	AA	1342	A
1	AA	1354	A

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Mol	Chain	Res	Type
1	AA	1355	C
1	AA	1357	U
1	AA	1358	G
1	AA	1359	C
1	AA	1362	A
1	AA	1364	U
1	AA	1366	G
1	AA	1371	A
1	AA	1372	U
1	AA	1376	C
1	AA	1380	U
1	AA	1381	U
1	AA	1382	U
1	AA	1383	G
1	AA	1384	G
1	AA	1387	G
1	AA	1391	A
1	AA	1393	U
1	AA	1396	C
1	AA	1398	U
1	AA	1399	C
1	AA	1405	G
1	AA	1410	U
1	AA	1413	U
1	AA	1418	U
1	AA	1431	A
1	AA	1432	G
1	AA	1433	U
1	AA	1435	U
1	AA	1447	A
1	AA	1448	G
1	AA	1452	U
1	AA	1455	G
1	AA	1464	A
1	AA	1465	G
1	AA	1466	A
1	AA	1479	C
1	AA	1489	A
1	AA	1494	G
1	AA	1498	G
1	AA	1500	G
1	AA	1502	C

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Mol	Chain	Res	Type
1	AA	1510	U
1	AA	1535	C
1	AA	1541	C
1	AA	1542	C
1	AA	1544	G
1	AA	1545	A
1	AA	1546	A
1	AA	1547	G
1	AA	1548	G
1	AA	1550	C
1	AA	1551	U
1	AA	1552	G
1	AA	1557	A
1	AA	1558	U
1	AA	1559	C
1	AA	1561	U
1	AA	1562	G
1	AA	1563	U
1	AA	1564	U
1	AA	1565	A
1	AA	1570	C
1	AA	1576	U
1	AA	1577	G
1	AA	1578	C
1	AA	1579	U
1	AA	1580	G
1	AA	1581	G
1	AA	1590	C
1	AA	1591	A
1	AA	1594	G
1	AA	1596	A
1	AA	1597	A
1	AA	1598	U
1	AA	1599	U
1	AA	1600	A
1	AA	1601	U
1	AA	1610	A
1	AA	1614	A
1	AA	1615	G
1	AA	1623	U
1	AA	1624	A
1	AA	1625	G

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Mol	Chain	Res	Type
1	AA	1642	G
1	AA	1657	G
1	AA	1659	C
1	AA	1660	C
1	AA	1662	U
1	AA	1676	A
1	AA	1682	C
1	AA	1698	U
1	AA	1699	G
1	AA	1700	A
1	AA	1701	A
1	AA	1702	U
1	AA	1720	G
1	AA	1721	G
1	AA	1726	G
1	AA	1755	U
1	AA	1756	U
1	AA	1757	G
1	AA	1759	C
1	AA	1760	G
1	AA	1772	A
1	AA	1786	A
1	AA	1791	A
1	AA	1795	A
1	AA	1797	A
1	AA	1798	A
1	AA	1800	U
1	AA	1801	C
1	AA	1802	G
1	AA	1803	U
1	AA	1804	A
1	AA	1809	G
1	AA	1811	U
1	AA	1822	G
1	AA	1824	A
1	AA	1825	C
1	AA	1834	G
1	AA	1835	G
1	AA	1836	A
1	AA	1838	C
1	AA	1840	U
1	AA	1841	U

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Mol	Chain	Res	Type
1	AA	1842	A
35	B2	14	U
35	B2	40	A
35	B2	43	A
35	B2	49	A
35	B2	60	A
35	B2	65	A
35	B2	66	A
35	B2	69	U
35	B2	73	C
35	B2	77	A
35	B2	92	G
35	B2	110	G
35	B2	111	C
35	B2	116	A
35	B2	118	U
35	B2	122	A
35	B2	156	A
35	B2	162	A
35	B2	163	A
35	B2	167	G
35	B2	170	G
35	B2	172	U
35	B2	174	U
35	B2	175	G
35	B2	176	A
35	B2	180	U
35	B2	181	A
35	B2	183	A
35	B2	184	C
35	B2	185	G
35	B2	187	U
35	B2	188	C
35	B2	189	G
35	B2	190	G
35	B2	191	U
35	B2	192	C
35	B2	193	U
35	B2	194	A
35	B2	197	U
35	B2	198	U
35	B2	207	C

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Mol	Chain	Res	Type
35	B2	213	G
35	B2	217	G
35	B2	218	A
35	B2	220	A
35	B2	225	G
35	B2	226	A
35	B2	239	U
35	B2	241	G
35	B2	246	U
35	B2	247	U
35	B2	248	G
35	B2	252	A
35	B2	253	U
35	B2	254	G
35	B2	255	C
35	B2	256	C
35	B2	257	A
35	B2	259	A
35	B2	260	U
35	B2	262	A
35	B2	263	A
35	B2	264	G
35	B2	269	U
35	B2	271	C
35	B2	272	G
35	B2	274	A
35	B2	277	G
35	B2	292	A
35	B2	303	A
35	B2	313	U
35	B2	331	A
35	B2	337	U
35	B2	347	C
35	B2	359	A
35	B2	360	A
35	B2	383	A
35	B2	384	G
35	B2	399	A
35	B2	406	U
35	B2	411	C
35	B2	429	G
35	B2	430	A

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Mol	Chain	Res	Type
35	B2	445	G
35	B2	446	U
35	B2	447	C
35	B2	448	U
35	B2	449	U
35	B2	450	A
35	B2	461	A
35	B2	462	U
35	B2	477	C
35	B2	500	U
35	B2	501	G
35	B2	504	A
35	B2	505	G
35	B2	509	A
35	B2	514	C
35	B2	522	G
35	B2	531	A
35	B2	532	A
35	B2	534	A
35	B2	540	A
35	B2	546	G
35	B2	547	G
35	B2	548	U
35	B2	549	G
35	B2	553	U
35	B2	554	U
35	B2	571	G
35	B2	572	A
35	B2	573	G
35	B2	575	G
35	B2	578	U
35	B2	579	A
35	B2	580	U
35	B2	581	A
35	B2	587	U
35	B2	588	G
35	B2	590	U
35	B2	591	G
35	B2	602	A
35	B2	603	C
35	B2	606	G
35	B2	613	A

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Mol	Chain	Res	Type
35	B2	625	U
35	B2	627	G
35	B2	628	U
35	B2	629	G
35	B2	634	G
35	B2	636	A
35	B2	637	U
35	B2	643	C
35	B2	645	U
35	B2	662	C
35	B2	674	A
35	B2	685	A
35	B2	702	A
35	B2	706	U
35	B2	708	U
35	B2	714	A
35	B2	715	U
35	B2	716	G
35	B2	717	A
35	B2	720	A
35	B2	732	A
35	B2	761	U
35	B2	763	G
35	B2	769	U
35	B2	770	G
35	B2	778	G
35	B2	786	C
35	B2	788	G
35	B2	789	A
35	B2	806	G
35	B2	813	G
35	B2	817	G
35	B2	838	A
35	B2	849	A
35	B2	862	A
35	B2	881	C
35	B2	889	G
35	B2	893	C
35	B2	903	U
35	B2	906	U
35	B2	911	U
35	B2	928	A

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Mol	Chain	Res	Type
35	B2	939	G
35	B2	940	G
35	B2	946	A
35	B2	948	G
35	B2	949	A
35	B2	953	A
35	B2	955	C
35	B2	969	G
35	B2	976	C
35	B2	981	C
35	B2	985	G
35	B2	991	C
35	B2	992	U
35	B2	993	C
35	B2	1009	C
35	B2	1011	G
35	B2	1012	A
35	B2	1015	A
35	B2	1033	G
35	B2	1034	A
35	B2	1047	C
35	B2	1049	U
35	B2	1050	G
35	B2	1051	G
35	B2	1053	G
35	B2	1056	G
35	B2	1057	G
35	B2	1058	A
35	B2	1059	A
35	B2	1060	U
35	B2	1061	U
35	B2	1062	U
35	B2	1064	C
35	B2	1067	A
35	B2	1079	A
35	B2	1081	C
35	B2	1095	G
35	B2	1096	A
35	B2	1098	G
35	B2	1100	C
35	B2	1101	C
35	B2	1104	G

