



Full wwPDB EM Validation Report ⓘ

Oct 13, 2024 – 03:45 AM EDT

PDB ID : 9AXV
EMDB ID : EMD-43976
Title : 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:

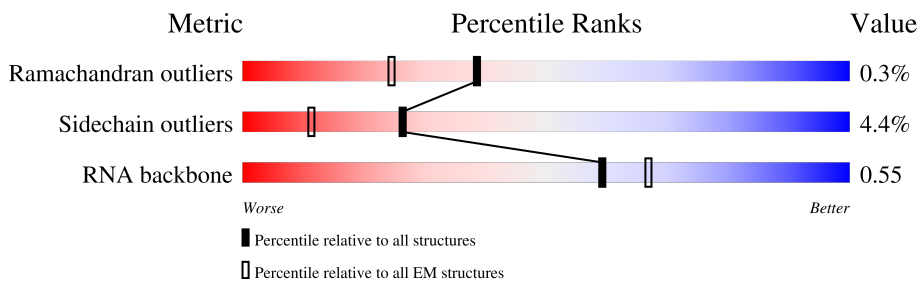
EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

1 Overall quality at a glance

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	
2	AD	292	
3	AE	252	
4	AF	253	
5	AG	249	
6	AH	262	
7	AI	203	
8	AJ	239	

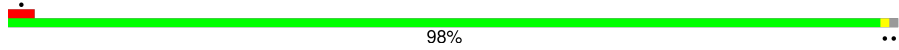



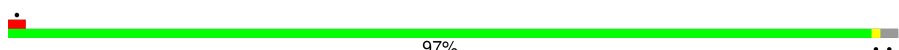
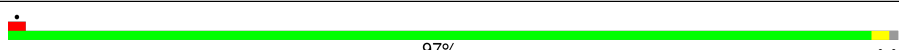
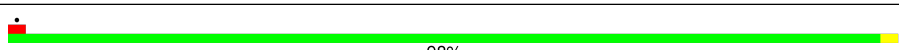
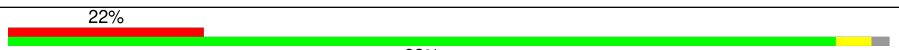
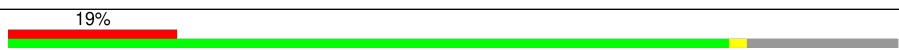

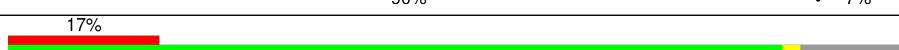



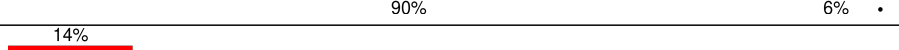
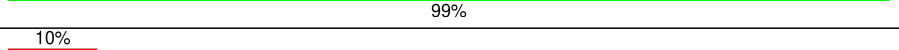
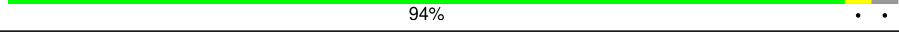
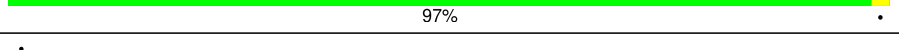
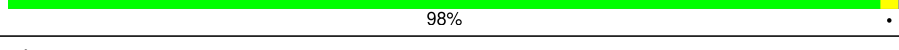

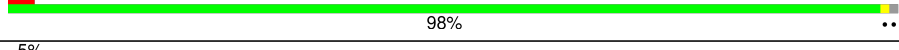
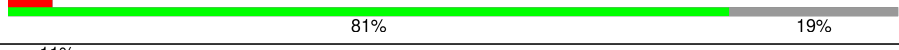
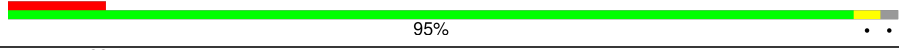
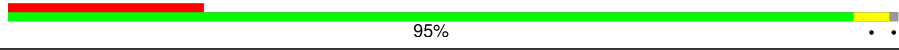

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Mol	Chain	Length	Quality of chain
9	AK	195	77% 96%
10	AL	200	54% 90% 6%
11	AM	192	53% 86% 6% 7%
12	AN	147	61% 60% 37%
13	AO	152	31% 88% 6% 6%
14	AP	145	83% 81% 17%
15	AQ	151	23% 96%
16	AR	139	27% 88% 8%
17	AS	154	66% 71% 6% 23%
18	AT	140	44% 97%
19	AU	131	52% 80% 10% 10%
20	AV	152	82% 88% 5% 7%
21	AW	144	41% 90% 8%
22	Aa	118	53% 78% 8% 14%
23	Ab	87	33% 99%
24	Ac	130	95% 5%
25	Ad	143	78% 94% 5%
26	Ae	134	85% 91% 8%
27	Af	89	63% 76% 22%
28	Ag	119	12% 78% 18%
29	Ah	83	70% 92% 6%
30	Ai	68	54% 90% 7%
31	Aj	56	43% 93% 5%
32	Ak	61	98% 95%
33	B0	106	84% 12%

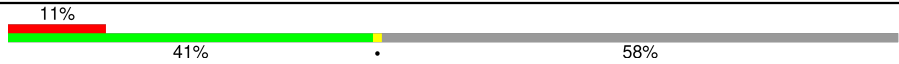

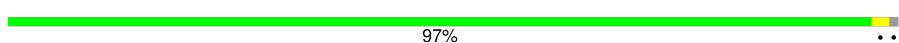
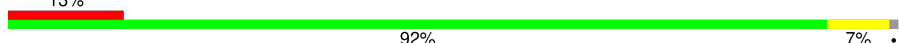



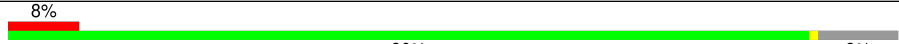
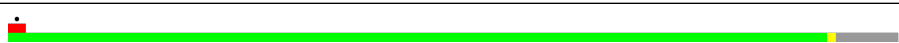

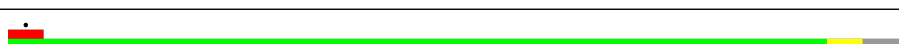

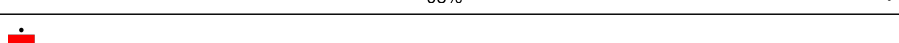
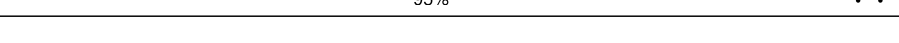
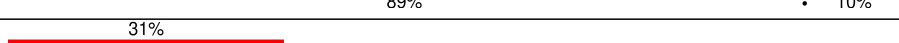
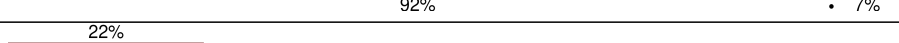
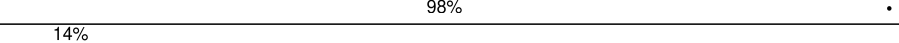
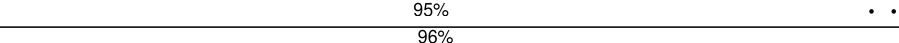
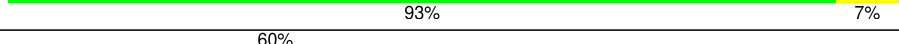
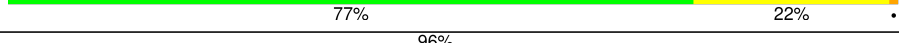

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Mol	Chain	Length	Quality of chain
34	B1	94	 98%
35	B2	3498	 72%
36	B3	246	 39%
37	B4	165	 76%
38	BN	253	 97%
39	BO	388	 97%
40	BP	363	 98%
41	BQ	294	 93%
42	BR	195	 81%
43	BS	251	 90%
44	BT	259	 87%
45	BU	189	 85%
46	BV	221	 81%
47	BW	174	 90%
48	BX	208	 99%
49	BY	134	 94%
50	BZ	201	 97%
51	Ba	197	 98%
52	Bb	187	 78%
53	Bc	187	 98%
54	Bd	193	 81%
55	Be	176	 95%
56	Bf	160	 95%
57	Bg	117	 82%
58	Bh	139	 92%

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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	
76	Am	314	
77	Sm	77	
78	Sn	75	
79	S3	10	

2 Entry composition [i](#)

There are 80 unique types of molecules in this entry. The entry contains 200604 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
14	AP	121	Total	C	N	O	S	0	0
			884	549	151	177	7		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
			Total	C	N	O	S		
28	Ag	97	795	491	167	132	5	0	0

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

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

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

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

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

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

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

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

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

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

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

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

- 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	133	Total	C	N	O	S	0	0
			1031	641	203	186	1		

- Molecule 76 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Am	314	Total	C	N	O	S	0	0
			2458	1549	422	478	9		

- Molecule 77 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
77	Sm	77	1625	722	292	534	77	0	0

- Molecule 78 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
78	Sn	75	1606	716	297	518	75	0	0

- Molecule 79 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
79	S3	10	204	92	27	75	10	0	0

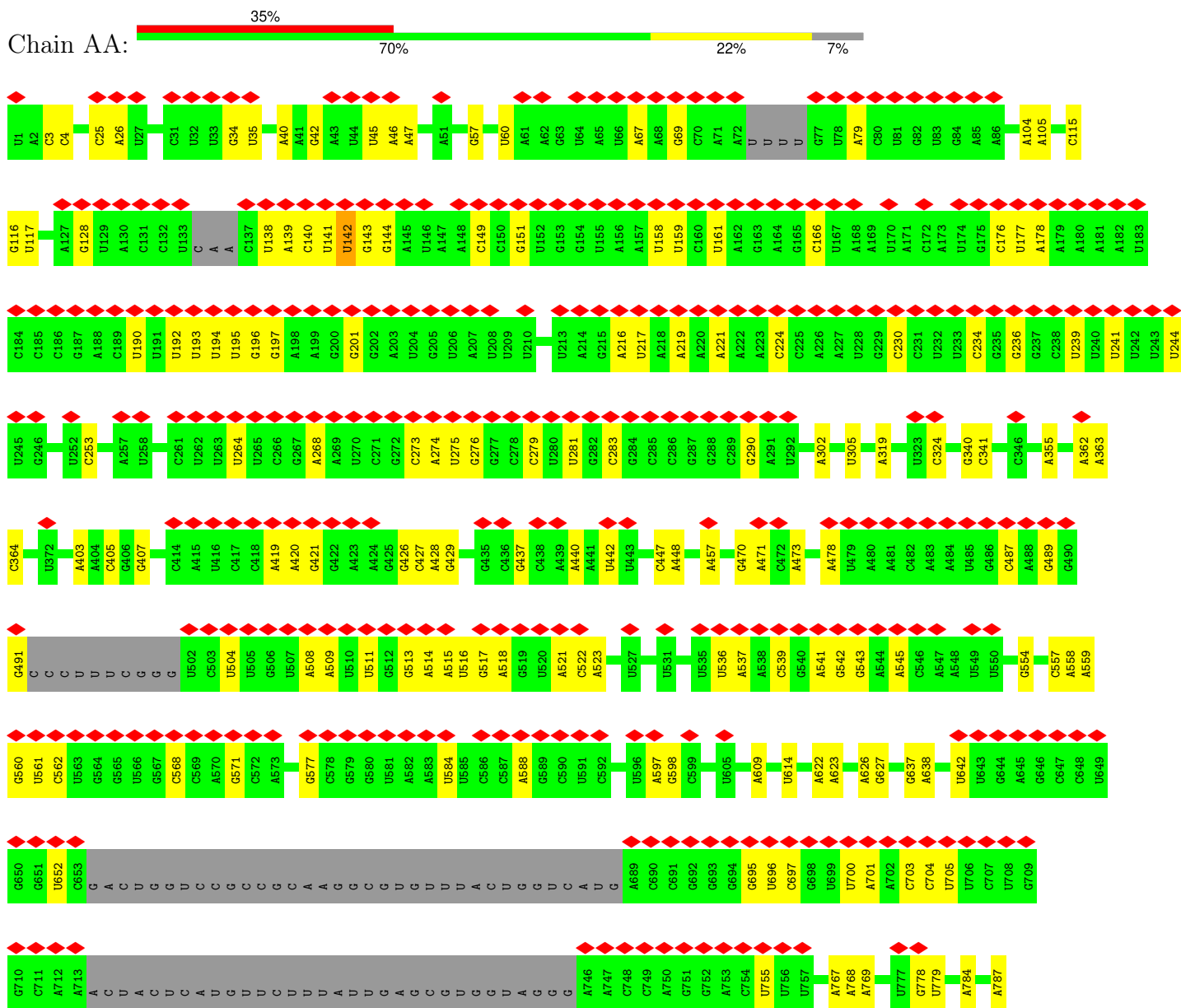
- Molecule 80 is ZINC ION (three-letter code: ZN) (formula: Zn).

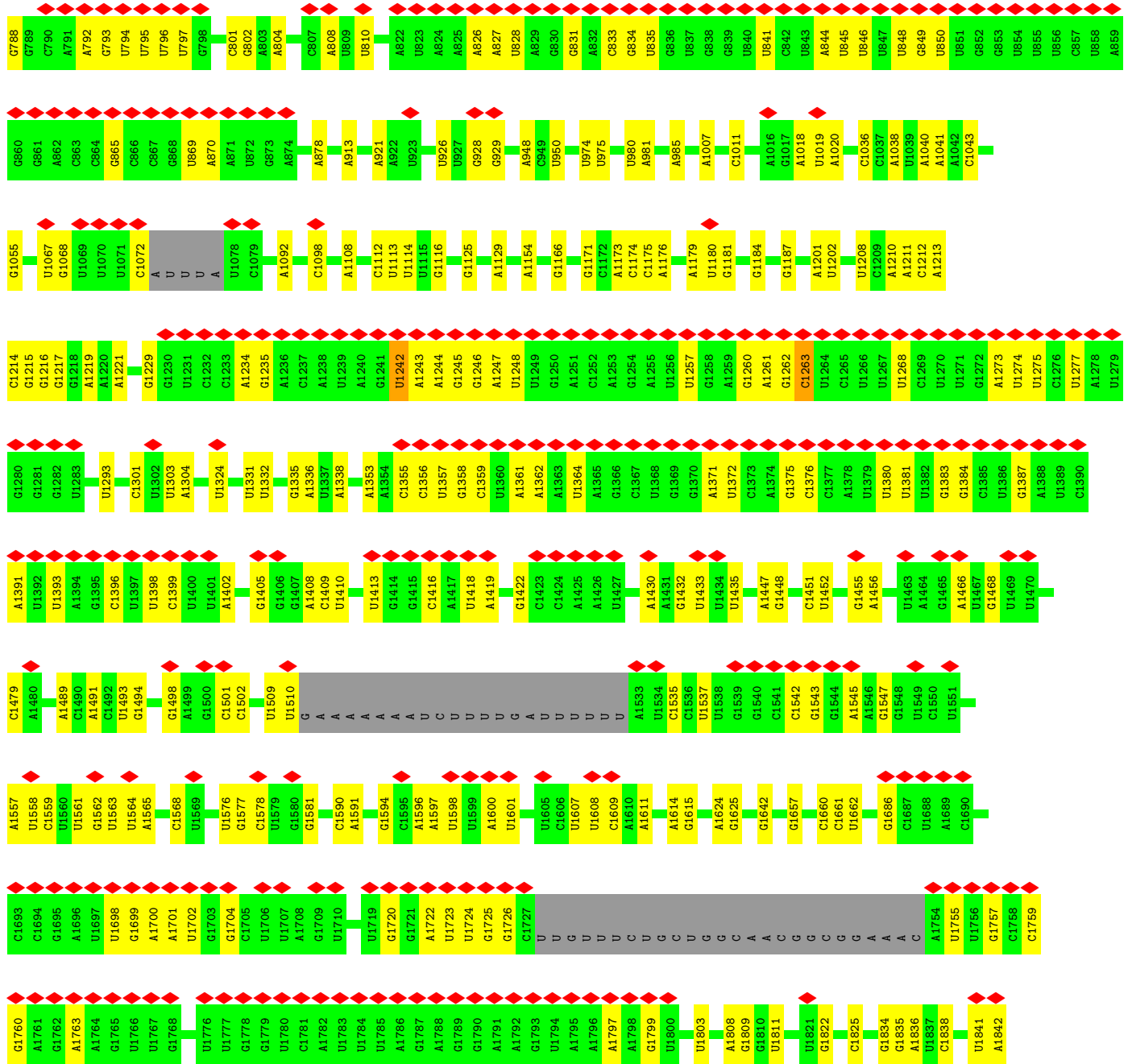
Mol	Chain	Residues	Atoms		AltConf
80	AA	1	Total	Zn	0
			1	1	
80	Ag	1	Total	Zn	0
			1	1	
80	Ah	1	Total	Zn	0
			1	1	
80	B0	1	Total	Zn	0
			1	1	
80	B1	1	Total	Zn	0
			1	1	
80	Bv	1	Total	Zn	0
			1	1	

3 Residue-property plots

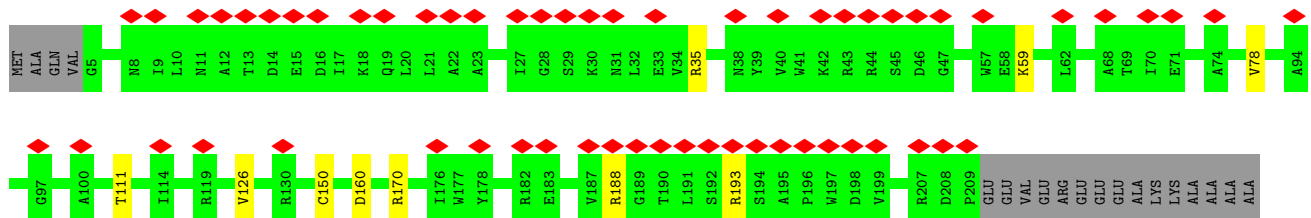
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

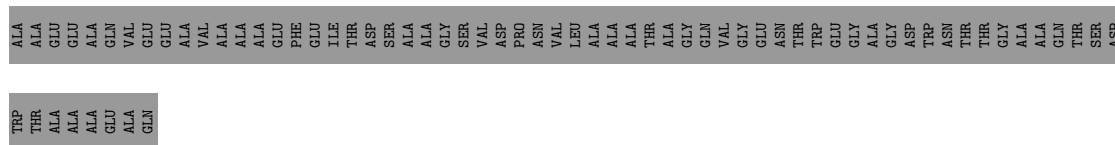
- Molecule 1: 18S ribosomal RNA



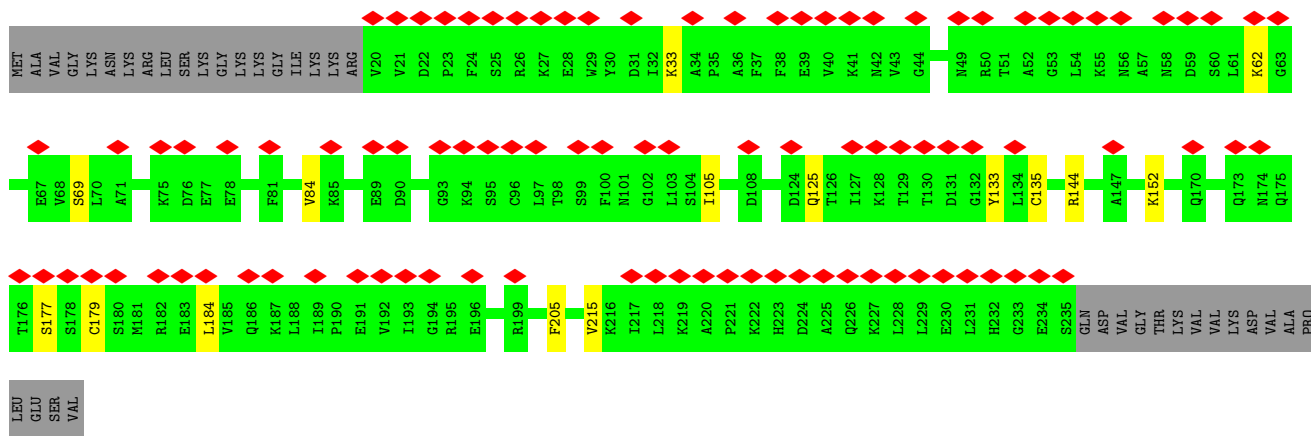
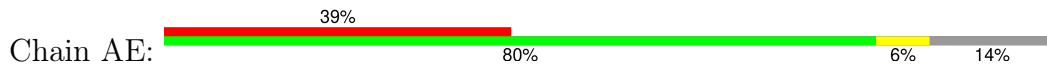


● Molecule 2: Small ribosomal subunit protein uS2A

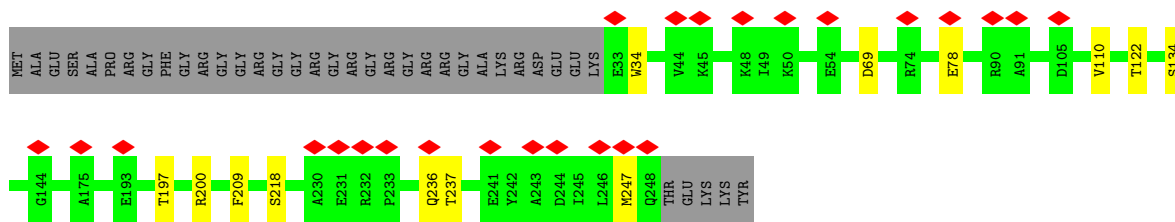
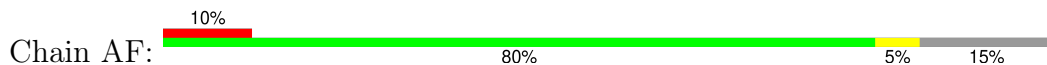




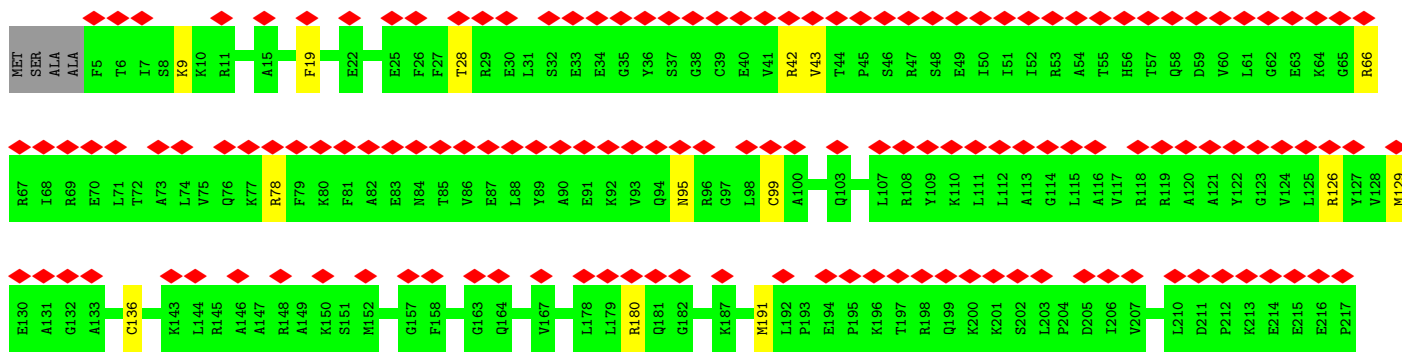
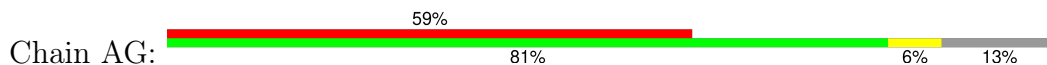
- Molecule 3: Small ribosomal subunit protein eS1B