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Mol	Chain	Res	Type
35	B2	1113	U
35	B2	1119	G
35	B2	1123	G
35	B2	1125	C
35	B2	1126	A
35	B2	1127	U
35	B2	1128	C
35	B2	1129	G
35	B2	1130	A
35	B2	1134	A
35	B2	1135	G
35	B2	1148	G
35	B2	1155	U
35	B2	1159	U
35	B2	1162	G
35	B2	1175	U
35	B2	1176	G
35	B2	1184	A
35	B2	1186	C
35	B2	1191	C
35	B2	1211	A
35	B2	1212	U
35	B2	1222	U
35	B2	1227	C
35	B2	1232	G
35	B2	1239	U
35	B2	1245	U
35	B2	1249	U
35	B2	1252	A
35	B2	1253	G
35	B2	1262	A
35	B2	1263	C
35	B2	1264	G
35	B2	1266	U
35	B2	1267	G
35	B2	1269	C
35	B2	1270	C
35	B2	1272	U
35	B2	1273	G
35	B2	1276	A
35	B2	1277	G
35	B2	1279	C

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Mol	Chain	Res	Type
35	B2	1289	U
35	B2	1292	G
35	B2	1293	G
35	B2	1294	A
35	B2	1297	G
35	B2	1300	U
35	B2	1302	A
35	B2	1303	C
35	B2	1304	A
35	B2	1310	C
35	B2	1313	G
35	B2	1316	G
35	B2	1317	A
35	B2	1318	A
35	B2	1319	U
35	B2	1323	C
35	B2	1333	A
35	B2	1334	A
35	B2	1336	U
35	B2	1338	G
35	B2	1340	U
35	B2	1361	A
35	B2	1379	U
35	B2	1380	A
35	B2	1381	G
35	B2	1388	G
35	B2	1389	A
35	B2	1420	U
35	B2	1426	G
35	B2	1433	U
35	B2	1451	G
35	B2	1452	A
35	B2	1453	A
35	B2	1468	G
35	B2	1470	U
35	B2	1471	C
35	B2	1515	A
35	B2	1521	G
35	B2	1522	G
35	B2	1530	C
35	B2	1542	C
35	B2	1557	U

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Mol	Chain	Res	Type
35	B2	1570	G
35	B2	1588	A
35	B2	1589	U
35	B2	1590	G
35	B2	1593	A
35	B2	1594	G
35	B2	1595	U
35	B2	1596	U
35	B2	1600	C
35	B2	1601	G
35	B2	1602	A
35	B2	1604	U
35	B2	1606	U
35	B2	1607	U
35	B2	1608	C
35	B2	1609	G
35	B2	1614	U
35	B2	1615	C
35	B2	1616	C
35	B2	1624	A
35	B2	1628	A
35	B2	1656	G
35	B2	1663	C
35	B2	1664	A
35	B2	1665	A
35	B2	1666	C
35	B2	1674	C
35	B2	1677	A
35	B2	1678	A
35	B2	1679	A
35	B2	1680	U
35	B2	1682	A
35	B2	1692	C
35	B2	1742	G
35	B2	1744	A
35	B2	1745	C
35	B2	1753	A
35	B2	1755	A
35	B2	1764	U
35	B2	1783	G
35	B2	1790	A
35	B2	1791	G

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Mol	Chain	Res	Type
35	B2	1800	G
35	B2	1801	C
35	B2	1803	U
35	B2	1806	U
35	B2	1811	A
35	B2	1816	G
35	B2	1819	G
35	B2	1821	G
35	B2	1837	G
35	B2	1838	A
35	B2	1849	G
35	B2	1853	A
35	B2	1854	A
35	B2	1855	U
35	B2	1856	G
35	B2	1869	C
35	B2	1871	U
35	B2	1876	U
35	B2	1894	A
35	B2	1896	A
35	B2	1897	A
35	B2	1901	C
35	B2	1904	C
35	B2	1921	C
35	B2	1933	G
35	B2	1934	A
35	B2	1935	U
35	B2	1941	A
35	B2	1961	G
35	B2	2005	U
35	B2	2007	G
35	B2	2182	C
35	B2	2183	A
35	B2	2185	C
35	B2	2188	A
35	B2	2190	U
35	B2	2200	U
35	B2	2201	A
35	B2	2209	G
35	B2	2210	G
35	B2	2219	A
35	B2	2228	U

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Mol	Chain	Res	Type
35	B2	2232	A
35	B2	2246	A
35	B2	2257	G
35	B2	2293	U
35	B2	2294	G
35	B2	2295	A
35	B2	2296	A
35	B2	2297	U
35	B2	2310	A
35	B2	2311	A
35	B2	2317	A
35	B2	2332	A
35	B2	2337	G
35	B2	2339	G
35	B2	2344	A
35	B2	2345	C
35	B2	2348	U
35	B2	2349	G
35	B2	2351	C
35	B2	2353	C
35	B2	2356	U
35	B2	2358	A
35	B2	2360	G
35	B2	2361	G
35	B2	2367	A
35	B2	2369	A
35	B2	2376	G
35	B2	2383	A
35	B2	2386	U
35	B2	2395	G
35	B2	2396	C
35	B2	2398	U
35	B2	2401	A
35	B2	2403	G
35	B2	2423	G
35	B2	2424	U
35	B2	2461	A
35	B2	2462	C
35	B2	2463	G
35	B2	2481	G
35	B2	2485	A
35	B2	2489	A

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Mol	Chain	Res	Type
35	B2	2490	A
35	B2	2491	G
35	B2	2492	A
35	B2	2499	U
35	B2	2523	G
35	B2	2527	A
35	B2	2528	G
35	B2	2529	A
35	B2	2530	G
35	B2	2601	U
35	B2	2602	U
35	B2	2603	C
35	B2	2606	U
35	B2	2607	A
35	B2	2610	U
35	B2	2611	A
35	B2	2619	A
35	B2	2620	A
35	B2	2622	C
35	B2	2627	U
35	B2	2628	U
35	B2	2629	G
35	B2	2630	G
35	B2	2632	A
35	B2	2633	U
35	B2	2635	U
35	B2	2636	A
35	B2	2638	U
35	B2	2642	C
35	B2	2643	A
35	B2	2644	U
35	B2	2645	A
35	B2	2648	C
35	B2	2649	U
35	B2	2650	A
35	B2	2656	A
35	B2	2657	A
35	B2	2660	U
35	B2	2661	U
35	B2	2662	U
35	B2	2664	U
35	B2	2665	U

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Mol	Chain	Res	Type
35	B2	2667	G
35	B2	2668	C
35	B2	2669	G
35	B2	2680	C
35	B2	2681	G
35	B2	2688	A
35	B2	2701	G
35	B2	2702	G
35	B2	2707	U
35	B2	2709	G
35	B2	2714	G
35	B2	2721	A
35	B2	2730	A
35	B2	2743	G
35	B2	2747	U
35	B2	2751	A
35	B2	2752	A
35	B2	2769	A
35	B2	2770	C
35	B2	2772	G
35	B2	2774	A
35	B2	2775	A
35	B2	2784	A
35	B2	2786	A
35	B2	2789	A
35	B2	2799	A
35	B2	2809	G
35	B2	2822	A
35	B2	2823	G
35	B2	2824	U
35	B2	2848	G
35	B2	2857	A
35	B2	2866	U
35	B2	2868	C
35	B2	2872	G
35	B2	2873	A
35	B2	2889	G
35	B2	2890	U
35	B2	2891	G
35	B2	2895	G
35	B2	2896	A
35	B2	2898	A

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Mol	Chain	Res	Type
35	B2	2903	A
35	B2	2905	C
35	B2	2909	G
35	B2	2912	A
35	B2	2913	U
35	B2	2918	G
35	B2	2923	G
35	B2	2934	G
35	B2	2937	U
35	B2	2938	U
35	B2	2940	A
35	B2	2942	A
35	B2	2944	C
35	B2	2955	U
35	B2	2957	U
35	B2	2962	C
35	B2	2966	G
35	B2	2967	A
35	B2	2982	A
35	B2	2984	C
35	B2	2992	A
35	B2	2993	G
35	B2	2994	C
35	B2	2996	G
35	B2	3001	C
35	B2	3002	G
35	B2	3003	G
35	B2	3018	U
35	B2	3030	U
35	B2	3031	A
35	B2	3036	A
35	B2	3040	G
35	B2	3042	G
35	B2	3046	G
35	B2	3050	U
35	B2	3051	A
35	B2	3066	A
35	B2	3067	G
35	B2	3078	C
35	B2	3085	G
35	B2	3091	G
35	B2	3093	G

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Mol	Chain	Res	Type
35	B2	3108	A
35	B2	3117	A
35	B2	3155	G
35	B2	3174	A
35	B2	3175	U
35	B2	3182	G
35	B2	3188	U
35	B2	3189	C
35	B2	3195	C
35	B2	3197	G
35	B2	3212	G
35	B2	3216	C
35	B2	3218	A
35	B2	3225	A
35	B2	3226	A
35	B2	3227	U
35	B2	3238	A
35	B2	3239	A
35	B2	3248	U
35	B2	3249	U
35	B2	3250	U
35	B2	3260	A
35	B2	3261	U
35	B2	3265	U
35	B2	3266	U
35	B2	3268	U
35	B2	3269	A
35	B2	3276	A
35	B2	3283	A
35	B2	3284	G
35	B2	3285	G
35	B2	3286	U
35	B2	3288	G
35	B2	3289	G
35	B2	3293	U
35	B2	3294	G
35	B2	3295	U
35	B2	3296	U
35	B2	3297	C
35	B2	3298	C
35	B2	3299	U
35	B2	3300	A

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Mol	Chain	Res	Type
35	B2	3301	C
35	B2	3302	U
35	B2	3304	U
35	B2	3305	C
35	B2	3306	C
35	B2	3307	U
35	B2	3310	A
35	B2	3315	A
35	B2	3317	A
35	B2	3318	A
35	B2	3319	G
35	B2	3327	A
35	B2	3328	U
35	B2	3329	G
35	B2	3338	A
35	B2	3343	A
35	B2	3345	G
35	B2	3347	G
35	B2	3359	U
35	B2	3360	G
35	B2	3363	C
35	B2	3371	U
35	B2	3372	C
35	B2	3373	C
35	B2	3374	A
35	B2	3375	U
35	B2	3376	U
35	B2	3377	G
35	B2	3382	C
35	B2	3388	C
35	B2	3390	G
35	B2	3391	A
35	B2	3392	A
35	B2	3393	U
35	B2	3394	C
35	B2	3405	C
35	B2	3408	A
35	B2	3418	U
35	B2	3419	G
35	B2	3420	U
35	B2	3435	U
35	B2	3442	U

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Mol	Chain	Res	Type
35	B2	3443	A
35	B2	3446	G
35	B2	3450	C
35	B2	3452	U
35	B2	3453	U
35	B2	3454	G
35	B2	3455	U
35	B2	3456	U
35	B2	3457	G
35	B2	3468	C
35	B2	3476	A
35	B2	3479	C
35	B2	3483	U
35	B2	3484	G
35	B2	3491	A
36	B3	7	G
36	B3	12	U
36	B3	13	A
36	B3	41	G
36	B3	45	A
36	B3	46	C
36	B3	53	U
36	B3	54	A
36	B3	55	A
36	B3	63	A
36	B3	64	G
36	B3	71	G
36	B3	75	G
36	B3	100	A
36	B3	110	G
36	B3	116	G
36	B3	119	U
37	B4	31	U
37	B4	42	U
37	B4	43	C
37	B4	47	G
37	B4	56	A
37	B4	59	G
37	B4	67	A
37	B4	70	C
37	B4	71	G
37	B4	88	A

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Mol	Chain	Res	Type
37	B4	89	U
37	B4	90	U
37	B4	91	C
37	B4	93	G
37	B4	94	U
37	B4	98	U
37	B4	103	G
37	B4	112	A
37	B4	114	C
37	B4	119	A
37	B4	121	U
37	B4	124	G
37	B4	133	U
37	B4	134	U
37	B4	135	C
37	B4	165	U

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	104	A
1	AA	140	C
1	AA	187	G
1	AA	275	U
1	AA	516	U
1	AA	558	A
1	AA	561	U
1	AA	747	A
1	AA	768	A
1	AA	1113	U
1	AA	1209	C
1	AA	1361	A
1	AA	1383	G
1	AA	1501	C
1	AA	1661	C
1	AA	1699	G
35	B2	188	C
35	B2	382	A
35	B2	446	U
35	B2	572	A
35	B2	589	U
35	B2	714	A

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Mol	Chain	Res	Type
35	B2	719	A
35	B2	948	G
35	B2	1059	A
35	B2	1094	A
35	B2	1103	U
35	B2	1133	G
35	B2	1269	C
35	B2	1272	U
35	B2	1854	A
35	B2	2200	U
35	B2	2661	U
35	B2	2993	G
35	B2	3001	C
35	B2	3217	U
35	B2	3260	A
35	B2	3292	U
35	B2	3295	U
35	B2	3328	U
35	B2	3362	C
35	B2	3373	C
36	B3	12	U
37	B4	88	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	9

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	537:A	O3'	538:A	P	4.50
1	AA	546:C	O3'	547:A	P	4.24
1	AA	1419:A	O3'	1420:A	P	4.11
1	AA	1359:C	O3'	1360:U	P	3.79
1	AA	1483:C	O3'	1484:G	P	3.67
1	AA	1605:U	O3'	1606:C	P	3.57
1	AA	524:A	O3'	525:U	P	3.42
1	AA	1574:C	O3'	1575:G	P	3.31
1	AA	1233:C	O3'	1234:A	P	3.28

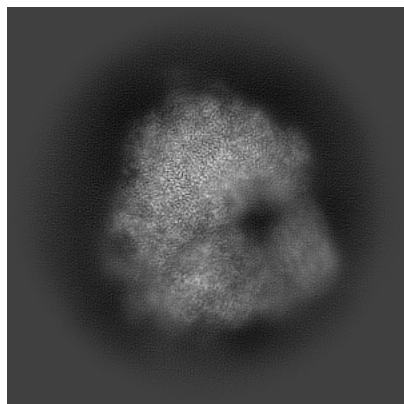
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43972. These allow visual inspection of the internal detail of the map and identification of artifacts.

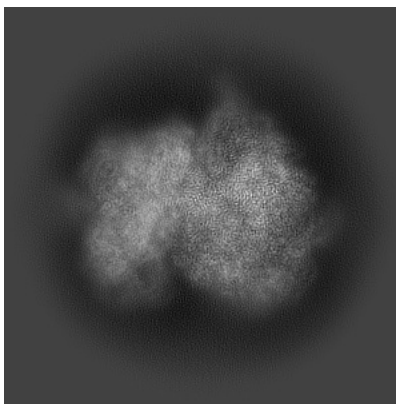
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

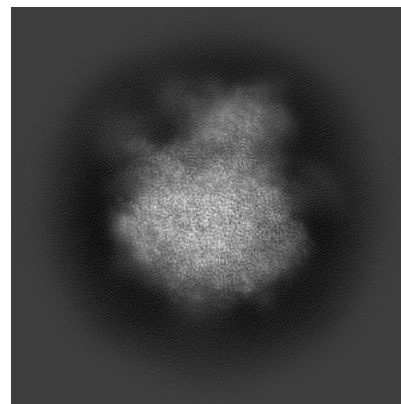
6.1.1 Primary map



X

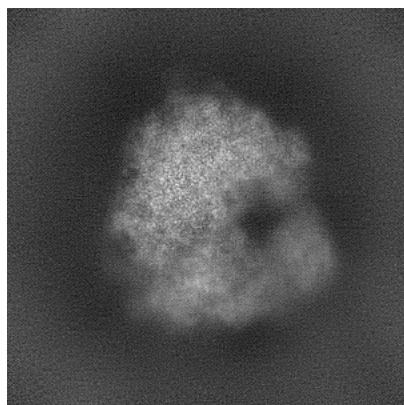


Y

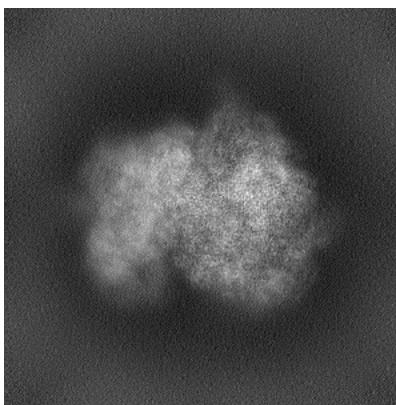


Z

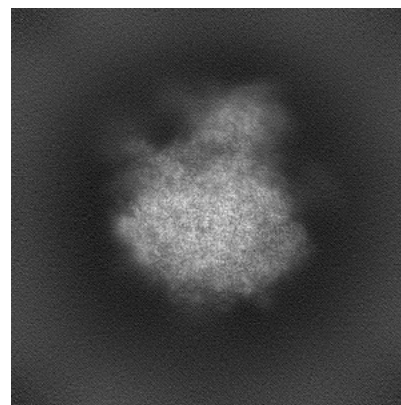
6.1.2 Raw map



X



Y

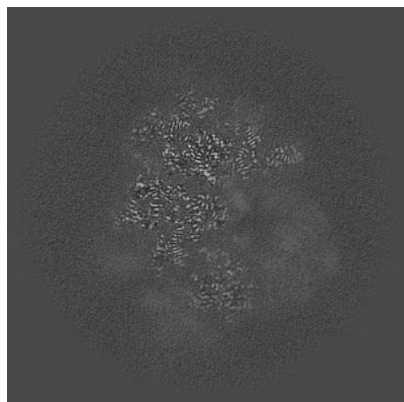


Z

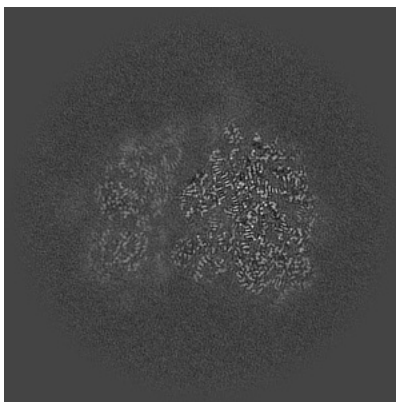
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