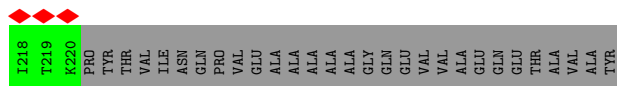


- Molecule 4: Small ribosomal subunit protein uS5

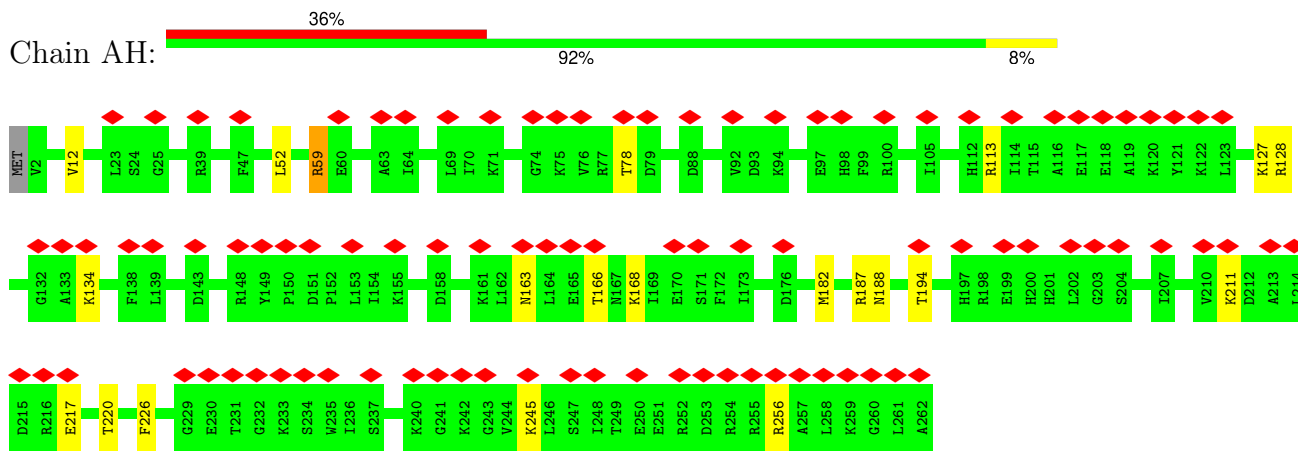


- Molecule 5: Small ribosomal subunit protein uS3

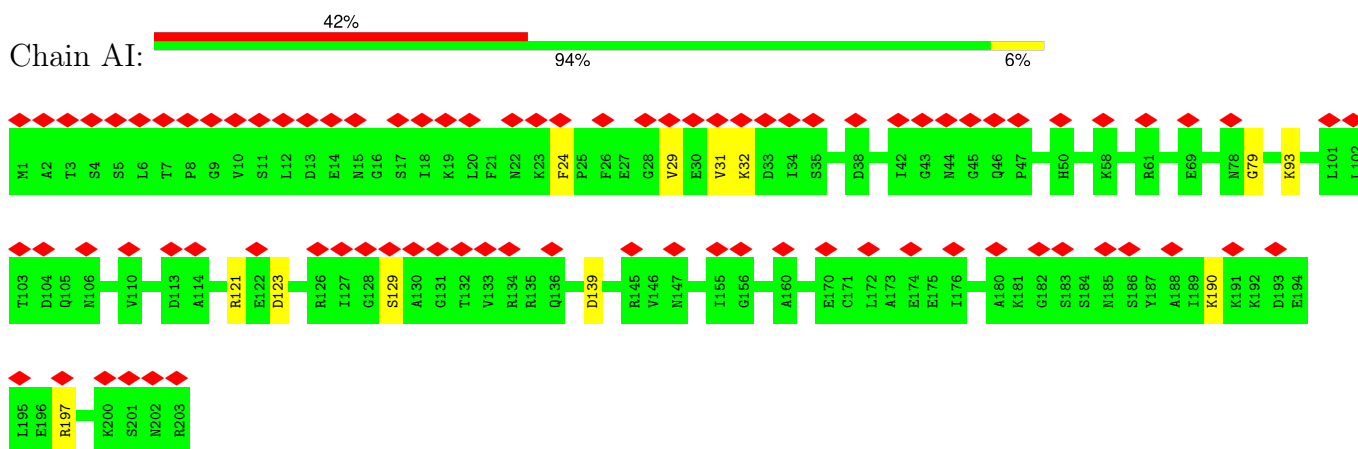




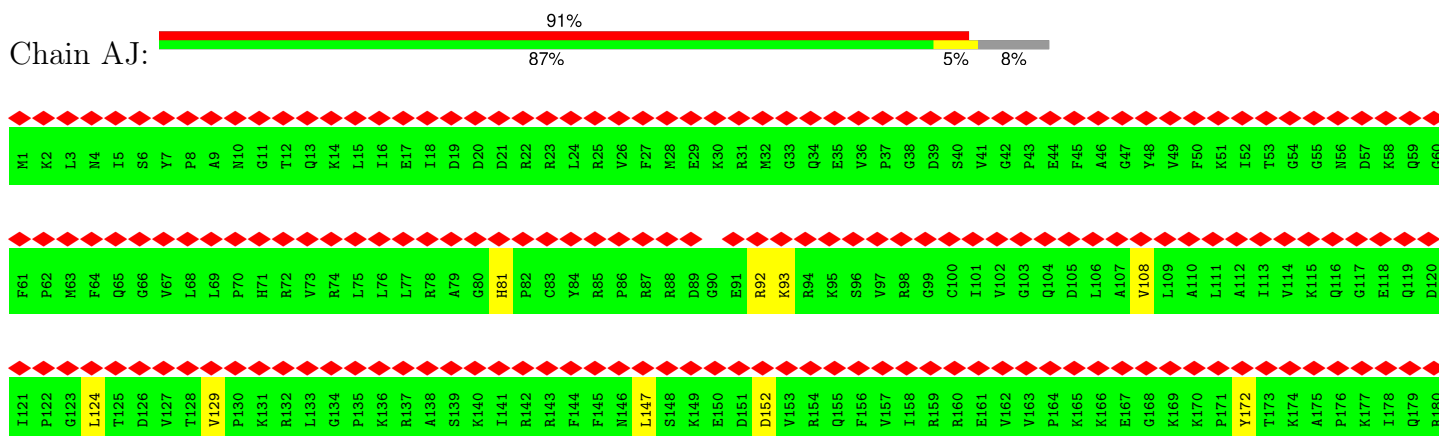
- Molecule 6: Small ribosomal subunit protein eS4C

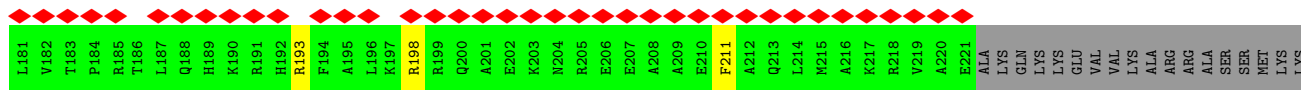


- Molecule 7: Small ribosomal subunit protein uS7A

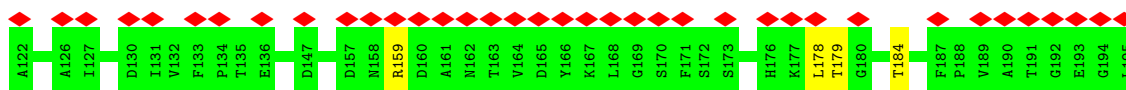
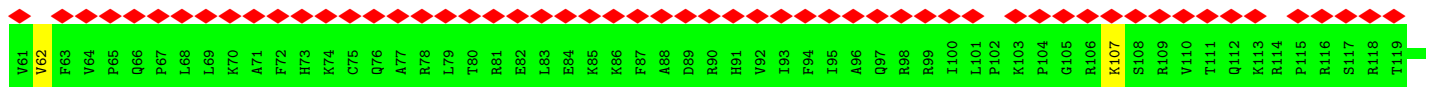
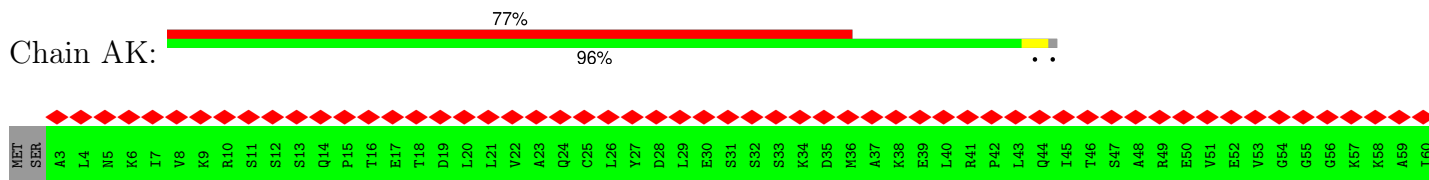


- Molecule 8: Small ribosomal subunit protein eS6B

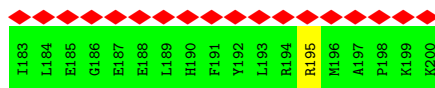
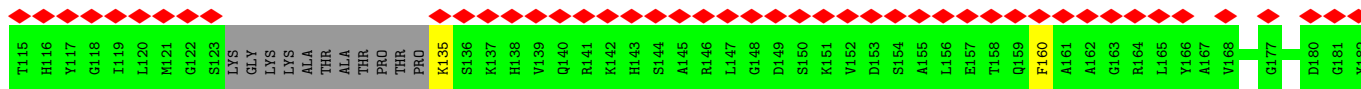
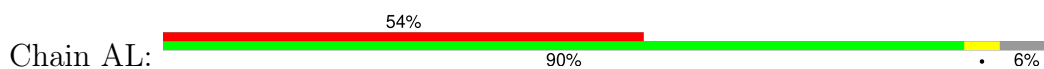




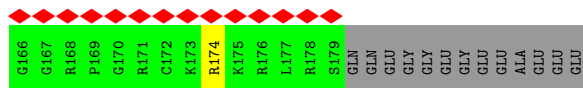
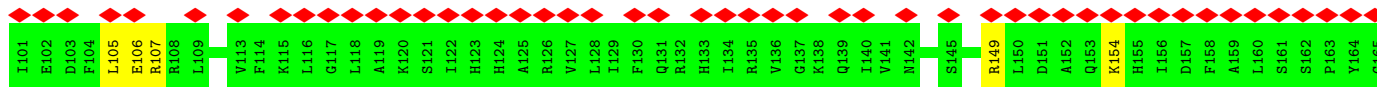
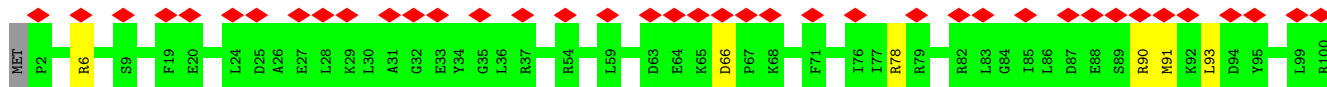
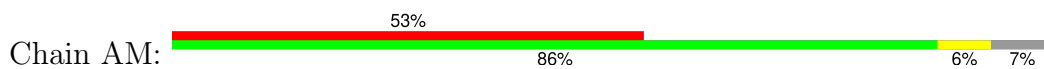
• Molecule 9: Small ribosomal subunit protein eS7



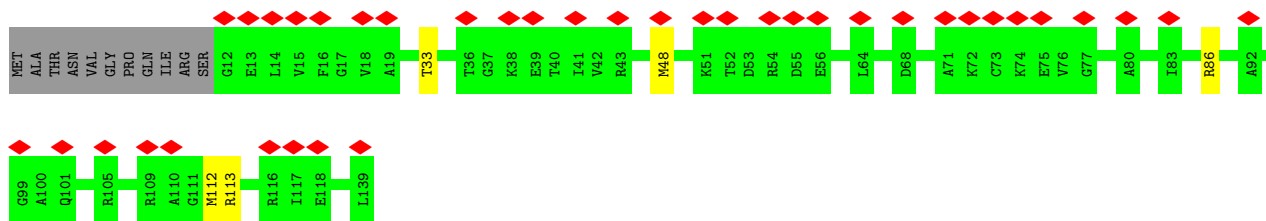
• Molecule 10: Small ribosomal subunit protein eS8B



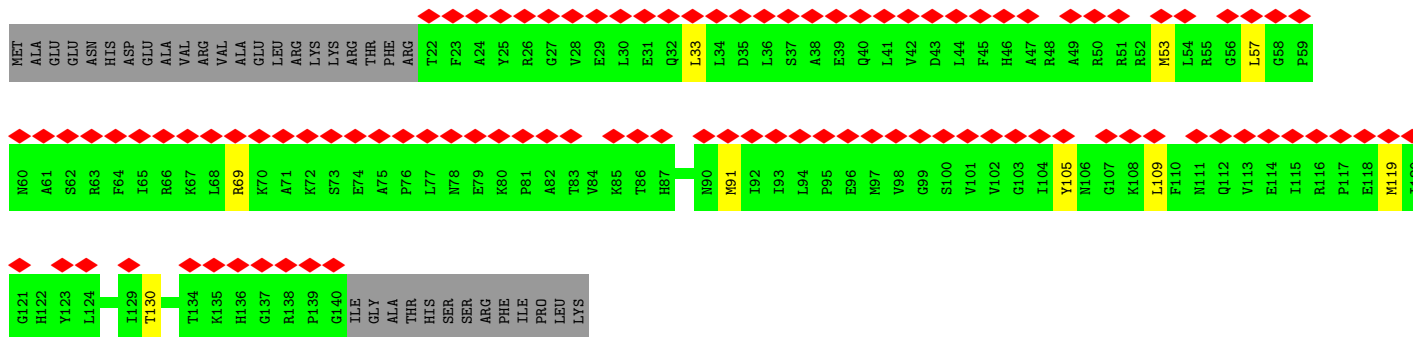
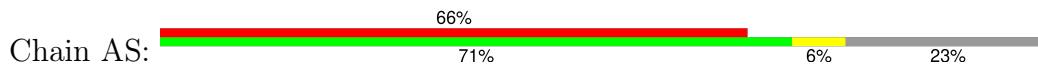
• Molecule 11: Small ribosomal subunit protein uS4B



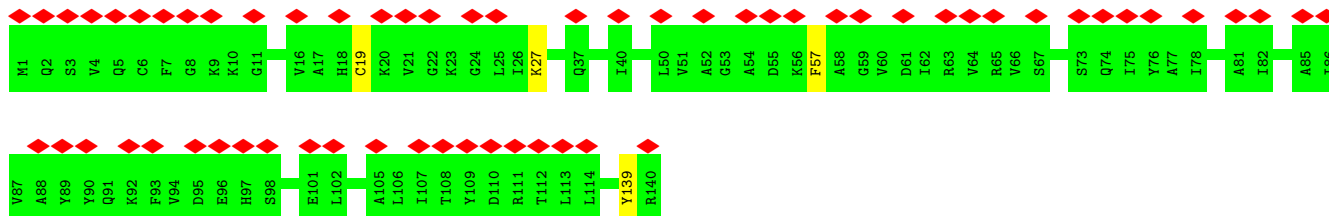
• Molecule 12: Small ribosomal subunit protein eS10B



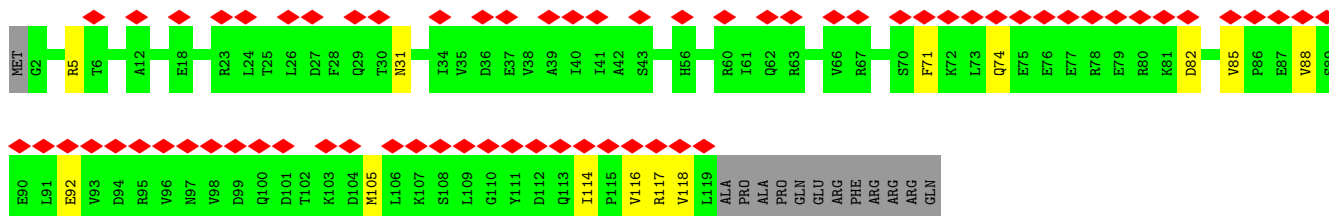
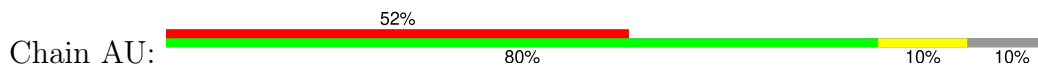
• Molecule 17: Small ribosomal subunit protein uS19B



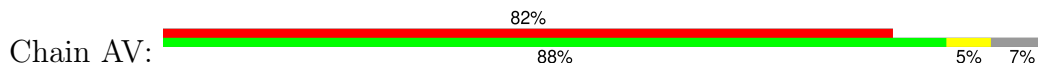
• Molecule 18: Small ribosomal subunit protein uS9A

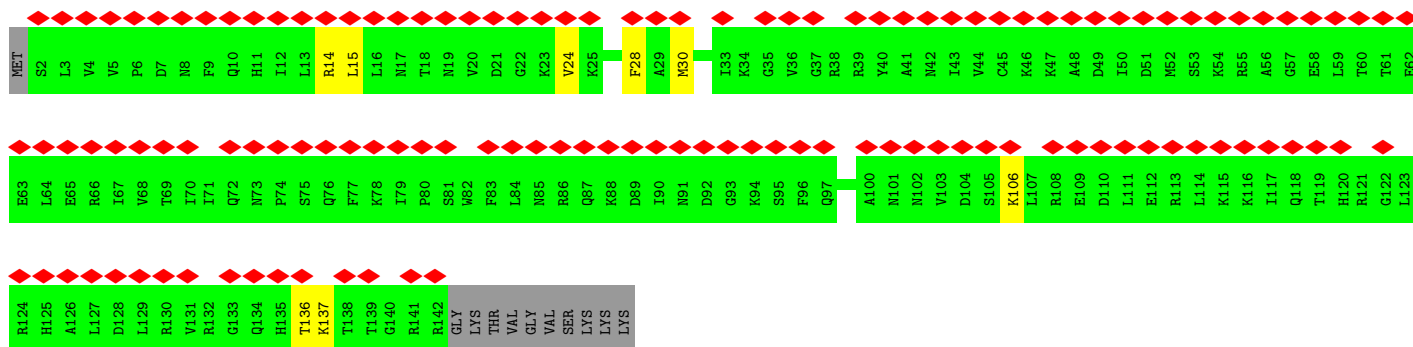


• Molecule 19: Small ribosomal subunit protein eS17A

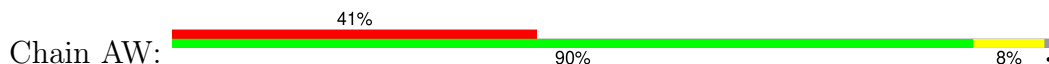


• Molecule 20: Small ribosomal subunit protein uS13B

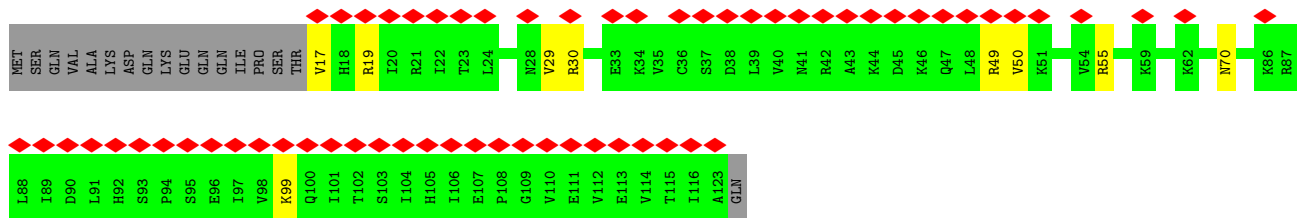
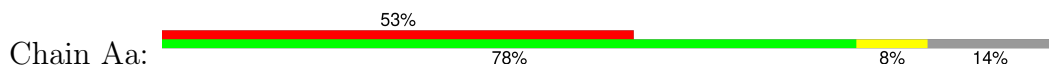




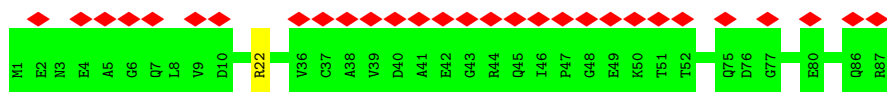
• Molecule 21: Small ribosomal subunit protein eS19A



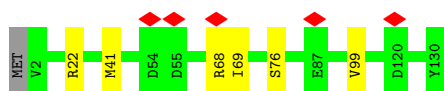
• Molecule 22: Small ribosomal subunit protein uS10



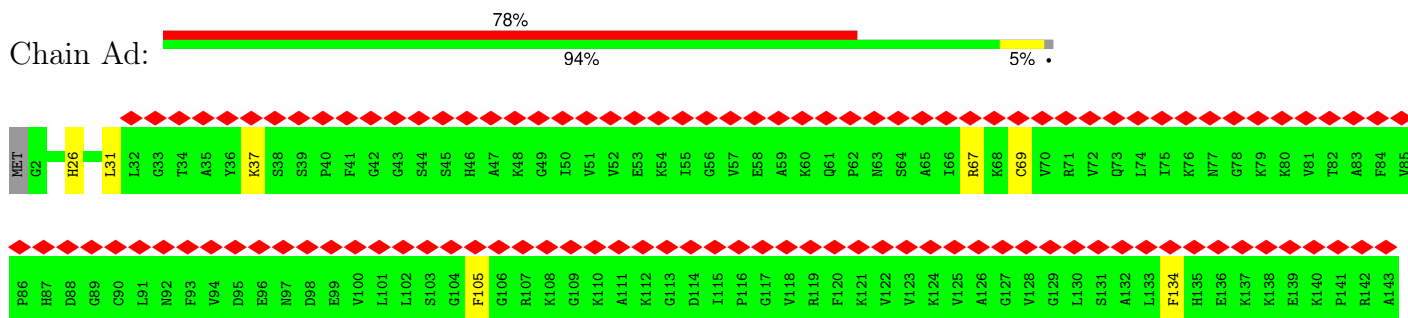
• Molecule 23: Small ribosomal subunit protein eS21



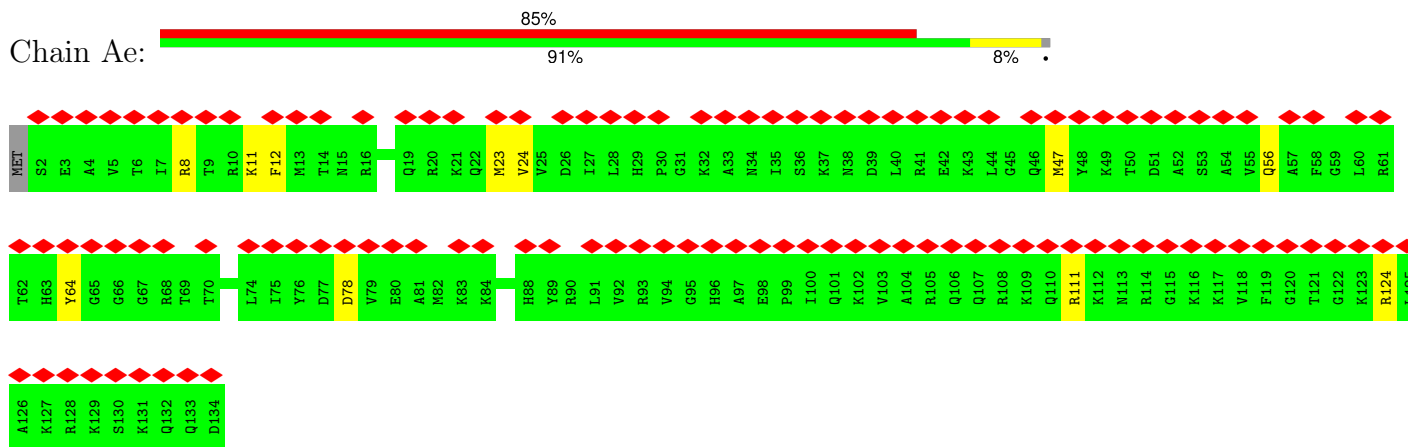
• Molecule 24: Small ribosomal subunit protein uS8A