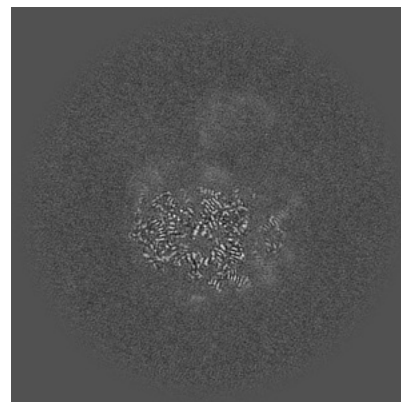
6.2.1 Primary map



X Index: 256

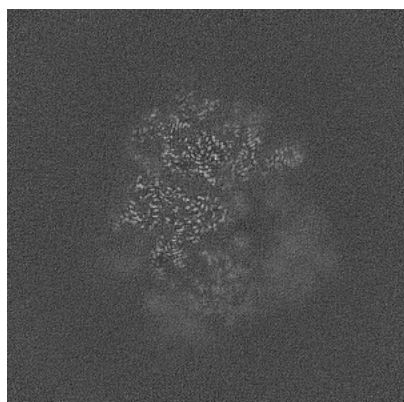


Y Index: 256

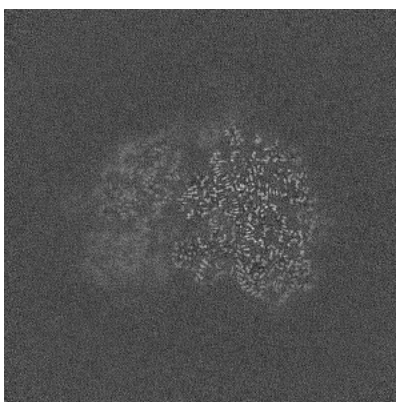


Z Index: 256

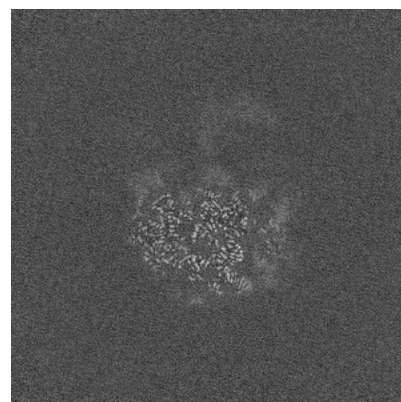
6.2.2 Raw map



X Index: 256



Y Index: 256

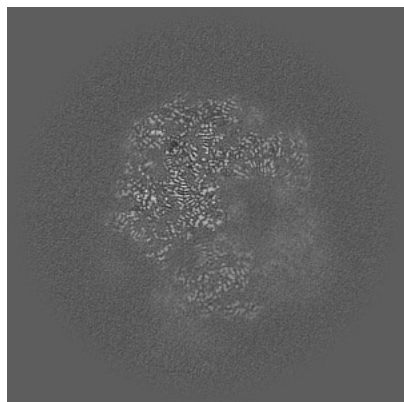


Z Index: 256

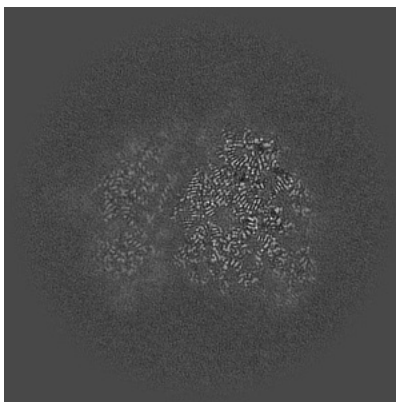
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

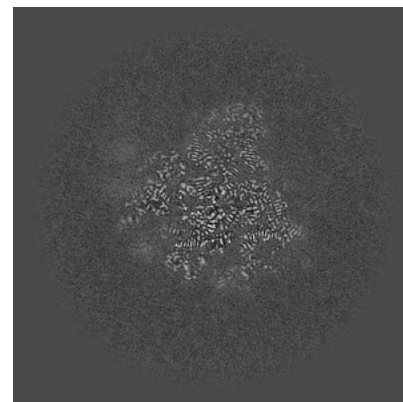
6.3.1 Primary map



X Index: 275

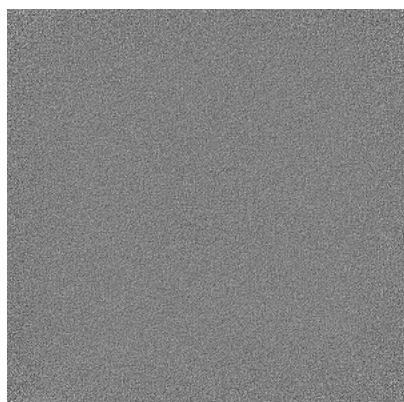


Y Index: 247

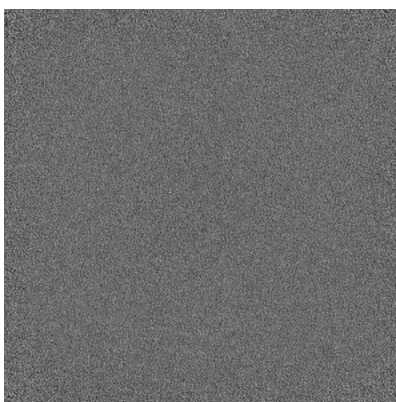


Z Index: 323

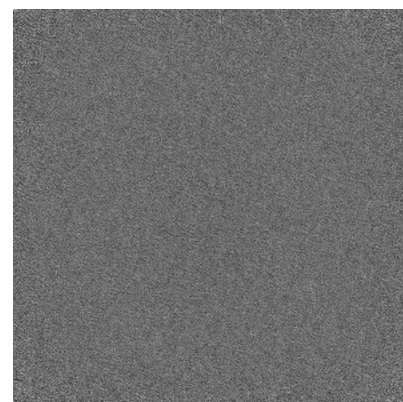
6.3.2 Raw map



X Index: 0



Y Index: 0

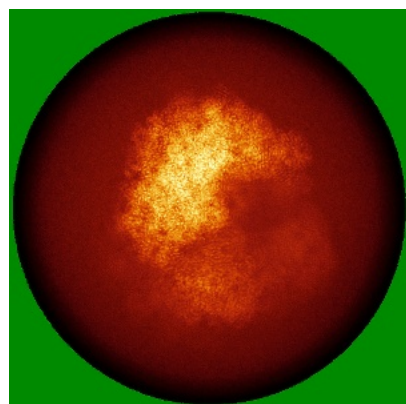


Z Index: 0

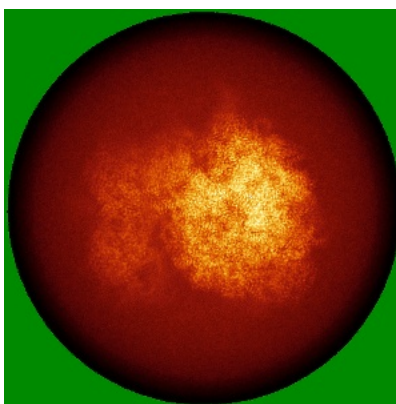
The images above show the largest variance slices of the map in three orthogonal directions.