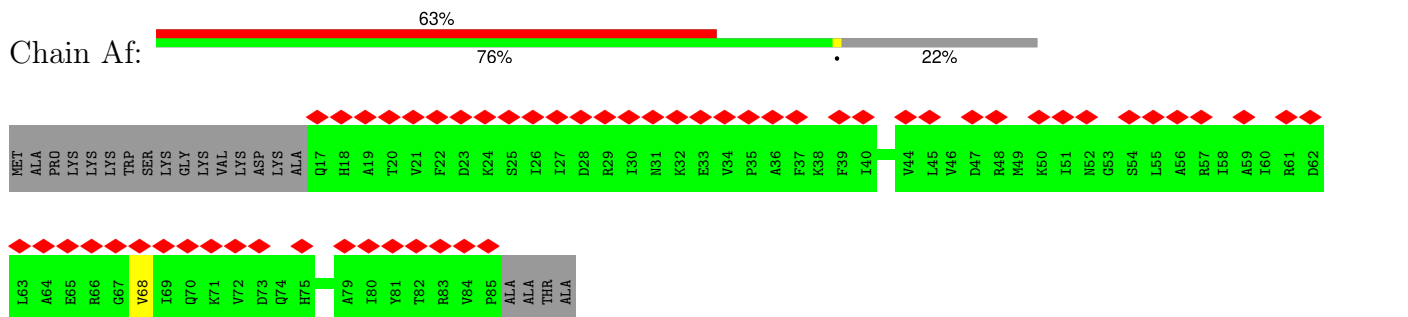
• Molecule 25: Small ribosomal subunit protein uS12A



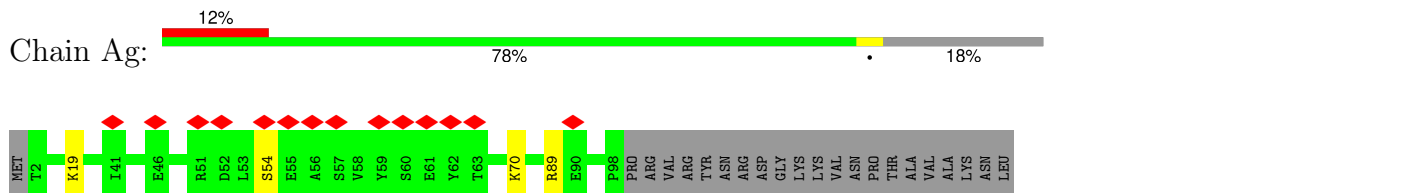
• Molecule 26: Small ribosomal subunit protein eS24A



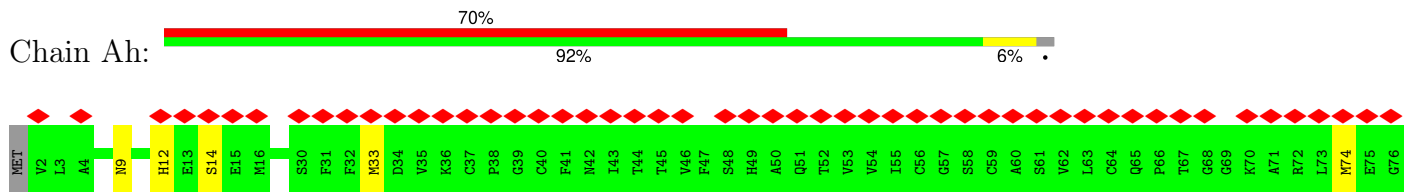
• Molecule 27: Small ribosomal subunit protein eS25A



• Molecule 28: Small ribosomal subunit protein eS26B

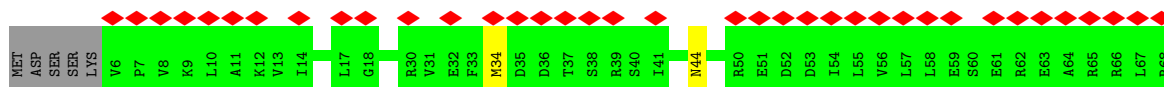
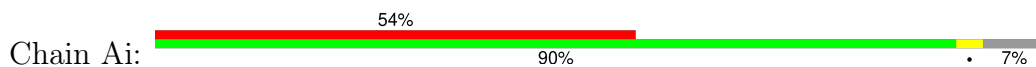


• Molecule 29: Small ribosomal subunit protein eS27

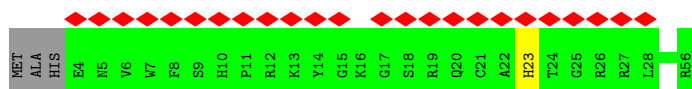
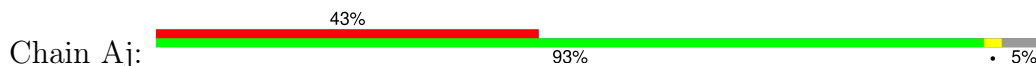




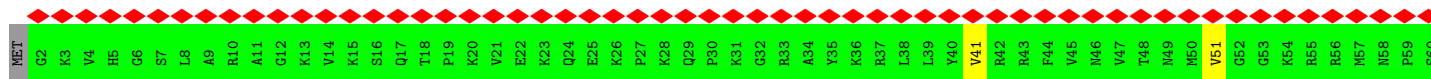
- Molecule 30: Small ribosomal subunit protein eS28A



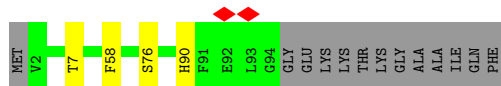
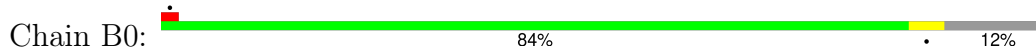
- Molecule 31: Small ribosomal subunit protein uS14



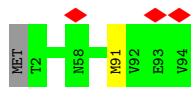
- Molecule 32: Small ribosomal subunit protein eS30B



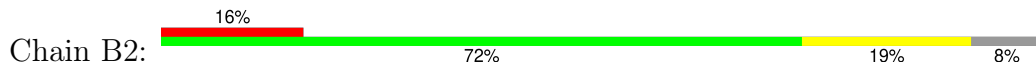
- Molecule 33: Large ribosomal subunit protein eL42

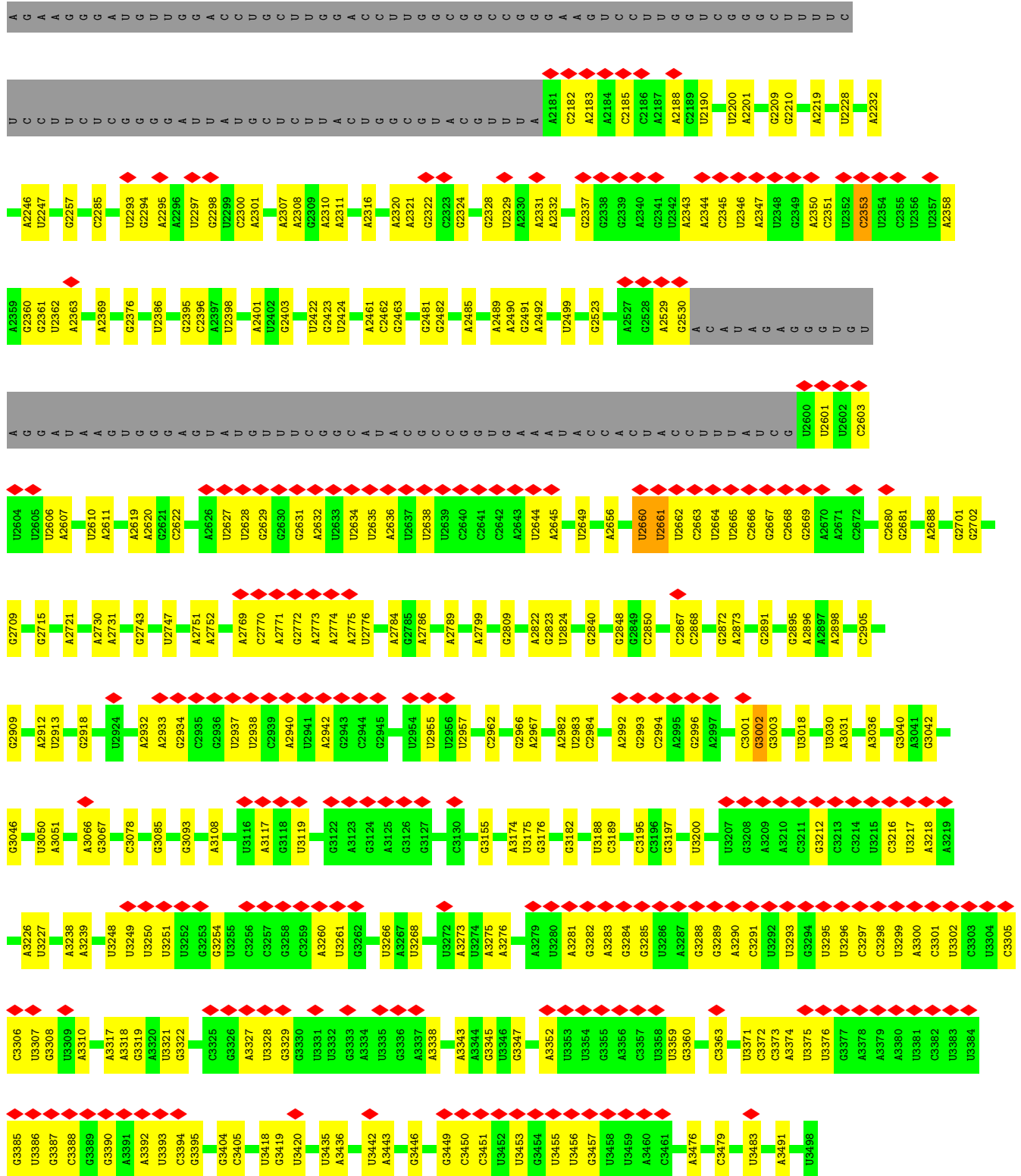


- Molecule 34: Large ribosomal subunit protein eL43A

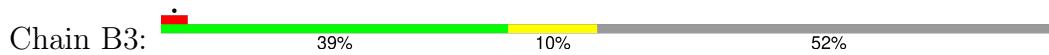


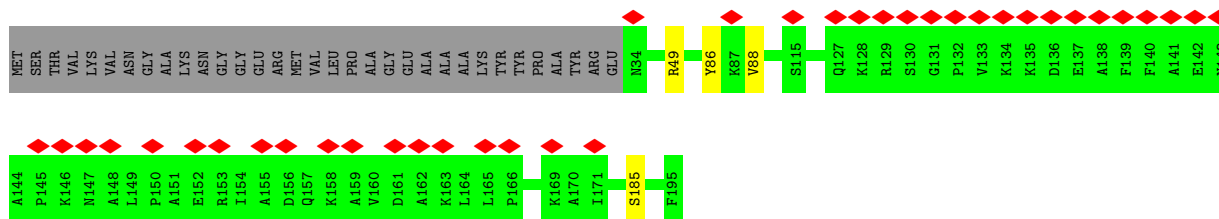
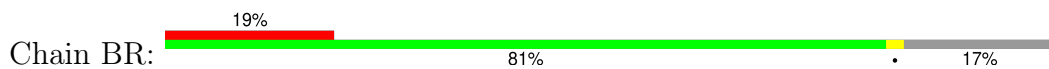
- Molecule 35: 28S ribosomal RNA



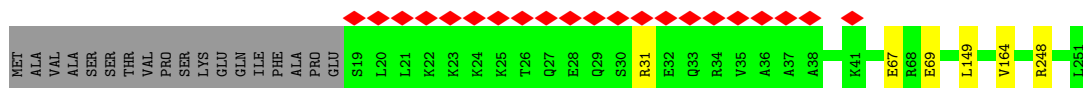


• Molecule 36: 5S ribosomal RNA

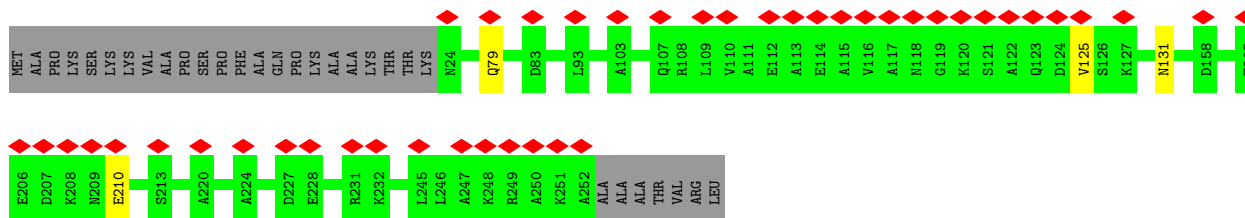
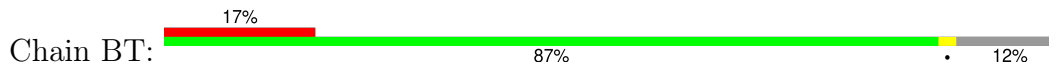




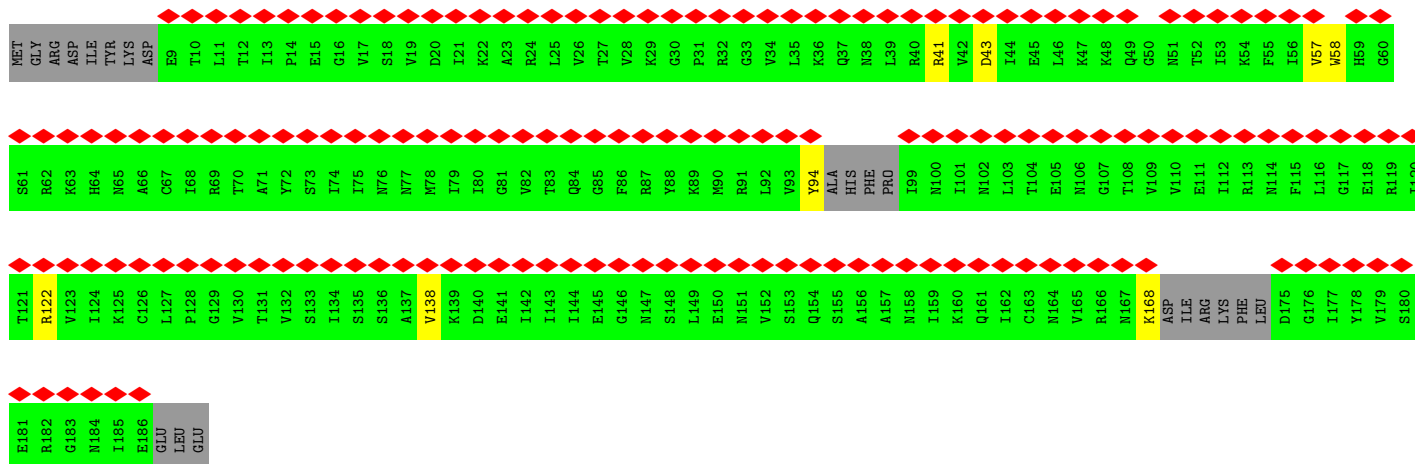
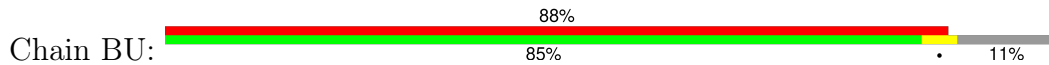
• Molecule 43: Large ribosomal subunit protein uL30C



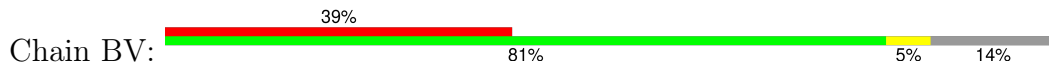
• Molecule 44: Large ribosomal subunit protein eL8

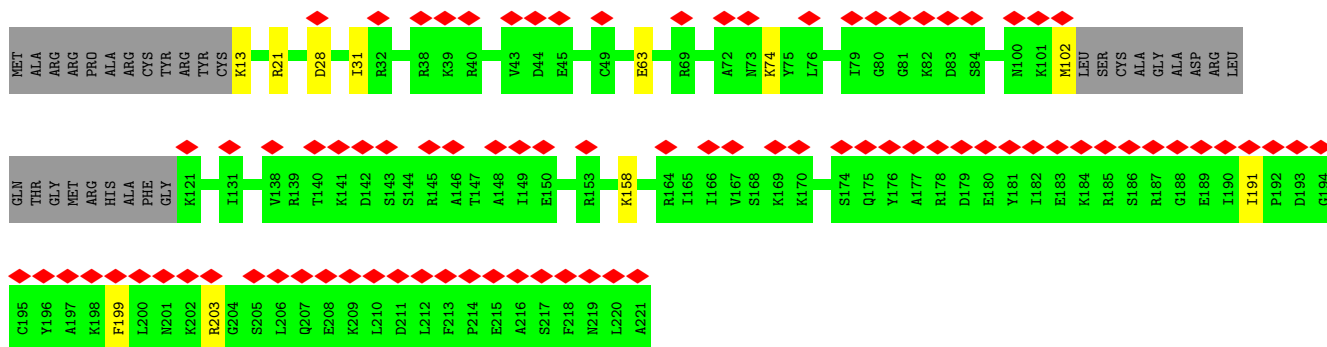


• Molecule 45: Large ribosomal subunit protein uL6B

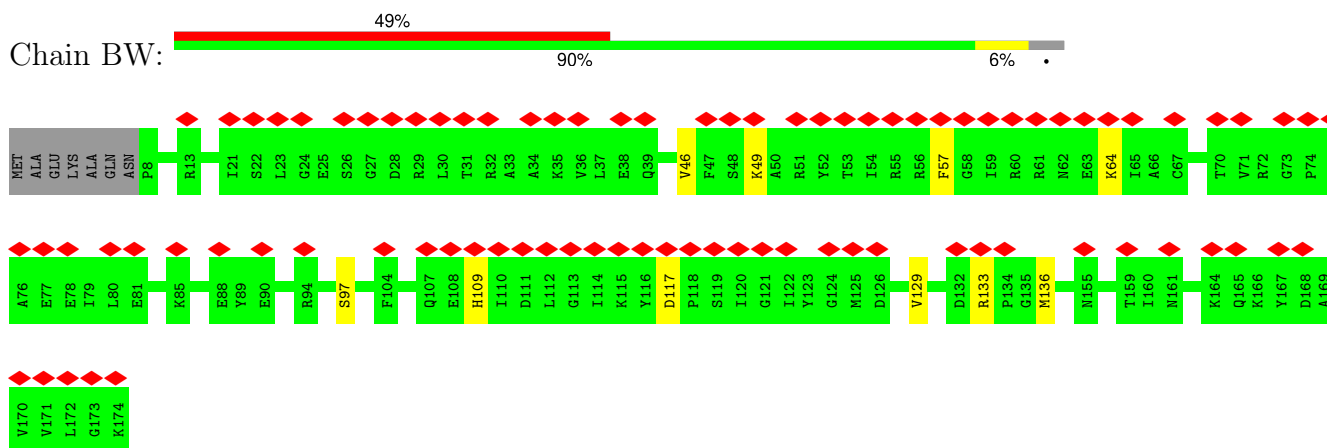


• Molecule 46: Large ribosomal subunit protein uL16A

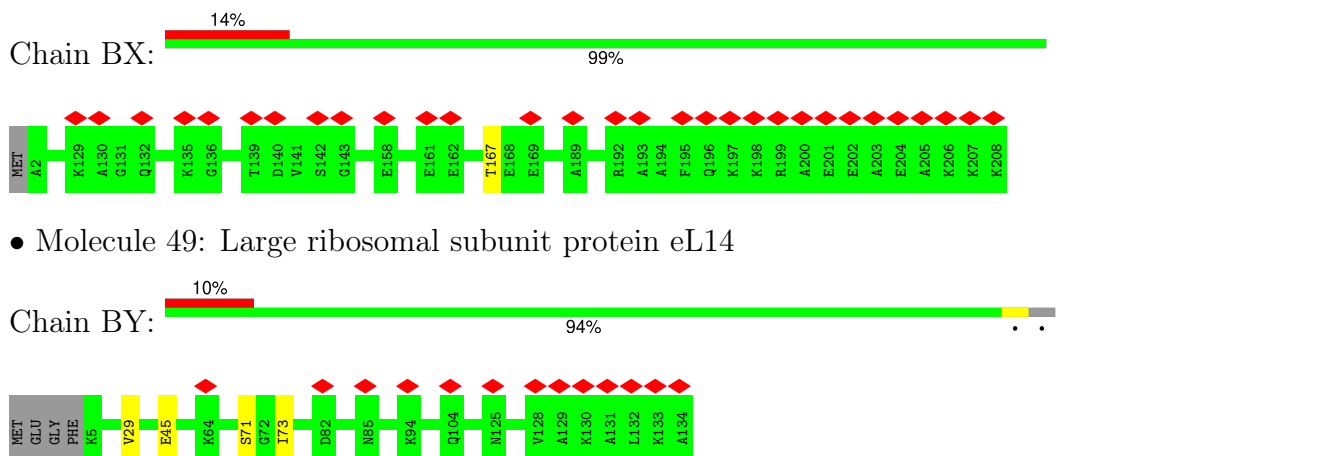




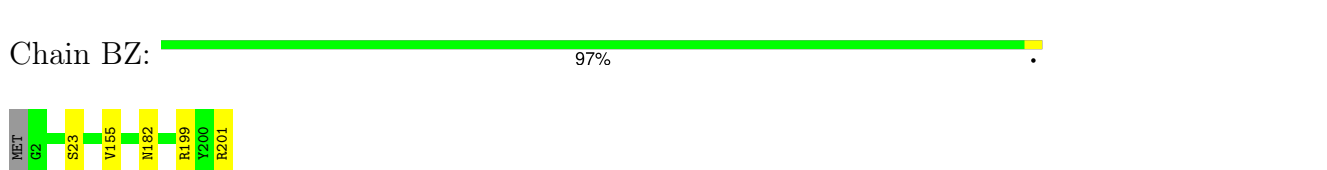
• Molecule 47: Large ribosomal subunit protein uL5A



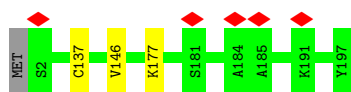
• Molecule 48: Large ribosomal subunit protein eL13



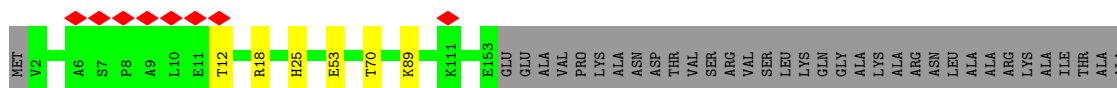
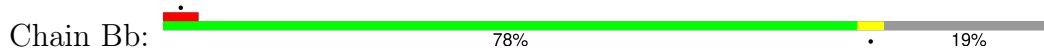
• Molecule 50: Large ribosomal subunit protein eL15B



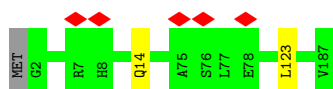
• Molecule 51: Large ribosomal subunit protein uL13A



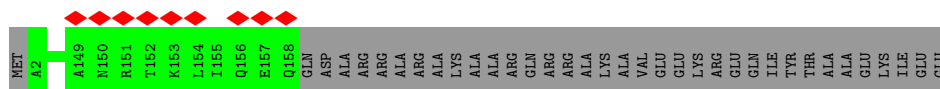
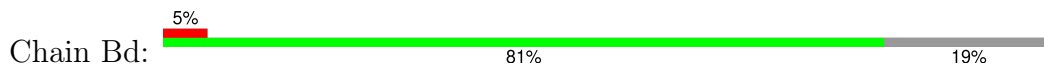
- Molecule 52: Large ribosomal subunit protein uL22A



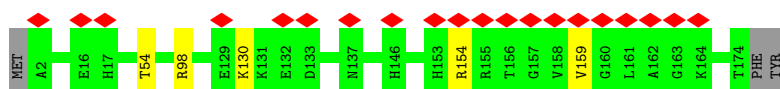
- Molecule 53: Large ribosomal subunit protein eL18B



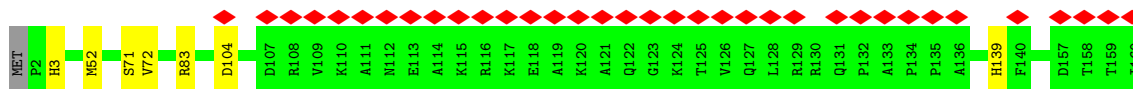
- Molecule 54: Large ribosomal subunit protein eL19B



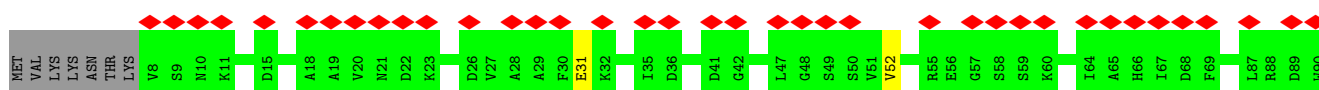
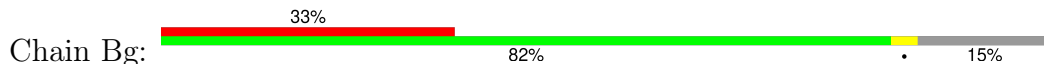
- Molecule 55: Large ribosomal subunit protein eL20A

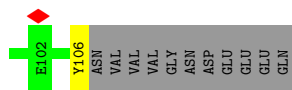


- Molecule 56: Large ribosomal subunit protein eL21B



- Molecule 57: Large ribosomal subunit protein eL22

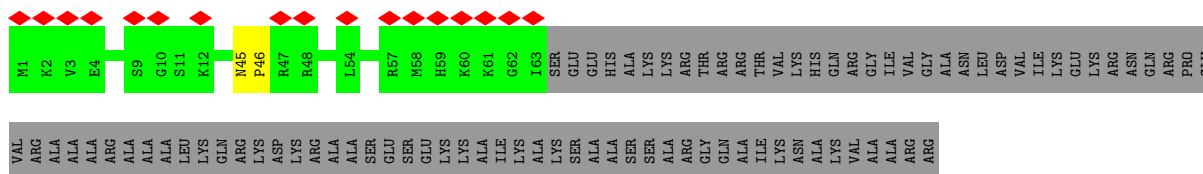




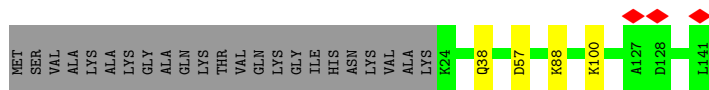
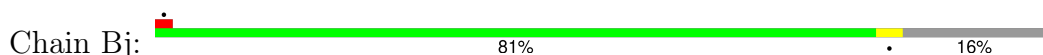
• Molecule 58: Large ribosomal subunit protein uL14B



• Molecule 59: Large ribosomal subunit protein eL24B



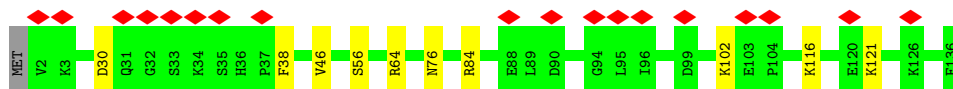
• Molecule 60: Large ribosomal subunit protein uL23A



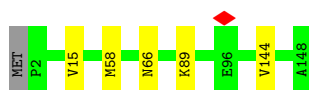
• Molecule 61: Large ribosomal subunit protein uL24



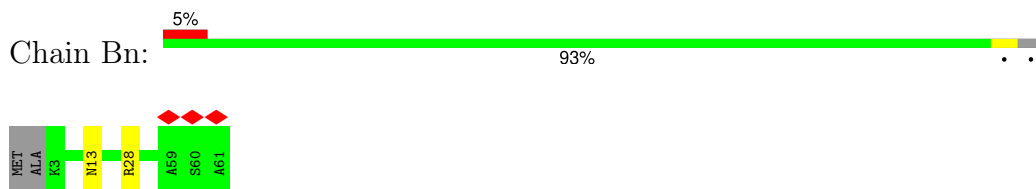
• Molecule 62: Large ribosomal subunit protein eL27A



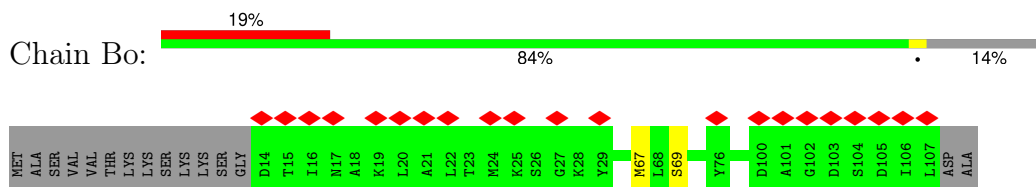
• Molecule 63: Large ribosomal subunit protein uL15B



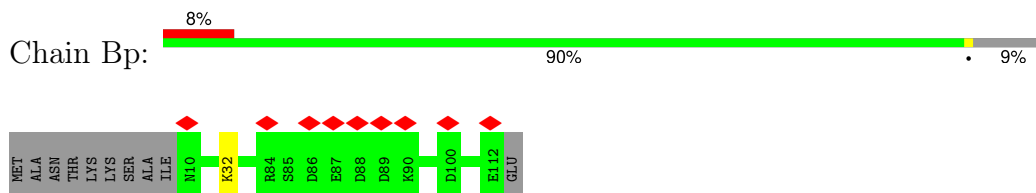
- Molecule 64: Large ribosomal subunit protein eL29



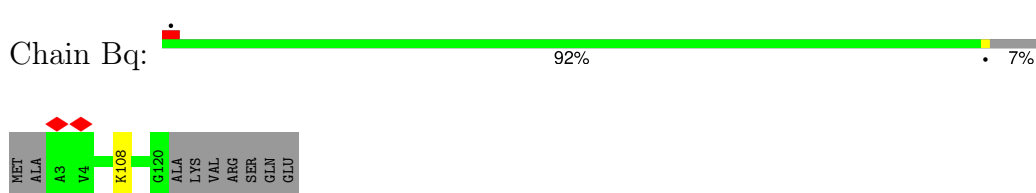
- Molecule 65: Large ribosomal subunit protein eL30A



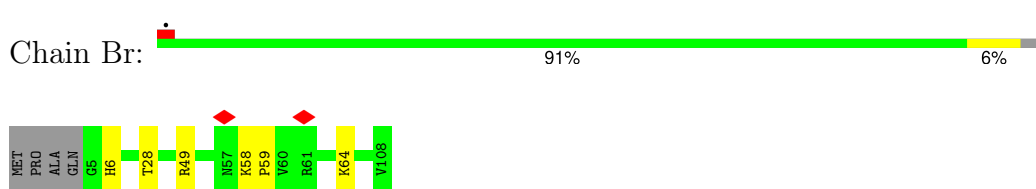
- Molecule 66: Large ribosomal subunit protein eL31



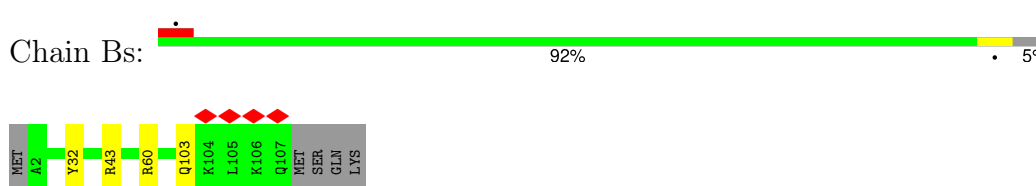
- Molecule 67: Large ribosomal subunit protein eL32A



- Molecule 68: Large ribosomal subunit protein eL33A

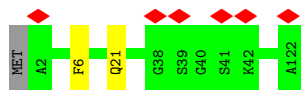


- Molecule 69: Large ribosomal subunit protein eL34B

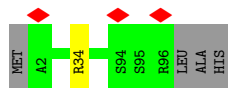


- Molecule 70: Large ribosomal subunit protein uL29

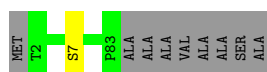




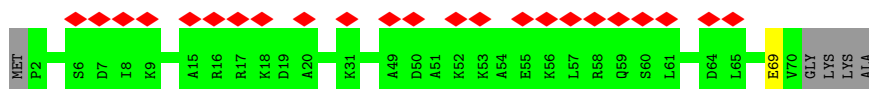
- Molecule 71: Large ribosomal subunit protein eL36B



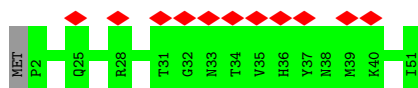
- Molecule 72: Large ribosomal subunit protein eL37B



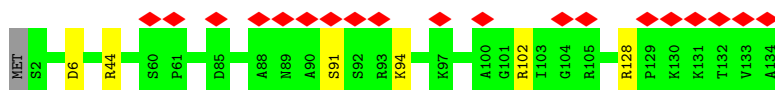
- Molecule 73: Large ribosomal subunit protein eL38A



- Molecule 74: Large ribosomal subunit protein eL39

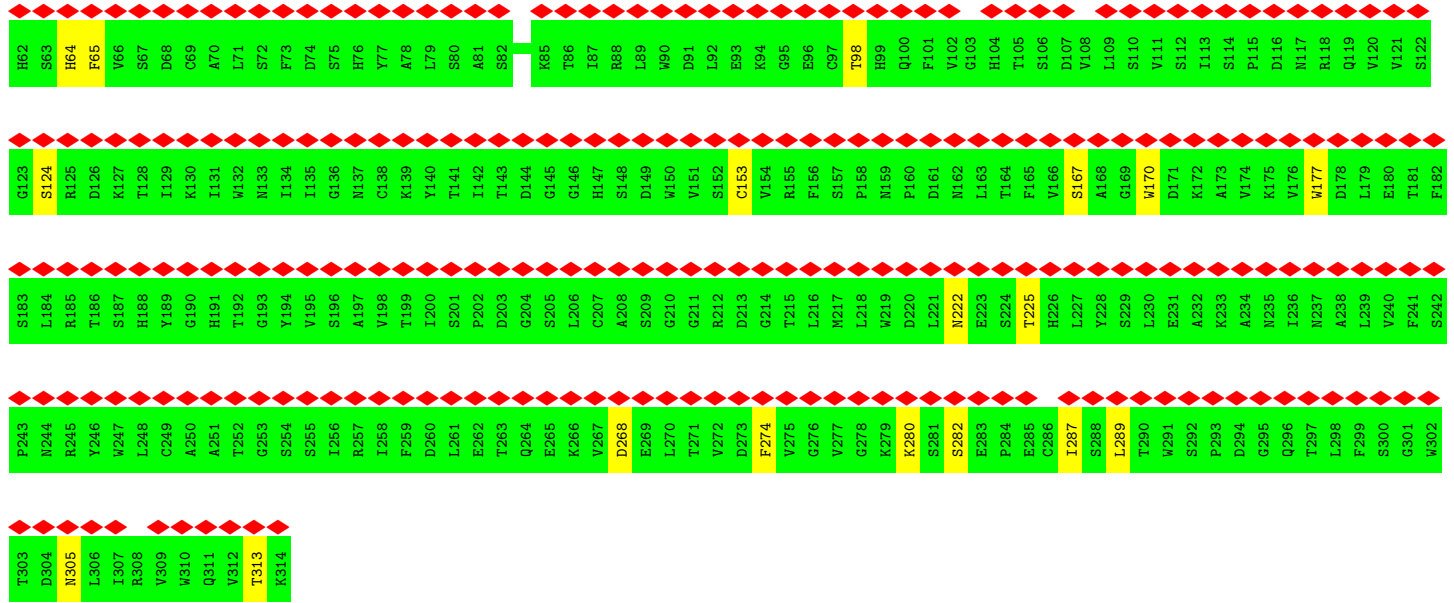


- Molecule 75: Large ribosomal subunit protein eL28

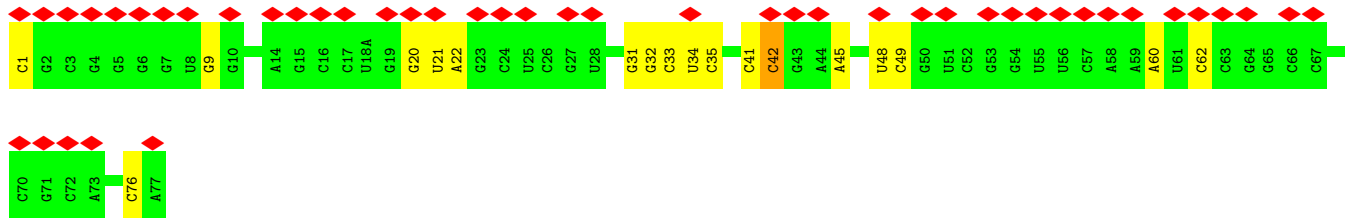
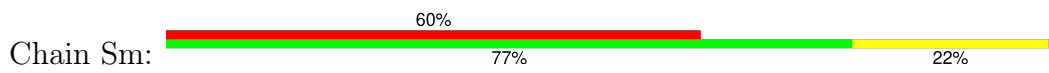


- Molecule 76: Small ribosomal subunit protein RACK1

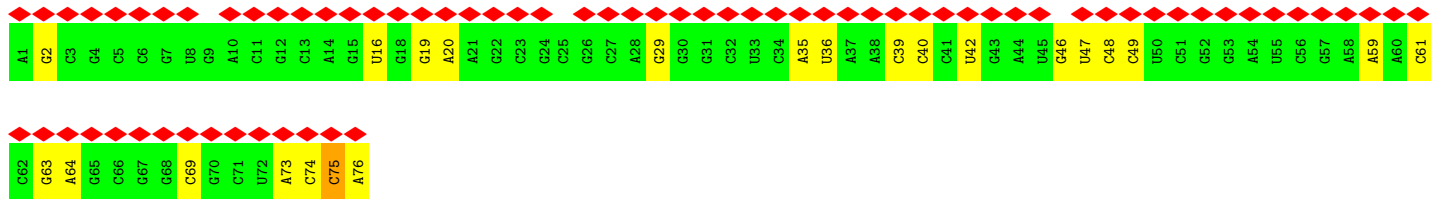




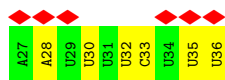
• Molecule 77: tRNA



• Molecule 78: A/P tRNA



• Molecule 79: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	58736	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	2.723	Depositor
Minimum map value	-1.267	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.090	Depositor
Recommended contour level	0.27	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	0/40663	0.76	12/63334 (0.0%)
2	AD	0.23	0/1635	0.52	0/2228
3	AE	0.24	0/1756	0.50	0/2358
4	AF	0.24	0/1695	0.51	1/2297 (0.0%)
5	AG	0.24	0/1726	0.53	0/2316
6	AH	0.25	0/2125	0.54	0/2858
7	AI	0.30	0/1577	0.58	2/2123 (0.1%)
8	AJ	0.26	0/1815	0.54	0/2428
9	AK	0.24	0/1554	0.52	0/2091
10	AL	0.25	0/1534	0.55	0/2050
11	AM	0.29	1/1487 (0.1%)	0.60	2/1990 (0.1%)
12	AN	0.24	0/769	0.46	0/1043
13	AO	0.25	0/1190	0.52	0/1602
14	AP	0.23	0/892	0.44	0/1208
15	AQ	0.24	0/1208	0.47	0/1624
16	AR	0.25	0/961	0.56	0/1293
17	AS	0.24	0/973	0.52	0/1307
18	AT	0.25	0/1100	0.49	0/1474
19	AU	0.23	0/983	0.54	0/1318
20	AV	0.26	0/1158	0.51	0/1552
21	AW	0.31	0/1139	0.51	0/1531
22	Aa	0.23	0/825	0.53	0/1111
23	Ab	0.23	0/680	0.51	0/918
24	Ac	0.23	0/1042	0.50	0/1399
25	Ad	0.24	0/1115	0.49	0/1489
26	Ae	0.24	0/1093	0.54	0/1453
27	Af	0.24	0/558	0.50	0/750
28	Ag	0.23	0/808	0.58	0/1083
29	Ah	0.32	0/630	0.53	0/845
30	Ai	0.22	0/500	0.59	0/669
31	Aj	0.24	0/458	0.55	0/610
32	Ak	0.23	0/482	0.52	0/639

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	B0	0.24	0/772	0.50	0/1025
34	B1	0.23	0/727	0.59	0/973
35	B2	0.20	0/76870	0.78	31/119823 (0.0%)
36	B3	0.18	0/2838	0.75	1/4422 (0.0%)
37	B4	0.18	0/3723	0.74	0/5796
38	BN	0.24	0/1910	0.53	0/2575
39	BO	0.24	0/3116	0.51	0/4190
40	BP	0.24	0/2852	0.49	0/3850
41	BQ	0.26	0/2361	0.51	0/3173
42	BR	0.25	0/1275	0.49	0/1719
43	BS	0.24	0/1929	0.47	0/2583
44	BT	0.24	0/1801	0.47	0/2430
45	BU	0.23	0/1330	0.50	0/1789
46	BV	0.24	0/1579	0.50	0/2115
47	BW	0.28	0/1369	0.55	0/1830
48	BX	0.24	0/1686	0.51	0/2267
49	BY	0.23	0/1054	0.49	0/1413
50	BZ	0.24	0/1717	0.53	0/2306
51	Ba	0.25	0/1575	0.48	0/2109
52	Bb	0.24	0/1237	0.48	0/1661
53	Bc	0.24	0/1511	0.54	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	0.48	0/1771
57	Bg	0.25	0/812	0.48	0/1090
58	Bh	0.25	0/1015	0.54	0/1369
59	Bi	1.23	4/534 (0.7%)	1.57	6/709 (0.8%)
60	Bj	0.24	0/963	0.51	0/1296
61	Bk	0.23	0/1008	0.54	0/1341
62	Bl	0.25	0/1101	0.50	0/1477
63	Bm	0.23	0/1200	0.52	0/1611
64	Bn	0.23	0/503	0.50	0/664
65	Bo	0.27	0/714	0.45	0/961
66	Bp	0.23	0/872	0.53	0/1172
67	Bq	0.24	0/958	0.53	0/1278
68	Br	0.71	2/853 (0.2%)	0.91	6/1146 (0.5%)
69	Bs	0.24	0/870	0.54	0/1165
70	Bt	0.23	0/1008	0.48	0/1340
71	Bu	0.23	0/766	0.54	0/1017
72	Bv	0.25	0/666	0.55	0/881
73	Bw	0.24	0/566	0.48	0/757
74	Bx	0.23	0/447	0.55	0/597
75	By	0.24	0/1045	0.51	0/1404

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Am	0.24	0/2520	0.50	0/3434
77	Sm	0.32	1/1812 (0.1%)	0.84	2/2816 (0.1%)
78	Sn	0.20	0/1796	0.83	3/2799 (0.1%)
79	S3	0.24	0/225	0.89	0/346
All	All	0.23	8/215709 (0.0%)	0.69	66/317220 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	Bi	46	PRO	CG-CD	-18.42	0.89	1.50
59	Bi	46	PRO	CB-CG	15.86	2.29	1.50
68	Br	59	PRO	N-CD	13.31	1.66	1.47
68	Br	59	PRO	CG-CD	-12.95	1.07	1.50
59	Bi	46	PRO	N-CD	10.75	1.62	1.47
77	Sm	1	C	OP3-P	-10.61	1.48	1.61
59	Bi	45	ASN	C-N	6.35	1.46	1.34
11	AM	149	ARG	CZ-NH1	-5.03	1.26	1.33

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	Bi	46	PRO	CB-CG-CD	-27.30	0.02	106.50
59	Bi	46	PRO	CA-N-CD	-18.33	85.84	111.50
68	Br	59	PRO	N-CD-CG	-17.31	77.24	103.20
59	Bi	45	ASN	C-N-CD	15.58	161.12	128.40
7	AI	121	ARG	NE-CZ-NH2	-11.29	114.66	120.30
68	Br	59	PRO	CA-N-CD	-9.99	97.51	111.50
1	AA	1409	C	C2-N1-C1'	9.00	128.70	118.80
68	Br	58	LYS	C-N-CD	8.95	147.20	128.40
1	AA	1409	C	N1-C2-O2	8.68	124.11	118.90
68	Br	59	PRO	CA-CB-CG	-8.65	87.57	104.00
35	B2	137	C	C2-N1-C1'	8.33	127.96	118.80
59	Bi	46	PRO	N-CA-CB	-8.22	93.44	103.30
35	B2	1639	U	C2-N1-C1'	8.21	127.56	117.70
35	B2	137	C	N1-C2-O2	8.13	123.78	118.90
59	Bi	46	PRO	N-CD-CG	-7.91	91.33	103.20
35	B2	1639	U	N1-C2-O2	7.38	127.97	122.80
35	B2	1529	U	C2-N1-C1'	7.01	126.12	117.70
35	B2	137	C	N3-C2-O2	-6.96	117.03	121.90
1	AA	1409	C	N3-C2-O2	-6.86	117.10	121.90
35	B2	1311	C	N3-C2-O2	-6.74	117.19	121.90
35	B2	1639	U	N3-C2-O2	-6.70	117.51	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	AI	121	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	AA	980	U	C2-N1-C1'	6.53	125.54	117.70
35	B2	1855	U	C2-N1-C1'	6.50	125.49	117.70
77	Sm	42	C	N3-C2-O2	-6.46	117.38	121.90
35	B2	2715	G	C5-C6-O6	6.42	132.45	128.60
59	Bi	46	PRO	CA-CB-CG	-6.38	91.88	104.00
35	B2	256	C	N3-C2-O2	-6.35	117.46	121.90
35	B2	3002	G	C4-N9-C1'	6.23	134.59	126.50
1	AA	1409	C	C6-N1-C1'	-6.20	113.36	120.80
1	AA	1409	C	C6-N1-C2	-6.04	117.88	120.30
35	B2	137	C	C6-N1-C2	-5.98	117.91	120.30
36	B3	46	C	C5'-C4'-O4'	-5.90	102.02	109.10
35	B2	1855	U	N1-C2-O2	5.89	126.92	122.80
78	Sn	75	C	C6-N1-C1'	5.84	127.81	120.80
35	B2	3002	G	C8-N9-C1'	-5.79	119.47	127.00
35	B2	3002	G	N3-C4-N9	5.79	129.47	126.00
11	AM	149	ARG	NE-CZ-NH1	5.73	123.17	120.30
78	Sn	75	C	C5-C4-N4	5.70	124.19	120.20
35	B2	414	G	O4'-C1'-N9	5.70	112.76	108.20
35	B2	256	C	N1-C2-O2	5.65	122.29	118.90
1	AA	142	U	P-O3'-C3'	5.61	126.43	119.70
35	B2	137	C	C6-N1-C1'	-5.59	114.09	120.80
35	B2	1529	U	N1-C2-O2	5.58	126.70	122.80
35	B2	1855	U	N3-C2-O2	-5.57	118.31	122.20
1	AA	1242	U	C2-N1-C1'	5.55	124.36	117.70
68	Br	59	PRO	N-CA-CB	-5.43	96.62	102.60
35	B2	1639	U	C6-N1-C1'	-5.39	113.66	121.20
35	B2	1064	C	N3-C2-O2	-5.36	118.15	121.90
11	AM	93	LEU	CA-CB-CG	5.35	127.61	115.30
4	AF	236	GLN	C-N-CA	5.33	135.03	121.70
1	AA	1263	C	C2-N1-C1'	5.30	124.63	118.80
1	AA	1409	C	C5-C6-N1	5.30	123.65	121.00
1	AA	224	C	N1-C2-O2	5.28	122.07	118.90
78	Sn	75	C	C2-N1-C1'	-5.25	113.02	118.80
77	Sm	42	C	N1-C2-O2	5.24	122.04	118.90
35	B2	2661	U	C2-N1-C1'	5.21	123.96	117.70
35	B2	2660	U	C2-N1-C1'	5.20	123.94	117.70
35	B2	1311	C	N1-C2-O2	5.19	122.01	118.90
35	B2	2715	G	N1-C6-O6	-5.17	116.80	119.90
68	Br	59	PRO	CB-CG-CD	-5.17	86.36	106.50
35	B2	2660	U	N1-C2-O2	5.16	126.41	122.80
35	B2	1529	U	N3-C2-O2	-5.15	118.59	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B2	1064	C	N1-C2-O2	5.15	121.99	118.90
1	AA	1263	C	N1-C2-O2	5.12	121.97	118.90
35	B2	2353	C	N3-C2-O2	-5.02	118.39	121.90