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

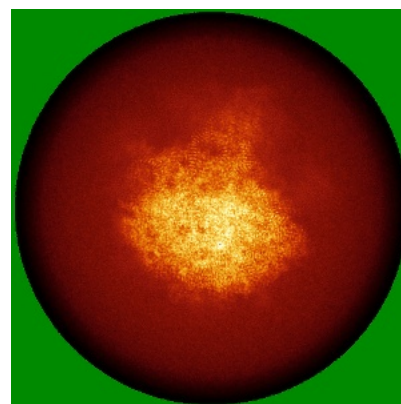
6.4.1 Primary map



X

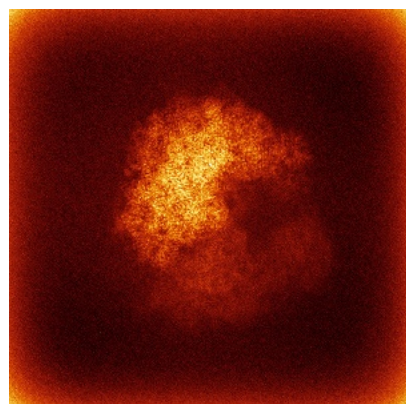


Y

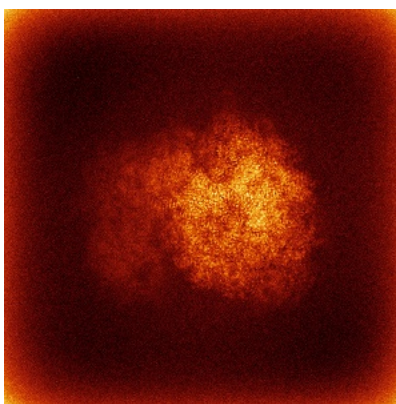


Z

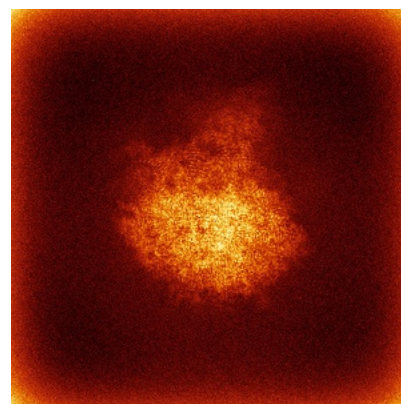
6.4.2 Raw map



X



Y

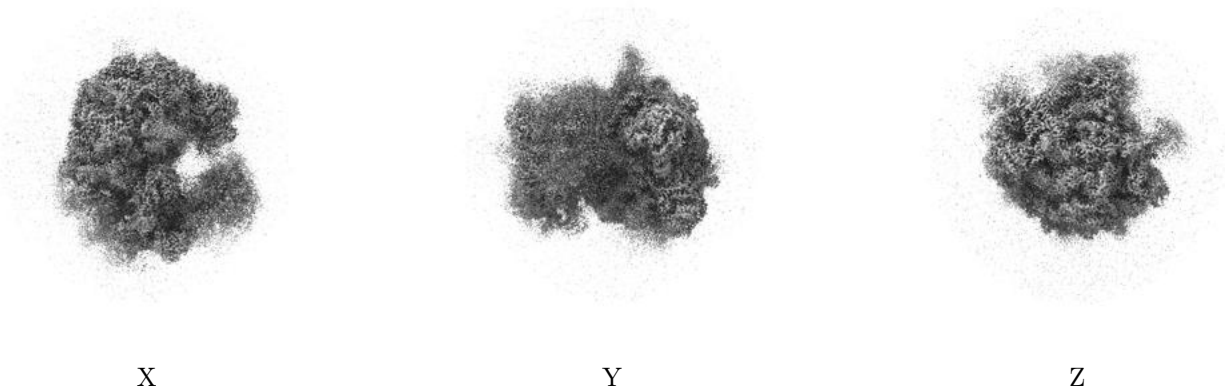


Z

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

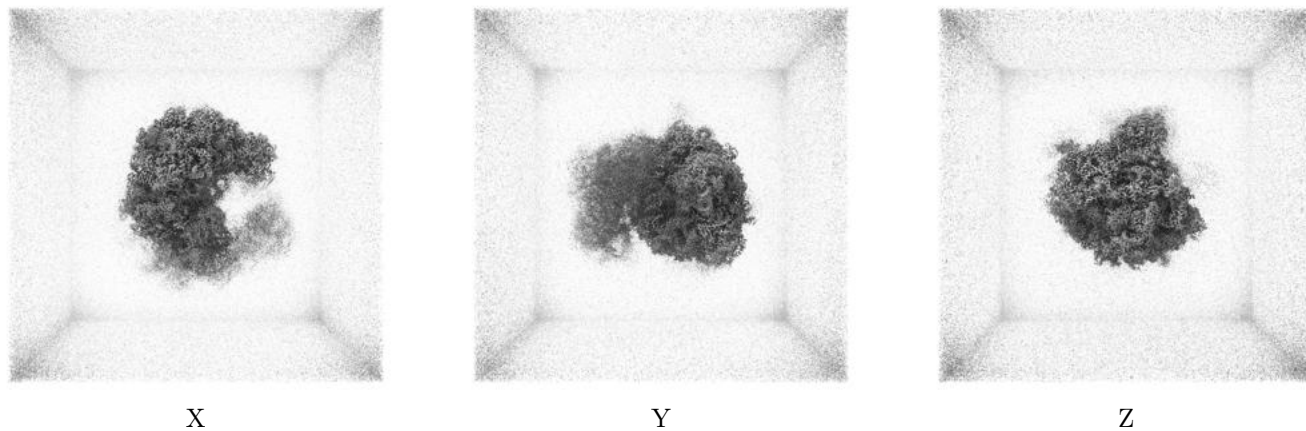
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.26. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

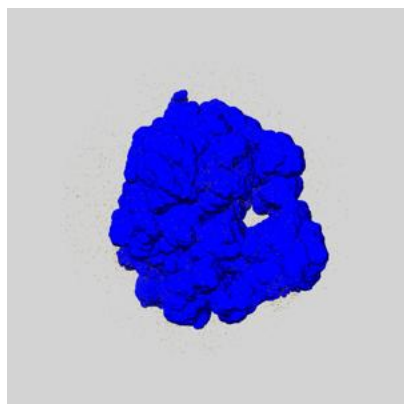
6.6 Mask visualisation [i](#)

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

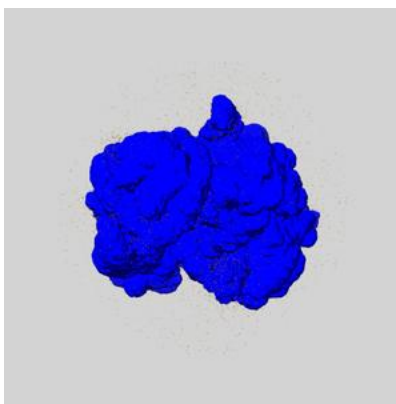
A mask typically either:

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

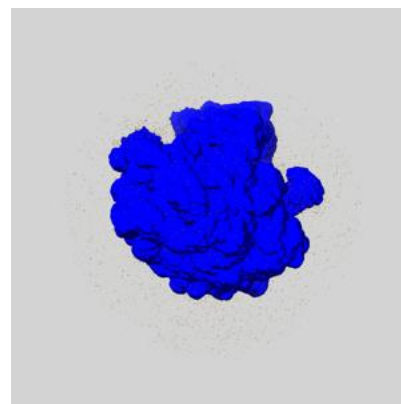
6.6.1 emd_43972_msk_1.map [i](#)



X



Y

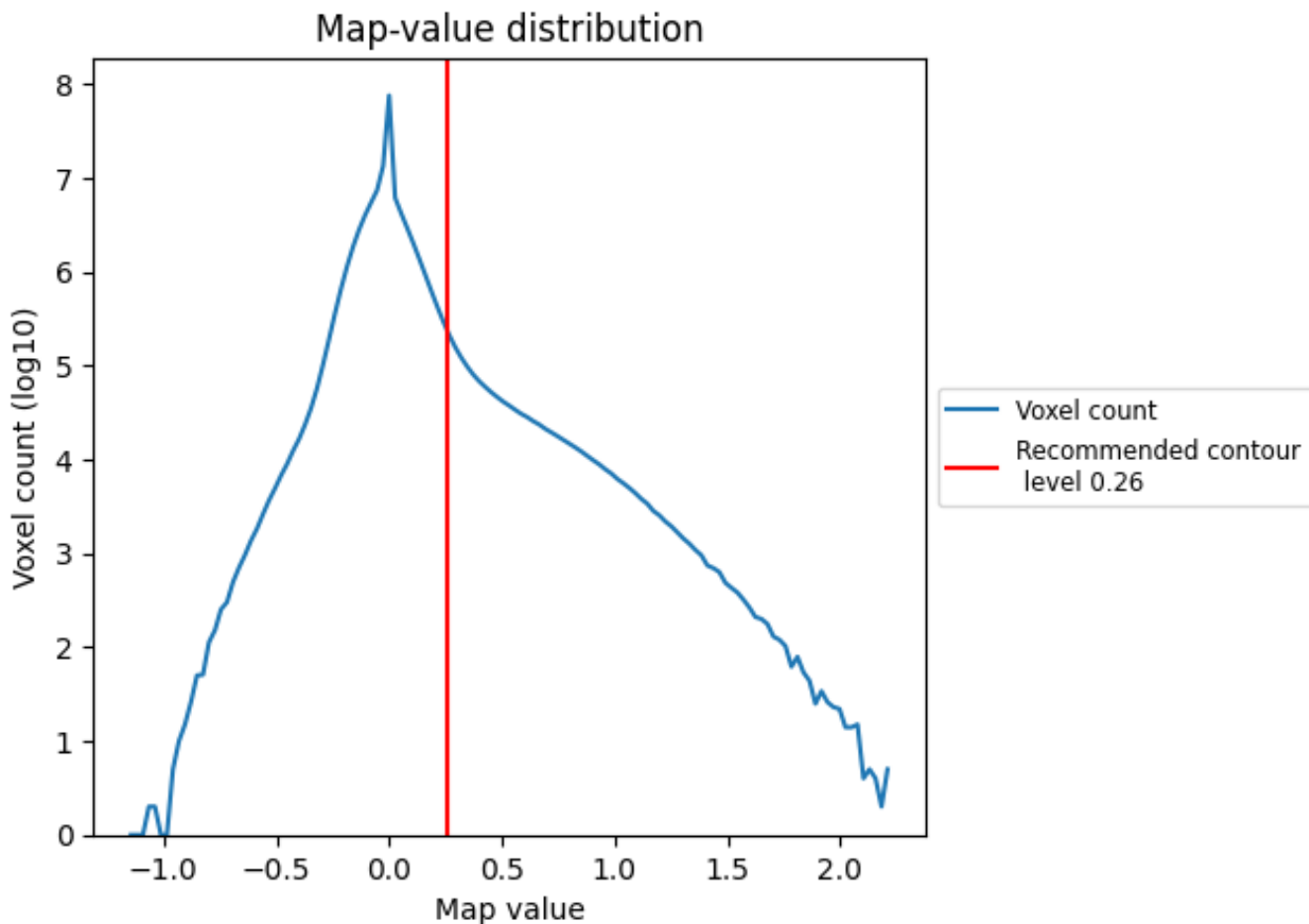


Z

7 Map analysis [i](#)

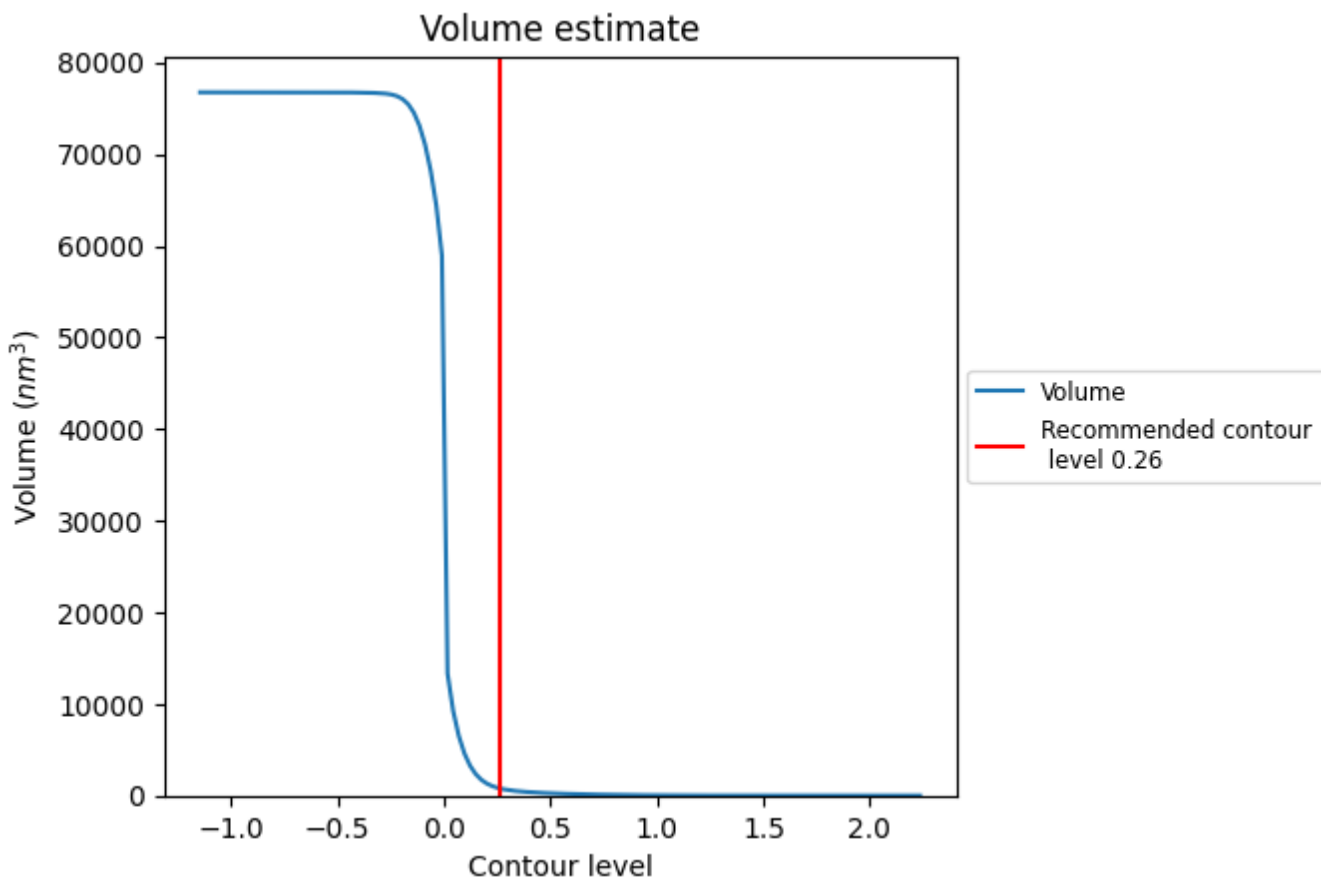
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

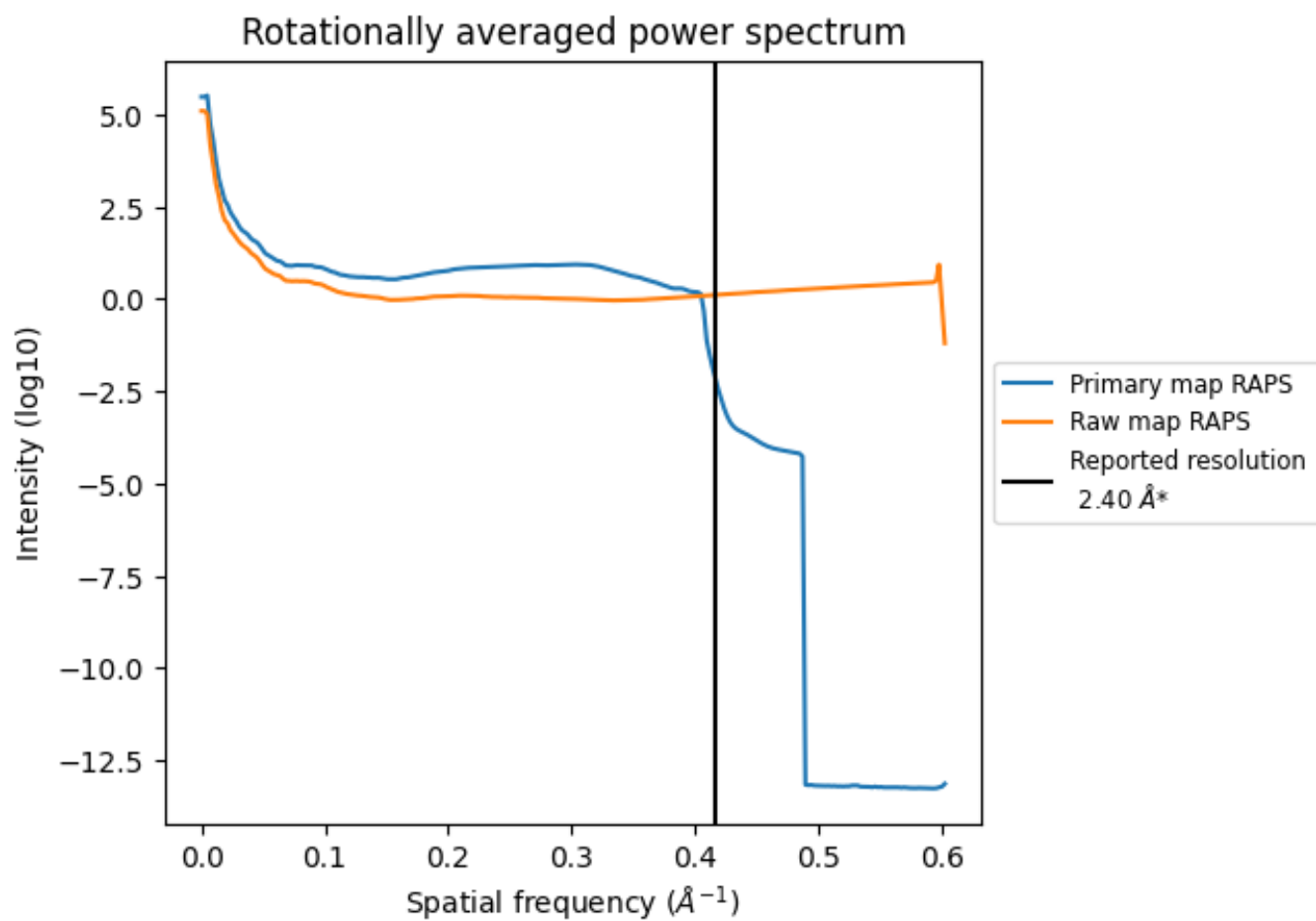
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 798 nm³; this corresponds to an approximate mass of 720 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](#)