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%)	180 (89%)	23 (11%)	0	100	100
3	AE	214/252 (85%)	200 (94%)	14 (6%)	0	100	100
4	AF	214/253 (85%)	207 (97%)	6 (3%)	1 (0%)	25	38
5	AG	214/249 (86%)	195 (91%)	18 (8%)	1 (0%)	25	38
6	AH	259/262 (99%)	231 (89%)	23 (9%)	5 (2%)	6	8
7	AI	201/203 (99%)	176 (88%)	21 (10%)	4 (2%)	6	8
8	AJ	219/239 (92%)	212 (97%)	7 (3%)	0	100	100
9	AK	191/195 (98%)	173 (91%)	18 (9%)	0	100	100
10	AL	184/200 (92%)	175 (95%)	9 (5%)	0	100	100
11	AM	176/192 (92%)	163 (93%)	13 (7%)	0	100	100
12	AN	90/147 (61%)	79 (88%)	10 (11%)	1 (1%)	12	18
13	AO	141/152 (93%)	131 (93%)	10 (7%)	0	100	100
14	AP	119/145 (82%)	106 (89%)	12 (10%)	1 (1%)	16	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	AQ	148/151 (98%)	142 (96%)	5 (3%)	1 (1%)	19	29
16	AR	126/139 (91%)	114 (90%)	12 (10%)	0	100	100
17	AS	117/154 (76%)	110 (94%)	7 (6%)	0	100	100
18	AT	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
19	AU	116/131 (88%)	99 (85%)	11 (10%)	6 (5%)	1	1
20	AV	139/152 (91%)	130 (94%)	9 (6%)	0	100	100
21	AW	140/144 (97%)	133 (95%)	7 (5%)	0	100	100
22	Aa	98/118 (83%)	90 (92%)	6 (6%)	2 (2%)	6	8
23	Ab	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
24	Ac	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
25	Ad	140/143 (98%)	136 (97%)	4 (3%)	0	100	100
26	Ae	131/134 (98%)	124 (95%)	6 (5%)	1 (1%)	16	26
27	Af	67/89 (75%)	61 (91%)	6 (9%)	0	100	100
28	Ag	95/119 (80%)	89 (94%)	6 (6%)	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%)	49 (96%)	2 (4%)	0	100	100
32	Ak	58/61 (95%)	53 (91%)	4 (7%)	1 (2%)	7	10
33	B0	91/106 (86%)	88 (97%)	3 (3%)	0	100	100
34	B1	91/94 (97%)	85 (93%)	6 (7%)	0	100	100
38	BN	246/253 (97%)	228 (93%)	18 (7%)	0	100	100
39	BO	382/388 (98%)	357 (94%)	25 (6%)	0	100	100
40	BP	360/363 (99%)	349 (97%)	11 (3%)	0	100	100
41	BQ	285/294 (97%)	257 (90%)	26 (9%)	2 (1%)	19	29
42	BR	160/195 (82%)	138 (86%)	22 (14%)	0	100	100
43	BS	231/251 (92%)	224 (97%)	7 (3%)	0	100	100
44	BT	227/259 (88%)	211 (93%)	16 (7%)	0	100	100
45	BU	162/189 (86%)	155 (96%)	7 (4%)	0	100	100
46	BV	187/221 (85%)	181 (97%)	6 (3%)	0	100	100
47	BW	165/174 (95%)	147 (89%)	16 (10%)	2 (1%)	11	16
48	BX	205/208 (99%)	201 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	BY	128/134 (96%)	125 (98%)	3 (2%)	0	100	100
50	BZ	198/201 (98%)	189 (96%)	9 (4%)	0	100	100
51	Ba	194/197 (98%)	191 (98%)	3 (2%)	0	100	100
52	Bb	150/187 (80%)	146 (97%)	4 (3%)	0	100	100
53	Bc	184/187 (98%)	178 (97%)	6 (3%)	0	100	100
54	Bd	155/193 (80%)	153 (99%)	2 (1%)	0	100	100
55	Be	171/176 (97%)	164 (96%)	6 (4%)	1 (1%)	22	33
56	Bf	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
57	Bg	97/117 (83%)	86 (89%)	11 (11%)	0	100	100
58	Bh	132/139 (95%)	125 (95%)	7 (5%)	0	100	100
59	Bi	61/149 (41%)	61 (100%)	0	0	100	100
60	Bj	116/141 (82%)	114 (98%)	2 (2%)	0	100	100
61	Bk	123/126 (98%)	122 (99%)	1 (1%)	0	100	100
62	Bl	133/136 (98%)	128 (96%)	5 (4%)	0	100	100
63	Bm	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
64	Bn	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
65	Bo	92/109 (84%)	92 (100%)	0	0	100	100
66	Bp	101/113 (89%)	98 (97%)	3 (3%)	0	100	100
67	Bq	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
68	Br	102/108 (94%)	100 (98%)	2 (2%)	0	100	100
69	Bs	104/111 (94%)	102 (98%)	2 (2%)	0	100	100
70	Bt	119/122 (98%)	115 (97%)	4 (3%)	0	100	100
71	Bu	93/99 (94%)	90 (97%)	3 (3%)	0	100	100
72	Bv	80/91 (88%)	75 (94%)	5 (6%)	0	100	100
73	Bw	67/74 (90%)	67 (100%)	0	0	100	100
74	Bx	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
75	By	131/134 (98%)	128 (98%)	3 (2%)	0	100	100
76	Am	312/314 (99%)	296 (95%)	16 (5%)	0	100	100
All	All	10699/11780 (91%)	10094 (94%)	576 (5%)	29 (0%)	38	51

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AH	245	LYS
19	AU	88	VAL
22	Aa	50	VAL
41	BQ	216	GLU
47	BW	46	VAL
47	BW	117	ASP
4	AF	237	THR
6	AH	12	VAL
6	AH	59	ARG
7	AI	31	VAL
7	AI	79	GLY
15	AQ	30	ALA
19	AU	92	GLU
19	AU	117	ARG
7	AI	24	PHE
7	AI	29	VAL
41	BQ	90	TRP
14	AP	134	ALA
26	Ae	56	GLN
32	Ak	51	VAL
19	AU	74	GLN
19	AU	118	VAL
22	Aa	19	ARG
5	AG	95	ASN
6	AH	168	LYS
6	AH	217	GLU
55	Be	159	VAL
19	AU	114	ILE
12	AN	37	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%)	160 (94%)	10 (6%)	16	28
3	AE	193/223 (86%)	178 (92%)	15 (8%)	10	17
4	AF	175/199 (88%)	164 (94%)	11 (6%)	15	25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	AG	181/203 (89%)	168 (93%)	13 (7%)	12	20
6	AH	226/227 (100%)	209 (92%)	17 (8%)	11	18
7	AI	169/169 (100%)	162 (96%)	7 (4%)	26	44
8	AJ	188/204 (92%)	176 (94%)	12 (6%)	14	24
9	AK	169/171 (99%)	163 (96%)	6 (4%)	30	49
10	AL	157/166 (95%)	150 (96%)	7 (4%)	23	40
11	AM	155/165 (94%)	145 (94%)	10 (6%)	14	24
12	AN	77/116 (66%)	74 (96%)	3 (4%)	27	46
13	AO	124/131 (95%)	115 (93%)	9 (7%)	11	20
14	AP	92/118 (78%)	89 (97%)	3 (3%)	33	53
15	AQ	127/128 (99%)	123 (97%)	4 (3%)	35	56
16	AR	95/104 (91%)	90 (95%)	5 (5%)	19	33
17	AS	101/131 (77%)	92 (91%)	9 (9%)	8	12
18	AT	111/111 (100%)	107 (96%)	4 (4%)	30	49
19	AU	107/120 (89%)	100 (94%)	7 (6%)	14	24
20	AV	127/136 (93%)	119 (94%)	8 (6%)	15	25
21	AW	117/119 (98%)	105 (90%)	12 (10%)	6	9
22	Aa	95/111 (86%)	88 (93%)	7 (7%)	11	19
23	Ab	73/73 (100%)	72 (99%)	1 (1%)	62	79
24	Ac	114/115 (99%)	108 (95%)	6 (5%)	19	33
25	Ad	112/113 (99%)	105 (94%)	7 (6%)	15	25
26	Ae	112/113 (99%)	102 (91%)	10 (9%)	8	12
27	Af	61/75 (81%)	60 (98%)	1 (2%)	58	76
28	Ag	87/106 (82%)	83 (95%)	4 (5%)	23	39
29	Ah	71/73 (97%)	66 (93%)	5 (7%)	12	21
30	Ai	56/61 (92%)	54 (96%)	2 (4%)	30	49
31	Aj	45/47 (96%)	44 (98%)	1 (2%)	47	67
32	Ak	51/52 (98%)	50 (98%)	1 (2%)	50	70
33	B0	84/93 (90%)	80 (95%)	4 (5%)	21	37
34	B1	74/75 (99%)	73 (99%)	1 (1%)	62	79
38	BN	188/192 (98%)	185 (98%)	3 (2%)	58	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	BO	318/326 (98%)	309 (97%)	9 (3%)	38	59
40	BP	293/294 (100%)	287 (98%)	6 (2%)	50	70
41	BQ	235/241 (98%)	222 (94%)	13 (6%)	18	31
42	BR	132/155 (85%)	128 (97%)	4 (3%)	36	57
43	BS	198/213 (93%)	192 (97%)	6 (3%)	36	57
44	BT	182/212 (86%)	178 (98%)	4 (2%)	47	67
45	BU	149/168 (89%)	141 (95%)	8 (5%)	18	32
46	BV	165/187 (88%)	154 (93%)	11 (7%)	13	23
47	BW	141/146 (97%)	133 (94%)	8 (6%)	17	29
48	BX	166/167 (99%)	165 (99%)	1 (1%)	84	92
49	BY	110/113 (97%)	106 (96%)	4 (4%)	30	49
50	BZ	175/176 (99%)	170 (97%)	5 (3%)	37	58
51	Ba	159/160 (99%)	156 (98%)	3 (2%)	52	72
52	Bb	124/149 (83%)	118 (95%)	6 (5%)	21	37
53	Bc	157/158 (99%)	155 (99%)	2 (1%)	65	81
54	Bd	136/163 (83%)	136 (100%)	0	100	100
55	Be	151/154 (98%)	147 (97%)	4 (3%)	41	62
56	Bf	138/139 (99%)	131 (95%)	7 (5%)	20	35
57	Bg	86/103 (84%)	83 (96%)	3 (4%)	31	51
58	Bh	103/107 (96%)	97 (94%)	6 (6%)	17	29
59	Bi	57/121 (47%)	57 (100%)	0	100	100
60	Bj	105/122 (86%)	101 (96%)	4 (4%)	28	47
61	Bk	110/111 (99%)	107 (97%)	3 (3%)	40	60
62	Bl	114/115 (99%)	104 (91%)	10 (9%)	8	13
63	Bm	122/123 (99%)	117 (96%)	5 (4%)	26	44
64	Bn	50/51 (98%)	48 (96%)	2 (4%)	27	45
65	Bo	75/87 (86%)	73 (97%)	2 (3%)	40	60
66	Bp	94/102 (92%)	93 (99%)	1 (1%)	70	84
67	Bq	100/107 (94%)	99 (99%)	1 (1%)	73	86
68	Br	91/94 (97%)	87 (96%)	4 (4%)	24	41
69	Bs	91/96 (95%)	87 (96%)	4 (4%)	24	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
70	Bt	106/107 (99%)	104 (98%)	2 (2%)	52	72
71	Bu	81/84 (96%)	80 (99%)	1 (1%)	67	82
72	Bv	68/71 (96%)	67 (98%)	1 (2%)	60	77
73	Bw	63/66 (96%)	62 (98%)	1 (2%)	58	76
74	Bx	46/47 (98%)	46 (100%)	0	100	100
75	By	112/113 (99%)	106 (95%)	6 (5%)	18	32
76	Am	276/276 (100%)	255 (92%)	21 (8%)	11	18
All	All	9163/9892 (93%)	8760 (96%)	403 (4%)	26	41

All (403) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	AD	35	ARG
2	AD	59	LYS
2	AD	78	VAL
2	AD	111	THR
2	AD	126	VAL
2	AD	150	CYS
2	AD	160	ASP
2	AD	170	ARG
2	AD	188	ARG
2	AD	193	ARG
3	AE	33	LYS
3	AE	62	LYS
3	AE	69	SER
3	AE	84	VAL
3	AE	105	ILE
3	AE	125	GLN
3	AE	133	TYR
3	AE	135	CYS
3	AE	144	ARG
3	AE	152	LYS
3	AE	177	SER
3	AE	179	CYS
3	AE	184	LEU
3	AE	205	PHE
3	AE	215	VAL
4	AF	34	TRP
4	AF	69	ASP
4	AF	78	GLU

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Mol	Chain	Res	Type
4	AF	110	VAL
4	AF	122	THR
4	AF	134	SER
4	AF	197	THR
4	AF	200	ARG
4	AF	209	PHE
4	AF	218	SER
4	AF	247	MET
5	AG	9	LYS
5	AG	19	PHE
5	AG	28	THR
5	AG	42	ARG
5	AG	43	VAL
5	AG	66	ARG
5	AG	78	ARG
5	AG	99	CYS
5	AG	126	ARG
5	AG	129	MET
5	AG	136	CYS
5	AG	180	ARG
5	AG	191	MET
6	AH	52	LEU
6	AH	59	ARG
6	AH	78	THR
6	AH	113	ARG
6	AH	127	LYS
6	AH	128	ARG
6	AH	134	LYS
6	AH	163	ASN
6	AH	166	THR
6	AH	182	MET
6	AH	187	ARG
6	AH	188	ASN
6	AH	194	THR
6	AH	211	LYS
6	AH	220	THR
6	AH	226	PHE
6	AH	256	ARG
7	AI	32	LYS
7	AI	93	LYS
7	AI	123	ASP
7	AI	129	SER

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Mol	Chain	Res	Type
7	AI	139	ASP
7	AI	190	LYS
7	AI	197	ARG
8	AJ	81	HIS
8	AJ	92	ARG
8	AJ	93	LYS
8	AJ	108	VAL
8	AJ	124	LEU
8	AJ	129	VAL
8	AJ	147	LEU
8	AJ	152	ASP
8	AJ	172	TYR
8	AJ	193	ARG
8	AJ	198	ARG
8	AJ	211	PHE
9	AK	62	VAL
9	AK	107	LYS
9	AK	159	ARG
9	AK	178	LEU
9	AK	179	THR
9	AK	184	THR
10	AL	29	LEU
10	AL	37	ARG
10	AL	64	ASN
10	AL	77	ARG
10	AL	135	LYS
10	AL	160	PHE
10	AL	195	ARG
11	AM	6	ARG
11	AM	66	ASP
11	AM	78	ARG
11	AM	90	ARG
11	AM	91	MET
11	AM	105	LEU
11	AM	106	GLU
11	AM	107	ARG
11	AM	154	LYS
11	AM	174	ARG
12	AN	1	MET
12	AN	15	LEU
12	AN	20	VAL
13	AO	21	GLN

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Mol	Chain	Res	Type
13	AO	62	SER
13	AO	64	ARG
13	AO	71	THR
13	AO	72	VAL
13	AO	108	VAL
13	AO	113	ARG
13	AO	128	LEU
13	AO	135	ASN
14	AP	41	LEU
14	AP	48	ARG
14	AP	92	ILE
15	AQ	45	MET
15	AQ	100	LYS
15	AQ	104	ARG
15	AQ	131	LYS
16	AR	33	THR
16	AR	48	MET
16	AR	86	ARG
16	AR	112	MET
16	AR	113	ARG
17	AS	33	LEU
17	AS	53	MET
17	AS	57	LEU
17	AS	69	ARG
17	AS	91	MET
17	AS	105	TYR
17	AS	109	LEU
17	AS	119	MET
17	AS	130	THR
18	AT	19	CYS
18	AT	27	LYS
18	AT	57	PHE
18	AT	139	TYR
19	AU	5	ARG
19	AU	31	ASN
19	AU	71	PHE
19	AU	82	ASP
19	AU	85	VAL
19	AU	105	MET
19	AU	116	VAL
20	AV	14	ARG
20	AV	15	LEU

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Mol	Chain	Res	Type
20	AV	24	VAL
20	AV	28	PHE
20	AV	30	MET
20	AV	106	LYS
20	AV	136	THR
20	AV	137	LYS
21	AW	6	VAL
21	AW	14	PHE
21	AW	28	MET
21	AW	51	ASP
21	AW	56	ARG
21	AW	74	ARG
21	AW	82	SER
21	AW	83	VAL
21	AW	84	ASN
21	AW	101	ARG
21	AW	121	ARG
21	AW	129	ARG
22	Aa	17	VAL
22	Aa	29	VAL
22	Aa	30	ARG
22	Aa	49	ARG
22	Aa	55	ARG
22	Aa	70	ASN
22	Aa	99	LYS
23	Ab	22	ARG
24	Ac	22	ARG
24	Ac	41	MET
24	Ac	68	ARG
24	Ac	69	ILE
24	Ac	76	SER
24	Ac	99	VAL
25	Ad	26	HIS
25	Ad	31	LEU
25	Ad	37	LYS
25	Ad	67	ARG
25	Ad	69	CYS
25	Ad	105	PHE
25	Ad	134	PHE
26	Ae	8	ARG
26	Ae	11	LYS
26	Ae	12	PHE

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Mol	Chain	Res	Type
26	Ae	23	MET
26	Ae	24	VAL
26	Ae	47	MET
26	Ae	64	TYR
26	Ae	78	ASP
26	Ae	111	ARG
26	Ae	124	ARG
27	Af	68	VAL
28	Ag	19	LYS
28	Ag	54	SER
28	Ag	70	LYS
28	Ag	89	ARG
29	Ah	9	ASN
29	Ah	12	HIS
29	Ah	14	SER
29	Ah	33	MET
29	Ah	74	MET
30	Ai	34	MET
30	Ai	44	ASN
31	Aj	23	HIS
32	Ak	41	VAL
33	B0	7	THR
33	B0	58	PHE
33	B0	76	SER
33	B0	90	HIS
34	B1	91	MET
38	BN	121	ASP
38	BN	139	ASP
38	BN	246	ARG
39	BO	5	LYS
39	BO	56	ILE
39	BO	59	ASP
39	BO	95	THR
39	BO	255	TRP
39	BO	289	ASP
39	BO	293	ASN
39	BO	377	LYS
39	BO	378	GLN
40	BP	29	LYS
40	BP	95	MET
40	BP	122	TYR
40	BP	179	ASP

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Mol	Chain	Res	Type
40	BP	343	LEU
40	BP	362	GLU
41	BQ	8	LYS
41	BQ	10	SER
41	BQ	23	ARG
41	BQ	61	THR
41	BQ	85	ARG
41	BQ	90	TRP
41	BQ	119	TYR
41	BQ	152	ARG
41	BQ	158	ARG
41	BQ	178	ASN
41	BQ	188	GLU
41	BQ	207	TYR
41	BQ	232	GLU
42	BR	49	ARG
42	BR	86	TYR
42	BR	88	VAL
42	BR	185	SER
43	BS	31	ARG
43	BS	67	GLU
43	BS	69	GLU
43	BS	149	LEU
43	BS	164	VAL
43	BS	248	ARG
44	BT	79	GLN
44	BT	125	VAL
44	BT	131	ASN
44	BT	210	GLU
45	BU	41	ARG
45	BU	43	ASP
45	BU	57	VAL
45	BU	58	TRP
45	BU	94	TYR
45	BU	122	ARG
45	BU	138	VAL
45	BU	168	LYS
46	BV	13	LYS
46	BV	21	ARG
46	BV	28	ASP
46	BV	31	ILE
46	BV	63	GLU

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Mol	Chain	Res	Type
46	BV	74	LYS
46	BV	102	MET
46	BV	158	LYS
46	BV	191	ILE
46	BV	199	PHE
46	BV	203	ARG
47	BW	49	LYS
47	BW	57	PHE
47	BW	64	LYS
47	BW	97	SER
47	BW	109	HIS
47	BW	129	VAL
47	BW	133	ARG
47	BW	136	MET
48	BX	167	THR
49	BY	29	VAL
49	BY	45	GLU
49	BY	71	SER
49	BY	73	ILE
50	BZ	23	SER
50	BZ	155	VAL
50	BZ	182	ASN
50	BZ	199	ARG
50	BZ	201	ARG
51	Ba	137	CYS
51	Ba	146	VAL
51	Ba	177	LYS
52	Bb	12	THR
52	Bb	18	ARG
52	Bb	25	HIS
52	Bb	53	GLU
52	Bb	70	THR
52	Bb	89	LYS
53	Bc	14	GLN
53	Bc	123	LEU
55	Be	54	THR
55	Be	98	ARG
55	Be	130	LYS
55	Be	154	ARG
56	Bf	3	HIS
56	Bf	52	MET
56	Bf	71	SER

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Mol	Chain	Res	Type
56	Bf	72	VAL
56	Bf	83	ARG
56	Bf	104	ASP
56	Bf	139	HIS
57	Bg	31	GLU
57	Bg	52	VAL
57	Bg	106	TYR
58	Bh	14	ARG
58	Bh	35	ASN
58	Bh	40	SER
58	Bh	60	VAL
58	Bh	70	ASP
58	Bh	133	SER
60	Bj	38	GLN
60	Bj	57	ASP
60	Bj	88	LYS
60	Bj	100	LYS
61	Bk	2	LYS
61	Bk	56	THR
61	Bk	73	TYR
62	Bl	30	ASP
62	Bl	38	PHE
62	Bl	46	VAL
62	Bl	56	SER
62	Bl	64	ARG
62	Bl	76	ASN
62	Bl	84	ARG
62	Bl	102	LYS
62	Bl	116	LYS
62	Bl	121	LYS
63	Bm	15	VAL
63	Bm	58	MET
63	Bm	66	ASN
63	Bm	89	LYS
63	Bm	144	VAL
64	Bn	13	ASN
64	Bn	28	ARG
65	Bo	67	MET
65	Bo	69	SER
66	Bp	32	LYS
67	Bq	108	LYS
68	Br	6	HIS

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Mol	Chain	Res	Type
68	Br	28	THR
68	Br	49	ARG
68	Br	64	LYS
69	Bs	32	TYR
69	Bs	43	ARG
69	Bs	60	ARG
69	Bs	103	GLN
70	Bt	6	PHE
70	Bt	21	GLN
71	Bu	34	ARG
72	Bv	7	SER
73	Bw	69	GLU
75	By	6	ASP
75	By	44	ARG
75	By	91	SER
75	By	94	LYS
75	By	102	ARG
75	By	128	ARG
76	Am	33	SER
76	Am	49	ASP
76	Am	60	THR
76	Am	64	HIS
76	Am	65	PHE
76	Am	98	THR
76	Am	124	SER
76	Am	153	CYS
76	Am	167	SER
76	Am	170	TRP
76	Am	177	TRP
76	Am	222	ASN
76	Am	225	THR
76	Am	268	ASP
76	Am	274	PHE
76	Am	280	LYS
76	Am	282	SER
76	Am	287	ILE
76	Am	289	LEU
76	Am	305	ASN
76	Am	313	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
2	AD	143	ASN
3	AE	49	ASN
3	AE	125	GLN
3	AE	173	GLN
5	AG	94	GLN
6	AH	163	ASN
6	AH	224	ASN
7	AI	15	ASN
10	AL	64	ASN
10	AL	80	GLN
11	AM	40	HIS
12	AN	91	HIS
15	AQ	78	ASN
21	AW	84	ASN
22	Aa	28	ASN
23	Ab	35	ASN
24	Ac	91	ASN
28	Ag	11	ASN
33	B0	3	ASN
34	B1	33	GLN
38	BN	85	GLN
39	BO	211	GLN
39	BO	212	ASN
41	BQ	63	GLN
42	BR	186	ASN
45	BU	100	ASN
45	BU	114	ASN
46	BV	14	ASN
46	BV	162	GLN
49	BY	123	GLN
50	BZ	156	HIS
51	Ba	27	GLN
51	Ba	32	GLN
51	Ba	47	HIS
55	Be	48	ASN
55	Be	87	HIS
56	Bf	95	HIS
58	Bh	134	ASN
60	Bj	86	HIS
62	Bl	106	GLN
65	Bo	74	HIS
66	Bp	48	HIS
69	Bs	69	GLN

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Mol	Chain	Res	Type
69	Bs	103	GLN
70	Bt	19	GLN
70	Bt	33	GLN
71	Bu	61	ASN
73	Bw	30	ASN
75	By	59	ASN
76	Am	4	GLN
76	Am	99	HIS
76	Am	244	ASN
76	Am	305	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1689/1842 (91%)	398 (23%)	15 (0%)
35	B2	3203/3498 (91%)	663 (20%)	26 (0%)
36	B3	118/246 (47%)	23 (19%)	1 (0%)
37	B4	156/165 (94%)	30 (19%)	1 (0%)
77	Sm	73/77 (94%)	17 (23%)	0
78	Sn	74/75 (98%)	23 (31%)	0
79	S3	9/10 (90%)	6 (66%)	1 (11%)
All	All	5322/5913 (90%)	1160 (21%)	44 (0%)

All (1160) 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	40	A
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	67	A
1	AA	69	G

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Mol	Chain	Res	Type
1	AA	79	A
1	AA	105	A
1	AA	115	C
1	AA	116	G
1	AA	117	U
1	AA	128	G
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	149	C
1	AA	151	G
1	AA	158	U
1	AA	159	U
1	AA	161	U
1	AA	166	C
1	AA	176	C
1	AA	177	U
1	AA	178	A
1	AA	190	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	201	G
1	AA	216	A
1	AA	217	U
1	AA	219	A
1	AA	221	A
1	AA	230	C
1	AA	234	C
1	AA	236	G
1	AA	239	U
1	AA	241	U
1	AA	244	U
1	AA	253	C
1	AA	264	U
1	AA	268	A

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Mol	Chain	Res	Type
1	AA	273	C
1	AA	274	A
1	AA	275	U
1	AA	276	G
1	AA	279	C
1	AA	281	U
1	AA	283	C
1	AA	290	G
1	AA	302	A
1	AA	305	U
1	AA	319	A
1	AA	324	C
1	AA	340	G
1	AA	341	C
1	AA	355	A
1	AA	362	A
1	AA	363	A
1	AA	364	C
1	AA	403	A
1	AA	405	C
1	AA	407	G
1	AA	419	A
1	AA	420	A
1	AA	421	G
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	470	G
1	AA	471	A
1	AA	473	A
1	AA	478	A
1	AA	487	C
1	AA	489	G
1	AA	491	G
1	AA	504	U

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Mol	Chain	Res	Type
1	AA	508	A
1	AA	509	A
1	AA	511	U
1	AA	513	G
1	AA	514	A
1	AA	515	A
1	AA	516	U
1	AA	517	G
1	AA	518	A
1	AA	521	A
1	AA	522	C
1	AA	523	A
1	AA	536	U
1	AA	537	A
1	AA	539	C
1	AA	541	A
1	AA	542	G
1	AA	543	G
1	AA	545	A
1	AA	554	G
1	AA	557	C
1	AA	558	A
1	AA	559	A
1	AA	560	G
1	AA	561	U
1	AA	562	C
1	AA	568	C
1	AA	571	G
1	AA	577	G
1	AA	584	U
1	AA	588	A
1	AA	597	A
1	AA	598	G
1	AA	609	A
1	AA	614	U
1	AA	622	A
1	AA	623	A
1	AA	626	A
1	AA	627	G
1	AA	637	G
1	AA	638	A
1	AA	642	U

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Mol	Chain	Res	Type
1	AA	652	U
1	AA	695	G
1	AA	696	U
1	AA	697	C
1	AA	700	U
1	AA	701	A
1	AA	703	C
1	AA	705	U
1	AA	755	U
1	AA	767	A
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
1	AA	794	U
1	AA	795	U
1	AA	796	U
1	AA	797	U
1	AA	801	C
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	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

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Mol	Chain	Res	Type
1	AA	865	G
1	AA	869	U
1	AA	870	A
1	AA	878	A
1	AA	913	A
1	AA	921	A
1	AA	926	U
1	AA	928	G
1	AA	929	G
1	AA	948	A
1	AA	950	U
1	AA	974	U
1	AA	975	U
1	AA	981	A
1	AA	985	A
1	AA	1007	A
1	AA	1011	C
1	AA	1018	A
1	AA	1019	U
1	AA	1020	A
1	AA	1036	C
1	AA	1038	A
1	AA	1040	A
1	AA	1041	A
1	AA	1043	C
1	AA	1055	G
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	1125	G
1	AA	1129	A
1	AA	1154	A
1	AA	1166	G
1	AA	1171	G
1	AA	1173	A

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Mol	Chain	Res	Type
1	AA	1174	C
1	AA	1175	C
1	AA	1176	A
1	AA	1179	A
1	AA	1180	U
1	AA	1181	G
1	AA	1184	G
1	AA	1187	G
1	AA	1201	A
1	AA	1202	U
1	AA	1208	U
1	AA	1210	A
1	AA	1211	A
1	AA	1212	C
1	AA	1213	A
1	AA	1214	C
1	AA	1215	G
1	AA	1216	G
1	AA	1217	G
1	AA	1219	A
1	AA	1221	A
1	AA	1229	G
1	AA	1234	A
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	1268	U
1	AA	1273	A
1	AA	1274	U
1	AA	1275	U
1	AA	1277	U
1	AA	1293	U

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Mol	Chain	Res	Type
1	AA	1301	C
1	AA	1303	U
1	AA	1304	A
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	1353	A
1	AA	1355	C
1	AA	1356	C
1	AA	1357	U
1	AA	1358	G
1	AA	1359	C
1	AA	1362	A
1	AA	1364	U
1	AA	1371	A
1	AA	1372	U
1	AA	1376	C
1	AA	1380	U
1	AA	1381	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	1402	A
1	AA	1405	G
1	AA	1408	A
1	AA	1410	U
1	AA	1413	U
1	AA	1416	C
1	AA	1418	U
1	AA	1419	A
1	AA	1422	G
1	AA	1430	A
1	AA	1432	G
1	AA	1433	U

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Mol	Chain	Res	Type
1	AA	1435	U
1	AA	1447	A
1	AA	1448	G
1	AA	1451	C
1	AA	1452	U
1	AA	1455	G
1	AA	1456	A
1	AA	1466	A
1	AA	1468	G
1	AA	1479	C
1	AA	1489	A
1	AA	1491	A
1	AA	1493	U
1	AA	1494	G
1	AA	1498	G
1	AA	1502	C
1	AA	1509	U
1	AA	1510	U
1	AA	1535	C
1	AA	1537	U
1	AA	1542	C
1	AA	1543	G
1	AA	1545	A
1	AA	1547	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	1568	C
1	AA	1576	U
1	AA	1577	G
1	AA	1578	C
1	AA	1581	G
1	AA	1590	C
1	AA	1591	A
1	AA	1594	G
1	AA	1596	A
1	AA	1597	A

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Mol	Chain	Res	Type
1	AA	1598	U
1	AA	1600	A
1	AA	1601	U
1	AA	1607	U
1	AA	1608	U
1	AA	1609	C
1	AA	1611	A
1	AA	1614	A
1	AA	1615	G
1	AA	1624	A
1	AA	1625	G
1	AA	1642	G
1	AA	1657	G
1	AA	1660	C
1	AA	1662	U
1	AA	1686	G
1	AA	1698	U
1	AA	1699	G
1	AA	1700	A
1	AA	1701	A
1	AA	1702	U
1	AA	1704	G
1	AA	1720	G
1	AA	1722	A
1	AA	1723	U
1	AA	1724	U
1	AA	1725	G
1	AA	1726	G
1	AA	1755	U
1	AA	1757	G
1	AA	1759	C
1	AA	1760	G
1	AA	1763	A
1	AA	1797	A
1	AA	1799	G
1	AA	1803	U
1	AA	1808	A
1	AA	1809	G
1	AA	1811	U
1	AA	1822	G
1	AA	1825	C
1	AA	1834	G

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Mol	Chain	Res	Type
1	AA	1835	G
1	AA	1836	A
1	AA	1838	C
1	AA	1841	U
1	AA	1842	A
35	B2	14	U
35	B2	26	A
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	77	A
35	B2	92	G
35	B2	109	A
35	B2	110	G
35	B2	111	C
35	B2	116	A
35	B2	118	U
35	B2	121	A
35	B2	122	A
35	B2	162	A
35	B2	163	A
35	B2	167	G
35	B2	169	U
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	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

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Mol	Chain	Res	Type
35	B2	194	A
35	B2	197	U
35	B2	198	U
35	B2	207	C
35	B2	213	G
35	B2	217	G
35	B2	220	A
35	B2	225	G
35	B2	226	A
35	B2	239	U
35	B2	241	G
35	B2	242	U
35	B2	247	U
35	B2	248	G
35	B2	249	G
35	B2	250	A
35	B2	252	A
35	B2	254	G
35	B2	255	C
35	B2	256	C
35	B2	257	A
35	B2	258	U
35	B2	259	A
35	B2	260	U
35	B2	269	U
35	B2	277	G
35	B2	291	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	446	U
35	B2	447	C
35	B2	449	U
35	B2	450	A
35	B2	452	C
35	B2	461	A
35	B2	462	U
35	B2	466	U
35	B2	486	G
35	B2	491	C
35	B2	501	G
35	B2	502	G
35	B2	503	U
35	B2	504	A
35	B2	505	G
35	B2	514	C
35	B2	532	A
35	B2	540	A
35	B2	541	G
35	B2	545	A
35	B2	546	G
35	B2	547	G
35	B2	548	U
35	B2	549	G
35	B2	553	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	589	U
35	B2	590	U
35	B2	591	G
35	B2	593	A
35	B2	594	A
35	B2	595	U
35	B2	602	A
35	B2	603	C

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Mol	Chain	Res	Type
35	B2	606	G
35	B2	613	A
35	B2	624	U
35	B2	625	U
35	B2	627	G
35	B2	628	U
35	B2	634	G
35	B2	636	A
35	B2	637	U
35	B2	645	U
35	B2	646	A
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	719	A
35	B2	720	A
35	B2	732	A
35	B2	760	C
35	B2	761	U
35	B2	762	U
35	B2	763	G
35	B2	764	U
35	B2	765	G
35	B2	766	G
35	B2	769	U
35	B2	770	G
35	B2	786	C
35	B2	788	G
35	B2	806	G
35	B2	812	A
35	B2	813	G
35	B2	817	G
35	B2	838	A
35	B2	849	A
35	B2	862	A

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Mol	Chain	Res	Type
35	B2	889	G
35	B2	893	C
35	B2	906	U
35	B2	911	U
35	B2	928	A
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	957	A
35	B2	969	G
35	B2	976	C
35	B2	985	G
35	B2	991	C
35	B2	992	U
35	B2	993	C
35	B2	1009	C
35	B2	1010	A
35	B2	1011	G
35	B2	1012	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	1052	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	1065	U
35	B2	1066	C
35	B2	1073	U
35	B2	1079	A

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Mol	Chain	Res	Type
35	B2	1081	C
35	B2	1095	G
35	B2	1096	A
35	B2	1101	C
35	B2	1104	G
35	B2	1113	U
35	B2	1119	G
35	B2	1123	G
35	B2	1124	C
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	1135	G
35	B2	1139	U
35	B2	1148	G
35	B2	1155	U
35	B2	1162	G
35	B2	1175	U
35	B2	1176	G
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	1240	G
35	B2	1245	U
35	B2	1251	U
35	B2	1252	A
35	B2	1260	G
35	B2	1262	A
35	B2	1263	C
35	B2	1264	G
35	B2	1266	U
35	B2	1267	G
35	B2	1270	C
35	B2	1272	U

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Mol	Chain	Res	Type
35	B2	1273	G
35	B2	1276	A
35	B2	1277	G
35	B2	1279	C
35	B2	1287	G
35	B2	1293	G
35	B2	1294	A
35	B2	1295	G
35	B2	1297	G
35	B2	1300	U
35	B2	1301	A
35	B2	1305	A
35	B2	1310	C
35	B2	1313	G
35	B2	1314	C
35	B2	1316	G
35	B2	1317	A
35	B2	1318	A
35	B2	1319	U
35	B2	1333	A
35	B2	1334	A
35	B2	1338	G
35	B2	1340	U
35	B2	1347	U
35	B2	1361	A
35	B2	1379	U
35	B2	1380	A
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	1471	C
35	B2	1515	A
35	B2	1521	G
35	B2	1522	G
35	B2	1530	C
35	B2	1542	C

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Mol	Chain	Res	Type
35	B2	1557	U
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	1602	A
35	B2	1604	U
35	B2	1606	U
35	B2	1607	U
35	B2	1608	C
35	B2	1609	G
35	B2	1612	C
35	B2	1613	C
35	B2	1614	U
35	B2	1615	C
35	B2	1616	C
35	B2	1624	A
35	B2	1628	A
35	B2	1640	A
35	B2	1656	G
35	B2	1657	U
35	B2	1664	A
35	B2	1665	A
35	B2	1666	C
35	B2	1672	A
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	1729	U
35	B2	1740	U
35	B2	1741	U
35	B2	1742	G
35	B2	1744	A
35	B2	1745	C

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Mol	Chain	Res	Type
35	B2	1755	A
35	B2	1756	U
35	B2	1764	U
35	B2	1783	G
35	B2	1790	A
35	B2	1791	G
35	B2	1800	G
35	B2	1806	U
35	B2	1807	G
35	B2	1811	A
35	B2	1816	G
35	B2	1821	G
35	B2	1837	G
35	B2	1838	A
35	B2	1853	A
35	B2	1854	A
35	B2	1855	U
35	B2	1856	G
35	B2	1857	G
35	B2	1869	C
35	B2	1870	U
35	B2	1871	U
35	B2	1875	U
35	B2	1876	U
35	B2	1894	A
35	B2	1897	A
35	B2	1901	C
35	B2	1904	C
35	B2	1905	A
35	B2	1921	C
35	B2	1933	G
35	B2	1934	A
35	B2	1935	U
35	B2	1941	A
35	B2	1948	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

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Mol	Chain	Res	Type
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
35	B2	2232	A
35	B2	2246	A
35	B2	2247	U
35	B2	2257	G
35	B2	2285	C
35	B2	2293	U
35	B2	2294	G
35	B2	2295	A
35	B2	2297	U
35	B2	2298	G
35	B2	2300	C
35	B2	2301	A
35	B2	2307	A
35	B2	2308	A
35	B2	2310	A
35	B2	2311	A
35	B2	2316	A
35	B2	2320	A
35	B2	2321	A
35	B2	2322	G
35	B2	2324	G
35	B2	2328	G
35	B2	2329	U
35	B2	2331	A
35	B2	2332	A
35	B2	2337	G
35	B2	2343	A
35	B2	2344	A
35	B2	2345	C
35	B2	2346	U
35	B2	2347	A
35	B2	2350	A
35	B2	2351	C
35	B2	2353	C
35	B2	2358	A

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Mol	Chain	Res	Type
35	B2	2360	G
35	B2	2361	G
35	B2	2362	U
35	B2	2363	A
35	B2	2369	A
35	B2	2376	G
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	2422	U
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	2482	G
35	B2	2485	A
35	B2	2489	A
35	B2	2490	A
35	B2	2491	G
35	B2	2492	A
35	B2	2499	U
35	B2	2523	G
35	B2	2529	A
35	B2	2530	G
35	B2	2601	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	2631	G

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Mol	Chain	Res	Type
35	B2	2632	A
35	B2	2634	U
35	B2	2635	U
35	B2	2636	A
35	B2	2638	U
35	B2	2644	U
35	B2	2645	A
35	B2	2649	U
35	B2	2656	A
35	B2	2660	U
35	B2	2661	U
35	B2	2662	U
35	B2	2663	C
35	B2	2664	U
35	B2	2665	U
35	B2	2666	C
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	2709	G
35	B2	2721	A
35	B2	2730	A
35	B2	2731	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	2771	A
35	B2	2772	G
35	B2	2773	A
35	B2	2774	A
35	B2	2775	A
35	B2	2776	U
35	B2	2784	A
35	B2	2786	A

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Mol	Chain	Res	Type
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	2840	G
35	B2	2848	G
35	B2	2850	C
35	B2	2868	C
35	B2	2872	G
35	B2	2873	A
35	B2	2891	G
35	B2	2895	G
35	B2	2896	A
35	B2	2898	A
35	B2	2905	C
35	B2	2909	G
35	B2	2912	A
35	B2	2913	U
35	B2	2918	G
35	B2	2932	A
35	B2	2933	A
35	B2	2934	G
35	B2	2937	U
35	B2	2938	U
35	B2	2940	A
35	B2	2942	A
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	2983	U
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

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Mol	Chain	Res	Type
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	3093	G
35	B2	3108	A
35	B2	3117	A
35	B2	3119	U
35	B2	3155	G
35	B2	3174	A
35	B2	3175	U
35	B2	3176	G
35	B2	3182	G
35	B2	3188	U
35	B2	3189	C
35	B2	3195	C
35	B2	3197	G
35	B2	3200	U
35	B2	3212	G
35	B2	3216	C
35	B2	3218	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	3251	U
35	B2	3254	G
35	B2	3260	A
35	B2	3261	U

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Mol	Chain	Res	Type
35	B2	3266	U
35	B2	3268	U
35	B2	3273	A
35	B2	3275	A
35	B2	3276	A
35	B2	3281	A
35	B2	3282	G
35	B2	3283	A
35	B2	3284	G
35	B2	3285	G
35	B2	3288	G
35	B2	3289	G
35	B2	3290	A
35	B2	3291	C
35	B2	3293	U
35	B2	3295	U
35	B2	3296	U
35	B2	3297	C
35	B2	3298	C
35	B2	3299	U
35	B2	3300	A
35	B2	3301	C
35	B2	3302	U
35	B2	3305	C
35	B2	3306	C
35	B2	3307	U
35	B2	3308	G
35	B2	3310	A
35	B2	3317	A
35	B2	3318	A
35	B2	3319	G
35	B2	3321	U
35	B2	3322	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	3352	A
35	B2	3359	U

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Mol	Chain	Res	Type
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	3385	G
35	B2	3386	U
35	B2	3387	G
35	B2	3388	C
35	B2	3390	G
35	B2	3392	A
35	B2	3393	U
35	B2	3394	C
35	B2	3395	G
35	B2	3404	G
35	B2	3405	C
35	B2	3418	U
35	B2	3419	G
35	B2	3420	U
35	B2	3435	U
35	B2	3436	A
35	B2	3442	U
35	B2	3443	A
35	B2	3446	G
35	B2	3449	G
35	B2	3450	C
35	B2	3451	C
35	B2	3453	U
35	B2	3455	U
35	B2	3456	U
35	B2	3457	G
35	B2	3476	A
35	B2	3479	C
35	B2	3483	U
35	B2	3491	A
36	B3	12	U
36	B3	13	A
36	B3	22	A
36	B3	31	G

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Mol	Chain	Res	Type
36	B3	42	A
36	B3	44	C
36	B3	45	A
36	B3	47	U
36	B3	49	C
36	B3	50	A
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	113	G
36	B3	116	G
36	B3	118	C
36	B3	119	U
37	B4	31	U
37	B4	42	U
37	B4	43	C
37	B4	46	U
37	B4	47	G
37	B4	56	A
37	B4	60	A
37	B4	67	A
37	B4	70	C
37	B4	71	G
37	B4	85	A
37	B4	89	U
37	B4	90	U
37	B4	91	C
37	B4	92	C
37	B4	93	G
37	B4	95	G
37	B4	98	U
37	B4	103	G
37	B4	112	A
37	B4	114	C
37	B4	119	A
37	B4	121	U

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Mol	Chain	Res	Type
37	B4	124	G
37	B4	133	U
37	B4	134	U
37	B4	135	C
37	B4	136	U
37	B4	164	U
37	B4	165	U
77	Sm	9	G
77	Sm	20	G
77	Sm	21	U
77	Sm	22	A
77	Sm	31	G
77	Sm	32	G
77	Sm	33	C
77	Sm	34	U
77	Sm	35	C
77	Sm	41	C
77	Sm	42	C
77	Sm	45	A
77	Sm	48	U
77	Sm	49	C
77	Sm	60	A
77	Sm	62	C
77	Sm	76	C
78	Sn	2	G
78	Sn	16	U
78	Sn	19	G
78	Sn	20	A
78	Sn	29	G
78	Sn	35	A
78	Sn	36	U
78	Sn	39	C
78	Sn	40	C
78	Sn	42	U
78	Sn	46	G
78	Sn	47	U
78	Sn	48	C
78	Sn	49	C
78	Sn	59	A
78	Sn	61	C
78	Sn	63	G
78	Sn	64	A

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Mol	Chain	Res	Type
78	Sn	69	C
78	Sn	73	A
78	Sn	74	C
78	Sn	75	C
78	Sn	76	A
79	S3	28	A
79	S3	30	U
79	S3	32	U
79	S3	33	C
79	S3	35	U
79	S3	36	U

All (44) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	AA	104	A
1	AA	140	C
1	AA	142	U
1	AA	275	U
1	AA	558	A
1	AA	561	U
1	AA	704	C
1	AA	768	A
1	AA	1113	U
1	AA	1361	A
1	AA	1375	G
1	AA	1383	G
1	AA	1501	C
1	AA	1661	C
1	AA	1699	G
35	B2	188	C
35	B2	290	G
35	B2	382	A
35	B2	572	A
35	B2	719	A
35	B2	948	G
35	B2	1094	A
35	B2	1103	U
35	B2	1244	G
35	B2	1269	C
35	B2	1272	U
35	B2	1608	C

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Mol	Chain	Res	Type
35	B2	1612	C
35	B2	1665	A
35	B2	1854	A
35	B2	2200	U
35	B2	2661	U
35	B2	2867	C
35	B2	2993	G
35	B2	3001	C
35	B2	3217	U
35	B2	3260	A
35	B2	3298	C
35	B2	3328	U
35	B2	3373	C
35	B2	3418	U
36	B3	12	U
37	B4	88	A
79	S3	35	U

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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	7
77	Sm	2
35	B2	1
22	Aa	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B2	2363:A	O3'	2364:G	P	6.70
1	Sm	17:C	O3'	18(A):U	P	4.09
1	Sm	18(A):U	O3'	19:G	P	4.09
1	AA	1419:A	O3'	1420:A	P	3.63
1	AA	1498:G	O3'	1499:A	P	3.41
1	AA	546:C	O3'	547:A	P	3.40
1	AA	1574:C	O3'	1575:G	P	3.31
1	Aa	116:ILE	C	123:ALA	N	3.26
1	AA	1605:U	O3'	1606:C	P	3.24
1	AA	1359:C	O3'	1360:U	P	3.23
1	AA	1483:C	O3'	1484:G	P	3.16

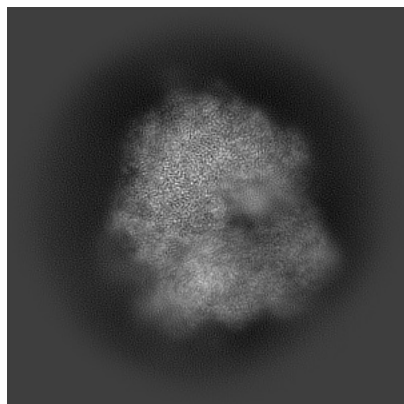
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43976. These allow visual inspection of the internal detail of the map and identification of artifacts.