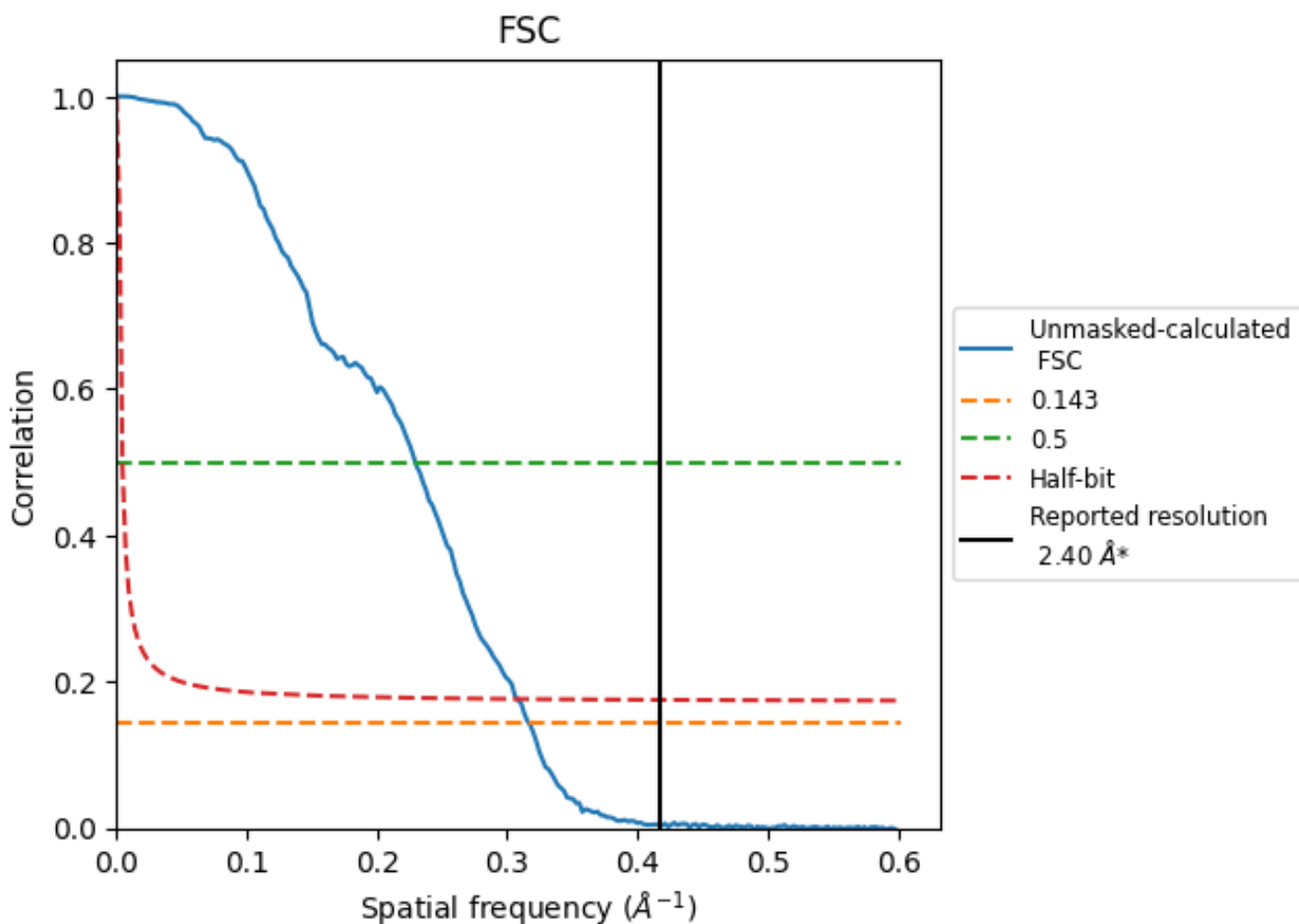


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

8.2 Resolution estimates [i](#)

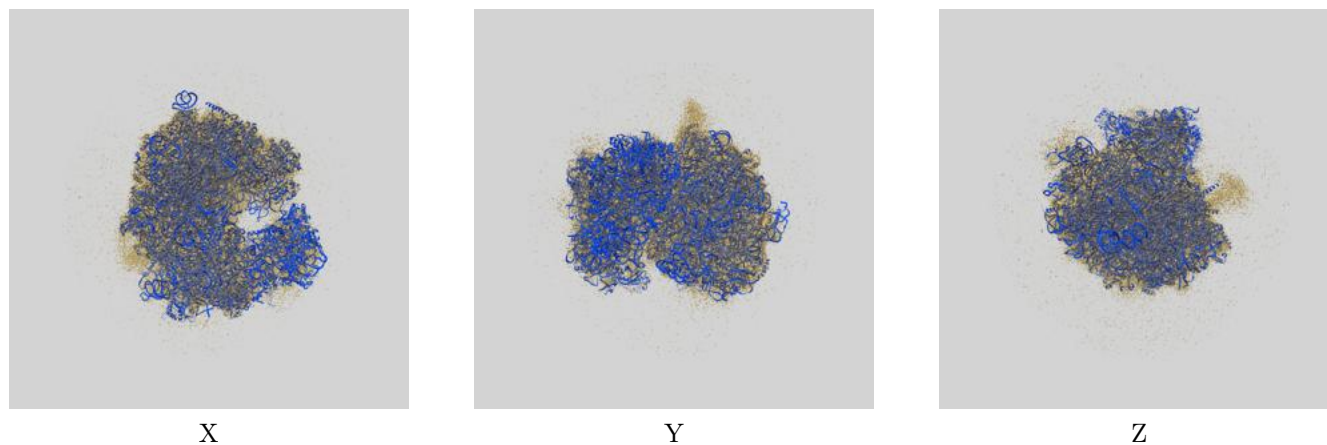
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	4.36	3.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.16 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

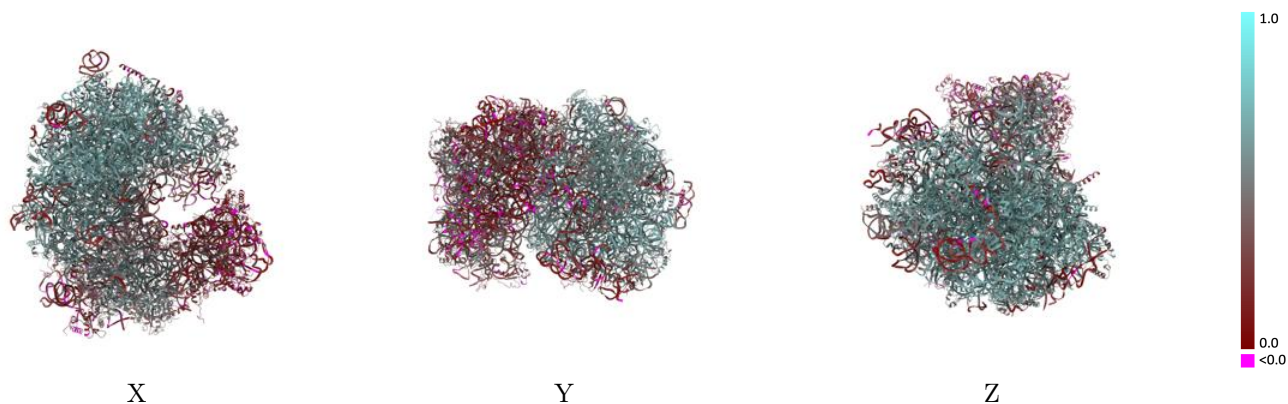
This section contains information regarding the fit between EMDB map EMD-43972 and PDB model 9AXT. Per-residue inclusion information can be found in section 3 on page 18.