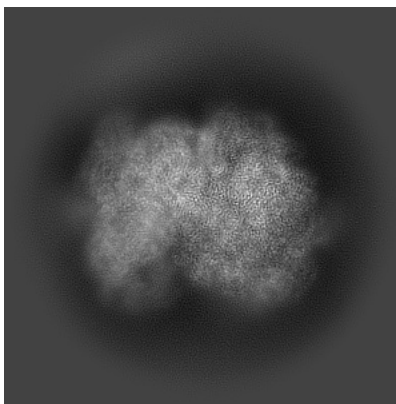
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

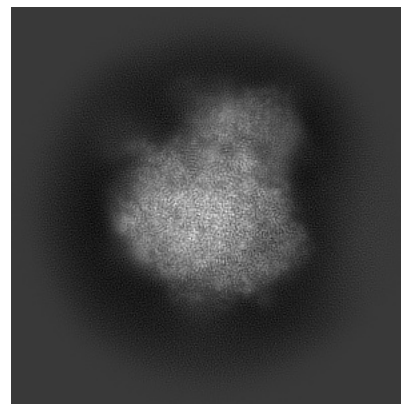
6.1.1 Primary map



X

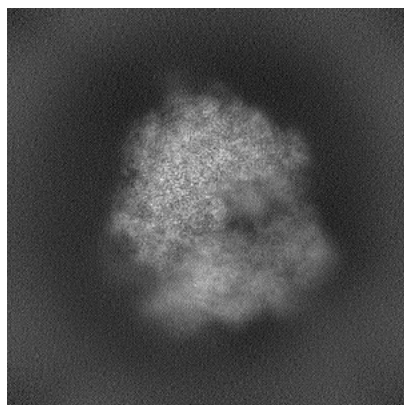


Y

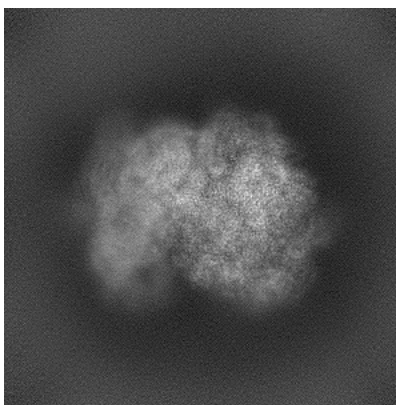


Z

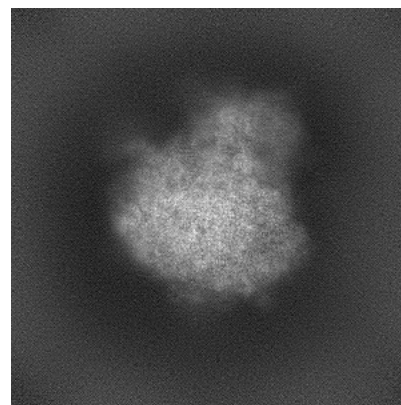
6.1.2 Raw map



X



Y

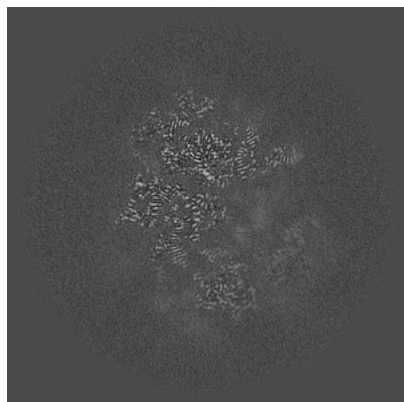


Z

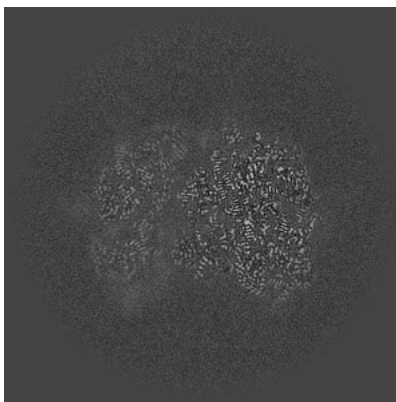
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

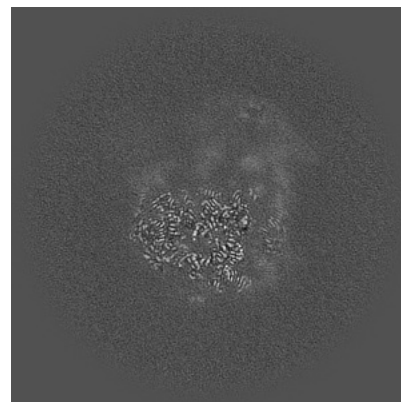
6.2.1 Primary map



X Index: 256



Y Index: 256

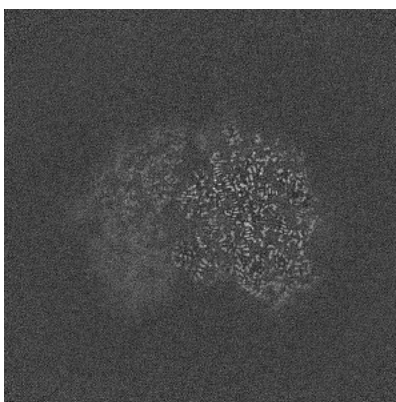


Z Index: 256

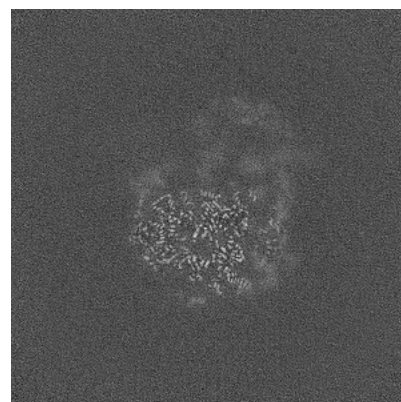
6.2.2 Raw map



X Index: 256



Y Index: 256

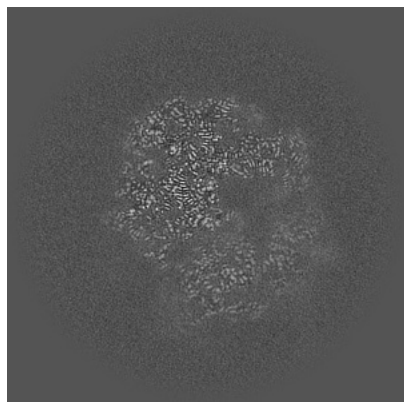


Z Index: 256

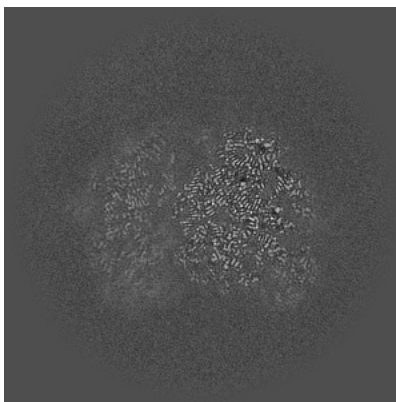
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

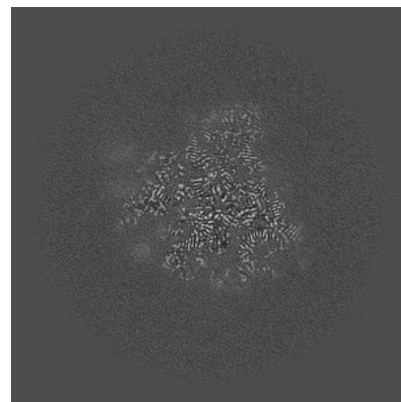
6.3.1 Primary map



X Index: 276

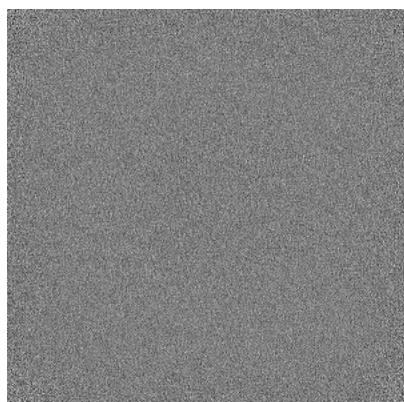


Y Index: 246

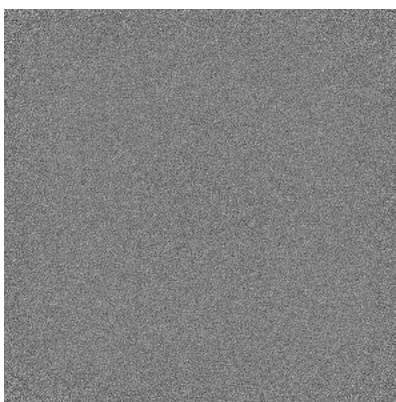


Z Index: 323

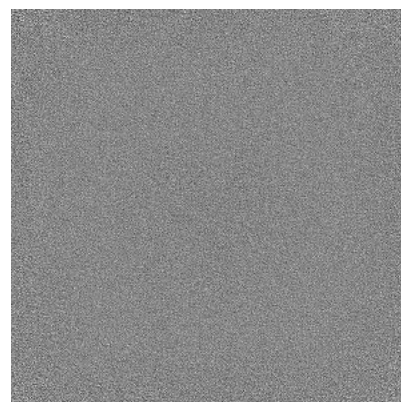
6.3.2 Raw map



X Index: 0



Y Index: 0

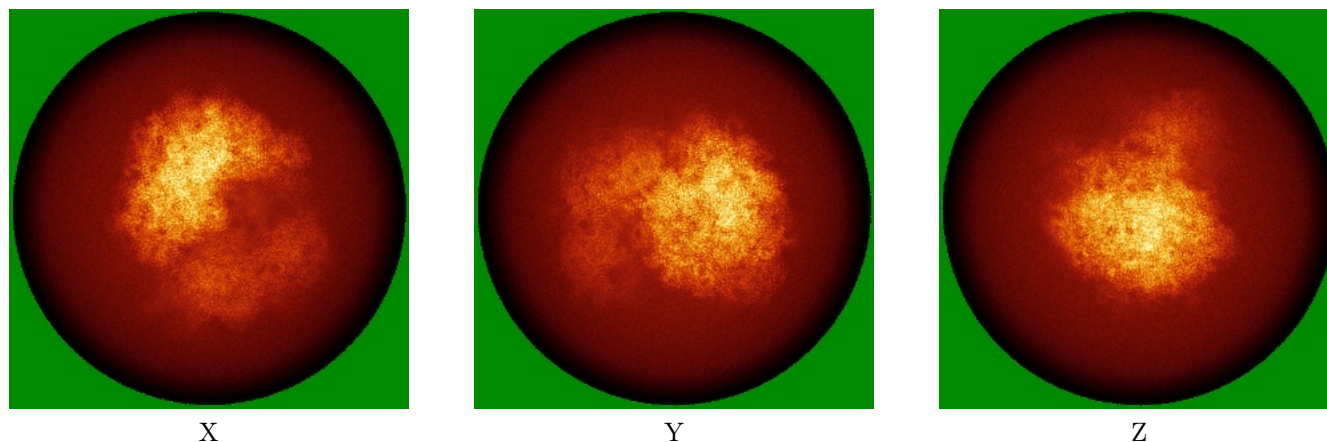


Z Index: 0

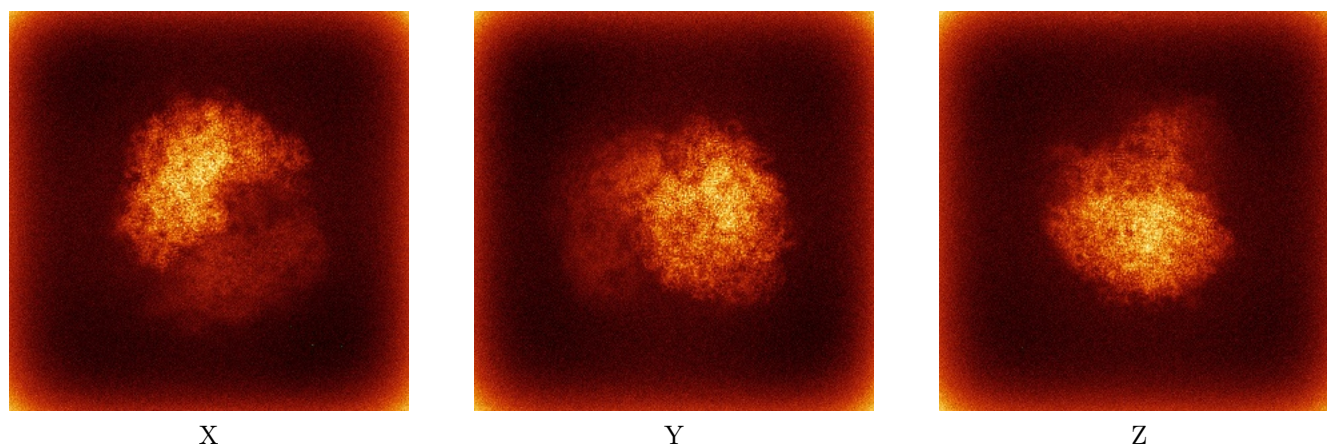
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



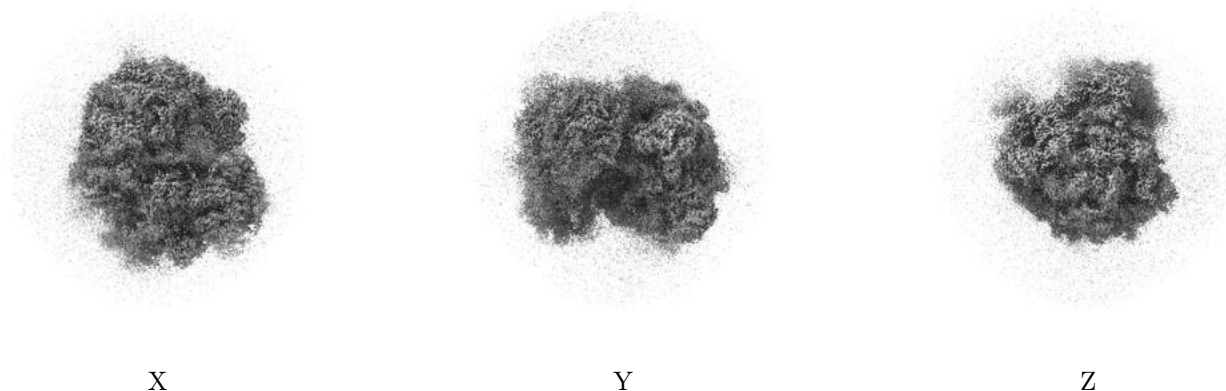
6.4.2 Raw map



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.

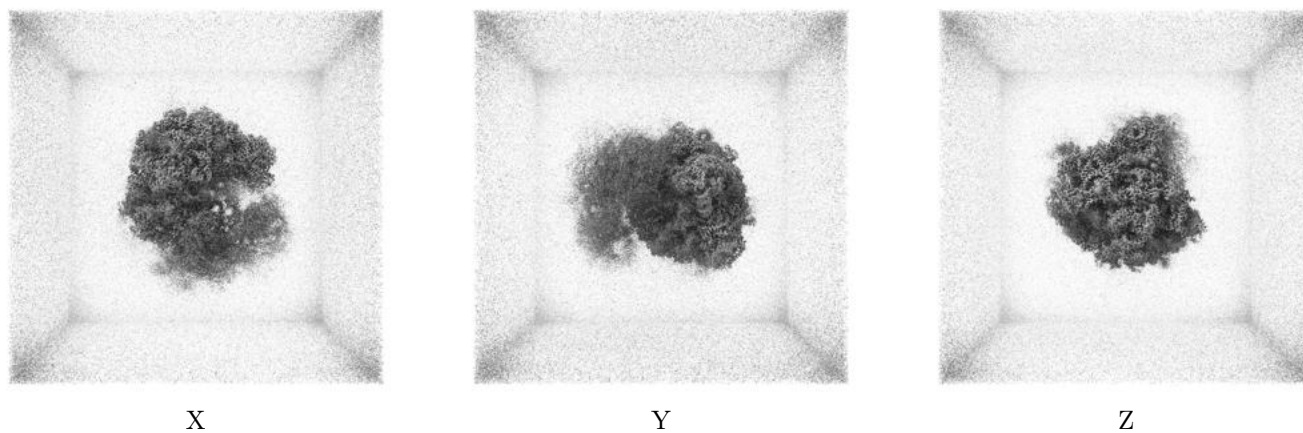
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.27. 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.

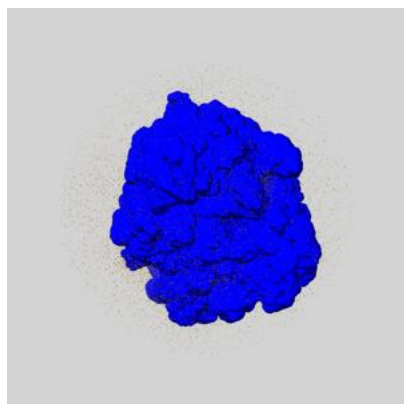
6.6 Mask visualisation [i](#)

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

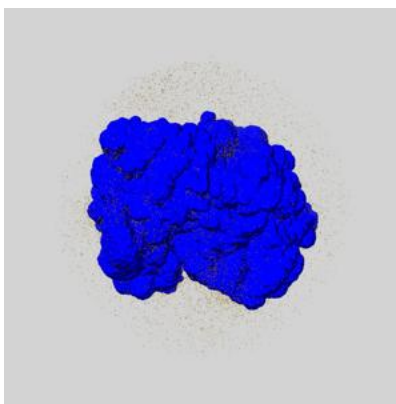
A mask typically either:

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

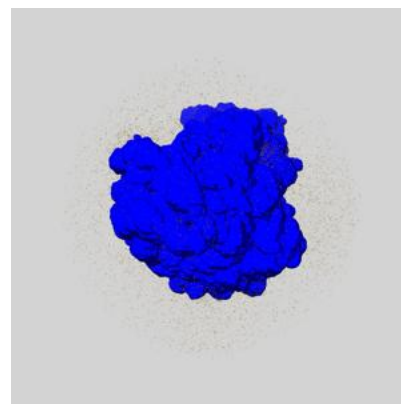
6.6.1 emd_43976_msk_1.map [i](#)



X



Y

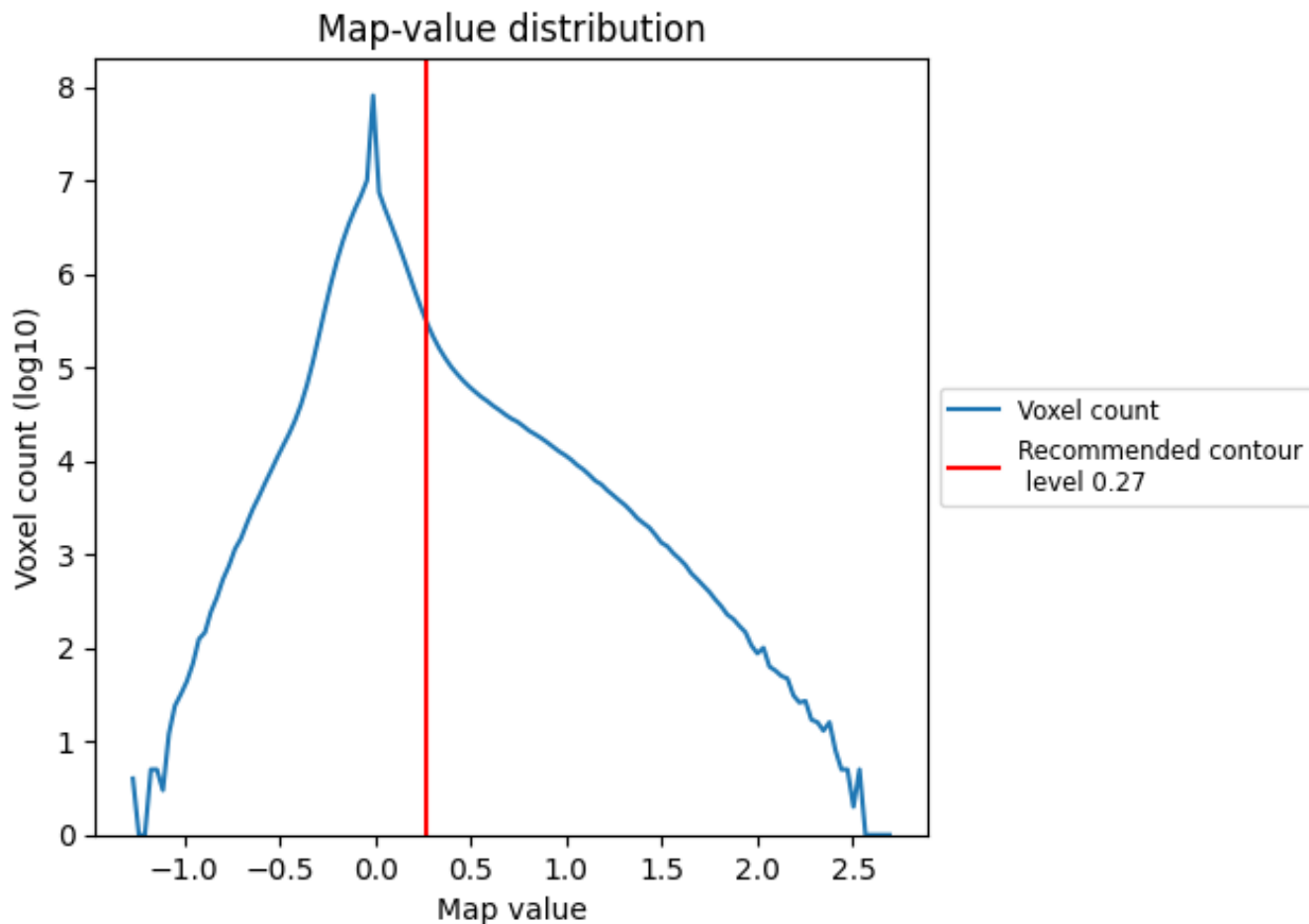


Z

7 Map analysis [i](#)

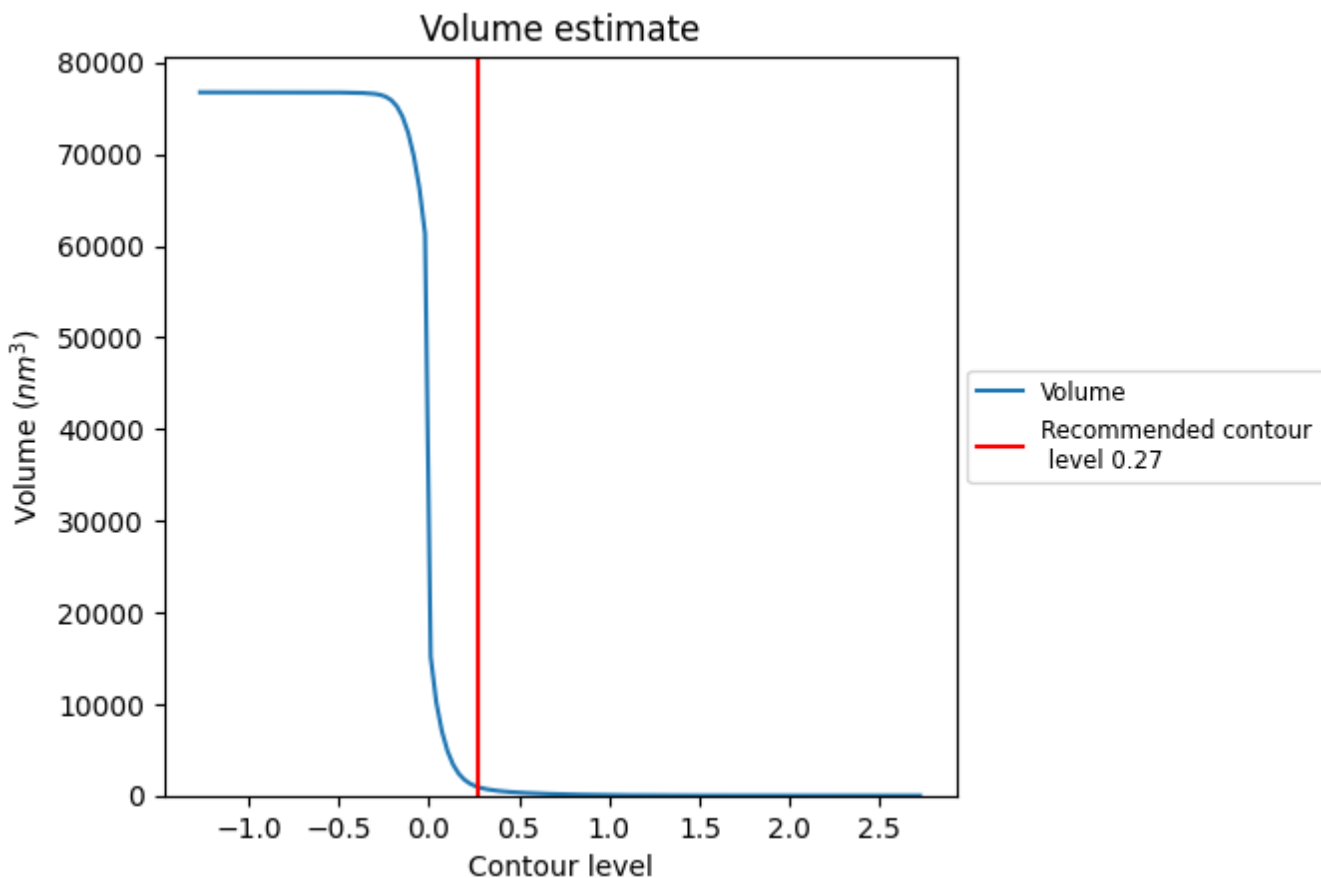
This section contains the results of statistical analysis of the map.

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.

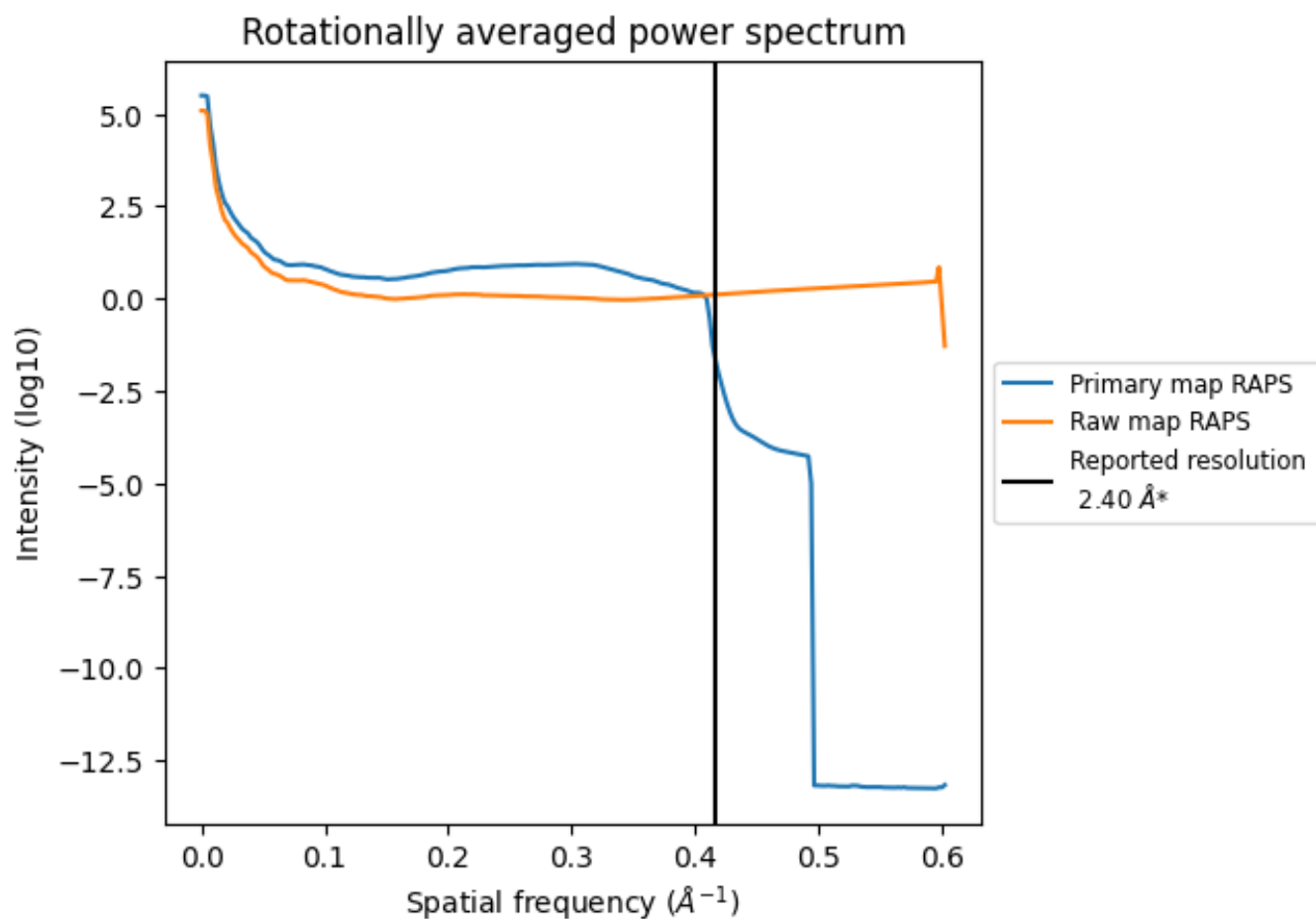
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 958 nm³; this corresponds to an approximate mass of 866 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](#)

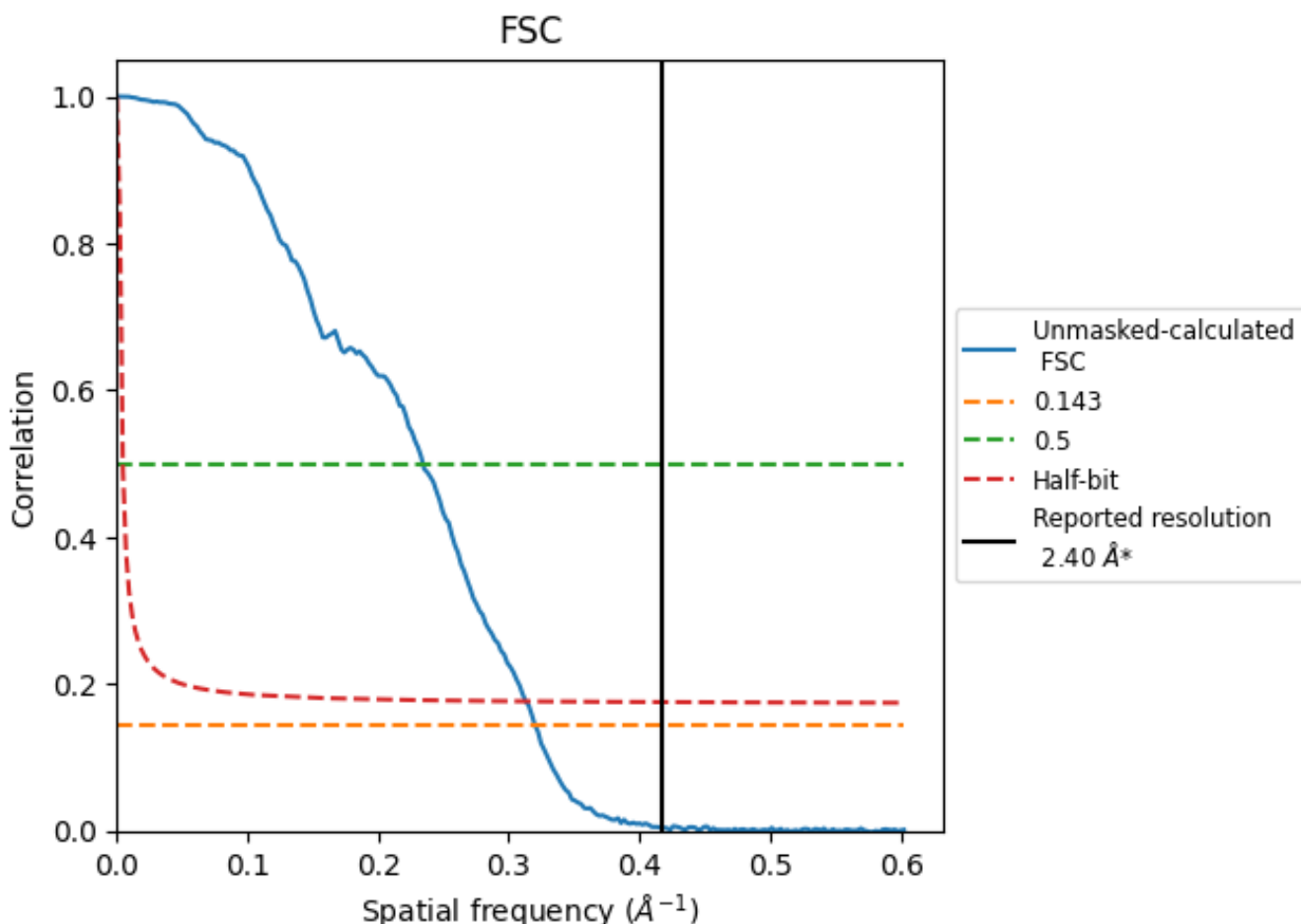


*Reported resolution corresponds to spatial frequency of 0.417 Å⁻¹

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 \AA^{-1}

8.2 Resolution estimates [i](#)

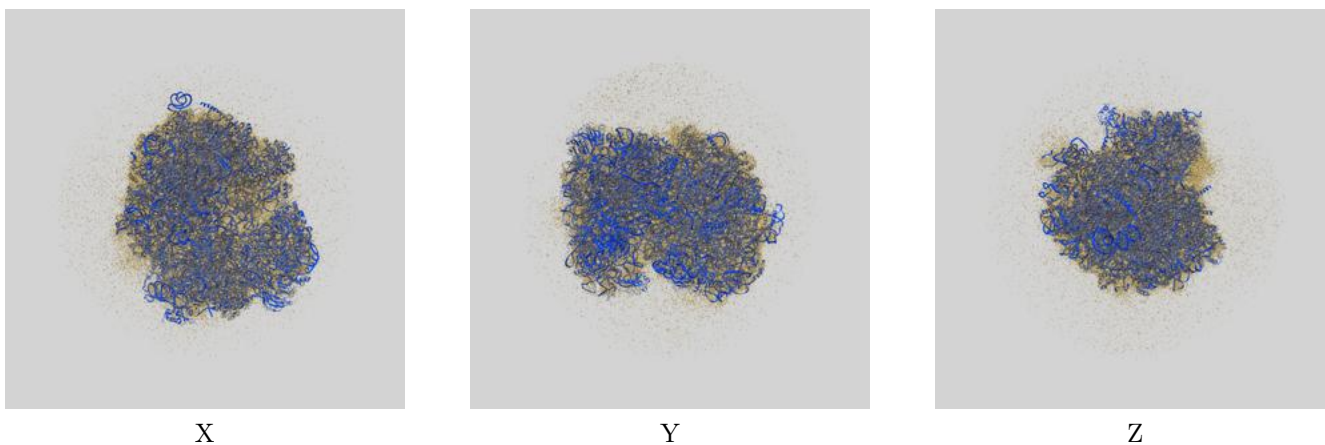
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.12	4.27	3.20

*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 3.12 differs from the reported value 2.4 by more than 10 %

9 Map-model fit [i](#)

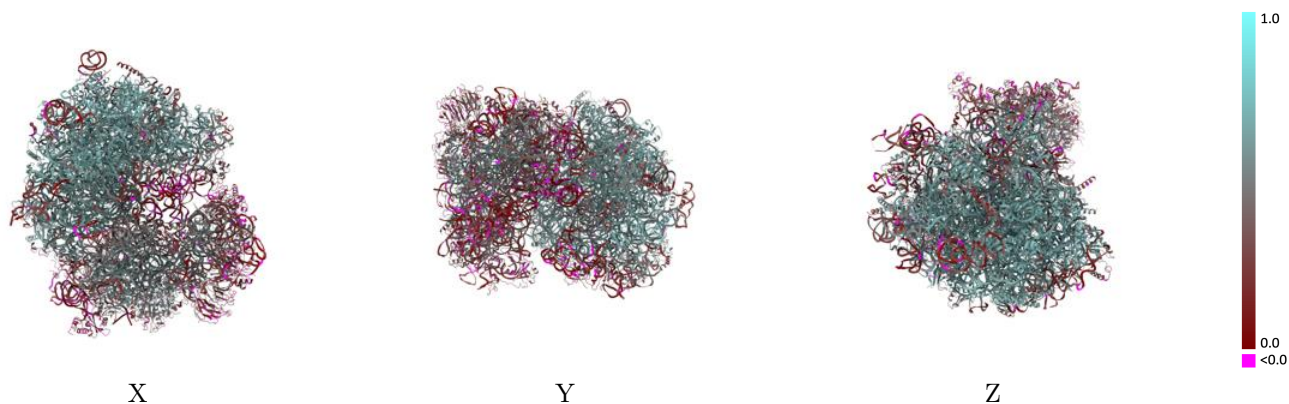
This section contains information regarding the fit between EMDB map EMD-43976 and PDB model 9AXV. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



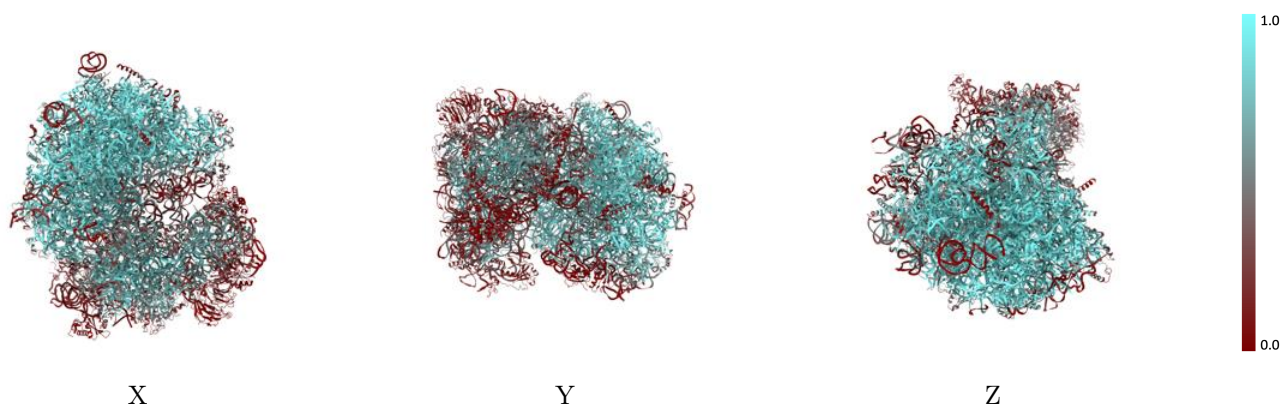
The images above show the 3D surface view of the map at the recommended contour level 0.27 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



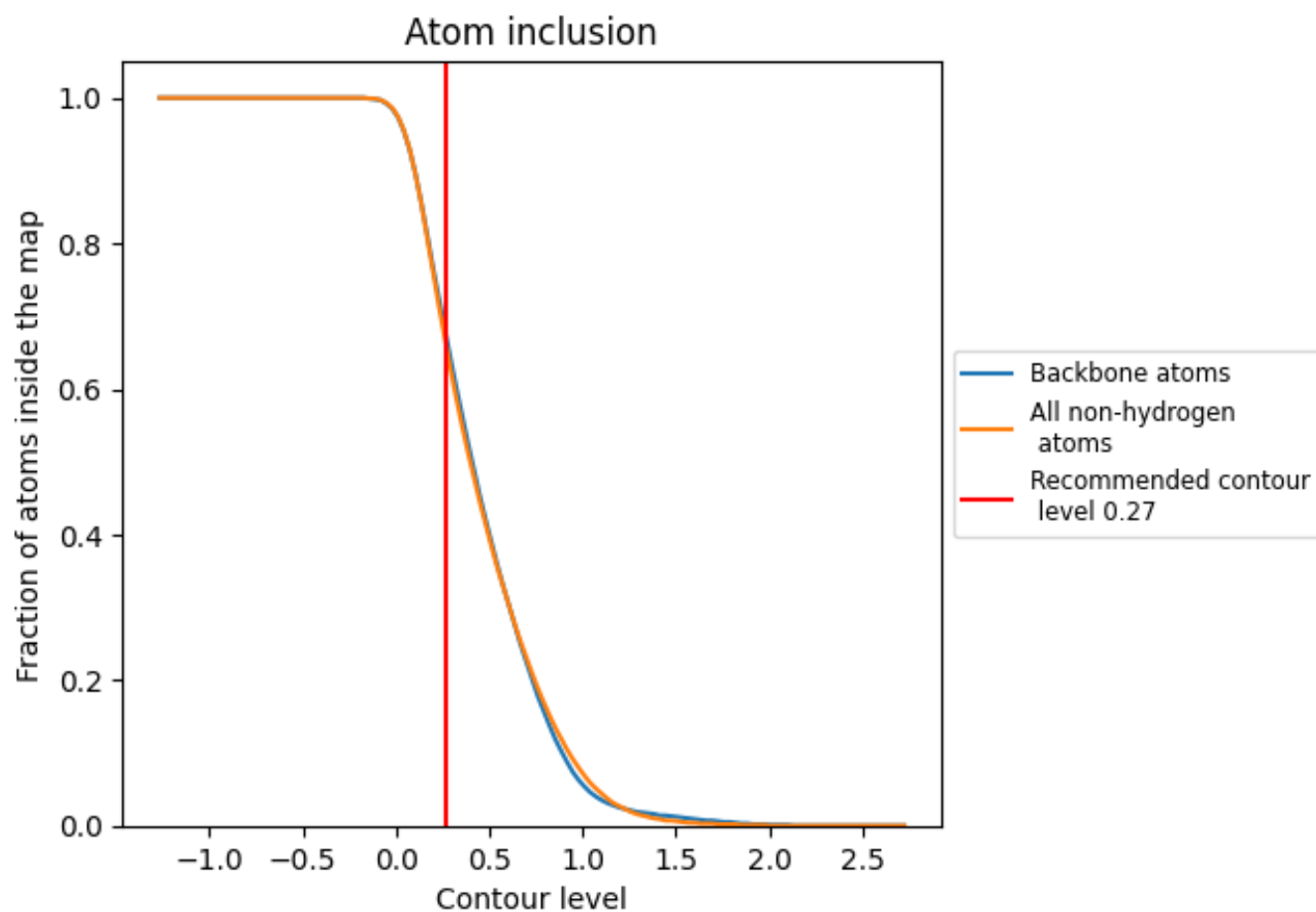
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.27).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 67% of all backbone atoms, 66% 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 (0.27) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6560	 0.4730
AA	 0.5230	 0.3480
AD	 0.5350	 0.4730
AE	 0.4340	 0.4290
AF	 0.6760	 0.5340
AG	 0.2910	 0.3540
AH	 0.4900	 0.4410
AI	 0.4620	 0.4050
AJ	 0.0630	 0.1850
AK	 0.1960	 0.2750
AL	 0.3600	 0.3340
AM	 0.3600	 0.3370
AN	 0.0850	 0.1680
AO	 0.5520	 0.4440
AP	 0.0020	 0.1390
AQ	 0.5880	 0.4850
AR	 0.5370	 0.4580
AS	 0.2010	 0.2310
AT	 0.4620	 0.3620
AU	 0.3630	 0.3510
AV	 0.1510	 0.2150
AW	 0.4610	 0.3840
Aa	 0.3570	 0.3620
Ab	 0.5380	 0.4800
Ac	 0.7930	 0.5670
Ad	 0.2370	 0.3260
Ae	 0.2100	 0.3000
Af	 0.2230	 0.3030
Ag	 0.6880	 0.5230
Ah	 0.3150	 0.3760
Ai	 0.3370	 0.2930
Aj	 0.4460	 0.3810
Ak	 0.0220	 0.1540
Am	 0.1060	 0.2800
B0	 0.8550	 0.6190









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Chain	Atom inclusion	Q-score
B1	0.8480	0.6040
B2	0.7900	0.5310
B3	0.8000	0.5050
B4	0.8730	0.5780
BN	0.9410	0.6560
BO	0.9040	0.6390
BP	0.9230	0.6530
BQ	0.6850	0.5290
BR	0.6610	0.5010
BS	0.8470	0.6180
BT	0.7280	0.5570
BU	0.0540	0.2100
BV	0.4470	0.4290
BW	0.4130	0.3620
BX	0.8090	0.6050
BY	0.7600	0.5640
BZ	0.9740	0.6720
Ba	0.9030	0.6380
Bb	0.9100	0.6510
Bc	0.9340	0.6550
Bd	0.8670	0.6190
Be	0.8310	0.6060
Bf	0.7570	0.5670
Bg	0.5120	0.4480
Bh	0.8640	0.6230
Bi	0.6170	0.5400
Bj	0.8700	0.6220
Bk	0.8740	0.6350
Bl	0.7340	0.5340
Bm	0.9440	0.6670
Bn	0.8890	0.6290
Bo	0.6960	0.5020
Bp	0.8610	0.6230
Bq	0.9340	0.6610
Br	0.9360	0.6540
Bs	0.8980	0.6460
Bt	0.8380	0.6200
Bu	0.8520	0.6140
Bv	0.9710	0.6740
Bw	0.5790	0.4740
Bx	0.7370	0.5270
By	0.7680	0.5840

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Chain	Atom inclusion	Q-score
S3	 0.4410	 0.2470
Sm	 0.3770	 0.1570
Sn	 0.1330	 0.0590