9.1 Map-model overlay [i](#)



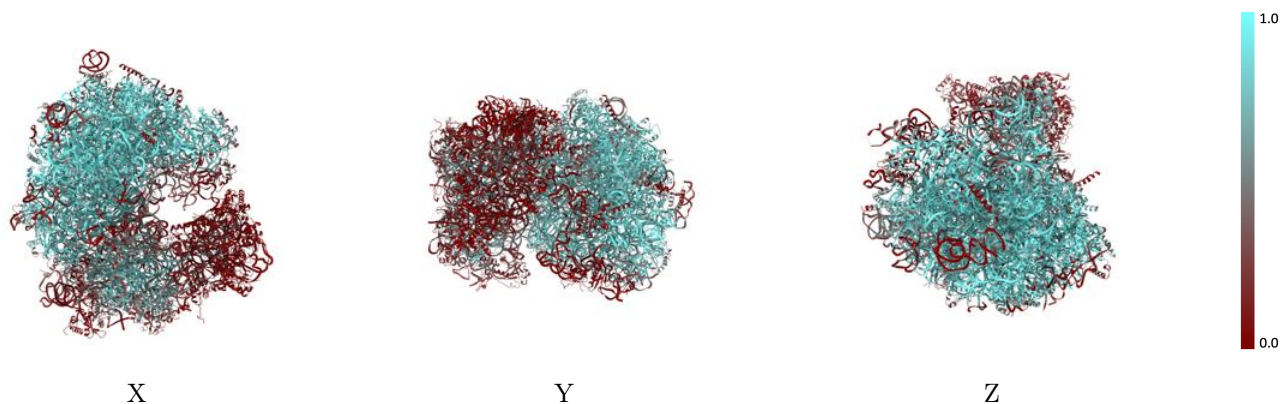
The images above show the 3D surface view of the map at the recommended contour level 0.26 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



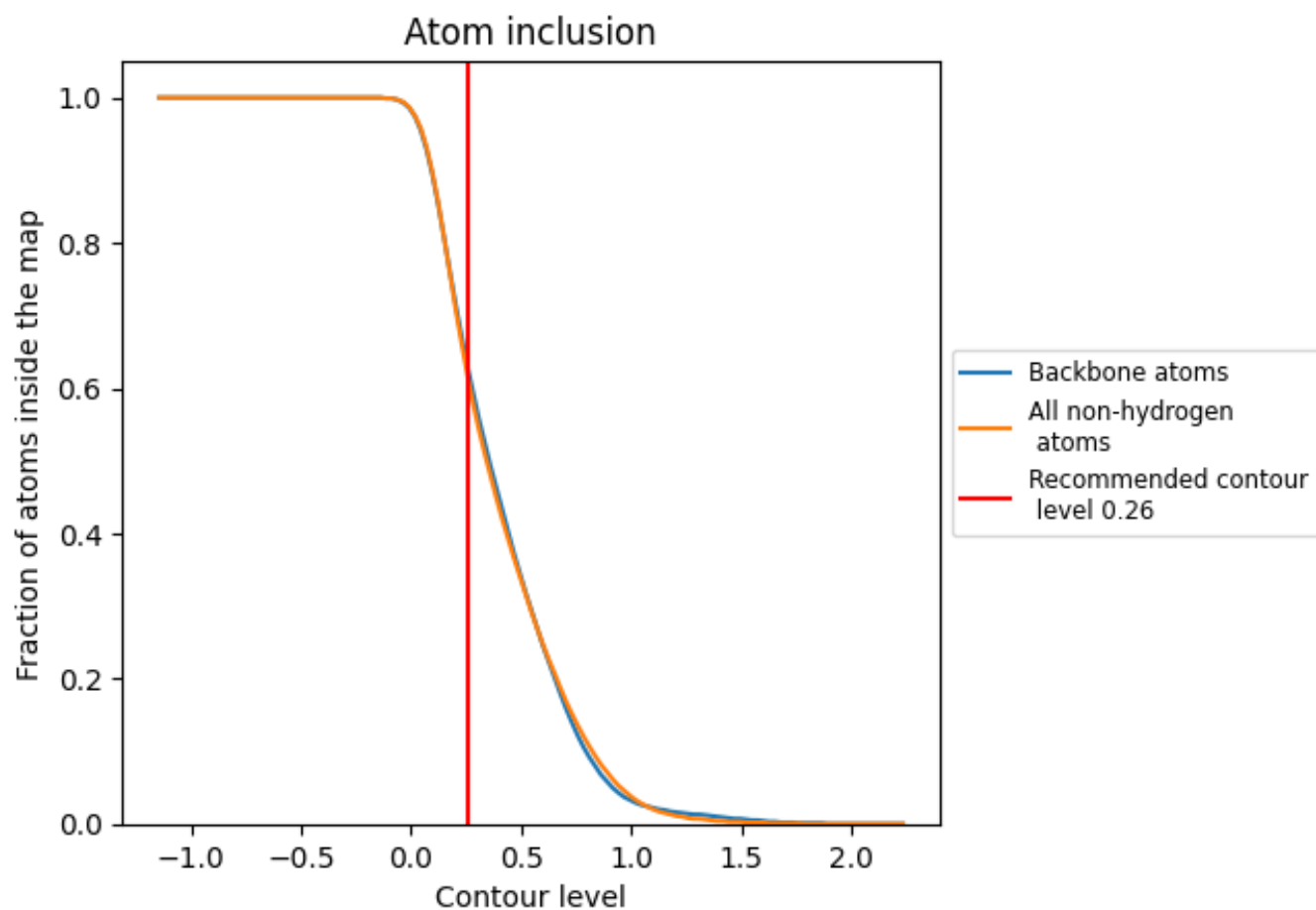
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.26).

9.4 Atom inclusion [i](#)



At the recommended contour level, 62% of all backbone atoms, 61% 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 (0.26) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6110	0.4710
AA	0.3830	0.3040
AD	0.4760	0.4750
AE	0.3310	0.4020
AF	0.5420	0.4860
AG	0.0350	0.1970
AH	0.5600	0.4930
AI	0.0700	0.2400
AJ	0.0850	0.2720
AK	0.1760	0.3090
AL	0.4000	0.4120
AM	0.3840	0.4250
AN	0.0180	0.1400
AO	0.5670	0.4850
AP	0.0020	0.1310
AQ	0.4300	0.4500
AR	0.3800	0.4060
AS	0.0380	0.1410
AT	0.0660	0.2240
AU	0.1050	0.2880
AV	0.0490	0.1830
AW	0.0630	0.2100
Aa	0.0760	0.2020
Ab	0.5120	0.4800
Ac	0.7430	0.5550
Ad	0.1950	0.3170
Ae	0.2370	0.3540
Af	0.0200	0.1580
Ag	0.4830	0.4510
Ah	0.2880	0.4020
Ai	0.0820	0.3060
Aj	0.0540	0.2630
Ak	0.0220	0.2230
B0	0.7550	0.5840
B1	0.7120	0.5720



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Chain	Atom inclusion	Q-score
B2	0.7780	0.5350
B3	0.8450	0.5590
B4	0.8680	0.5760
BN	0.9080	0.6490
BO	0.9010	0.6430
BP	0.8980	0.6450
BQ	0.6680	0.5380
BR	0.6630	0.5350
BS	0.8430	0.6070
BT	0.7310	0.5850
BU	0.0610	0.2580
BV	0.1460	0.3590
BW	0.3270	0.3660
BX	0.7540	0.5940
BY	0.7320	0.5710
BZ	0.9730	0.6700
Ba	0.8950	0.6410
Bb	0.9090	0.6520
Bc	0.9020	0.6490
Bd	0.8390	0.6140
Be	0.8170	0.6100
Bf	0.7600	0.5740
Bg	0.5590	0.5040
Bh	0.8420	0.6260
Bi	0.7280	0.5810
Bj	0.8640	0.6230
Bk	0.8030	0.6140
Bl	0.7320	0.5650
Bm	0.9360	0.6580
Bn	0.8620	0.6210
Bo	0.6070	0.5150
Bp	0.8550	0.6230
Bq	0.9110	0.6470
Br	0.9230	0.6500
Bs	0.8970	0.6480
Bt	0.8000	0.6100
Bu	0.8170	0.6170
Bv	0.9600	0.6670
Bw	0.5920	0.5100
Bx	0.7080	0.5240
By	0.6030	0.5620